Nitrogen Efficiency of Winter Oilseed Rape and its Prediction by Hyperspectral Canopy Reflectance and Electrical Capacitance

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Abbreviations

Base	Baseline offset correction
$DD90_{max}$	Maximal diameter at 90 % depth
Delta Nup	Nitrogen uptake after flowering
$Dens_{Av}$	Average root density
DH	Doubled haploid
DM	Dry matter
$DM\%_{EOF}$	DM content of aboveground biomass
$DM\%_{Seed}$	DM content of seeds
$DM\%_{Straw}$	DM content of straw
EC	Electrical capacitance
EC_{EOF}	Electrical capacitance at end of flowering
EC_{FRUIT}	Electrical capacitance during fruit development
EOF	End of flowering
FL	Begin of flowering
FM	Fresh matter
HI	Harvest index
Lat_{FM}	Lateral root mass FM
MAT	Maturity
$N\%_{EOF}$	Nitrogen content of aboveground biomass DM at end of flowering
$N\%_{Seed}$	Nitrogen content of seeds DM
$N\%_{Straw}$	Nitrogen content of straw DM
NHI	Nitrogen harvest index
NIPALS	Non-linear iterative partial least squares
Norris	Norris gap derivative transformation
NUE	Nitrogen use efficiency
$NupEff_{EOF}$	Nitrogen uptake efficiency at end of flowering
$NupEff_{MAT}$	Nitrogen uptake efficiency at maturity
Nup_{EOF}	Nitrogen uptake of aboveground biomass DM at end of flowering
Nup_{MAT}	Nitrogen uptake of aboveground biomass DM at maturity
Nup_{Seed}	Nitrogen uptake of seeds DM
Nup_{Straw}	Nitrogen uptake of straw DM
NutEff	Nitrogen utilisation efficiency
Oil yield	Oil yield DM
Oil%	Oil content of seeds DM
PL	Plant length
PLSR	Partial least squares regression

RM_{0-20}	Root mass in horizon 0-20 cm DM
RM_{20-40}	Root mass in horizon 20-40 cm DM
RM_{40-60}	Root mass in horizon 40-60 cm DM
RootArea	Projected root area
RootDia	Root diameter
RS_{FM}	Root system mass FM
RTP	Number of root tip paths
SaGo	Savitzky-Golay derivative transformation
Seed 9%	Seed yield at 9% moisture
Seed DM	Seed yield DM
SNV	Standard normal variate transformation
StemDia	Stem diameter
Straw DM	Straw yield DM
Tap_{FM}	Taproot mass FM
TD_M	Mean tip diameter
TD_{Med}	Median tip diameter
W_{Max}	Maximal root system width
W_{Med}	Median root system width
$Yield_{EOF}$	Aboveground biomass yield DM at end of flowering

GENERAL INTRODUCTION

Oilseed rape (*Brassica napus* L.)

Oilseed rape (*Brassica napus* ssp. *napus* L.) is an amphidiploid species. It originated from a natural hybridisation between turnip rape (*Brassica rapa* L.) and cabbage (*Brassica oleracea* L.) followed by chromosome doubling. Therefore, oilseed rape carries the A-genome (2n = 20) of turnip rape and the C-genome of cabbage (2n = 18). Relevant cultivation only started in the 18th century (Friedt & Snowdon 2009). But it was not before the mid-1970s when it reached a large scale worldwide. By this time the first varieties with double low quality of seeds were released. Their seed oil contained zero erucic acid and their seed meal only low amounts of glucosinolates. Erucic acid causes heart damages while glucosinolates are not only known to decrease the palatability of oilseed rape in feed but also to harm thyroid, hepatic and kidney. Thus, double low quality was the prerequisite for the use of oilseed rape in food and feed (Friedt & Snowdon 2009). With a production of 26.5 Mt oil in season 2013/14 oilseed rape is the third most important oil crop worldwide (USDA 2015). In EU-27 its seed oil is mainly used for industrial purposes (7.1 Mt, market year 2013/14) and food (2.3 Mt, market year 2013/14). Within industrial use biofuels play the most important role (6.6 Mt, market year 2013/14) (USDA 2013).

Self-pollination dominates in oilseed rape but outcrossing is observed from 10 % to more than 50 % (Friedt & Snowdon 2009, Becker 2011). Two variety types exist – open pollinated (or line) varieties and hybrid varieties. Line varieties result from crossings of different parents and are propagated by self-pollination. Therefore, they are characterised by a high degree of homozygosity. Hybrid varieties result from crosses of parental inbred lines. In contrast to line varieties they cannot be propagated by self-pollination. Instead the parents are maintained as inbred lines and used as parental components to produce hybrids. Therefore, hybrids are highly heterozygous. Compared to their inbred parents hybrids show an improved yield and yield stability. This phenomenon is known as heterosis and either defined as the difference between hybrid performance and the mean performance of its parents (mid-parent heterosis) or as difference to the better parent (better parent heterosis) (Bernardo 2010 a). In oilseed rape production hybrid varieties dominate. In 2013 hybrids were grown at 80 % of the oilseed rape cropping area in Germany

(Kleffmann-Group n.D.). Budewig & Leon (2003) and Friedt et al. (2003) confirmed higher yields and improved yield stability of hybrid varieties compared to line varieties of winter oilseed rape.

Nitrogen and nitrogen efficiency

Together with sulphur, phosphorous, potassium, sodium and magnesium nitrogen belongs to the macronutrients of plants. Nitrogen is the nutrient which is required in largest amounts by plants. As constituent of amino acids, peptides, proteins, nucleic acids, chlorophyll, co-enzymes, phytohormones and secondary metabolites it is essential for plants. When nitrogen is limited photosynthesis, chlorophyll synthesis and protein synthesis can be down regulated while pathways of the secondary metabolism or protein degradation are up regulated or vice versa at sufficient nitrogen supply. That also concerns up and down regulation of transport systems. Also root architecture is altered when availability of nitrogen changes. Generally, root branching is supressed at high nitrogen supply. At nitrogen limitation development of lateral roots is enhanced. Adaptions to changes in nitrogen availability also involve root axis number, rooting depths, rooting density and root longevity (Miller & Cramer 2004, Hawkesford et al. 2012).

There are several definitions of nitrogen efficiency (Fig. 1). It can be defined as unit grain yield per unit nitrogen supply (nitrogen use efficiency NUE). It is of agronomic importance as it describes the ratio between output (yield) to fertiliser input. Graham et al. (1984) defined genotypes nitrogen efficient when they produced high yields at nitrogen limitation. Sattelmacher et al. (1994) suggested that not only genotypes that perform well at nitrogen limitation but also those with a high response to additional nitrogen supply to be considered as nitrogen efficient. A nitrogen efficient genotype may also be one that shows no or only little decline in yield at nitrogen limitation. Moll et al. (1982) defined two components of nitrogen use efficiency. Uptake efficiency (NupEff) refers to the ratio between the amount of nitrogen which is taken up (total uptake) to the amount of available nitrogen. Utilisation efficiency (NutEff) on the other hand describes the ability to convert total nitrogen uptake into seed yield. Both contributed to different portions to variation in nitrogen use efficiency depending on level of N supply (Moll et al. 1982, Kessel et al. 2012, Nyikako et al. 2014). Apparent

nitrogen use (ANU) and agronomic nitrogen efficiency (ANE) consider the realised advantage of fertilisation. They compare nitrogen uptake and seed yield, respectively, between fertilisation and non-fertilisation at a given level of soil nitrogen. Physiological nitrogen efficiency describes the ratio of the difference in seed yield under fertilisation and non-fertilisation to the difference in nitrogen uptake under nitrogen fertilisation and non-fertilisation (Craswell & Godwind 1984).

$\mathbf{NUE = Seed\ DM \times N\ supply^{-1}}$	N use efficiency concerning seed yield [1]
$\mathbf{NupEff = N_{Plant} \times N\ supply^{-1}}$	N uptake efficiency [1]
$\mathbf{NutEff = Seed\ DM \times N_{Plant}^{-1}}$	N utilisation efficiency [1]
$\mathbf{ANE = (Seed\ DM_{+} - Seed\ DM_{0}) \times N\ fertiliser^{-1}}$	Agronomic N efficiency [2]
$\mathbf{ANU = (N_{Plant,+} - N_{Plant,0}) \times N\ supply^{-1}}$	Apparent N use [2]
$\mathbf{PNE = (Seed\ DM_{+} - Seed\ DM_{0}) \times (N_{Plant,+} - N_{Plant,0})^{-1}}$	Physiological N efficiency [2]

Seed DM Seed yield dry matter • **N supply** N supply of plant/stand • $\mathbf{N_{Plant}}$ N uptake of plant • $\mathbf{Seed\ DM_{+}}$ Seed yield dry matter when fertilised • $\mathbf{Seed\ DM_{0}}$ Seed yield dry matter when unfertilised • **N fertiliser** N applied with fertiliser • $\mathbf{N_{Plant,+}}$ N uptake of plant when fertilised • $\mathbf{N_{Plant,0}}$ N uptake of plant when unfertilised

Fig. 1: Some definitions of nitrogen efficiency
According to [1] Moll et al. 1982 and [2] Craswell & Godwind 1984

The current study addressed nitrogen use efficiency (NUE), nitrogen uptake efficiency (NupEff) and nitrogen utilisation efficiency (NutEff) as defined by Moll et al. (1982). When examined at low nitrogen supply it is possible to identify nitrogen efficient genotypes as such that achieve high yields. Genotypes that show low yields at low nitrogen supply are nitrogen inefficient either with regards to low seed yield per unit available nitrogen or with regards to their yield decline at decreasing nitrogen supply or both. It is necessary to test genotypes at low and high nitrogen supply to distinguish genotypes that perform poor at low and high levels of nitrogen supply and ones that perform poor at low but well at high nitrogen supply. Genotypes that produce high yields at low and high nitrogen levels can be assigned nitrogen efficient independent from differences in yield between nitrogen levels. Genotypes performing poor at low and high nitrogen supply on the other hand have a general low yield

potential. Although the difference between yield at high and low nitrogen supply is low they cannot be assigned nitrogen efficient. A genotype which performs well at high but bad at low nitrogen supply can be assigned nitrogen inefficient as it reacts very sensitive to decreasing nitrogen supply and is low yielding at low nitrogen supply. Accordingly genotypes were tested at contrasting nitrogen levels in the current study. The question of “N supply” (Fig. 1) arises. Next to fertiliser nitrogen soil mineral nitrogen (SMN) can be considered when defining nitrogen supply. Analyses of SMN only reflect the amount of available nitrogen at time of sampling. Plant available nitrogen underlies alteration, degradation and losses in the soil. Therefore, it is difficult to predict the amount of nitrogen which is available from SMN. Thus, the current study did not consider SMN when defining nitrogen supply. Instead the amount of nitrogen taken up by the plot with highest nitrogen uptake at low nitrogen supply and fertiliser nitrogen were used to compute available nitrogen.

Nitrogen efficiency and breeding

Oilseed rape suffers from low nitrogen efficiency compared to other crops (Sylvester-Bradley & Kindred 2009). The crop reacts very sensitive to nitrogen limitation. Möllers et al. (2000) reported a yield decline from 40.8 dt ha^{-1} at high nitrogen supply to 26.3 dt ha^{-1} at low nitrogen supply. At low nitrogen supply 57 % to 70 % of yield at high nitrogen supply were realised depending on the genotype. Berry et al. (2010) reported a yield decline from 41.1 dt ha^{-1} at high to 29.7 dt ha^{-1} at low nitrogen supply Among environments yield decline ranged from 9 % to 54 %. Schulte auf’m Erley et al. (2011) observed a decline in seed yield from 38.9 dt ha^{-1} at high to 24.4 dt ha^{-1} at low nitrogen supply. At low nitrogen supply genotypes produced 52 % to 70 % of seed yield at high nitrogen supply. EU regulations have moved N efficiency of winter oilseed rape into focus of plant breeders. EU directive 2009/28/EG regulates amongst other things greenhouse gas emissions of biofuel production. According to that directive biodiesel production of rapeseed must not exceed an emission of 42 g CO_2 $(MJ)^{-1}$ from 2018. Current estimations assume that 52 g CO_2 $(MJ)^{-1}$ are emitted during cultivation of oilseed rape (56 %), transport (2 %) and production of biodiesel (42 %) (Ufop 2015). Another regulation that concerns cultivation of rapeseed in general is the EU nitrate directive from 1991. It was transposed into

German law by “Düngeverordnung” (fertiliser act). The version of 2012 regulates that the three years average of nitrogen surplus must not exceed 60 kg N ha^{-1} per year (Federal Ministry of Justice and Consumer Protection & juris GmbH 2012).

To breed nitrogen efficient cultivars one must decide about the traits to select for. Next to seed yield itself possible parameters are nitrogen use efficiency or its components (nitrogen uptake efficiency and nitrogen utilisation efficiency according to Moll et al. 1982) but also nitrogen uptake at different growth stages or nitrogen harvest index. A suitable trait should show significant genetic variation and stable expression across environments, i.e. high heritability. But not only the trait to be selected for is to be decided but also the condition under which selection is conducted needs to be considered particularly regarding nitrogen fertilisation/availability. Another aspect is the method of selection. It may be necessary to grow large numbers of genotypes until harvest and analyse seeds and straw for nitrogen. But it may also be possible to apply methods for indirect selection that allow selection early during growth. Three studies were conducted concerning different aspects of nitrogen efficiency of winter oilseed rape as a trait in plant breeding.

The first study (chapter A) analysed genetic variation of nitrogen efficiency parameters of genetic diverse genotypes and of DH lines and test hybrids. It addressed several questions.

1. How large is the genetic variation in nitrogen efficiency in winter oilseed rape that can be exploited for breeding?
2. How stable are nitrogen efficiency parameters expressed across environments?
3. Is it necessary to test genotypes at different levels of nitrogen supply?
4. Do DH lines and test hybrids perform different with regards to nitrogen efficiency parameters?
5. Does heterosis for nitrogen efficiency parameters exist?

To answer these questions a diverse set of 30 genotypes and 30 DH lines and 30 descending test hybrids were tested for nitrogen efficiency parameters at two nitrogen levels in field trials at three locations in one to two years.

In the second study (chapter B) hyperspectral canopy reflectance was tested as method to predict nitrogen uptake and seed yield of winter oilseed rape and thus, to facilitate selection. Several questions were to be answered.

1. Can hyperspectral canopy reflectance in principal be applied to predict nitrogen uptake and/or seed yield?
2. Is it necessary to develop different calibrations for different levels of nitrogen supply?
3. What is the best plant developmental stage to measure with regards to predictive ability of calibration?

To answer these questions hyperspectral canopy reflectance was measured twice in the field trials mentioned above. Reflectance was used to develop calibrations across and within nitrogen levels for nitrogen uptake and seed yield.

The third study (chapter C) examined electrical capacitance of winter oilseed rape for its relationship to nitrogen efficiency parameters and/or root characteristics to answer three questions.

1. Is there genetic variation for electrical capacitance in winter oilseed rape and how stable is the trait expressed?
2. Does electrical capacitance correlate with nitrogen efficiency parameters and thus, can be applied as selection criterion in breeding?
3. Is electrical capacitance of winter oilseed rape related to root characteristics?

To answer the first and second question electrical capacitance was measured twice in the field trials of the first study and tested for its phenotypic and genetic correlation to nitrogen efficiency parameters. The second question was addressed in experiments with ten genotypes that were tested in field trials and under controlled conditions in the greenhouse. Next to electrical capacitance root characteristics were determined directly or based on digital images.

CHAPTER A - NITROGEN EFFICIENCY AND RELATED TRAITS OF WINTER OILSEED RAPE

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Introduction

Nitrogen efficiency of oilseed rape

Winter oilseed rape receives nitrogen fertiliser most often in two applications. At begin of vegetation after winter nitrogen fertilisation enhances regrowth of rosette leaves and supports primordia of flowers and leaves. At beginning of stem extension it provides the high amounts of nitrogen required during flowering and fruit development. Only if development before winter is weak, e.g. due to late sowing, nitrogen fertilisers are applied in autumn (Weimar 2015). Nitrogen demand depends on expected seed yield. It is estimated that about 6 kg N ha^{-1} are accumulated by the crop to produce 100 kg seed ha^{-1} (Rathke et al. 2006). Legislative regulations like EU Directive 2009/28/EG and EU nitrate directive (Federal Ministry of Justice and Consumer Protection & juris GmbH 2012, Ufop 2015) have moved nitrogen efficiency of winter oilseed rape into focus of plant breeders.

Oilseed rape suffers from low nitrogen efficiency. With flowering oilseed rape starts to shed leaves. The translocation of leaf nitrogen is incomplete. Malagoli et al. (2005) reported that dropped leaves contain 0.7 – 3.5 % nitrogen. Nitrogen content was higher during the first phase of leaf shedding when pods have not yet started to develop. When developing pods provided a strong sink lower nitrogen contents were observed in dropped leaves. Next to growth stage translocation is influenced by nitrogen fertilisation. At low nitrogen levels more nitrogen is remobilised from leaves than at higher nitrogen levels (Schjoerring et al. 1995, Ulas et al. 2013). After flowering only little nitrogen is taken up, though contradicting results exist. An increase of the amount of nitrogen between 4 kg N ha^{-1} and 60 kg N ha^{-1} was described in the plant between flowering and maturity by several authors (Aniol 1993, Hocking et al. 1997, Malagoli et al. 2005, Berry et al. 2010, Ulas et al. 2013). But also net nitrogen losses were observed (Aufhammer et al. 1994). When comparing low and high nitrogen supply, it appears that at high nitrogen supply plants take up less nitrogen after flowering than at low nitrogen or even loose nitrogen. Therefore, at low nitrogen supply net nitrogen accumulation was observed (Aufhammer et al. 1994, Schjoerring et al. 1995, Schulte auf'm Erley et al. 2011). Nitrogen uptake after

flowering (if existing) is low compared to nitrogen uptake until flowering (up to 200 kg N ha^{-1}). Most of nitrogen in reproductive tissues is endogenous, i.e. is translocated from vegetative tissues. Experiments with ^{15}N labelling revealed that 60 - 70% of nitrogen in flowers and pods is derived from the stem and leaves and not from nitrogen which was taken up after flowering (Schjoerring et al. 1995, Malagoli et al. 2005). Similar to remobilisation of leaf nitrogen remobilisation of stem nitrogen to pods and seeds increases with decreasing nitrogen supply (Ulas et al. 2013).

It is estimated that a maximum of 50 % of nitrogen applied with fertiliser is recovered by the crop (Schjoerring et al. 1995, Jensen et al. 1997, Leleu et al. 2000). Nitrogen harvest index of oilseed rape varies from 0.7 to 0.8 (Schulte auf'm Erley et al. 2011, Ulas et al. 2013, Koeslin-Findeklee et al. 2014), i.e. at least 20 – 30 % of nitrogen in the plant remain on the field after harvest and add up to residual fertiliser nitrogen and lost leaf nitrogen. Nitrogen surpluses of more than 90 – 100 kg N ha^{-1} were reported after cultivation of winter oilseed rape (Henke et al. 2007, Sieling & Kage 2010). These high surpluses cause problems in crop rotations containing winter oilseed rape as it may lead to three years averages of nitrogen surplus above the legislative threshold of 60 kg N ha^{-1} a^{-1} specified in the German fertiliser act. High nitrogen surpluses lead to pollution of groundwater by nitrate due to leaching (Henke et al. 2007, Federal Ministry of Justice and Consumer Protection & juris GmbH 2012).

Schulte auf'm Erley et al. (2011) conducted experiments with winter oilseed rape at three nitrogen levels. They observed significant genetic variation for seed yield, nitrogen uptake, nitrogen uptake after begin of flowering, nitrogen utilisation efficiency and nitrogen harvest index at all nitrogen levels. Nitrogen uptake was considered as a trait closely associated to seed yield at all nitrogen levels. Kessel et al. (2012) examined 36 genotypes of winter oilseed rape including hybrid cultivars, old and new line cultivars and resynthesised lines in field trials at two nitrogen levels. Significant genetic variation was detected for nitrogen yield and nitrogen efficiency. Nitrogen uptake efficiency was more important for nitrogen use efficiency than nitrogen utilisation efficiency at low nitrogen supply. At high nitrogen supply nitrogen utilisation efficiency was more important. Nyikako et al. (2014) analysed genetic variation of nitrogen use efficiency, nitrogen uptake efficiency and nitrogen utilisation efficiency of a DH population of winter oilseed rape at two nitrogen levels. They observed significant genetic variation for nitrogen uptake and nitrogen utilisation efficiency. Nitrogen uptake efficiency was more important for variation in nitrogen use

efficiency than nitrogen utilisation efficiency at low nitrogen supply. At high nitrogen supply this was true for two environments while in other two environments nitrogen utilisation efficiency was more important.

Only few studies examined nitrogen efficiency of DH lines and test hybrids of winter oilseed rape. Friedt et al. (2003) reported that hybrids showed higher seed yield at low and high nitrogen supply compared to DH lines, line varieties and semi-synthetics. The difference between hybrid mean and mean of DH lines increased with increasing nitrogen supply. Nitrogen harvest index was lower for hybrids than for DH lines at low nitrogen supply but revealed no difference at higher nitrogen levels. Gehringer et al. (2007) compared seed yield of DH lines and test hybrids at two sites. On average test hybrids outperformed DH lines in seed yield at both sites. Heterosis for seed yield was higher and always positive under poor soil conditions. At good soil conditions heterosis was low and sometimes negative. In a further study of Koeslin-Findeklee et al. (2014) seed yield and nitrogen utilisation efficiency of hybrids was higher than that of DH lines at low and high nitrogen supply. No differences were found for nitrogen concentration in seeds and nitrogen harvest index at both nitrogen levels. Nitrogen uptake at maturity was lower for DH lines at low nitrogen supply while at high nitrogen supply DH lines and hybrids did not differ in nitrogen uptake.

Objectives of the study

The current study wants to answer the following questions.

1. How large is the genetic variation in nitrogen efficiency and related traits in winter oilseed rape?
2. How stable are nitrogen efficiency and related traits expressed across environments?
3. Must selection environments for nitrogen efficiency resemble nitrogen supply of target environments?

To answer these questions, field trials with 30 genetically diverse genotypes were conducted at two nitrogen levels.

4. Do DH lines and test hybrids differ in their reaction to different levels of nitrogen supply?
5. Does heterosis for nitrogen efficiency parameters exist?

Therefore, DH lines and their test hybrids were examined in field trials at two nitrogen levels.

Materials and Methods

In 2011/12 and 2012/13 30 genotypes were tested in two parallel field trials differing in time of harvest – end of flowering (EOF) and maturity (MAT). In 2013/14 two DH populations were tested together with their testcrosses in two MAT trials – MAT007 and MAT029.

Genotypes

Diversity set

Thirty adapted genotypes of winter oilseed rape, representing a broad genetic diversity, were tested 2011/12 and 2012/13 (Tab. A 1). Their genetic diversity was assessed by Bus et al. (2011). The set contained double low, high erucic acid and glucosinolate containing genotypes. Next to old and new line varieties resynthesised lines were included.

Tab. A 1: Genotypes of diversity set

Genotype	Type	Country	C22:1	GSL	Release period *	Remarks
PBY001	L	Germany	+	+	NA	EC10
PBY002	L	Germany	+	+	NA	
PBY003	L	Sweden	0	+	NA	
PBY004	L	Czech Republic	+	+	1954-1979	
PBY005	L	Germany	0	0	1980-1989	
PBY006	L	Germany	0	0	1980-1989	
PBY007	L	France	+	+	NA	P_{DH}, EC10
PBY008	L	France	+	+	NA	EC10
PBY009	L	Russia	+	+	1954-1979	
PBY010	L	Russia	+	+	1980-1989	
PBY011	L	Poland	0	0	NA	
PBY012	L	Germany	0	0	2000-2007	
PBY013	L	Germany	0	0	2000-2007	
PBY014	L	Italy	NA	NA	1954-1979	
PBY015	L	Germany	0	0	1990-1999	EC10
PBY017	DH	United Kingdom	NA	NA	NA	
PBY018	L	France	0	0	1980-1989	
PBY019	L	Germany	0	0	1980-1989	
PBY020	R	NA	+	+	NA	
PBY021	R	NA	+	+	NA	EC10
PBY022	L	United Kingdom	0	0	1990-1999	EC10
PBY023	L	France	0	0	1990-1999	
PBY024	L	France	0	0	1990-1999	
PBY025	L	France	0	0	2000-2007	
PBY026	L	France	0	0	2000-2007	EC10
PBY027	L	Germany	0	0	1990-1999	EC10
PBY028	L	Germany	0	0	1990-1999	
PBY029	L	unknown	0	0	2000-2007	P_{DH}, EC10
PBY061	DH	Germany	0	0	NA	S_{DH}, EC10
PBY062	MS	Germany	0	0	NA	S_{TH}, EC10

* Release period as given in Bus et al. (2011), L line variety, DH double haploid line, R resynthesized line, MS male sterile line, C22:1 erucic acid content, GSL total glucosinolate content, 0 < 2 % erucic acid in seed oil and < 25 µmol glucosinolate (g seeds)$^{-1}$ at 9% moisture, respectively, + > 2 % erucic acid in seed oil and > 25 µmol glucosinolate (g seeds)$^{-1}$ at 9% moisture, respectively, NA data not available, EC10 genotypes selected from field trials 2011/12 for testing in additional electrical capacitance trials described in chapter C, P_{DH} used as pollinator to produce DH populations tested 2013/14, S_{DH} Common seed parent used to develop DH populations tested 2013/14, S_{TH} Common seed parent of test hybrids tested 2013/14 (tester)

DH lines and test hybrids

Two genotypes of the diversity set (PBY007, PBY029) were crossed to PBY061 (Tab. A 1) to develop two DH populations. Subsequently DH lines were crossed to a common tester (PBY062) to produce test hybrids. Fifteen DH lines, their descending test hybrids as well as the DH parents (PBY007, PBY029 and PBY061) and the male sterile tester (PBY062) were tested for each population.

Experimental design

Diversity set

In 2011/12 and 2012/13 two parallel trials were run. One was harvested at end of flowering (EOF) the other one at maturity (MAT). Both were designed as two-factorial split plots with nitrogen levels (N1 and N0) as whole plot factor and genotype as subplot factor. Genotypes were randomised in alpha lattice design. Each trial was replicated twice. For similar neighbour effects between trials and nitrogen levels the same randomisation was used for the two trials and the two nitrogen levels within environments and replications.

DH lines and test hybrids

In 2013/14 genotypes were tested in two trials at two nitrogen levels (N1 and N0) which were harvested at maturity (MAT). One trial was conducted for each population. Population 007 (Pop007) contained 15 DH lines derived from PBY007, their test hybrids and parental genotypes PBY007, PBY061 and PBY062 (Tab. A 1). It was tested in MAT007. Population 029 (Pop029) contained 15 DH lines derived from PBY029, their test hybrids and parental genotypes PBY029, PBY061 and PBY062 (Tab. A 1). It was tested in MAT029. For a better comparison of DH lines and test hybrids a DH line and its descending test hybrid were treated as one randomisation unit (descent) (Fig. A 1). As for the three parental genotypes no corresponding test hybrids existed they were paired with three commercial hybrids – Artoga (Limagrain GmbH, Edemissen, Germany), Titan (W. von Borries-Eckendorf GmbH & Co KG, Leopoldshöhe, Germany) and Visby (Saatzucht Hans Lembke KG, Malchow/Poel, Germany). The trials were set up as three-factorial split-split plots with

nitrogen level as whole plot factor, variety type (DH line or test hybrid) as subplot factor and descent as sub-subplot factor. Factors were randomised to whole plots, subplots and sub-subplots. To prevent competition between hybrids and DH lines both were grown in alternating rows (Fig. A 1). For similar neighbour effects between trials and nitrogen levels the same randomisation was used for the two trials and the two nitrogen levels within environments and replications.

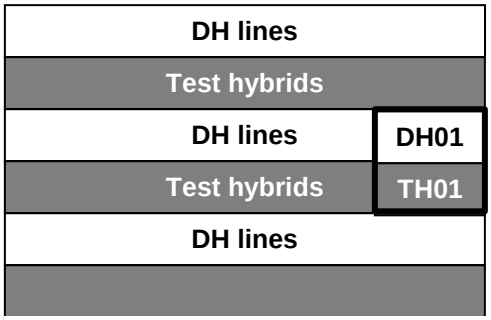

Fig. A 1: Arrangement of DH lines and test hybrids in MAT trials 2013/14
Alternating rows of DH lines and test hybrids and DH line (DH01) with corresponding test hybrid (TH01) as one randomisation unit

Cultivation

Field trials were conducted at two locations in 2011/12 and at three locations in 2012/13 and 2013/14 in Central and Northern Germany (Tab. A 2). That resulted in five combinations (environments) of location and year for the diversity set (2011/12 and 2012/2013) (Tab. A 2). DH lines and test hybrids were tested in three environments (2013/14) (Tab. A 2). Season 2013/14 was characterised by a warm winter (4.3 °C in Lower Saxony LS, 3.7 °C Hesse H) compared to long term means (LS 1.2 °C, H 0.3 °C) (DWD 2014 a) and an early and warm spring (LS 10.4 °C, H 10.3 °C) compared to long term means (LS 7.9 °C, H 7.8 °C) (DWD 2014 b).

Genotypes were tested at two nitrogen fertilisation levels. At N1 160 – 180 kg N ha^{-1} were applied in two portions (Tab. A 3) while at N0 no nitrogen fertiliser was applied. Trials with the diversity set were sown from August 22nd to August 28th except in season 2012/13 where sowing in Göttingen took place at September 3rd. DH lines and test hybrids were sown from August 30th to September 4th. Information about plot size, sowing density and number of rows is given in Tab. A 4.

Plant protection followed common practice. To facilitate harvest of MAT trials, non-selective herbicides were applied two weeks before harvest in EIN2012, EIN2013, EIN2014, GOE2012, GOE2013 and GOE2014 but not in GIE2013 and GIE2014.

Tab. A 2: Environments of field trials

Environment	Location	Season	Prec[6] [mm]	T[7] [°C]	Height[8] [m]	Latitude[8]	Longitude[8]
EIN2012[1]	Rotenkirchen (near Einbeck)	2011/12	843	8,4	150	51°46'50.09"N	9°49'23.64"E
EIN2013[1]	Rotenkirchen (near Einbeck)	2012/13	843	8,4	145	51°46'33.69"N	9°50'16.76"E
EIN2014[1]	Markoldendorf (near Einbeck)	2013/14	843	8,4	135	51°48'45.39"N	9°47'6.59"E
GIE2013[2]	Rauischholzhausen (near Marburg)	2012/13	707	9,3	220	50°45'40.22"N	8°52'9.77"E
GIE2014[2]	Rauischholzhausen[4] (near Marburg)	2013/14	707	9,3	220	50°45'55.04"N	8°52'44.04"E
GIE2014[2]	Mardorf[5] (near Marburg)	2013/14	707	9,3	200	50°45'58.85"N	8°55'52.09"E
GOE2012[3]	Reinshof (near Göttingen)	2011/12	651	8,7	150	51°30'4.10"N	9°55'45.52"E
GOE2013[3]	Reinshof (near Göttingen)	2012/13	651	8,7	155	51°29'27.18"N	9°55'36.01"E
GOE2014[3]	Reinshof (near Göttingen)	2013/14	651	8,7	160	51°29'17.69"N	9°56'0.93"E

[1] Fields of KWS Saat AG, Einbeck/Germany, [2] Fields of university Gießen/Germany, [3] Fields of university Göttingen/Germany, [4] Experiments on electrical capacitance (EC007 and EC029, chapter C) were conducted in this environment, [5]MAT007 and MAT029 were conducted in this environment, [6]Mean precipitation and [7]Mean temperature from 1981 – 2010 based on data from German Meteorological Service weather stations ID3348 (EIN), ID3164 (GIE), ID 1691 (GOE), [8]Height above sea level, latitude and longitude of a point in the centre of the field

Tab. A 3: Nitrogen fertilisation

Environment	Nitrogen fertilisation in N1 [kg N ha^{-1}] (Portions, Fertiliser)	Available nitrogen [kg ha^{-1}] [1]			
		EOF		MAT	
		N0	N1	N0	N1
2011/12 and 2012/13					
EIN2012	158 (99 + 59, Piamon 33-S)	57	215	- [2]	
EIN2013	158 (99 + 59, Piamon 33-S)	89	247	95	253
GIE2013	180 (100 + 80, ASN + CAN)	117	297	144	324
GOE2012	177 (42/54 + 81, ASA/CAN + CAN)	38	215	60	237
GOE2013	177 (42/54 + 81, ASA/CAN + CAN)	123	300	137	314
2013/14					
EIN2014	158 (99 + 59, Piamon 33-S)			216	374
GIE2014	180 (100 + 80, ASN + CAN)	- [3]		157	337
GOE2014	177 (42/54 + 81, ASA/CAN + CAN)			258	435

Nitrogen fertilisation total amount of N, amount of nitrogen and type of fertiliser applied with each portion are given in brackets, ASN ammonium sulphate nitrate, CAN calcium ammonium nitrate, ASA ammonium sulphate ammoniac, EOF EOF trial, MAT MAT trial, [1] For computation of available nitrogen see equation 8, [2] trial conducted but not harvested (hail damage), [3] trial not conducted

Tab. A 4: Plots and sowing of field trial in seasons 2011/12, 2012/13 and 2013/14

Location	Plot size (Length/width)	Number of rows	Between rows distance	Seeds m^{-2} at sowing
EIN	18 m² (10/1.8)	6	30 cm	50
GIE	8.75 m² (7/1.25)	8	16 cm	60
GOE	11.25 m² (7.5/1.5)	6	25 cm	83

EIN Fields of KWS Saat AG Einbeck/Germany, GIE Fields of university Gießen/Germany, GOE Fields of university Göttingen/Germany,

Assessment of traits

An overview about captured traits can be found in Tab. A 5.

Tab. A 5: Captured traits and abbreviations

Date	Trait	Abbreviation	Diversity set captured in	DH lines and test hybrids captured in
EOF	DM content of aboveground biomass	$DM\%_{EOF}$	5 env	Not captured
	Aboveground biomass yield DM	$Yield_{EOF}$		
	Nitrogen content of aboveground biomass DM	$N\%_{EOF}$		
	Nitrogen uptake of aboveground biomass DM	Nup_{EOF}		
	Nitrogen uptake efficiency	$NupEff_{EOF}$		
MAT	DM content of seeds	$N\%_{Seed}$	4 env	3 env
	Seed yield DM	Seed DM		
	Seed yield at 9% moisture	Seed 9%		
	Nitrogen content of seeds DM	$N\%_{Seed}$		
	Nitrogen uptake of seeds DM	Nup_{Seed}		
	Oil content of seeds DM	Oil%		
	Oil yield DM	Oil yield		
	DM content of straw	$DM\%_{Straw}$		
	Straw yield DM	Straw DM		
	Nitrogen content of straw DM	$N\%_{Straw}$		
	Nitrogen uptake of straw DM	Nup_{Straw}		
	Nitrogen uptake of aboveground biomass	Nup_{MAT}		
	Nitrogen uptake efficiency	$NupEff_{MAT}$		
	Nitrogen utilisation efficiency	NutEff		
	Nitrogen use efficiency	NUE		
	Harvest index	HI		
	Nitrogen harvest index	NHI		
	Nitrogen uptake after flowering [1]	Delta Nup	4 env	Not captured
	Begin of flowering [2]	FL	4 env	2 env
	Plant length [2]	PL	5 env	2 env

EOF end of flowering, MAT maturity, [1] EOF and MAT were necessary to capture the trait (see under "Nitrogen efficiency parameters"), [2] in 2011/12 and 2012/13 trait was captured in EOF or MAT, env environments

Begin of flowering and plant length

During vegetation begin of flowering (number of days after January 1st when 10 % of plants flowered) and plant length (in cm) after end of length growth were captured but not in all environments (Tab. A 5).

Yield

Aboveground biomass at end of flowering ($Yield_{EOF}$)

Total aboveground biomass was harvested at end of flowering with a grass harvester. Therefore, plants were cut above soil level. Fresh biomass was weighed immediately and a subsample was taken.

Seed yield and Straw yield at maturity

MAT trial in EIN2012 could not be harvested due to severe hail damage. In all other MAT trials seed and straw were harvested at maturity with a plot-combiner (Hege 160). Therefore, plants were cut above soil level. Straw was collected with a tarpaulin which was attached to the back of the harvester and weighed with a crane scale immediately after harvest (Fig. A 2). A subsample of straw containing stem, branches and pod walls was taken for further analyses. Seed yield was computed for 9 % moisture (Seed 9%) and as dry matter (Seed DM). Seed 9% is of interest for breeders while Seed DM was used for computations of nitrogen efficiency parameters.

Dry matter content of aboveground biomass, straw and seeds

The subsamples of aboveground biomass taken at end of flowering and the subsamples of straw taken at maturity were dried at 60 °C overnight followed by 105 °C until constant weight. Subsamples of seeds were dried at 40 °C overnight followed by 105 °C until constant weight.

Oil content

About 2 g of seeds were analysed for oil content using near-infrared reflectance of intact seeds (NIRS monochromator model 6500, NIRSystems, Inc., Silversprings, MD, USA, calibrations raps2012.eqa, raps2013.eqa and raps2014.eqa provided by VDLUFA Qualitätssicherung NIRS GmbH).

Fig. A 2: Harvest of MAT trial with plot-combiner (left) and weighing straw (right)

Nitrogen efficiency

Sample preparation

Two tablespoons of the dried subsample of aboveground biomass were milled to a particle size of 0.2 mm with a centrifugal mill (ZM 100, Retsch, Haan/Germany). The dried subsample of straw was milled to a particle size of 4 mm with a cutting mill (SM 100, Retsch, Haan/Germany). Two tablespoons were then milled to a particle size of 0.2 mm with a centrifugal mill (ZM 100, Retsch, Haan/Germany). About 2 g of seeds were milled for 1 min with an electric blade grinder.

Nitrogen analysis

Nitrogen content of dry matter of aboveground biomass at end of flowering ($N\%_{EOF}$), seed ($N\%_{Seed}$) and straw ($N\%_{Straw}$) was analysed following Dumas method. Due to issues of measurement capacity analyses were run in two laboratories (Tab. A 6).

Tab. A 6: Nitrogen analysis

Laboratory	Trials	Analysed quantity	Nitrogen elemental analyser	Details
Göttingen[1]	EOF 2011/12 MAT 2011/12 MAT 2012/13	16 - 19 mg	Vario EL[3]	$T_{Oxidation}$ = 950 °C $T_{Reduction}$ = 500 °C Thermal conductivity detector Standard Acetanilide
Vechta[2]	EOF 2012/13 MAT007 MAT029	500 mg	Vario Max CN[3]	$T_{Oxidation}$ = 900 °C $T_{Reduction}$ = 830 °C Thermal conductivity detector Standard L-Glutamic acid

[1] Georg-August-Universität Göttingen, Abteilung Pflanzenbau, Göttingen/Germany, [2] Georg-August-Universität Göttingen, Außenstelle Vechta, Vechta/Germany, [3] Elementar Analysensysteme GmbH, Hanau/Germany

Nitrogen efficiency parameters

Nitrogen uptake of total aboveground biomass at end of flowering (Nup_{EOF}), seeds (Nup_{Seed}), straw (Nup_{Straw}) and total aboveground biomass (NupMAT) at maturity, nitrogen uptake after flowering (Delta Nup), harvest index (HI), nitrogen harvest index (NHI), nitrogen uptake efficiency at end of flowering ($NupEff_{EOF}$) and at maturity ($NupEff_{MAT}$), nitrogen utilisation efficiency (NutEff) and nitrogen use efficiency (NUE) were computed using equations A 1 – A 11. The contribution of the variances of $NupEff_{MAT}$ and NutEff to the variance of NUE was estimated according to Moll et al. (1982).

Equation A 1

$$\mathbf{Nup_{EOF} = N\%_{EOF} \times Yield_{EOF}}$$

Nup_{EOF} [dt ha^{-1}] = Amount of nitrogen taken up by total aboveground biomass dry matter at EOF

$N\%_{EOF}$ = Nitrogen content of total aboveground biomass dry matter at EOF

Yield $_{EOF}$ [dt ha^{-1}) = Total aboveground biomass dry matter

Equation A 2

$$\mathbf{Nup_{Seed} = N\%_{Seed} \times Seed\ DM}$$

Nup_{Seed} [dt ha^{-1}] = Amount of nitrogen taken up by seeds at maturity

$N\%_{Seed}$ = Nitrogen content of seeds dry matter at maturity

Seed DM [dt ha^{-1}] = Seed yield dry matter at maturity

Equation A 3

$$\mathbf{Nup_{Straw} = N\%_{Straw} \times Straw\ DM}$$

Nup_{Straw} [dt ha^{-1}] = Amount of nitrogen taken up by straw at maturity

$N\%_{Straw}$ = nitrogen content of straw dry matter at maturity

Straw [dt ha^{-1}] = Straw yield dry matter at maturity

Equation A 4

$$\mathbf{Nup_{MAT} = Nup_{Seed} + Nup_{Straw}}$$

Nup_{MAT} [dt ha^{-1}] = Amount of nitrogen taken up by total aboveground biomass at maturity

Nup_{Seed} [dt ha^{-1}] = Amount of nitrogen taken up by seeds at maturity

Nup_{Straw} [dt ha^{-1}] = Amount of nitrogen taken up by straw at maturity

Equation A 5

$$\mathbf{Delta\ Nup = Nup_{MAT} - Nup_{EOF}}$$

Delta Nup = Nitrogen uptake between end of flowering and maturity

Equation A 6

$$\mathbf{HI = Seed\ DM \times (Seed\ DM + Straw\ DM)^{-1}}$$

HI = Harvest index

Seed DM [dt ha^{-1}] = Seed yield dry matter at maturity

Straw [dt ha^{-1}] = Straw yield dry matter at maturity

Equation A 7

$$\mathbf{NHI = Nup_{Seed} \times Nup_{MAt}^{-1}}$$

NHI = nitrogen harvest index

Equation A 8

$$\mathbf{NupEff_{EOF} = Nup_{EOF} \times Available\ nitrogen\ EOF^{-1}}$$

$NupEff_{EOF}$ = Nitrogen uptake efficiency at EOF

Nup_{EOF} [dt ha^{-1}] = Amount of nitrogen taken up by total aboveground biomass dry matter at EOF

Available nitrogen EOF [dt ha^{-1}]

For N0 = For each environment plot at N0 with highest Nup EOF in replication 1 and plot with highest Nup EOF in replication 2 are averaged

For N1 = Available nitrogen EOF at N0 + Fertiliser nitrogen

Equation A 9

$$\mathbf{NupEff_{MAT} = Nup_{MAT} \times Available\ nitrogen\ MAT^{-1}}$$

$NupEff_{MAT}$ = Nitrogen uptake efficiency of total aboveground biomass at maturity

Nup_{MAT} [dt ha-^{1}] = Amount of nitrogen taken up by total aboveground biomass at maturity

Available nitrogen MAT [dt ha^{-1}]

For N0 = For each environment at N0 plot with highest Nup MAT in replication 1 and plot with highest Nup MAT in replication 2 are averaged

For N1 = Available nitrogen MAT for N0 + Fertiliser N

Equation A 10

$$\mathbf{NutEff = Seed\ DM \times Nup_{MAT}^{-1}}$$

NutEff = Nitrogen utilisation efficiency

Seed yield [dt ha^{-1}] = Seed yield dry matter at maturity

Equation A 11

$$\mathbf{NUE = NupEff_{MAT} \times NutEff = Seed\ DM \times Available\ nitrogen\ MAT^{-1}}$$

NUE [dt Seed (dt Available nitrogen MAT)$^{-1}$] = nitrogen use efficiency of total aboveground biomass at maturity

$NupEff_{MAT}$ = Nitrogen uptake efficiency of total aboveground biomass at maturity

NutEff = Nitrogen utilisation efficiency

Statistical analysis

Plabstat (version 3A, Utz 2011, https://plant-breeding.uni-hohenheim.de/software.html) was used for analysis of variance.

Diversity set

In order to correct plot values for spatial variation a lattice analysis was applied to each nitrogen level in each environment to data derived from EOF and MAT trials. During that procedure two cases of missing values were distinguished. Case 1 was true for genotypes with only one missing plot whereas in case 2 both plots of a genotype were missing. For case 1 the computation of the missing value was accepted whereas for case 2 it was not. The latter were computed by applying model A 1 to each nitrogen level. One genotype (PBY014) did not survive winter and thus, was not considered in further analyses. Split-plot analysis (model A 2) was then applied to the lattice corrected and computed missing plot values. The split-plot ANOVA was corrected for degrees of freedom which were used up by lattice correction (if efficiency > 100%) and computation of missing values in lattice and model A 1. For EOF split-plot analysis (model A 2) was conducted across all five environments. MAT trials were analysed across the four available environments (Tab. A 5). As Nup_{EOF} and Nup_{MAT} were captured at different plots Delta Nup could not be analysed plot-wise. Instead there was one value per genotype, environment and nitrogen level. Delta Nup was analysed based on these values by applying model A 3.

Model A 1

$$Y_{abc} = m + e_a + r_{b(a)} + g_c + (eg)_{ac} + (rg)_{bc(a)}$$

Y_{abc} = Observation for c^{th} genotype in a^{th} environment and b^{th} replication

m = Overall mean

e_a = Random effect of a^{th} environment

$r_{b(a)}$ = Random effect of b^{th} replication within a^{th} environment

g_c = Fixed effect of c^{th} genotype

$(eg)_{ac}$ = Effect of interaction between a^{th} environment and c^{th} genotype

$(rg)_{bc(a)}$ = Error (Interaction effect between b^{th} replication and c^{th} genotype within a^{th} environment)

Model A 2

$$Y_{abcd} = m + e_a + r_{b(a)} + n_c + (en)_{ac} + (rn)_{bc(a)} + g_d + (eg)_{ad} + (ng)_{cd} + (eng)_{acd} + (rng)_{bcd(a)}$$

Y_{abcd} = Observation for d^{th} genotype in a^{th} environment in b^{th} replication and c^{th} nitrogen level

m = Overall mean

e_a = Random effect of a^{th} environment

$r_{b(a)}$ = Whole plot error (Random effect of b^{th} replication within a^{th} environment)

n_c = Fixed effect of c^{th} nitrogen level

$(en)_{ac}$ = Effect of interaction between a^{th} environment and c^{th} nitrogen level

$(rn)_{bc(a)}$ = Effect of interaction between b^{th} replication and c^{th} nitrogen level within a^{th} environment

g_d = Fixed effect of d^{th} genotype

$(eg)_{ad}$ = Effect of interaction between a^{th} environment and d^{th} genotype

$(ng)_{cd}$ = Interaction effect between c^{th} nitrogen level and d^{th} genotype

$(eng)_{acd}$ = Effect of interaction between a^{th} environment, c^{th} nitrogen level and d^{th} genotype

$(rng)_{bcd(a)}$ = Subplot error (Interaction effect between b^{th} replication, c^{th} nitrogen level and d^{th} genotype within a^{th} environment)

Model A 3

$$Y_{abc} = m + e_a + n_b + (en)_{ab} + g_c + (eg)_{ac} + (ng)_{bc} + (eng)_{abc}$$

Y_{abcd} = Observation for c^{th} genotype in a^{th} environment and b^{th} nitrogen level

m = Overall mean

e_a = Random effect of a^{th} environment

n_b = Fixed effect of b^{th} nitrogen level

$(en)_{ab}$ = Effect of interaction between a^{th} environment a and b^{th} nitrogen level

g_c = Fixed effect of c^{th} genotype

$(eg)_{ac}$ = Effect of interaction between a^{th} environment and c^{th} genotype

$(ng)_{bc}$ = Effect of interaction between b^{th} nitrogen level and c^{th} genotype

$(eng)_{abc}$ = Interaction effect between a^{th} environment, b^{th} nitrogen level and c^{th} genotype

Model A 4

$$Y_{ab} = m + e_a + g_b + (eg)_{ab}$$

Y_{ab} = Observation for the b^{th} genotype at the a^{th} environment

m = Overall mean

e_a = Random effect of a^{th} environment

g_b = Fixed effect of b^{th} genotype

$(eg)_{ab}$ = Interaction effect between a^{th} environment and b^{th} genotype

DH lines and test hybrids

Statistical analysis was conducted for DH lines and test hybrids but not for parental genotypes. For the latter simple means across environments were computed. MAT007 and MAT029 were analysed independently. In a first step missing values were computed separate for N1 and N0 (split-plot analysis, model A 5). Afterwards a split-split plot analysis (model A 6) was applied to MAT007 and MAT029 to compute ANOVA. To estimate heritabilities model A 7 was applied and heritability was estimated for effect of genotype within variety type.

Model A 5

$$Y_{abcf} = m + e_a + r_{b(a)} + t_c + (et)_{ac} + (rt)_{bc(a)} + d_f + (ed)_{af} + (td)_{cf} + (etd)_{acf} + (rtd)_{bc(a)}$$

Y_{abcf} = Observation for f^{th} descent in a^{th} environment, b^{th} replication and of c^{th} type

m = Overall mean

e_a = Random effect of a^{th} environment

$r_{b(a)}$= Random effect of b^{th} replication with a^{th} environment

t_c = Fixed effect of c^{th} variety type

$(et)_{ac}$ = Effect of interaction between a^{th} environment and c^{th} variety type

$(rt)_{bc(a)}$ = Whole plot error (Effect of interaction between b^{th} replication and c^{th} variety type within a^{th} environment)

d_f = Fixed effect of f^{th} descent

$(ed)_{af}$ = Effect of interaction between a^{th} environment and f^{th} variety type

$(td)_{cf}$ = Effect of interaction between c^{th} variety type and f^{th} descent

$(etd)_{acf}$ = Effect of interaction between a^{th} environment, c^{th} variety type and f^{th} descent

$(rtd)_{bcf(a)}$ = Subplot error (Effect of interaction between b^{th} replication, c^{th} variety type and f^{th} descent within a^{th} environment)

Model A 6

$$Y_{abcfg} = m + e_a + r_{b(a)} + n_c + (en)_{ac} + (rn)_{bc(a)} + t_f + (et)_{af} + (nt)_{cf} + (ent)_{acf} + (rnt)_{bc(a)} + d_g + (ed)_{ag} + (nd)_{cg} + (td)_{fg} + (end)_{acg} + (etd)_{afg} + (entd)_{acfg} + (rntd)_{bcfg(a)}$$

Y_{abcfg} = Observation of g^{th} descent at a^{th} environment, b^{th} replication, c^{th} nitrogen level and of f^{th} variety type

m = Overall mean

e_a = Random effect of a^{th} environment

$r_{b(a)}$ = Random effect of b^{th} replication within a^{th} environment

n_c = Fixed effect of c^{th} nitrogen level

$(en)_{ac}$ = Effect of interaction between a^{th} environment and c^{th} nitrogen level

$(rn)_{bc(a)}$ = Whole plot error (Effect of interaction between b^{th} replication and c^{th} nitrogen level within a^{th} environment)

t_f = Fixed effect of f^{th} variety type

$(et)_{af}$ = Effect of interaction between a^{th} environment and f^{th} variety type

$(nt)_{cf}$ = Effect of interaction between c^{th} nitrogen level and f^{th} variety type

$(ent)_{acf}$ = Effect of interaction between a^{th} environment, c^{th} nitrogen level and f^{th} variety type

$(rnt)_{bcf(a)}$ = Subplot error (Effect of interaction between b^{th} replication, c^{th} nitrogen level and f^{th} variety type with a^{th} environment)

d_g = Fixed effect of g^{th} descent

$(ed)_{ag}$ = Effect of interaction between a^{th} environment and g^{th} descent

$(nd)_{cg}$ = Effect of interaction between c^{th} nitrogen level and g^{th} descent

$(td)_{fg}$ = Effect of interaction between f^{th} type and g^{th} descent

$(end)_{acg}$ = Effect of interaction between a^{th} environment, c^{th} nitrogen level and g^{th} descent

$(etd)_{afg}$ = Effect of interaction between a^{th} environment, f^{th} variety type and g^{th} descent

$(entd)_{acfg}$ = Effect of interaction between a^{th} environment, c^{th} nitrogen level, f^{th} variety type and g^{th} descent

$(rntd)_{bcfg(a)}$ = Sub-subplot error (Effect of interaction between b^{th} replication, c^{th} nitrogen level, f^{th} variety type and g^{th} descent within a^{th} environment)

Model A 7

$$\mathbf{Y_{abcd} = m + e_a + r_{b(a)} + n_c + (en)_{ac} + (rn)_{bc(a)} + t_d + (et)_{ad} + (nt)_{cd} + (ent)_{acd} + (rnt)_{bcd(a)} + g_{f(d)} + (eg)_{af(d)} + (ng)_{cf(d)} + (eng)_{acf(d)} + (rng)_{bcf(ad)}}$$

Y_{abcdf} = Observation of the f^{th} genotype of the d^{th} type at a^{th} environment, b^{th} replication and c^{th} nitrogen level

m = Overall mean

e_a = Random effect of a^{th} environment

$r_{b(a)}$ = Random effect of b^{th} replication within a^{th} environment

n_c = Fixed effect of c^{th} nitrogen level

$(en)_{ac}$ = Effect of interaction between a^{th} environment and c^{th} nitrogen level

$(rn)_{bc(a)}$ = Whole plot error (Effect of interaction between b^{th} replication and c^{th} nitrogen level within a^{th} environment)

t_d = Fixed effect of d^{th} variety type

$(et)_{ad}$ = Effect of interaction between a^{th} environment and d^{th} variety type

$(nt)_{cd}$ = Effect of interaction between c^{th} nitrogen level and d^{th} variety type

$(ent)_{acd}$ = Effect of interaction between a^{th} environment, c^{th} nitrogen level and d^{th} variety type

$(rnt)_{bcd(a)}$ = Subplot error (Effect of interaction between b^{th} replication, c^{th} nitrogen level and d^{th} variety type within a^{th} environment)

$g_{f(d)}$ = Fixed effect of f^{th} genotype within d^{th} variety type

$(eg)_{af(d)}$ = Effect of interaction between a^{th} environment and f^{th} genotype within d^{th} variety type

$(ng)_{cf(d)}$ = Effect of interaction between c^{th} nitrogen level and f^{th} genotype within d^{th} variety type

$(eng)_{acf(d)}$ = Effect of interaction between a^{th} environment, c^{th} nitrogen level and f^{th} genotype within d^{th} variety type

$(rng)_{bcf(ad)}$ = Sub-subplot error (Effect of interaction between b^{th} replication, c^{th} nitrogen level and f^{th} genotype within a^{th} environment and d^{th} variety type)

Heterosis

Heterosis of test hybrids was computed within nitrogen levels. Simple mean was computed for the common tester PBY062 within nitrogen levels across all trials and environments. Means for DH lines across all environments within nitrogen levels derive from model 6. The mean of the common tester and the respective DH line is the mid-parent performance. Relative heterosis was calculated as difference between hybrid and mid-parent performance (equation A 13) expressed in percentage of mid-parent performance.

Equation A 13

$$Het = [(P_H - P_{MP}) \times P_{MP}^{-1}] \times 100\%$$

Het = Relative heterosis

P_H = Hybrid performance

P_{MP} = Mid-parent performance (mean of hybrid parents)

Results

Diversity set

End of flowering trial (EOF)

The following section describes $Yield_{EOF}$, Nup_{EOF} and $NupEff_{EOF}$. Information about other traits captured in EOF (Tab. A 5) can be found in the appendix (Tab. I, Tab. II).

$Yield_{EOF}$

$Yield_{EOF}$ showed significant genetic variation and a heritability of 0.86 (Tab. A 7). The overall experimental mean was 49 dt ha^{-1}. The difference between N1 (57 dt ha^{-1}) and N0 (40 dt ha^{-1}) was significant. PBY012 showed highest yield at N1 (64 dt ha^{-1}) and N0 (49 dt ha^{-1}) (Fig. A 3). Lowest yield under N1 (35 dt ha^{-1}) and N0 (27 dt ha^{-1}) was detected for PBY009 (Fig. A 3). A significant interaction between genotype and nitrogen level was detected. Nitrogen level explained more variance than genotype and interaction between genotype and nitrogen level. The latter contributed only little to total variance (Tab. A 7).

Tab. A 7: ANOVA for $Yield_{EOF}$ of diversity set

Source	DF	MS	Var.cp	F	
E	4	50721.92	436.46	547.58	**
R:E	5	92.63	-1.15	0.58	*ns*
N	1	40858.80	135.63	26.76	**
EN	4	1527.04	23.58	9.58	*
RN:E	5	159.33	4.55	5.82	**
G	28	534.34	23.01	7.20	**
EG	112	74.18	11.70	2.71	**
NG	28	61.20	2.89	1.89	*
ENG	112	32.34	2.48	1.18	*ns*
RNG:E	176	27.38	27.38		
Total	475				
h^2		0.73 – **0.86** – 0.92			

DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N nitrogen level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) with 0.95 confidence interval

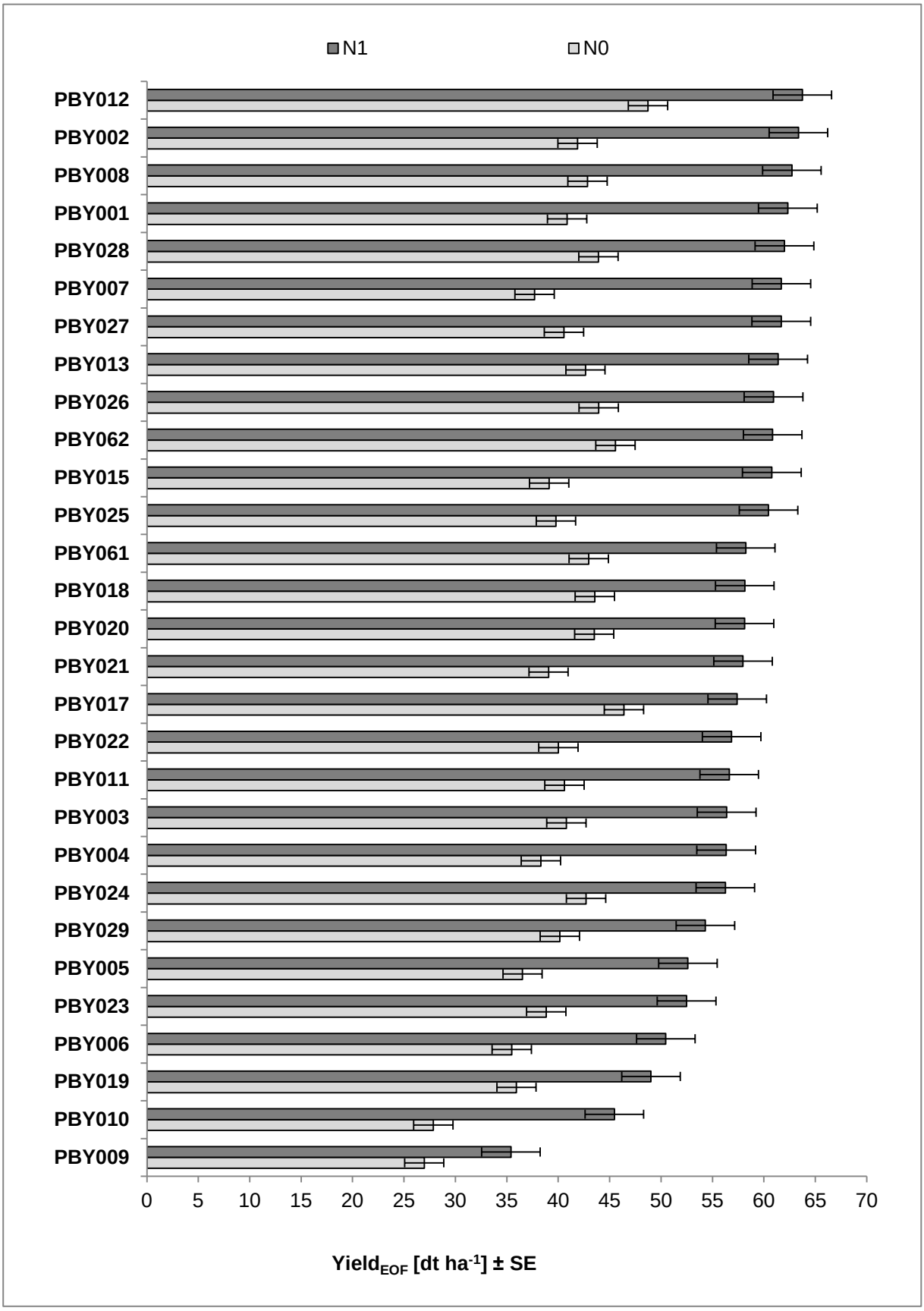

Fig. A 3: Yield$_{EOF}$ of diversity set
Means of genotypes across five environments for N1 and N0 with standard error SE

Nup_{EOF}

For Nup_{EOF} significant genetic variation and a heritability of 0.81 were observed (Tab. A 8). The overall mean was 1.05 dt ha^{-1}. At N1 1.47 dt nitrogen ha^{-1} and at N0 0.63 dt nitrogen ha^{-1} were taken up on average. This difference was significant (Tab. A 8). Nup_{EOF} at N1 ranged from 1.06 dt ha^{-1} (PBY009) to 1.71 dt ha^{-1} (PBY012, PBY028) (Fig. A 4). At N0 Nup_{EOF} ranged from 0.48 dt ha^{-1} (PBY009) to 0.79 dt ha^{-1} (PBY017). The interaction between genotype and nitrogen level was significant. The contribution of genotype to total variance is more than twice as high as the contribution of genotype by nitrogen level interaction. (Tab. A 8).

Tab. A 8: ANOVA for Nup_{EOF} of diversity set

Source	DF	MS	Var.cp	F	
E	4	16.34	0.1400	166.45	**
R:E	5	0.10	-0.0001	0.92	*ns*
N	1	101.26	0.3443	71.34	**
EN	4	1.42	0.0226	13.31	**
RN:E	5	0.11	0.0031	6.19	**
G	28	0.18	0.0074	5.35	**
EG	112	0.03	0.0042	1.96	**
NG	28	0.06	0.0034	2.30	**
ENG	112	0.03	0.0047	1.54	**
RNG:E	174	0.02	0.0172		
Total	473				
h^2		0.64 - **0.81** - 0.89			

DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N nitrogen level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for $\alpha = 0.01$, *ns* not significant for $\alpha = 0.05$, h^2 heritability (bold) with 0.95 confidence interval

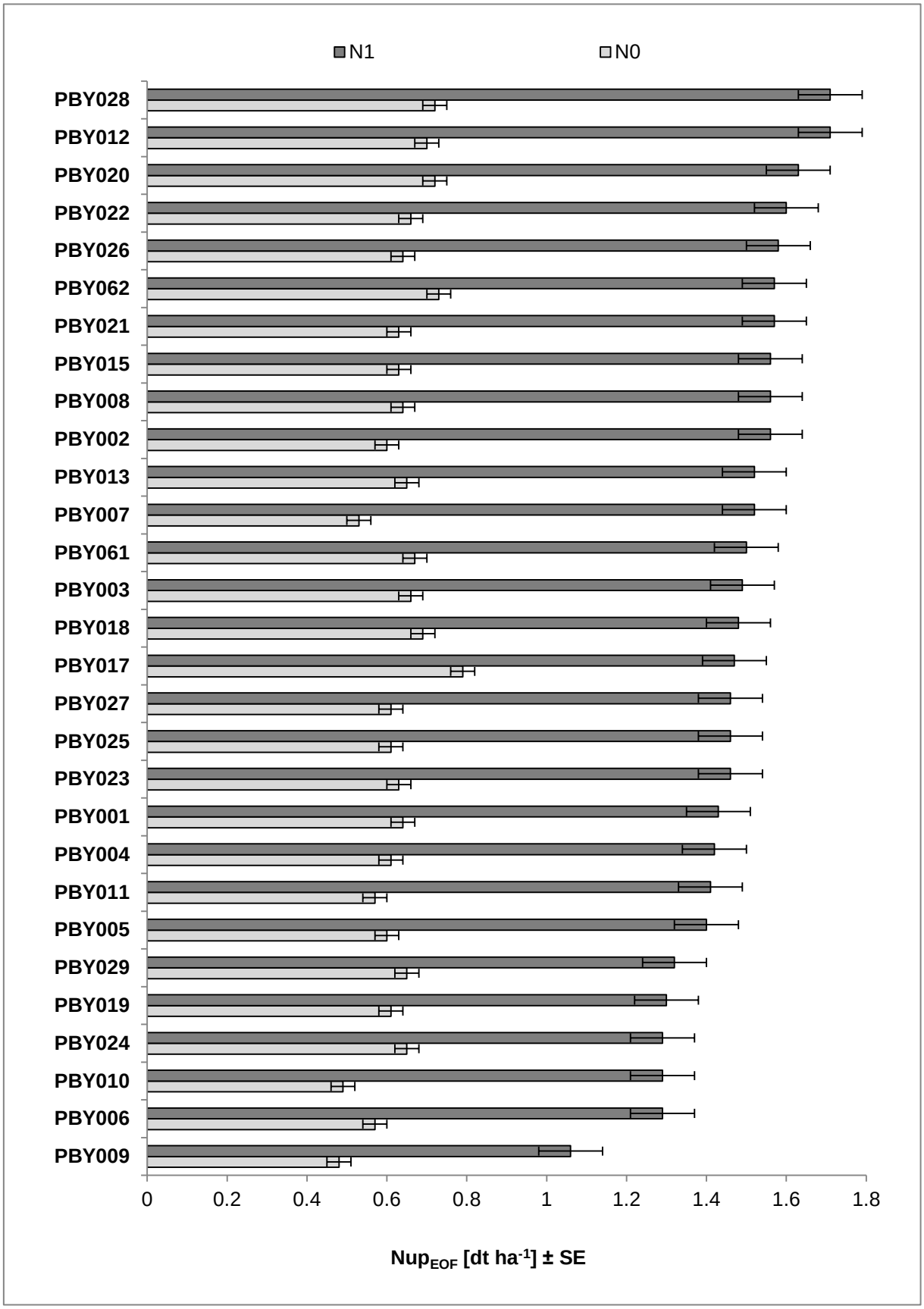

Fig. A 4: Nup$_{EOF}$ of diversity set
Means of genotypes across five environments for N1 and N0 with standard error SE

$NupEff_{EOF}$

$NupEff_{EOF}$ showed significant genetic variation and a heritability of 0.81 (Tab. A 9). The mean across nitrogen levels was 0.65. With 0.56 $NupEff_{EOF}$ was significantly lower at N1 than with 0.74 at N0. $NupEff_{EOF}$ at N1 ranged from 0.42 (PBY009) to 0.65 (PBY012 and PBY028) (Fig. A 5). At N0 it ranged from 0.60 (PBY009 and PBY010) to 0.88 (PBY017). A significant interaction between genotype and nitrogen level was observed. The contribution of genotype by nitrogen level interaction to total variance was one third of the contribution of genotype. (Tab. A 9).

Tab. A 9: ANOVA for $NupEff_{EOF}$ of diversity set

Source	DF	MS	Var.cp	F	
E	4	0.35	0.0026	7.74	*
R:E	5	0.05	0.0001	1.17	*ns*
N	1	4.53	0.0145	14.07	*
EN	4	0.32	0.0049	8.24	*
RN:E	5	0.04	0.0011	5.68	**
G	28	0.06	0.0025	5.35	**
EG	112	0.01	0.0012	1.68	**
NG	28	0.02	0.0008	2.09	**
ENG	112	0.01	0.0002	1.05	*ns*
RNG:E	173	0.01	0.0069		
Total	472				
h^2		0.64 - **0.81** - 0.89			

DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N nitrogen level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) with 0.95 confidence interval

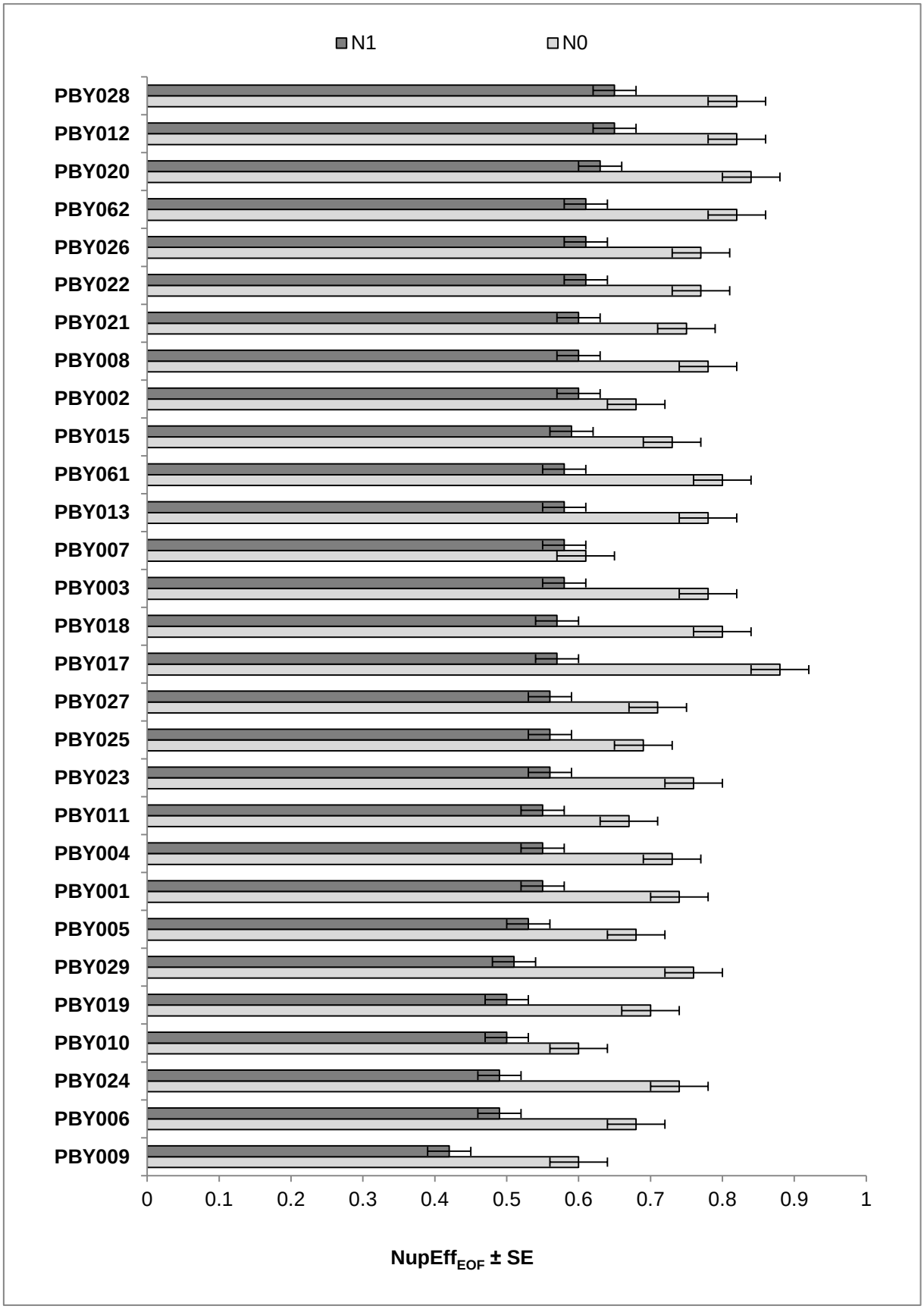

Fig. A 5: NupEff$_{EOF}$ of diversity set
Means of genotypes across five environments for N1 and N0 with standard error SE

Maturity trial (MAT)

In the following Seed 9%, Nup_{MAT}, $NupEff_{MAT}$, NutEff, NUE and NHI will be described. Information about other traits captured in MAT (Tab. A 5) can be found in the appendix (Tab. I, Tab. II).

Seed 9%

For Seed 9% significant genetic variation and a heritability of 0.92 were detected (Tab. A 10). The overall mean was 26 dt ha^{-1}. The difference between N1 (31 dt ha^{-1}) and N0 (21 dt ha^{-1}) was significant. At N1 Seed 9% ranged from 17 dt ha^{-1} (PBY009) to 39 dt ha^{-1} (PBY023) and at N0 from 9 dt ha^{-1} (PBY011) to 27 dt ha^{-1} (PBY023) (Fig. A 6). The genotype by nitrogen level interaction was significant. Nitrogen level and genotype contributed to a high degree to total variance while contribution of interaction between genotype and nitrogen level was comparable small (Tab. A 10).

Tab. A 10: ANOVA for Seed 9% of diversity set

Source	DF	MS	Var.cp	F	
E	3	5975.37	50.55	53.45	**
R:E	4	111.80	1.49	4.42	*ns*
N	1	11054.66	46.40	38.14	**
EN	3	289.82	4.56	11.46	*
RN:E	4	25.30	0.52	2.45	*
G	28	499.99	28.60	11.81	**
EG	84	42.32	8.00	4.10	**
NG	28	53.49	4.45	2.99	**
ENG	84	17.88	3.78	1.73	**
RNG:E	129	10.31	10.31		
Total	368				
h^2		0.84 - **0.92** - 0.95			

DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N nitrogen level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) with 0.95 confidence interval

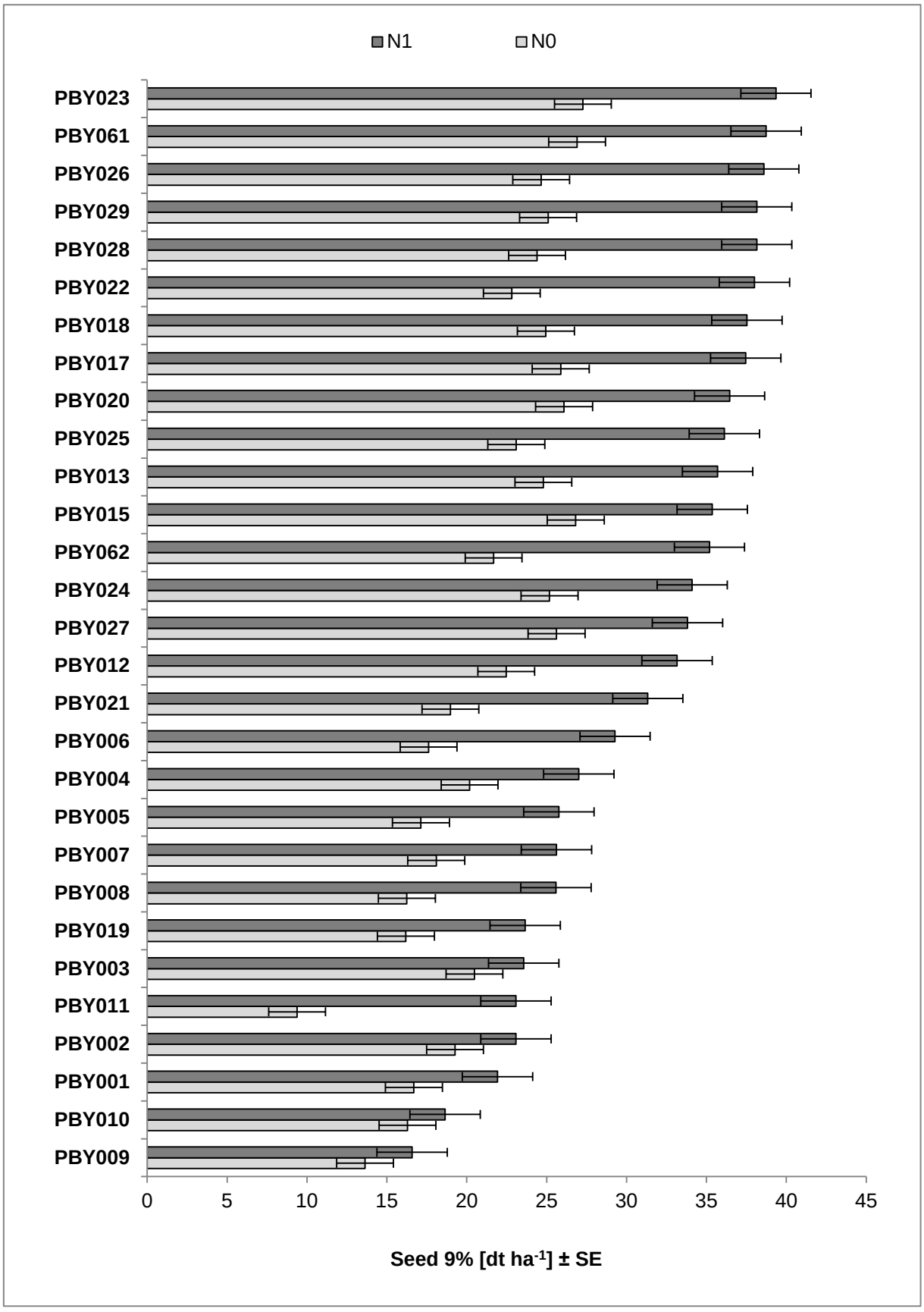

Fig. A 6: Seed 9% of diversity set
Means of genotypes across four environments for N1 and N0 with standard error SE

Nup_{MAT}

Significant genetic variation and a heritability of 0.85 were observed for Nup_{MAT} (Tab. A 11). On average 1.18 dt nitrogen ha^{-1} were taken up. The difference between N1 (1.53 dt ha^{-1}) and N0 (0.83 dt ha^{-1}) was significant (Tab. A 11). Nup_{MAT} at N1 ranged from 0.97 dt ha^{-1} (PBY009) to 1.88 dt ha^{-1} (PBY062) and from 0.62 dt ha^{-1} (PBY009) to 0.99 dt ha^{-1} (PBY013). The interaction between genotype and nitrogen level was significant. Nitrogen level explained most of the observed variance. Contribution of genotype was nearly three times higher than contribution of interaction between genotype and nitrogen level (Fig. A 7).

Tab. A 11: ANOVA for Nup_{MAT} of diversity set

Source	DF	MS	Var.cp	F	
E	3	9.75	0.0813	30.71	**
R:E	4	0.32	0.0003	1.05	*ns*
N	1	56.51	0.2400	67.56	**
EN	3	0.84	0.0092	2.76	*ns*
RN:E	4	0.30	0.0097	13.64	**
G	28	0.24	0.0129	6.85	**
EG	84	0.04	0.0033	1.59	**
NG	28	0.06	0.0047	2.55	**
ENG	84	0.02	0.0011	1.10	*ns*
RNG:E	125	0.02	0.0222		
Total	364				
h^2		0.72 - **0.85** - 0.92			

DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N nitrogen level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for $\alpha = 0.01$, *ns* not significant for $\alpha = 0.05$, h^2 heritability (bold) with 0.95 confidence interval

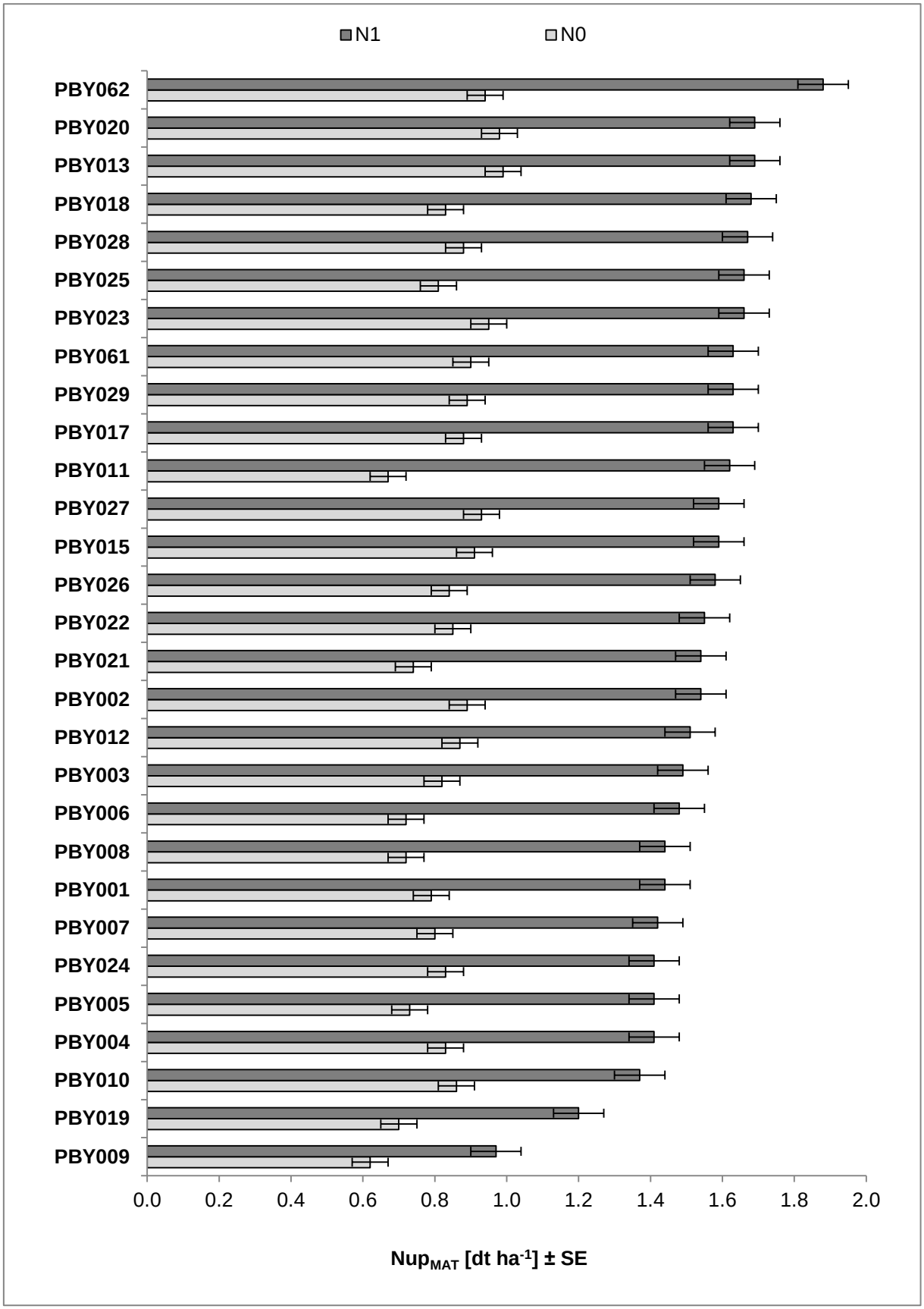

Fig. A 7: Nup$_{MAT}$ of diversity set
Means of genotypes across four environments for N1 and N0 with standard error SE

$NupEff_{MAT}$

$NupEff_{MAT}$ revealed significant genetic variation and a heritability of 0.76 (Tab. A 12). The overall mean was 0.65 . The difference between N1 (0.54) and N0 (0.76) was significant (Tab. A 12). At N1 $NupEff_{MAT}$ ranged from 0.36 (PBY009) to 0.66 (PBY062) and from 0.60 (PBY009) to 0.90 (PBY013) at N0 (Fig. A 8). The interaction between genotype and nitrogen level was not significant. Genotype explained eight times more variance than interaction between genotype and nitrogen level (Tab. A 12).

Tab. A 12: ANOVA for $NupEff_{MAT}$ of diversity set

Source	DF	MS	Var.cp	F	
E	3	0.28	0.00168	3.21	*ns*
R:E	4	0.09	-0.00023	0.87	*ns*
N	1	5.54	0.02346	55.87	**
EN	3	0.10	-0.00004	0.98	*ns*
RN:E	4	0.10	0.00331	18.97	**
G	28	0.06	0.00302	4.25	**
EG	84	0.01	0.00239	2.79	**
NG	28	0.01	0.00039	1.29	*ns*
ENG	84	0.01	0.00277	2.04	**
RNG:E	125	0.01	0.00534		
Total	364				
h^2		0.54 - **0.76** - 0.87			

DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N nitrogen level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for $\alpha = 0.01$, *ns* not significant for $\alpha = 0.05$, h^2 heritability (bold) with 0.95 confidence interval

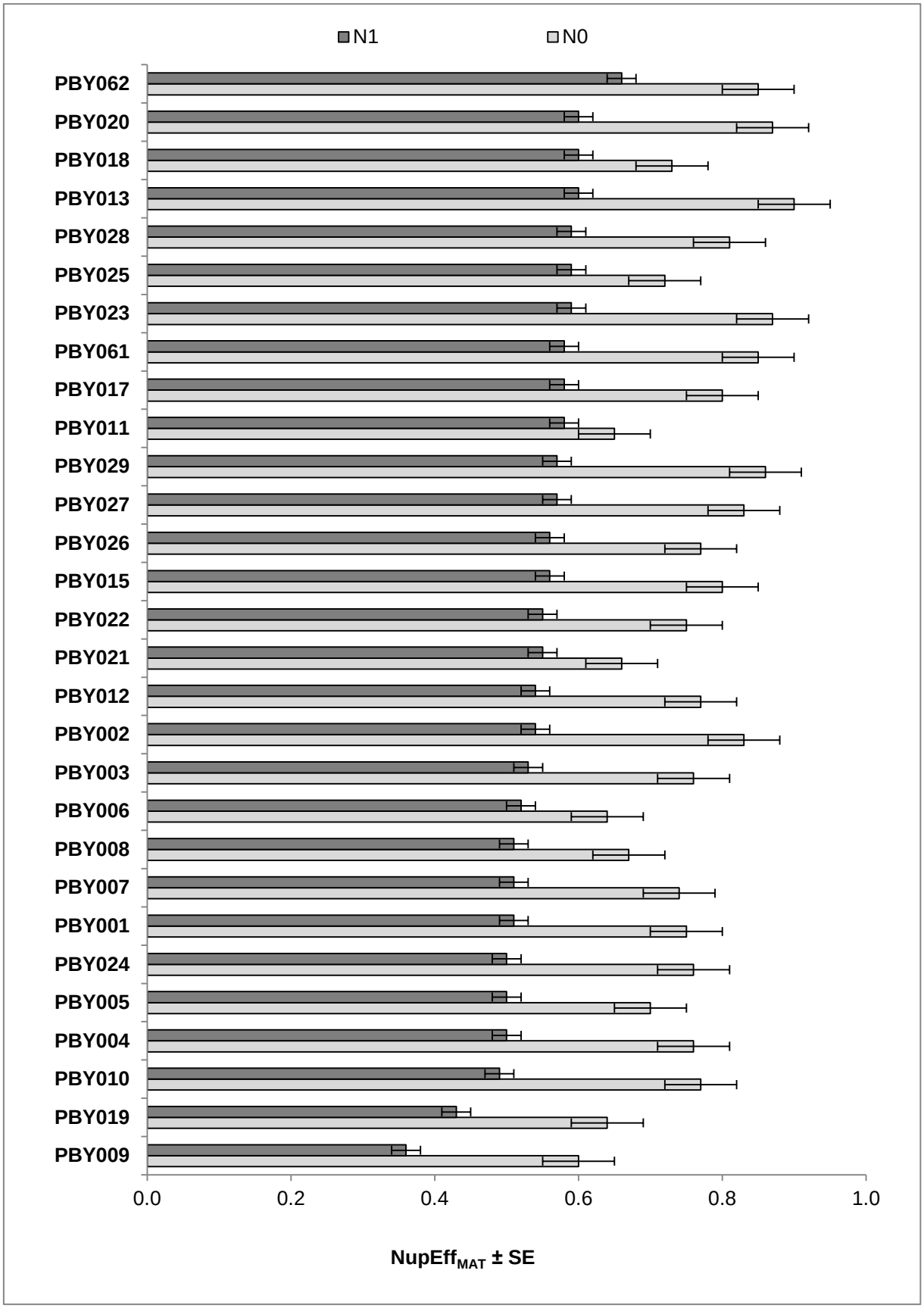

Fig. A 8: NupEff$_{MAT}$ of diversity set
Means of genotypes across four environments for N1 and N0 with standard error SE

NutEff

Significant genetic variation and a heritability of 0.92 were detected for NutEff (Tab. A 13). The overall mean was 21 dt dt^{-1}. NutEff under N1 (18 dt dt^{-1}) was significantly lower than under N0 (23 dt dt^{-1}). At N1 it ranged from 13 dt dt^{-1} (PBY010) to 22 dt dt^{-1} (PBY022) and at N0 from 15 dt dt^{-1} (PBY011) to 28 dt dt^{-1} (PBY024) (Fig. A 9). The interaction between genotype and nitrogen level was significant. Most of variance was explained by nitrogen level and genotype while inter-action between genotype and nitrogen level explained only little of total variance (Tab. A 13).

Tab. A 13: ANOVA for NutEff of diversity set

Source	DF	MS	Var.cp	F	
E	3	16.48	-0.20	0.42	*ns*
R:E	4	39.25	-0.05	0.93	*ns*
N	1	2733.32	11.66	94.22	**
EN	3	29.01	-0.23	0.69	*ns*
RN:E	4	42.24	1.36	15.44	**
G	28	136.81	7.87	12.65	**
EG	84	10.82	2.02	3.96	**
NG	28	7.89	0.53	2.16	**
ENG	84	3.64	0.45	1.33	*ns*
RNG:E	115	2.74	2.74		
Total	354				
h^2		0.85 - **0.92** - 0.96			

DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N nitrogen level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for $\alpha = 0.01$, *ns* not significant for $\alpha = 0.05$, h^2 heritability (bold) with 0.95 confidence interval

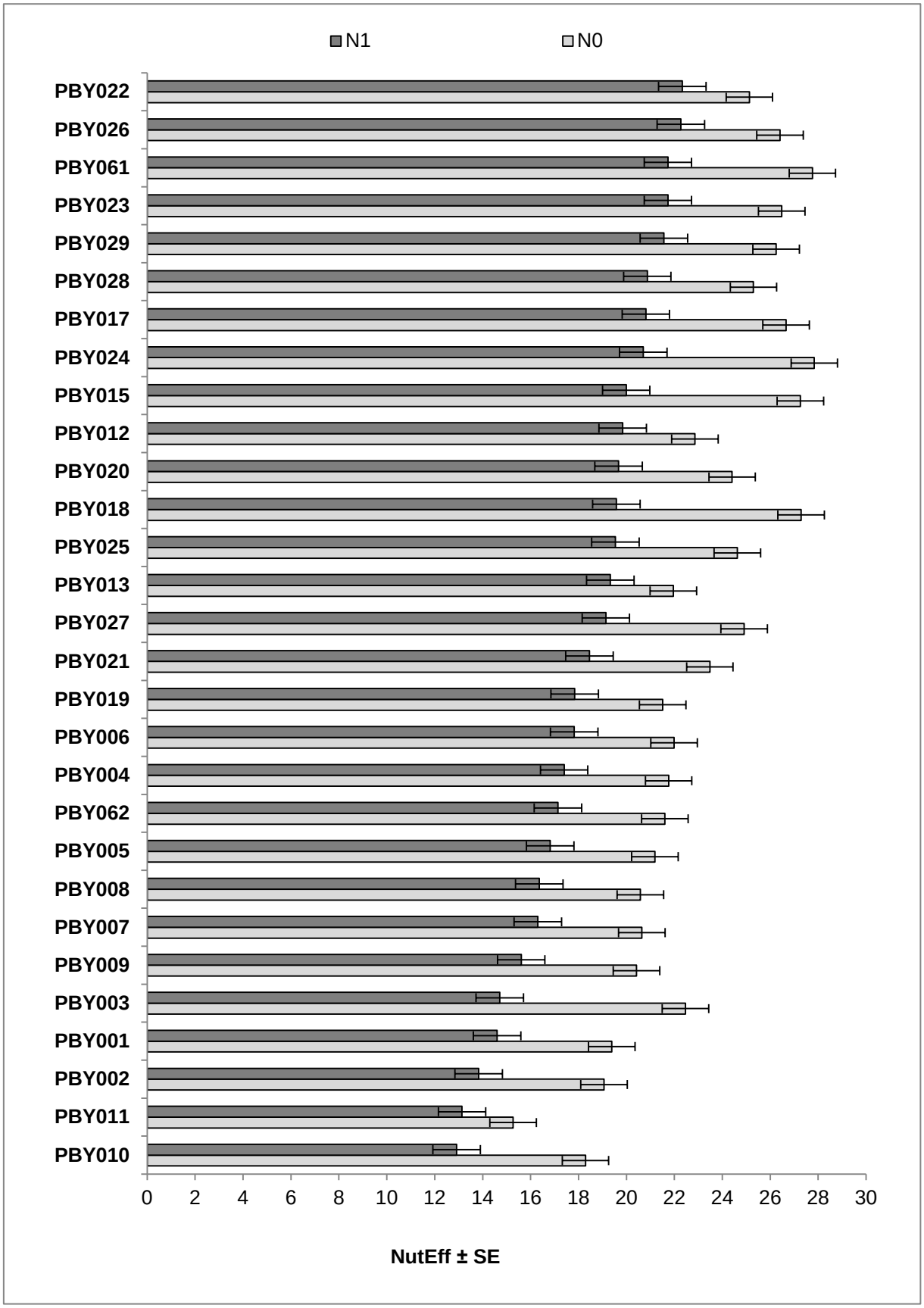

Fig. A 9: NutEff of diversity set
Means of genotypes across four environments for N1 and N0 with standard error SE

NUE

For NUE significant genetic variation and a heritability of 0.90 were observed. The overall mean was 14. At N1 (10) NUE was significantly lower than at N0 (18) (Tab. A 14). NUE at N1 ranged from 6 (PBY009) to 13 (PBY023) and from 9 (PBY011) to 23 (PBY023) at N0 (Fig. A 10). Significant interaction between genotype and nitrogen level was detected. Nitrogen level contributed most to total variance followed by contribution of genotype. Interaction between genotype and nitrogen level explained less variance (Tab. A 14).

Tab. A 14: ANOVA for NUE of diversity set

Source	DF	MS	Var.cp	F	
E	3	194.54	1.28	4.18	*ns*
R:E	4	46.59	0.48	2.46	*ns*
N	1	6908.86	29.59	155.61	**
EN	3	44.40	0.44	2.34	*ns*
RN:E	4	18.96	0.57	8.08	**
G	28	121.83	6.83	9.76	**
EG	84	12.49	2.54	5.33	**
NG	28	16.19	1.24	2.60	**
ENG	84	6.23	1.94	2.66	**
RNG:E	125	2.35	2.35		
Total	364				
h^2		0.80 - **0.90** - 0.94			

DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N nitrogen level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for $\alpha = 0.01$, *ns* not significant for $\alpha = 0.05$, h^2 heritability (bold) with 0.95 confidence interval

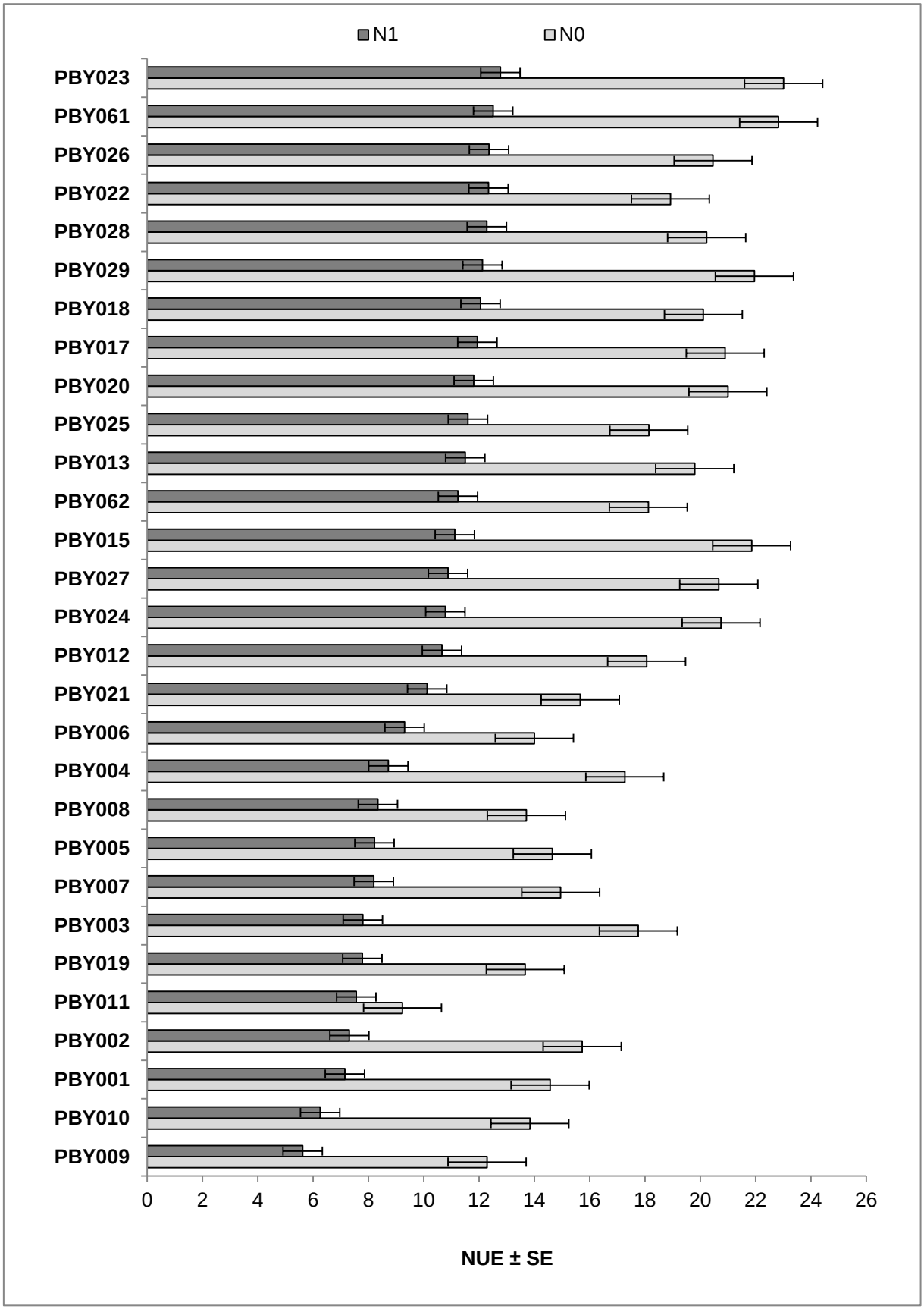

Fig. A 10: NUE of diversity set
Means of genotypes across four environments for N1 and N0 with standard error SE

NHI

NHI showed significant genetic variation and a heritability of 0.87 (Tab. A 15). The overall mean was 0.68. N1 revealed a significant lower NHI (0.65) than N0 (0.72) (Tab. A 15). NHI at N1 ranged from 0.51 (PBY11) to 0.76 (PBY028) and from 0.55 (PBY011) to 0.80 (PBY028) (Fig. A 11). The interaction between genotype and nitrogen level was significant. Genotype and nitrogen level contributed most to total variance while contribution of interaction between genotype and nitrogen level was very small (Tab. A 15).

Tab. A 15: ANOVA for NHI of diversity set

Source	DF	MS	Var.cp	F	
E	3	0.063	0.0003	2.10	*ns*
R:E	4	0.030	-0.0002	0.70	*ns*
N	1	0.469	0.0020	30.78	*
EN	3	0.015	-0.0005	0.35	*ns*
RN:E	4	0.043	0.0014	20.69	**
G	28	0.056	0.0030	7.54	**
EG	84	0.007	0.0013	3.56	**
NG	28	0.006	0.0004	2.14	**
ENG	84	0.003	0.0003	1.30	*ns*
RNG:E	145	0.002	0.0021		
Total	384				
h^2		0.74 - **0.87** - 0.92			

DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N nitrogen level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) with 0.95 confidence interval

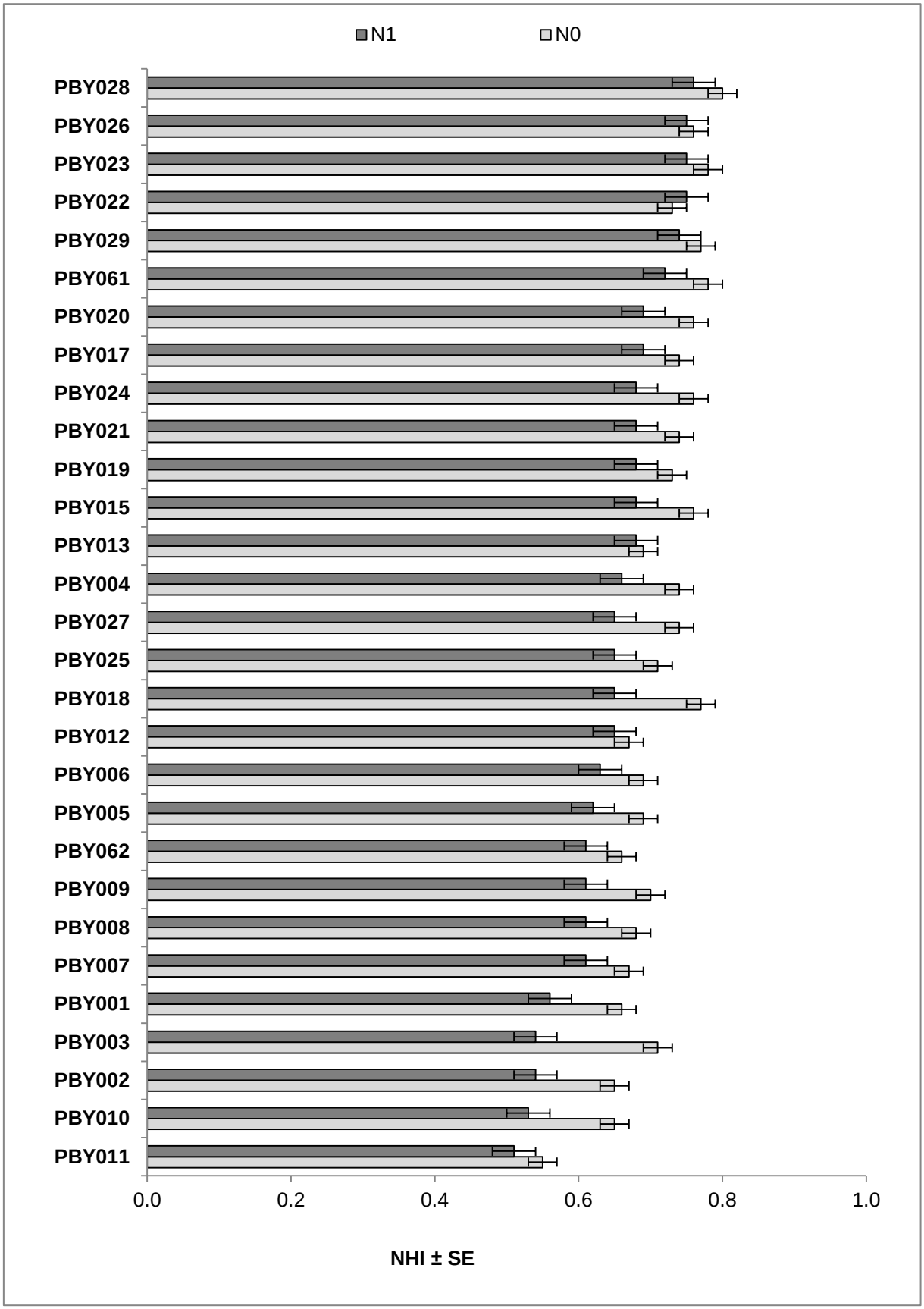

Fig. A 11: NHI of diversity set
Means of genotypes across four environments for N1 and N0 with standard error SE

Delta Nup

Delta Nup describes nitrogen uptake after flowering. It was calculated as difference between Nup_{MAT} and Nup_{EOF} of genotype per environment and nitrogen level. Significant genetic variation and a heritability of 0.67 were observed. Overall 6.5 kg N ha^{-1} were taken up between end of flowering and maturity. At N1 genotypes lost 0.76 kg N ha^{-1}. At N0 genotypes took up 13.7 kg N ha^{-1}. But the difference was not significant (Tab. A 16). At N1 Delta Nup ranged from -30.0 kg ha^{-1} (PBY012) to 24.5 kg ha^{-1} (PBY029), at N0 from 1.8 kg ha^{-1} (PBY008) to 30.5 kg ha^{-1} (PBY029) (Fig. A 12). The interaction between genotype and nitrogen level was significant. Genotype and interaction between genotype and nitrogen level contributed to a high degree to total variance while the effect of nitrogen level was not significant (Tab. A 16).

Tab. A 16: ANOVA for Delta Nup of diversity set

Source	DF	MS	Var.cp	F	
E	3	8061.33	135.03	35.14	**
N	1	12107.66	1.89	1.02	*ns*
EN	3	11888.07	402.02	51.81	**
G	28	680.14	56.70	3.00	**
EG	84	226.54	-1.45	0.99	*ns*
NG	28	387.99	39.64	1.69	*
ENG	84	229.44	229.44		
Total	231				
h^2		0.35 – **0.67** – 0.81			

DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, N nitrogen level, G genotype, EN, EG, NG interactions, ENG error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) with 0.95 confidence interval

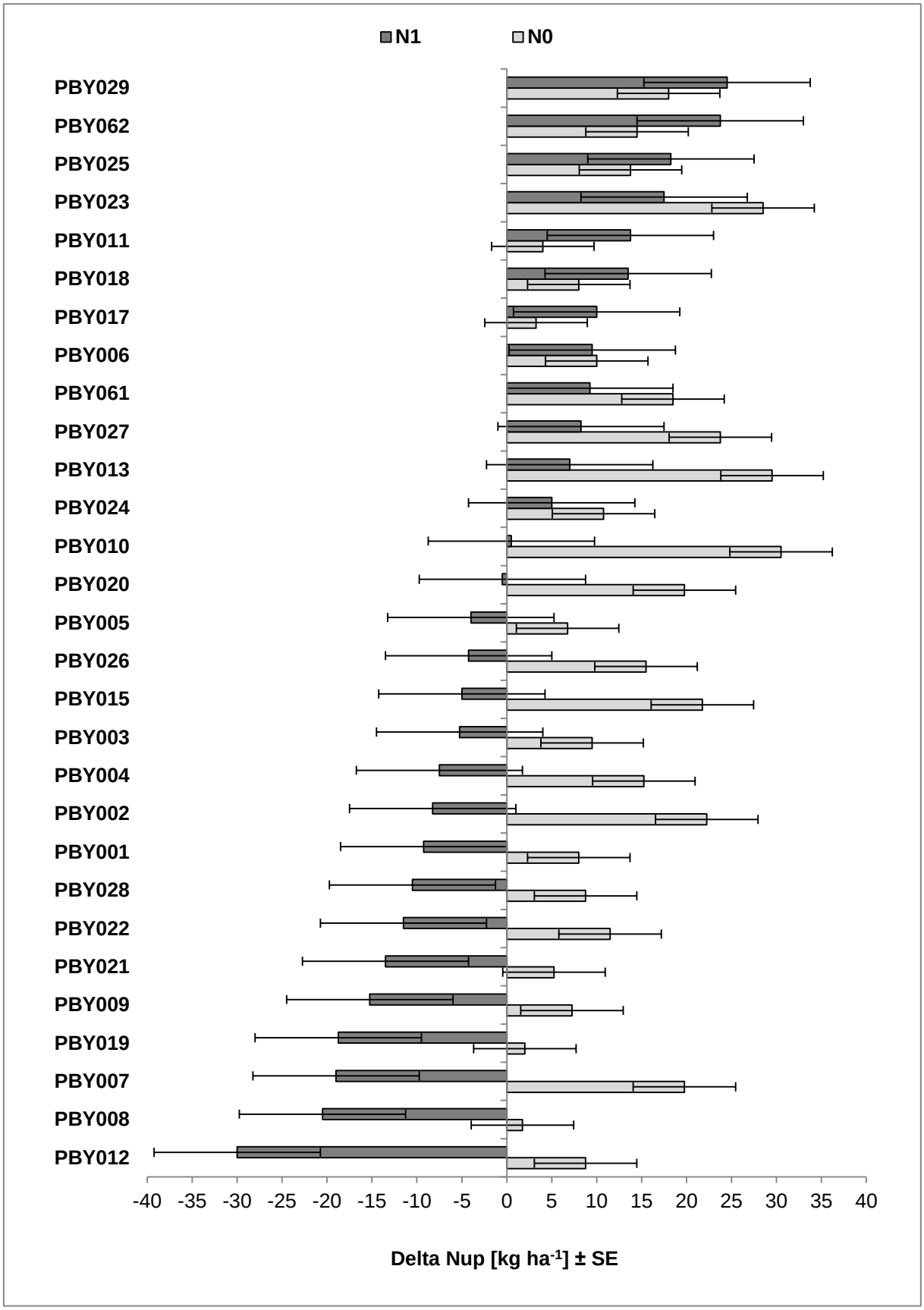

Fig. A 12: Delta Nup of diversity set
Means of genotypes across four environments for N1 and N0 with standard error SE

Contribution of $NupEff_{MAT}$ and NutEff to NUE

Under N1 and N0 variance of NutEff contributed to higher portion to variance of NUE than variance of $NupEff_{MAT}$. At both nitrogen levels the respective contributions were the same (Fig. A 13).

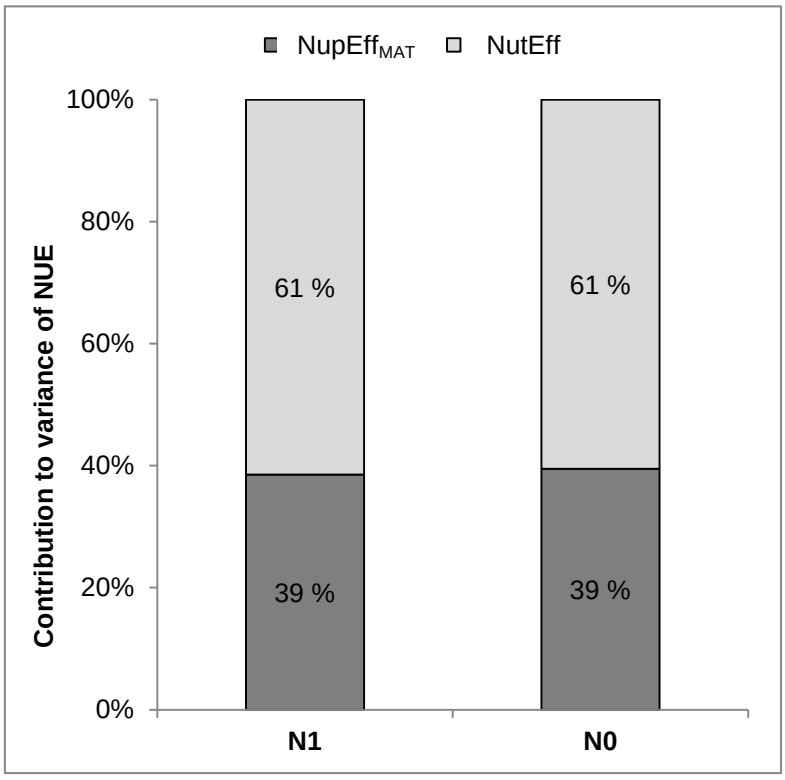

Fig. A 13: Contribution of variances of $NupEff_{MAT}$ and NutEff to variance of NUE of diversity set at N1 and N0

Selection of DH parents

Based on results of 2011/12 PBY007 and PBY029 were selected as parents of two DH populations to be tested in MAT007 and MAT029. Differences in $NupEff_{EOF}$, $NupEff_{MAT}$ (Fig. A 14), NutEff and NUE (Fig. A 15) were one selection criteria. But it was also to be considered that genotypes were selected which were also tested in experiments of other project partners. Therefore the selected genotypes did not always represent the extremes (Fig. A 14, Fig. A 15).

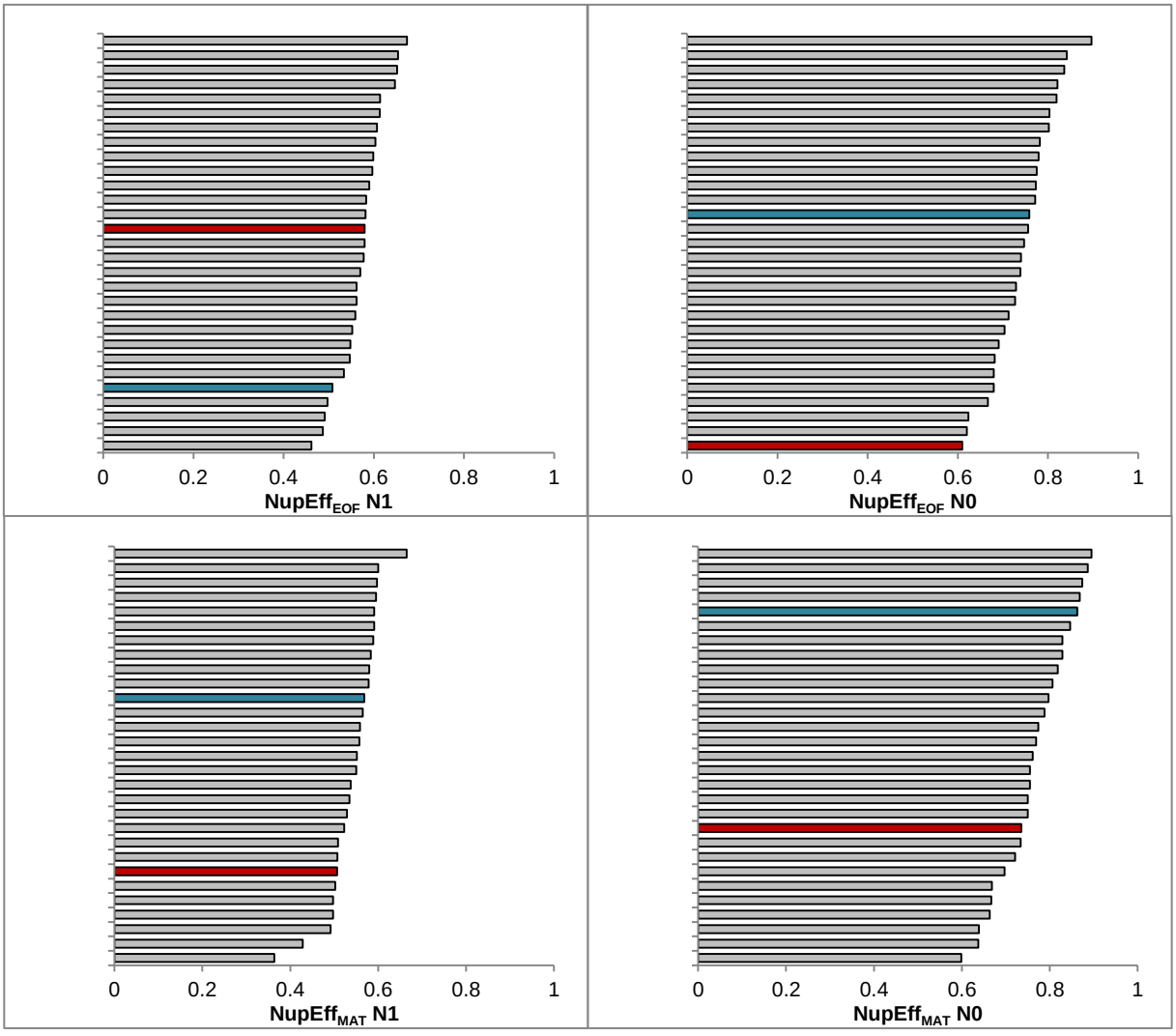

Fig. A 14: $NupEff_{EOF}$ (top) and $NupEff_{MAT}$ (bottom) of diversity set 2011/12
Means of genotypes across two environments for N1 (left) and N0 (right), red PBY007, blue PBY029

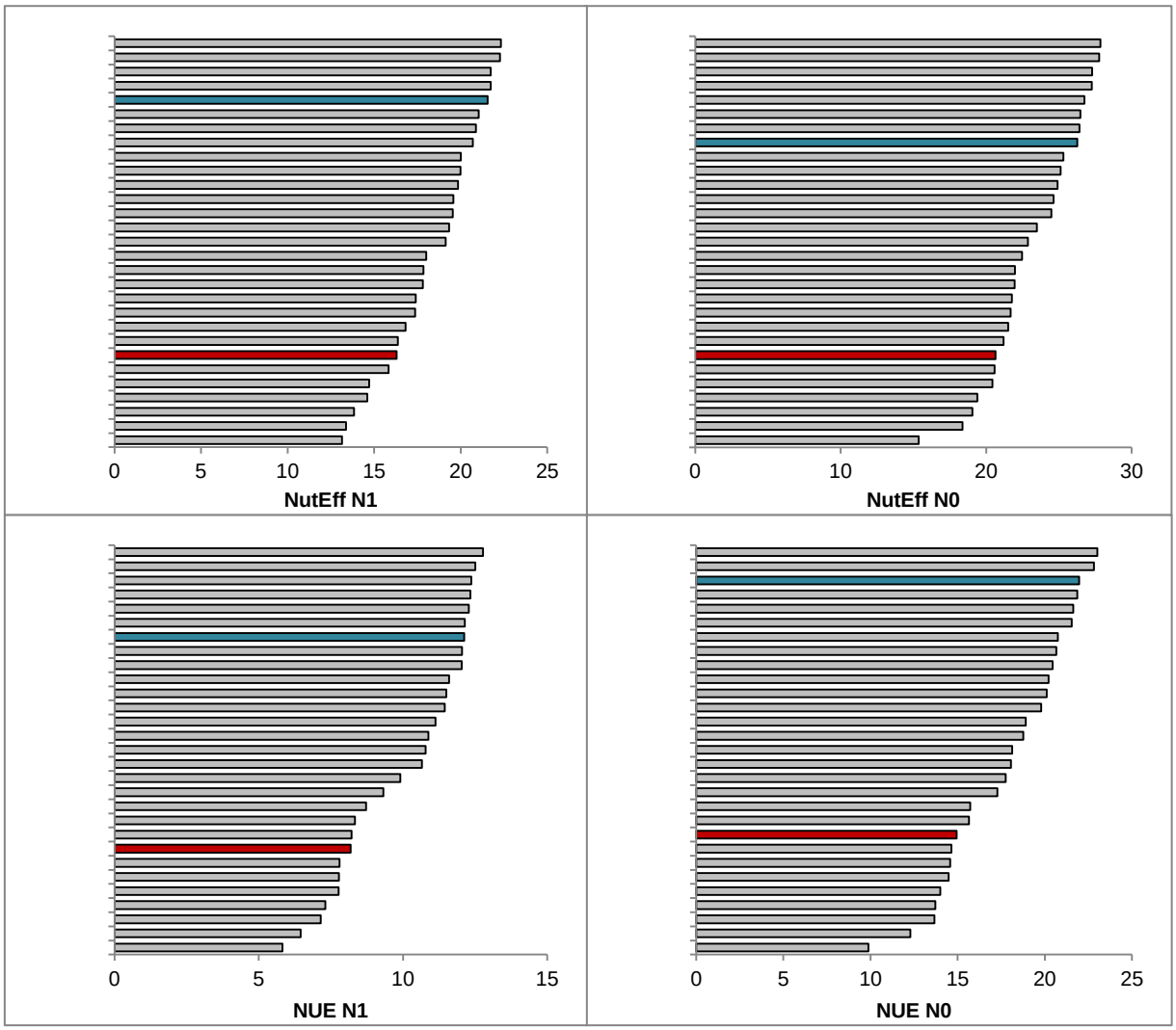

Fig. A 15: NutEff (top) and NUE (bottom) of diversity set 2011/12
Means of genotypes across two environments for N1 (left) and N0 (right), red PBY007, blue PBY029

DH lines and test hybrids

In the following section Seed 9%, Nup_{MAT}, $NupEff_{MAT}$, NutEff, NUE and NHI and heterosis for these traits will be described for Population 007 and Population 029. As the male sterile female parent (PBY062) of the test hybrids was the same for both populations its means are given here: Seed 9% 26.92 dt ha^{-1} (N0) and 33.27 dt ha^{-1}, Nup_{MAT} 1.66 dt ha^{-1}(N0) and 1.89 dt ha^{-1} (N1), $NupEff_{MAT}$ 0.79 (N0) and 0.51 (N1), $NutEff_{MAT}$ 15.88 (N0) and 15.97 (N1), NUE 12.38 (N0) and 8.19 (N1) and NHI 0.62 (N0) and 0.65 (N1). Details about other traits (Tab. A 5) are given in appendix (Tab. III, Tab. IV, Tab. V, Tab. VI).

Population 007 (Pop007)

Seed 9%

Seed 9% was significantly influenced by descent and interaction between descent and variety type (Tab. A 17). Effects of nitrogen level, interaction between variety type and nitrogen level and interaction between descent and variety type were not significant (Tab. A 17). Heritability was 0.72 (Tab. A 17). DH lines at N1 showed seed 9% from 30 dt ha^{-1} to 43 dt ha^{-1} and at N0 from 29 dt ha^{-1} to 41 dt ha^{-1} (Fig. A 16). Hence, at both nitrogen levels some exceeded their better parent none fell below the lower one. Test hybrids revealed seed 9% from 38 dt ha^{-1} to 50 dt ha^{-1} at N1 and from 33 dt ha^{-1} to 40 dt ha^{-1} at N0 (Fig. A 16). Most test hybrid performed worse than current hybrid cultivars at N1 and N0, but some showed comparable seed yields. At N1 one test hybrid (TH020) exceeded commercial hybrids.

All test hybrids showed positive heterosis for seed 9%. At N1 it was higher than at N0. At N1 it ranged from 8 % to 31%, at N0 from 6 % to 23 % (Fig. A 17).

Tab. A 17: ANOVA for Seed 9% of Pop007

Source	DF	MS	Var.cp	F	
E	2	765.74	6.21	38.14	**
R:E	3	20.08	-0.22	0.60	*ns*
N	1	2112.27	3.38	1.40	*ns*
EN	2	1503.85	24.51	45.23	**
RN:E	3	33.25	-0.11	0.91	*ns*
T	1	641.23	3.24	10.96	*ns*
ET	2	58.50	0.36	1.59	*ns*
NT	1	486.79	3.04	2.29	*ns*
ENT	2	212.90	5.87	5.80	*
RNT:E	7	36.68	1.60	2.89	**
D	14	105.31	3.12	3.46	**
ED	28	30.39	2.22	2.40	**
ND	14	28.20	1.00	1.74	*ns*
TD	14	41.71	2.59	3.91	**
END	28	16.18	0.88	1.28	*ns*
ETD	28	10.66	-0.50	0.84	*ns*
NTD	14	8.52	-0.05	0.97	*ns*
ENTD	28	8.80	-1.94	0.69	*ns*
RNTD:E	167	12.67	12.67		
Total	359				
h^2		0.44 – **0.72** – 0.85			

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, N nitrogen level, T variety type, D descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval

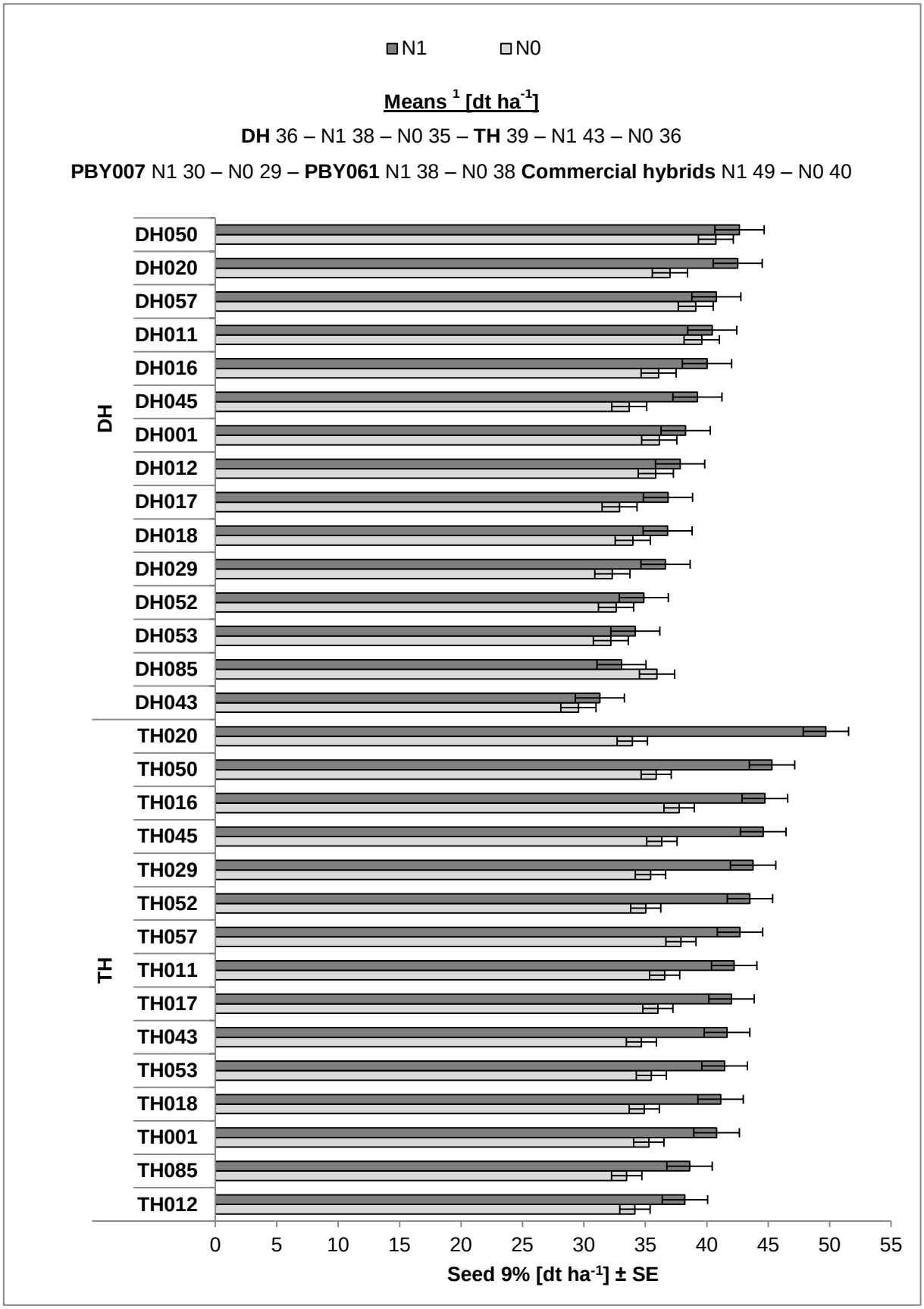

Fig. A 16: Seed 9% of Pop007
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, [1] Means for DH and TH across both nitrogen levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0

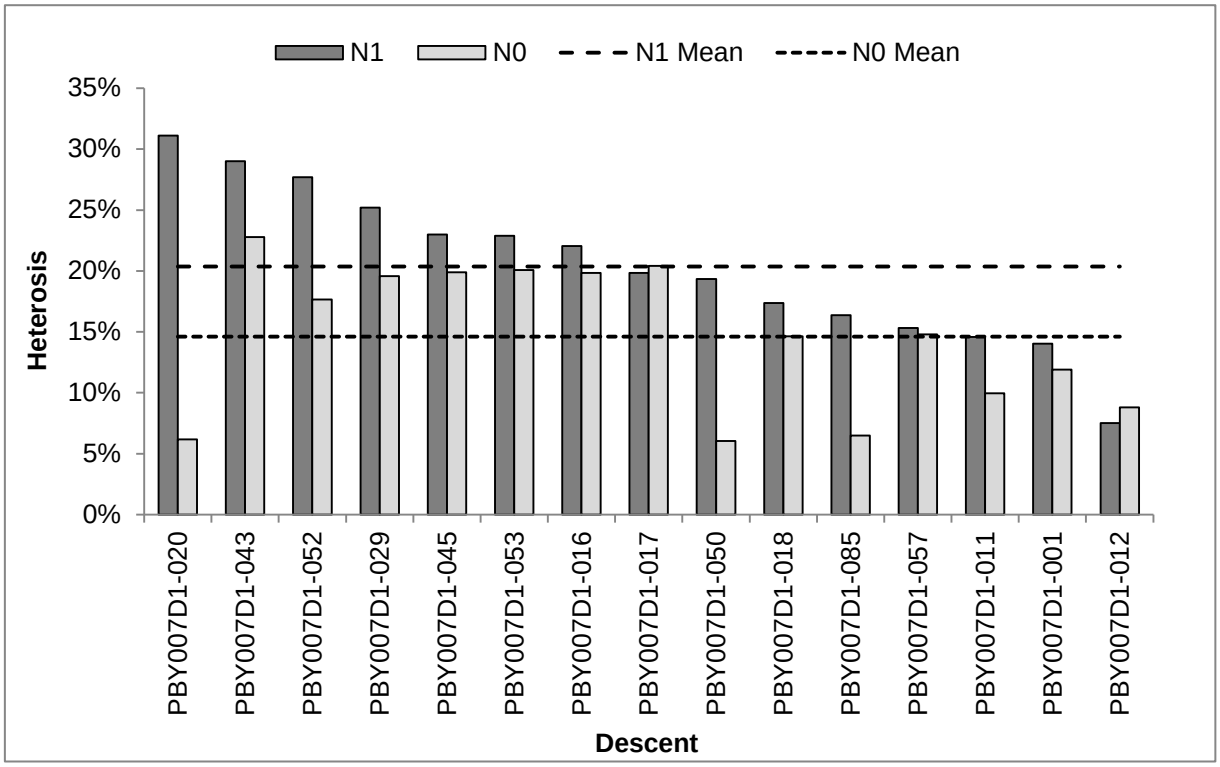

Fig. A 17: Heterosis for Seed 9% of Pop007
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

Nup_{MAT}

Nup_{MAT} was significantly affected by descent and the interaction between descent and variety type. Nitrogen level, variety type, the interaction between variety type and nitrogen level and the interaction between descent and nitrogen level had no significant effect. Heritability was 0.73 (Tab. A 18). At N1 DH lines took up 1.53 dt ha^{-1} to 2.08 dt ha^{-1}. At N0 Nup_{MAT} of DH lines ranged from 1.47 dt ha^{-1} to 1.99 dt ha^{-1}. No DH line fell below the parental genotypes but some exceeded them at both nitrogen levels (Fig. A 18). With Nup_{MAT} from 1.85 dt ha^{-1} to 2.39 dt ha^{-1} at N1 and from 1.31 dt ha^{-1} to 1.55 dt ha^{-1} at N0 test hybrids took up more nitrogen than DH lines. At N1 TH020 outperformed commercial hybrids but at N0 all test hybrids showed lower Nup_{MAT} than commercial ones (Fig. A 18).

Positive heterosis was observed at N1 whereas heterosis at N0 was negative. At N1 it ranged from 2 % to 21 %, at N0 from -23 % to -8 % (Fig. A 19).

Tab. A 18: ANOVA for Nup_{MAT} of Pop007

Source	DF	MS	Var.cp	F	
E	2	6.44	0.0520	31.99	**
R:E	3	0.20	0.0013	1.63	*ns*
N	1	8.85	0.0284	2.37	*ns*
EN	2	3.74	0.0602	30.19	**
RN:E	3	0.12	0.0007	1.21	*ns*
T	1	0.05	-0.0007	0.30	*ns*
ET	2	0.18	0.0013	1.78	*ns*
NT	1	5.84	0.0111	1.21	*ns*
ENT	2	4.85	0.1582	47.46	**
RNT:E	7	0.10	0.0051	3.90	**
D	14	0.23	0.0074	4.28	**
ED	28	0.05	0.0035	2.06	**
ND	14	0.05	0.0014	1.47	*ns*
TD	14	0.07	0.0034	2.53	*
END	28	0.04	0.0024	1.36	*ns*
ETD	28	0.03	0.0002	1.03	*ns*
NTD	14	0.03	0.0014	1.40	*ns*
ENTD	28	0.02	-0.0026	0.80	*ns*
RNTD:E	167	0.03	0.0262		
Total	359				
h^2			0.46 - **0.73** - 0.85		

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, N nitrogen level, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval

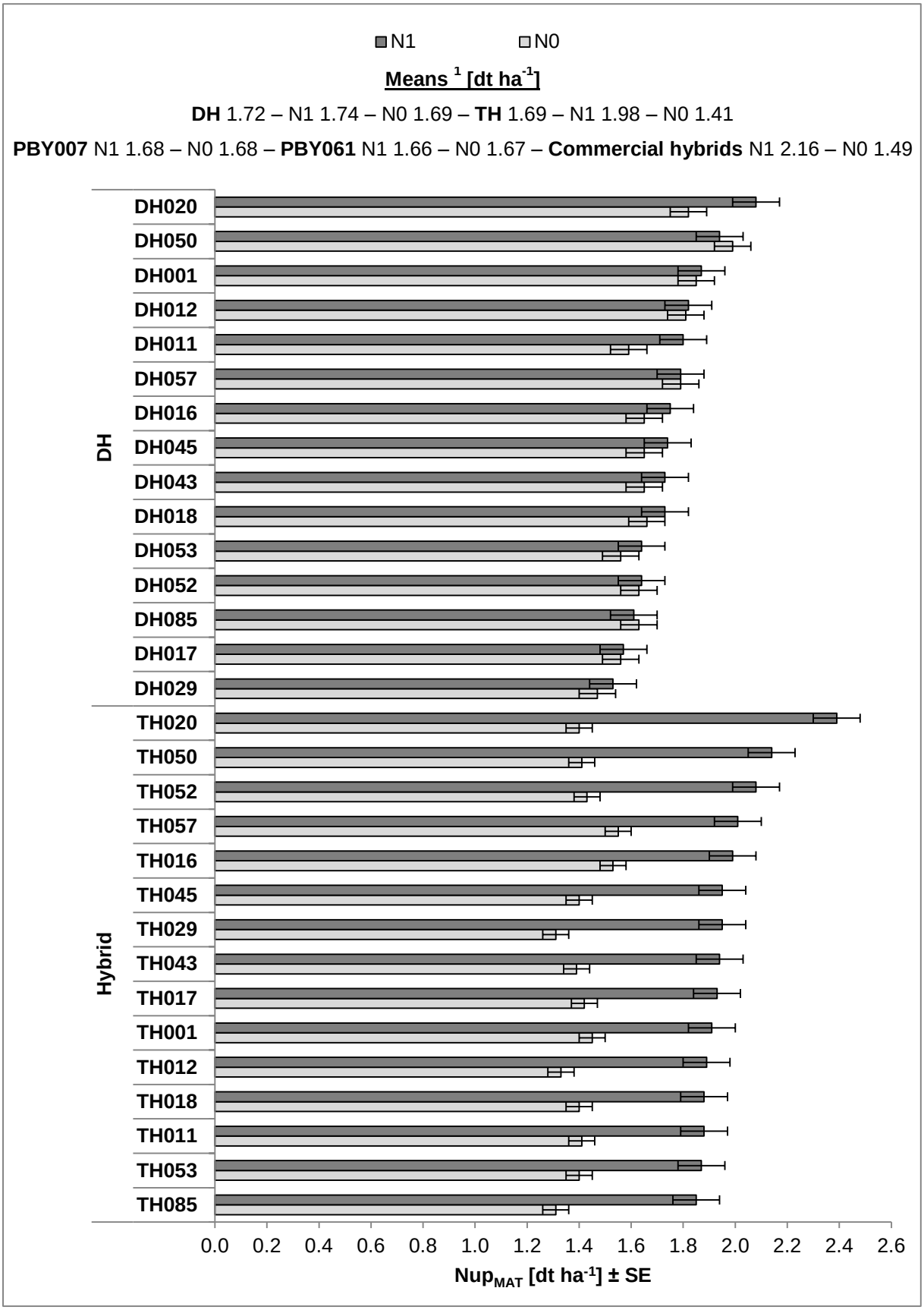

Fig. A 18: Nup_{MAT} of Pop007
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, [1] Means for DH and TH across both nitrogen levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0

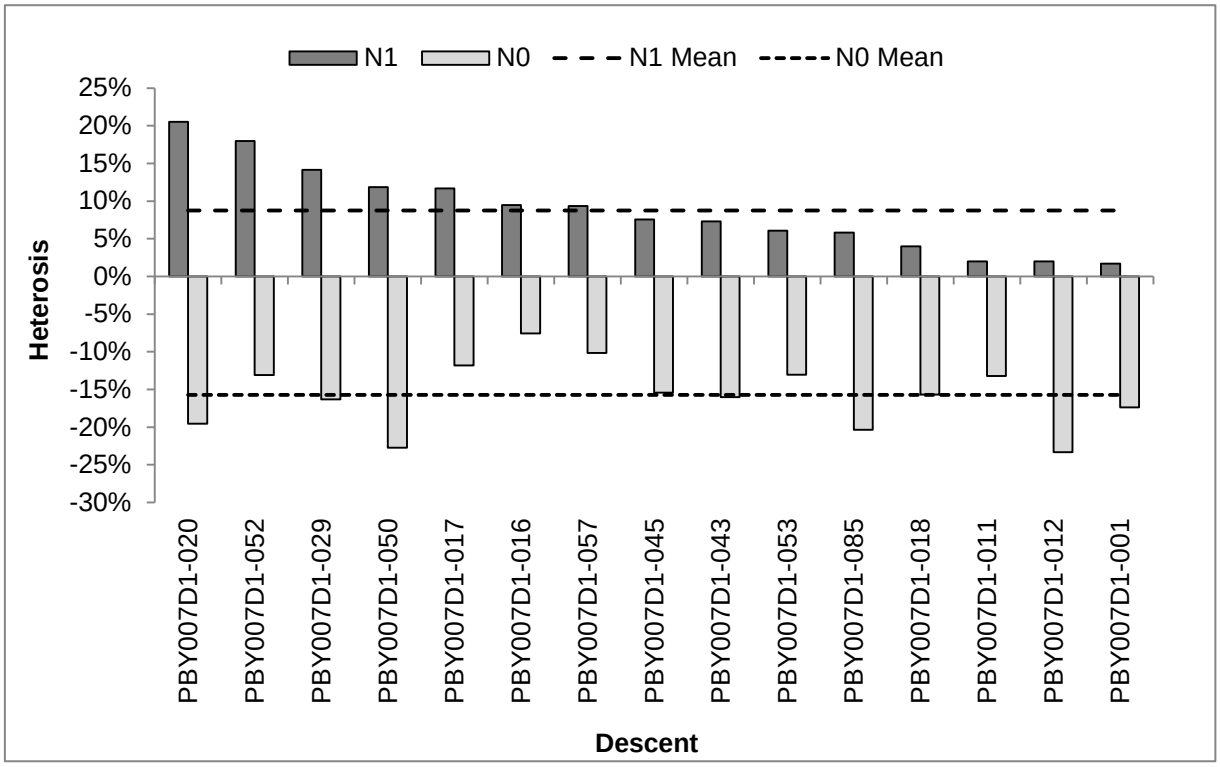

Fig. A 19: Heterosis for Nup_{MAT} of Pop007
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

$NupEff_{MAT}$

$NupEff_{MAT}$ was significantly affected by nitrogen level, descent and the interaction between descent and variety type. Variety type, the interactions between variety type and nitrogen level and between descent and variety type had no significant effect on $NupEff_{MAT}$. Heritability was 0.68 (Tab. A 19). At N1 $NupEff_{MAT}$ of DH lines ranged from 0.41 to 0.55, at N0 from 0.68 to 0.95 . Some DH lines exceeded the better parent but none fell below the lower one (Fig. A 20). Test hybrids at N1 showed $NupEff_{MAT}$ in the range from 0.49 to 0.63 at N0 from 0.63 to 0.74. No test hybrid exceeded commercial ones but some showed comparable $NupEff_{MAT}$ (Fig. A 20).

Heterosis was positive at N1 and negative at N0. At N1 it ranged from -2 % to 19 %, at N0 from -22 % to -5 % (Fig. A 21).

Tab. A 19: ANOVA for $NupEff_{MAT}$ of Pop007

Source	DF	MS	Var.cp	F	
E	2	0.300	0.0022	8.46	*ns*
R:E	3	0.036	0.0002	1.36	*ns*
N	1	5.317	0.0286	31.00	*
EN	2	0.172	0.0024	6.56	*ns*
RN:E	3	0.026	0.0001	1.10	*ns*
T	1	0.091	0.0005	10.69	*ns*
ET	2	0.009	-0.0003	0.36	*ns*
NT	1	0.634	0.0025	1.55	*ns*
ENT	2	0.408	0.0128	17.19	**
RNT:E	7	0.024	0.0013	5.66	**
D	14	0.030	0.0009	3.25	**
ED	28	0.009	0.0006	2.22	**
ND	14	0.007	0.0000	1.06	*ns*
TD	14	0.011	0.0006	2.83	**
END	28	0.006	0.0005	1.49	*ns*
ETD	28	0.004	-0.0001	0.94	*ns*
NTD	14	0.005	0.0005	2.55	*
ENTD	28	0.002	-0.0010	0.50	*ns*
RNTD:E	167	0.004	0.0042		
Total	359				
h^2			0.36 - **0.68** - 0.83		

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, N nitrogen level, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval

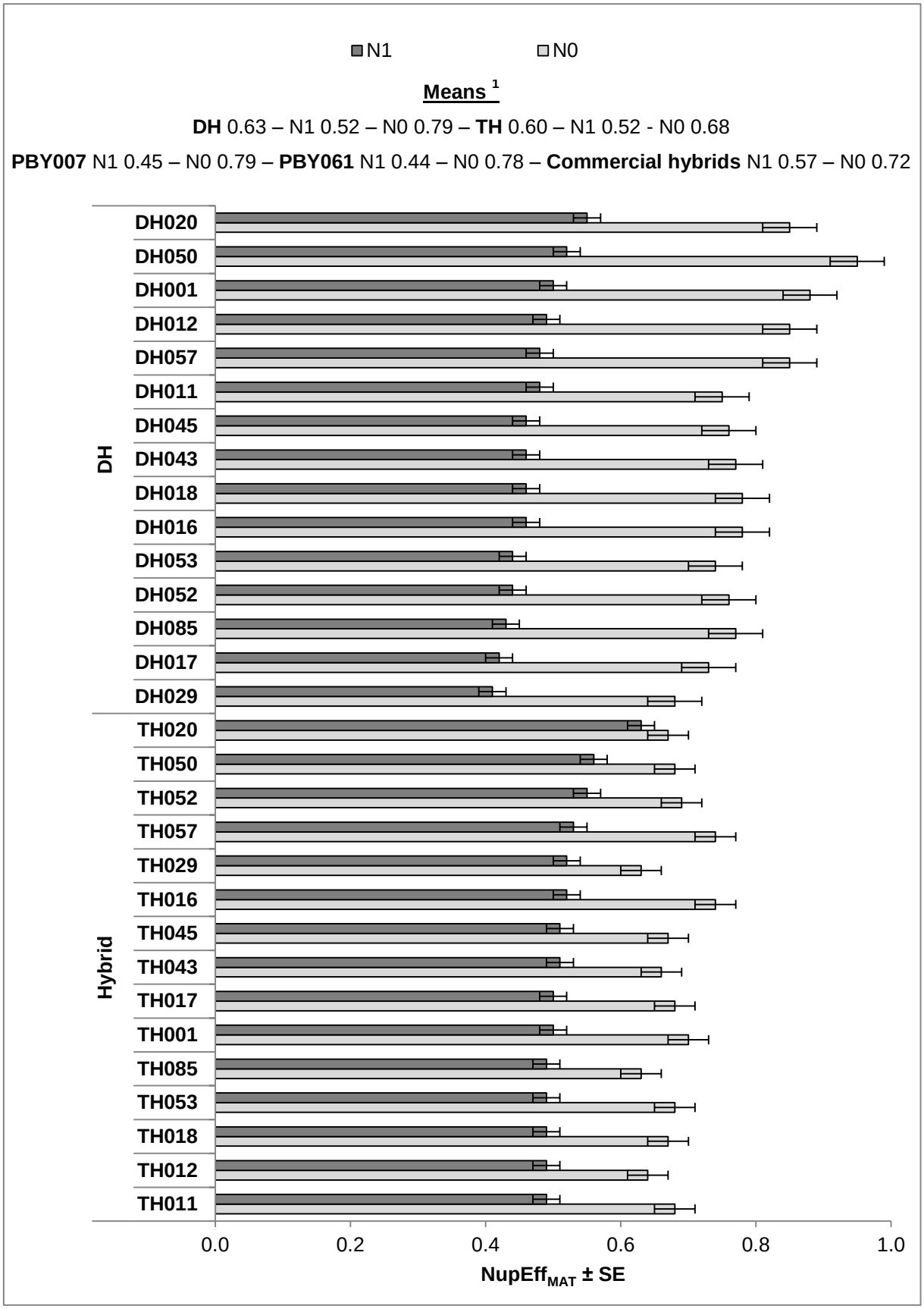

Fig. A 20: $NupEff_{MAT}$ of Pop007
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, [1] Means for DH and TH across both nitrogen levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0

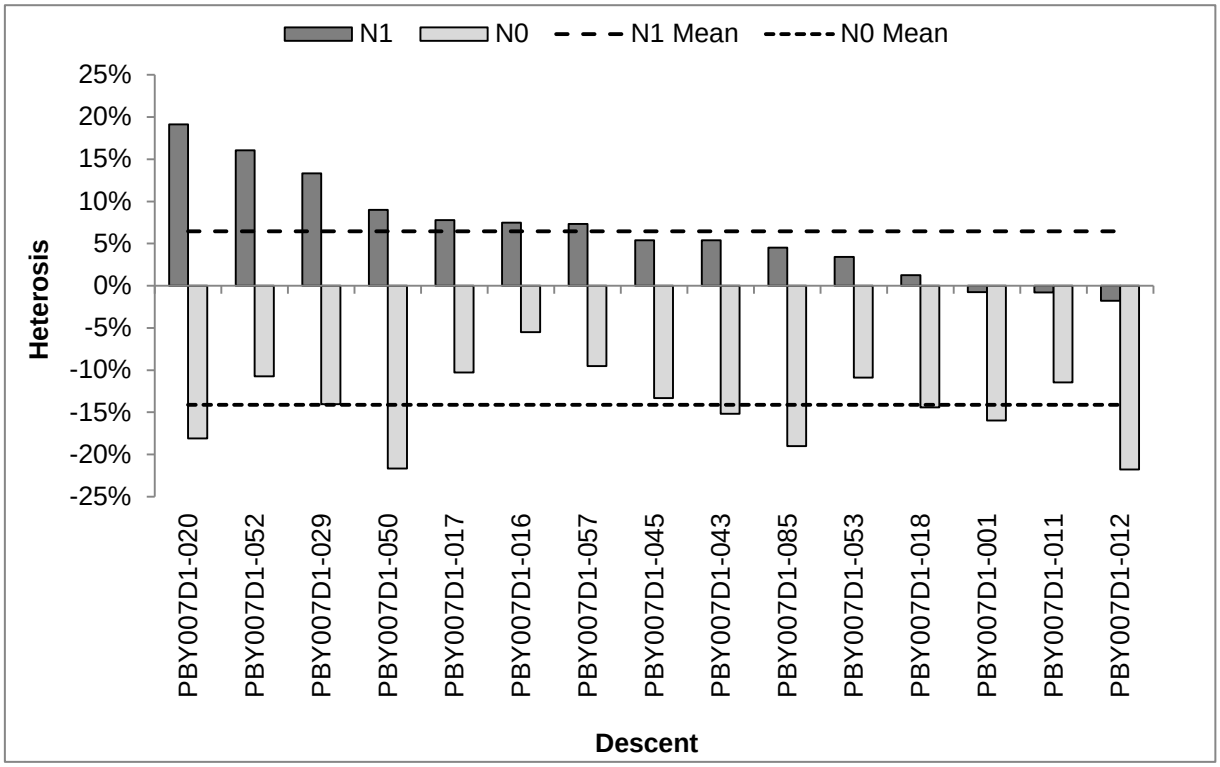

Fig. A 21: Heterosis for $NupEff_{MAT}$ of Pop007
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

NutEff

Variety type, descent and the interaction between descent and variety type had significant influence on NutEff. Nitrogen level, variety type and the interaction between descent and nitrogen level did not significantly affect NutEff. Heritability was 0.76 dt dt^{-1} (Tab. A 20). At N1 NutEff of DH lines ranged from 17 to 22, at N0 from 17 to 23. The better DH parent was outperformed by some DH lines at N1 and N0. No DH line fell below the lower parent PBY007 (N1 17, N0 16). For test hybrids NutEff at N1 ranged from 19 to 21, at N0 from 22 to 25. No test hybrid exceeded commercial hybrids but some showed comparable NutEff (Fig. A 22).

Heterosis was positive for NutEff at N1 and N0. At N1 it was lower than at N0. It ranged from 5 % to 20 % at N1 and from at N0 23 % to 39 % (Fig. A 23).

Tab. A 20: ANOVA for NutEff of Pop007

Source	DF	MS	Var.cp	F	
E	2	345.78	2.69	15.28	*
R:E	3	22.64	0.27	3.37	*ns*
N	1	254.03	1.08	4.26	*ns*
EN	2	59.64	0.88	8.89	*ns*
RN:E	3	6.71	0.16	3.75	*ns*
T	1	262.91	1.42	36.78	*
ET	2	7.15	0.09	3.99	*ns*
NT	1	293.02	0.13	1.04	*ns*
ENT	2	281.37	9.32	157.11	**
RNT:E	7	1.79	0.01	1.11	*ns*
D	14	17.38	0.58	4.87	**
ED	28	3.57	0.24	2.21	**
ND	14	2.98	0.05	1.26	*ns*
TD	14	6.54	0.36	2.90	**
END	28	2.36	0.19	1.46	*ns*
ETD	28	2.25	0.16	1.39	*ns*
NTD	14	2.24	0.17	1.84	*ns*
ENTD	28	1.22	-0.20	0.75	*ns*
RNTD:E	167	1.62	1.62		
Total	359				
h^2		0.52 - 0.**76** - 0.87			

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, N nitrogen level, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval

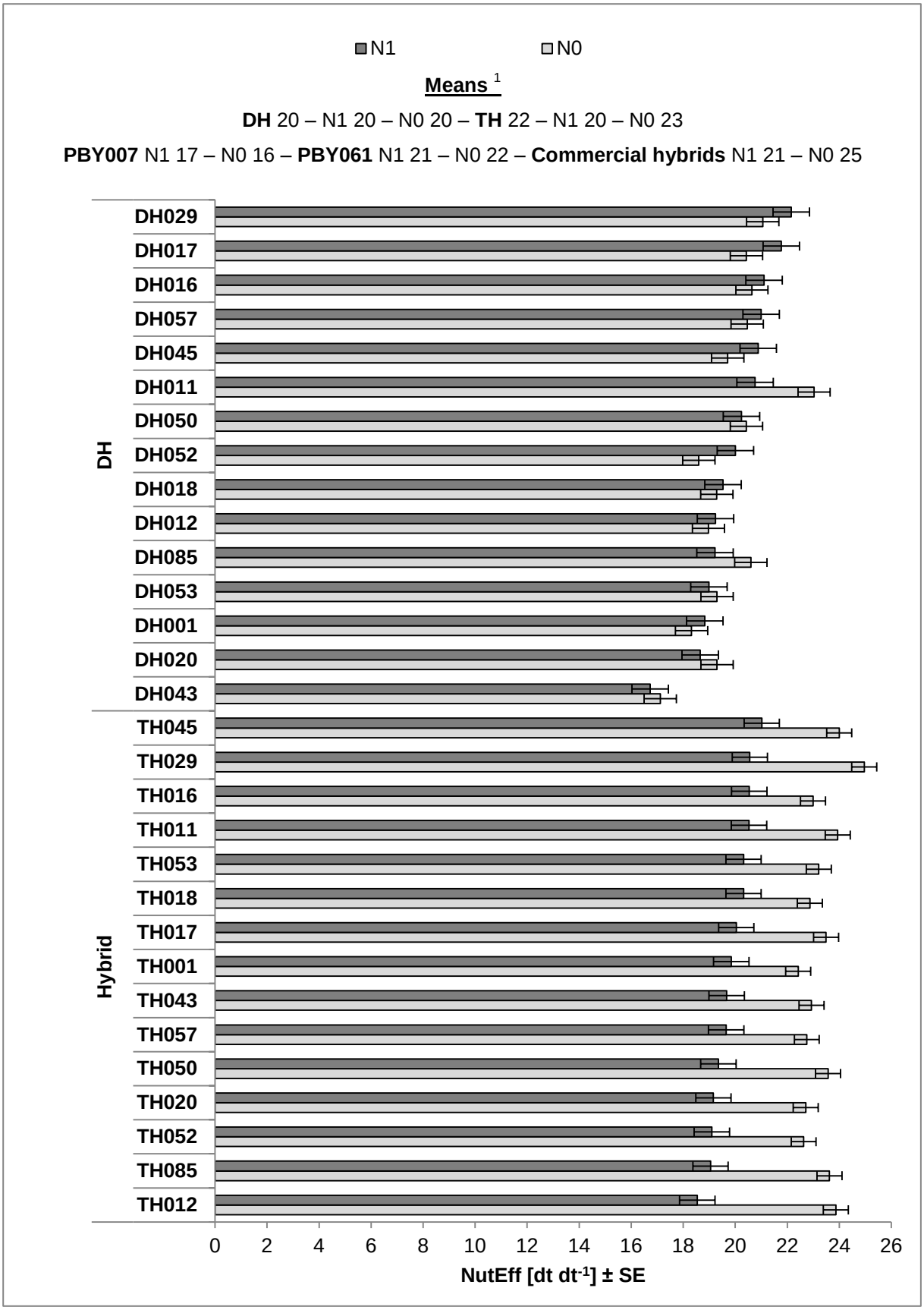

Fig. A 22: NutEff of Pop007
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, [1] Means for DH and TH across both nitrogen levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0

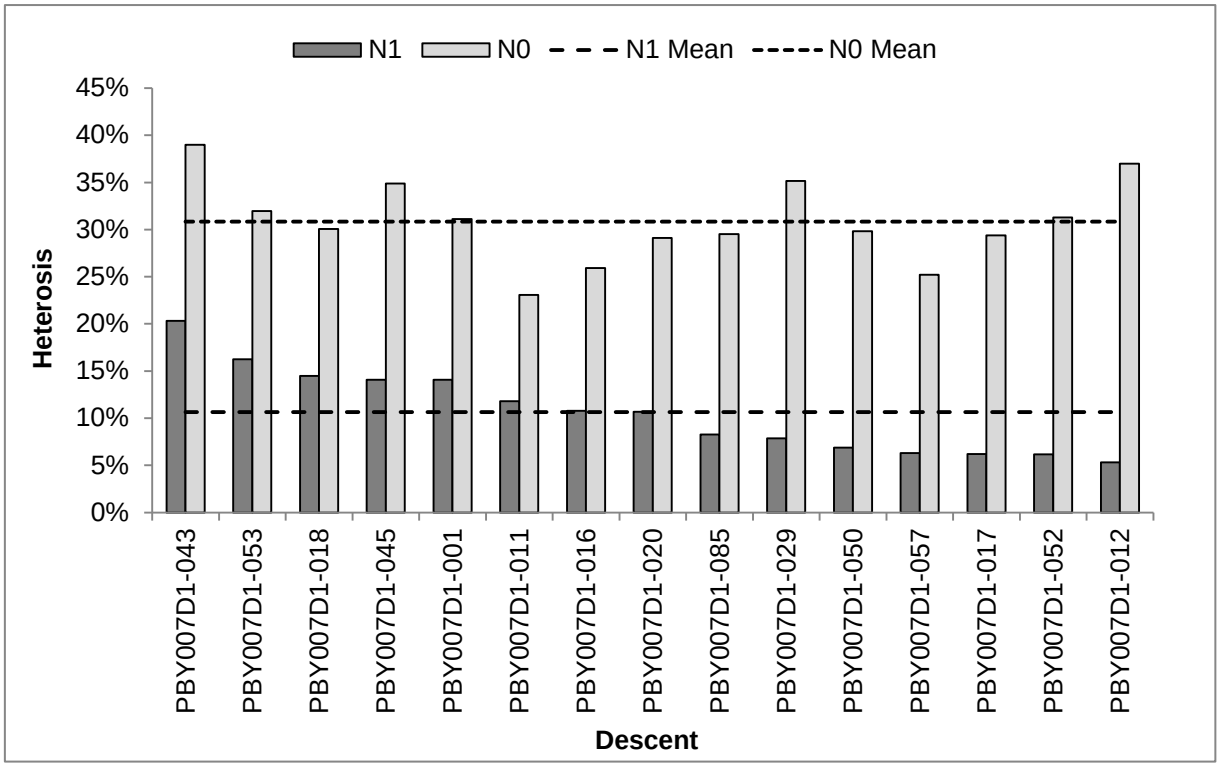

Fig. A 23: Heterosis for NutEff of Pop007
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

NUE

NUE was significantly affected by nitrogen level, variety type, descent and the interaction between descent and variety type. The interactions between variety type and nitrogen level and between descent and variety type were not significant. Heritability was 0.66 (Tab. A 21). At N1 NUE of DH lines ranged from 8 to 10, at N0 from 13 to 19. Some DH lines showed higher NUE than the better DH parent. No DH line fell below the lower parent (Fig. A 24). NUE of test hybrids at N1 ranged from 9 to 12 and from 15 to 17 at N0. Although test hybrid did not exceed commercial ones some test hybrids showed comparable NUE (Fig. A 24).

Positive heterosis was observed for NUE at N1 and N0. At N1 it was higher than at N0. It ranged from 6 % to 30 % at N1 and from 0 % to 19 % at N0 (Fig. A 25).

Tab. A 21: ANOVA for NUE of Pop007

Source	DF	MS	Var.cp	F	
E	2	240.05	1.97	65.70	**
R:E	3	3.65	-0.03	0.71	*ns*
N	1	3091.91	17.10	210.09	**
EN	2	14.72	0.16	2.85	*ns*
RN:E	3	5.16	-0.11	0.60	*ns*
T	1	35.45	0.19	37.43	*
ET	2	0.95	-0.13	0.11	*ns*
NT	1	22.28	0.12	1.92	*ns*
ENT	2	11.58	0.10	1.35	*ns*
RNT:E	7	8.60	0.46	4.90	**
D	14	13.42	0.34	2.55	*
ED	28	5.27	0.44	3.00	**
ND	14	3.58	0.12	1.71	*ns*
TD	14	6.08	0.40	4.54	**
END	28	2.10	0.09	1.19	*ns*
ETD	28	1.34	-0.10	0.76	*ns*
NTD	14	2.21	0.25	3.04	**
ENTD	28	0.73	-0.52	0.41	*ns*
RNTD:E	167	1.76	1.76		
Total	359				
h^2		0.32 - **0.66** - 0.82			

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, N nitrogen level, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, ** significant for $\alpha = 0.01$, * significant for $\alpha = 0.05$, *ns* not significant for $\alpha = 0.05$, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval

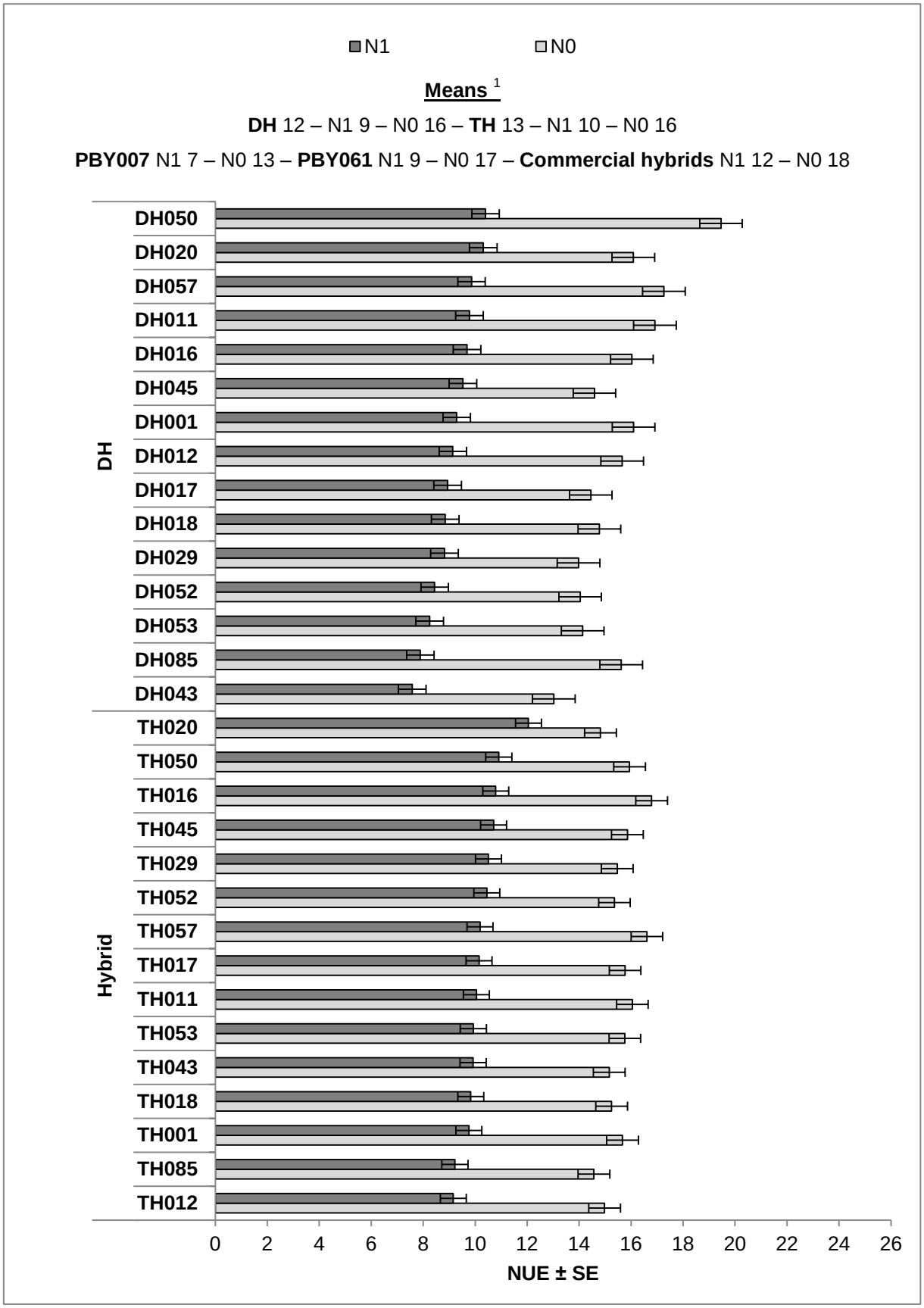

Fig. A 24: NUE of Pop007
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, [1] Means for DH and TH across both nitrogen levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0

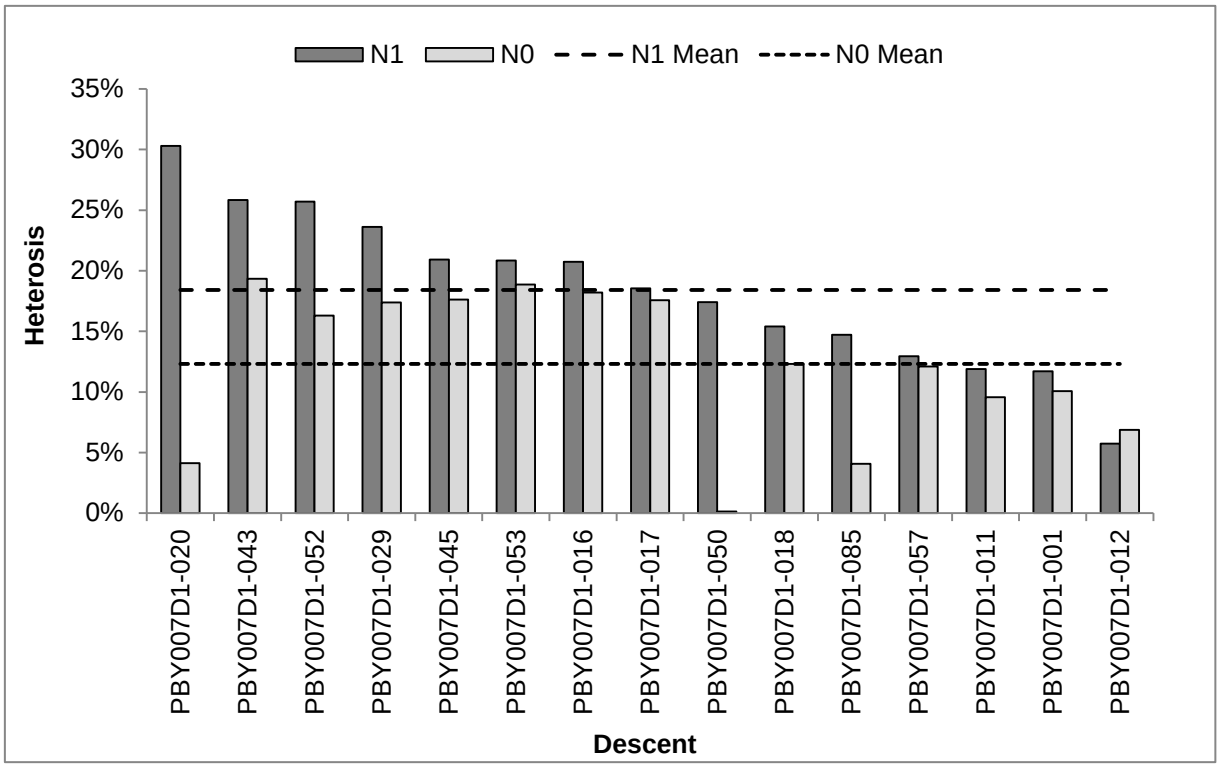

Fig. A 25: Heterosis for NUE of Pop007
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

NHI

NHI was not significantly affected by nitrogen level, variety type, descent and the interactions between variety type and nitrogen level, between descent and nitrogen level and between descent and variety type. Heritability was 0.46 (Tab. A 22). NHI ranged from 0.69 to 0.79 for DH lines at N1 and from 0.69 to 0.81 at N0. Their parents showed similar NHI (Fig. A 26).Test hybrids at N1 showed NHI from 0.70 to 0.77, at N0 all from 0.75 to 0.79. Hence test hybrids showed same NUE as commercial ones (Fig. A 26).

NHI showed positive heterosis at N1 and N0. At N1 it was lower than at N0. It ranged from 1 % to 11 % at N1 and from 7 % to 18 % at N0 (Fig. A 27).

Tab. A 22: ANOVA for NHI of Pop007

Source	DF	MS	Var.cp	F	
E	2	0.148	0.0012	22.01	*
R:E	3	0.007	0.0000	1.36	*ns*
N	1	0.015	0.0001	3.72	*ns*
EN	2	0.004	0.0000	0.81	*ns*
RN:E	3	0.005	0.0001	5.49	*
T	1	0.030	0.0001	2.85	*ns*
ET	2	0.011	0.0002	11.76	**
NT	1	0.017	0.0000	1.11	*ns*
ENT	2	0.015	0.0005	17.09	**
RNT:E	7	0.001	0.0000	0.60	*ns*
D	14	0.005	0.0001	1.89	*ns*
ED	28	0.003	0.0001	1.65	*
ND	14	0.002	0.0000	0.88	*ns*
TD	14	0.003	0.0001	1.78	*ns*
END	28	0.003	0.0003	1.72	*
ETD	28	0.002	0.0000	1.13	*ns*
NTD	14	0.002	0.0002	2.01	*ns*
ENTD	28	0.001	-0.0002	0.77	*ns*
RNTD:E	167	0.002	0.0015		
Total	359				
h^2			0.08 - **0.46** - 0.71		

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, N nitrogen level, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval

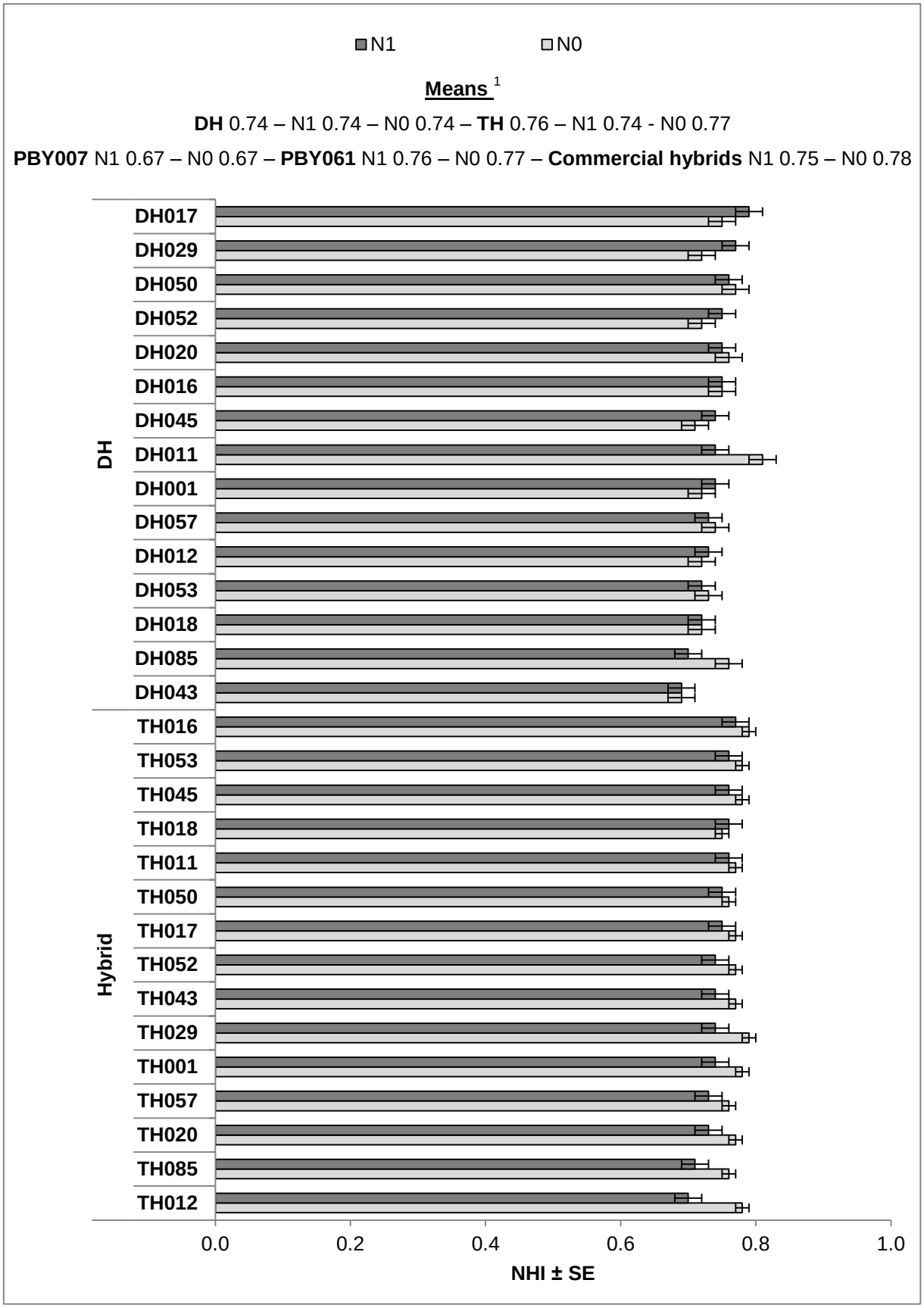

Fig. A 26: NHI of Pop007
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, [1] Means for DH and TH across both nitrogen levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0

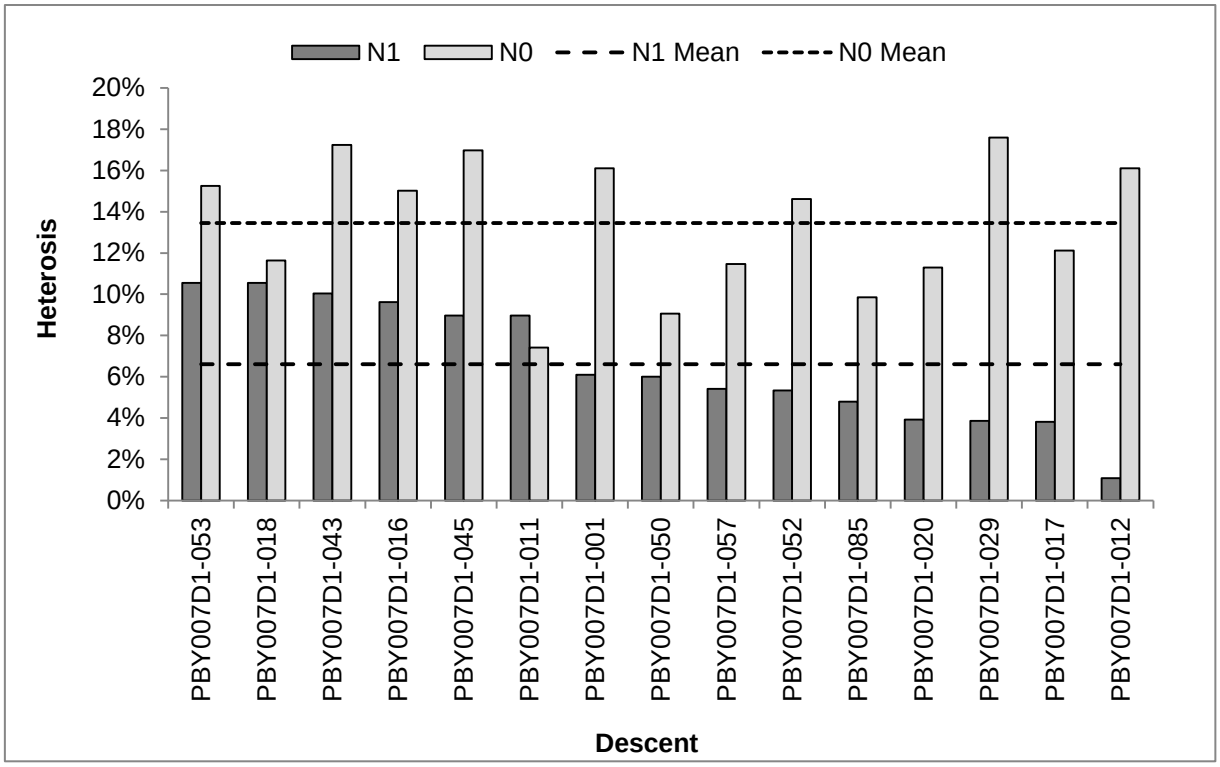

Fig. A 27: Heterosis for NHI of Pop007
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

Contribution of $NupEff_{MAT}$ and NutEff to NUE

Variance of NUE was dominated by variance of $NupEff_{MAT}$ both for DH lines and test hybrids at N1 and N0. This was even clearer at N0 than at N1. Variance of NUE of test hybrids was to a higher portion dominated by variance of $NupEff_{MAT}$ than that of DH lines (Fig. A 28).

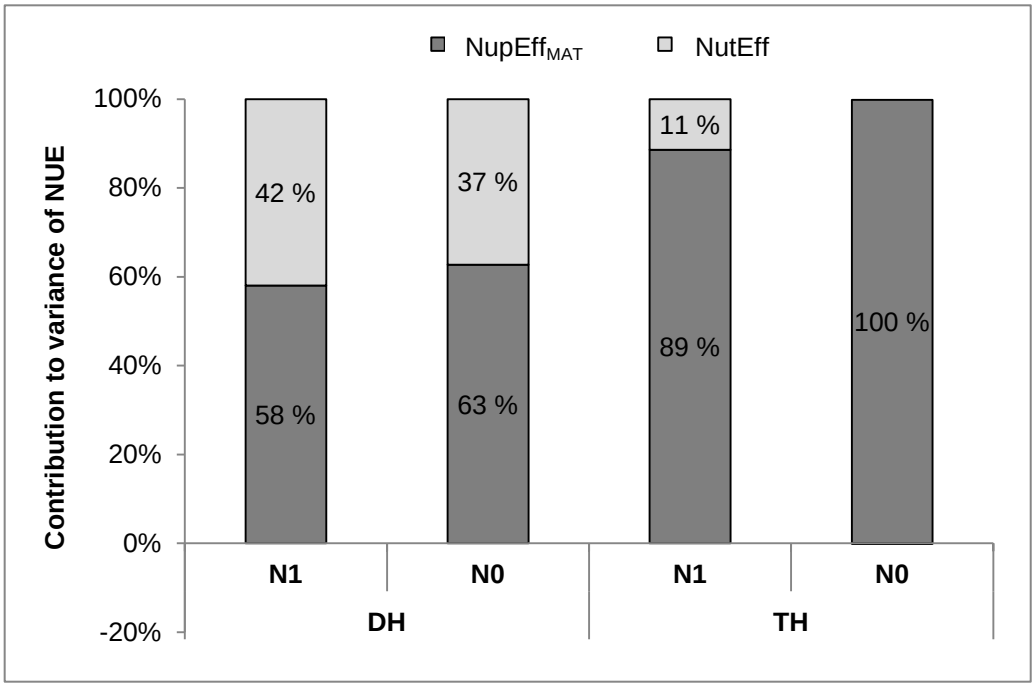

Fig. A 28: Contribution of variances of $NupEff_{MAT}$ and NutEff to variance of NUE of Pop007

Population 029 (Pop029)

Seed 9%

Seed 9% was significantly affected by descent and the interaction between descent and variety type. Nitrogen level, variety type and interactions between variety type and nitrogen level and between descent and nitrogen level had no significant effect. Heritability was 0.80 (Tab. A 23). DH lines at N1 showed seed 9% from 33 dt ha^{-1} to 48 dt ha^{-1} and at N0 from 30 dt ha^{-1} to 47 dt ha^{-1}. Some DH lines exceeded the better parent and all exceeded the lower parent (Fig. A 29). Seed 9% of test hybrids at N1 ranged from 40 dt ha^{-1} to 46 dt ha^{-1} and at N0 from 32 dt ha^{-1} to 38 dt ha^{-1}. No test hybrid exceeded commercial hybrids (Fig. A 29).

Heterosis was detected for all test hybrids at N1 and N0. Except for one test hybrid at N0 it was always positive. At N1 heterosis was higher than at N0. It ranged from 6 % to 26 % at N1 and from -5 % to 20 % at N0 (Fig. A 30).

Tab. A 23: ANOVA for Seed 9% of Pop029

Source	DF	MS	Var.cp	F	
E	2	1773.97	14.51	53.24	**
R:E	3	33.32	-0.96	0.37	*ns*
N	1	2647.56	7.23	1.97	*ns*
EN	2	1345.86	20.91	14.79	*
RN:E	3	91.00	1.94	2.76	*ns*
T	1	1.85	-0.12	0.08	*ns*
ET	2	24.31	-0.14	0.74	*ns*
NT	1	556.02	3.42	2.24	*ns*
ENT	2	248.51	7.19	7.54	*
RNT:E	7	32.94	1.53	3.30	**
D	14	127.76	4.05	4.19	**
ED	28	30.49	2.56	3.05	**
ND	14	12.33	-0.01	0.99	*ns*
TD	14	77.50	5.62	7.73	**
END	28	12.40	0.60	1.24	*ns*
ETD	28	10.03	0.01	1.00	*ns*
NTD	14	4.18	-0.98	0.42	*ns*
ENTD	28	10.04	0.02	1.00	*ns*
RNTD:E	167	9.99	9.99		
Total	359				
h^2		0.61 - **0.80** - 0.89			

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, N nitrogen level, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval

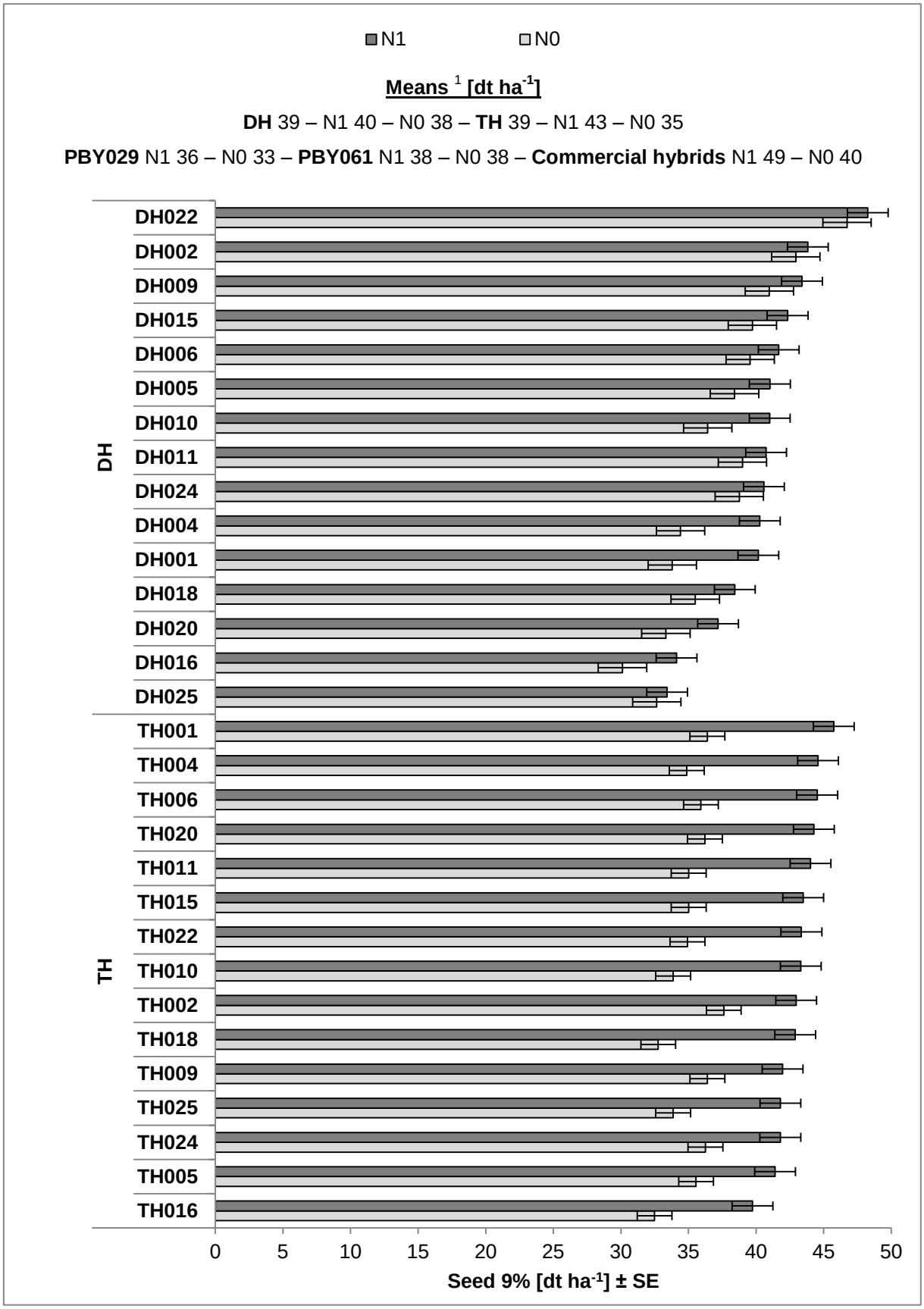

Fig. A 29: Seed 9% of Pop029
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, [1] Means for DH and TH across both nitrogen levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0

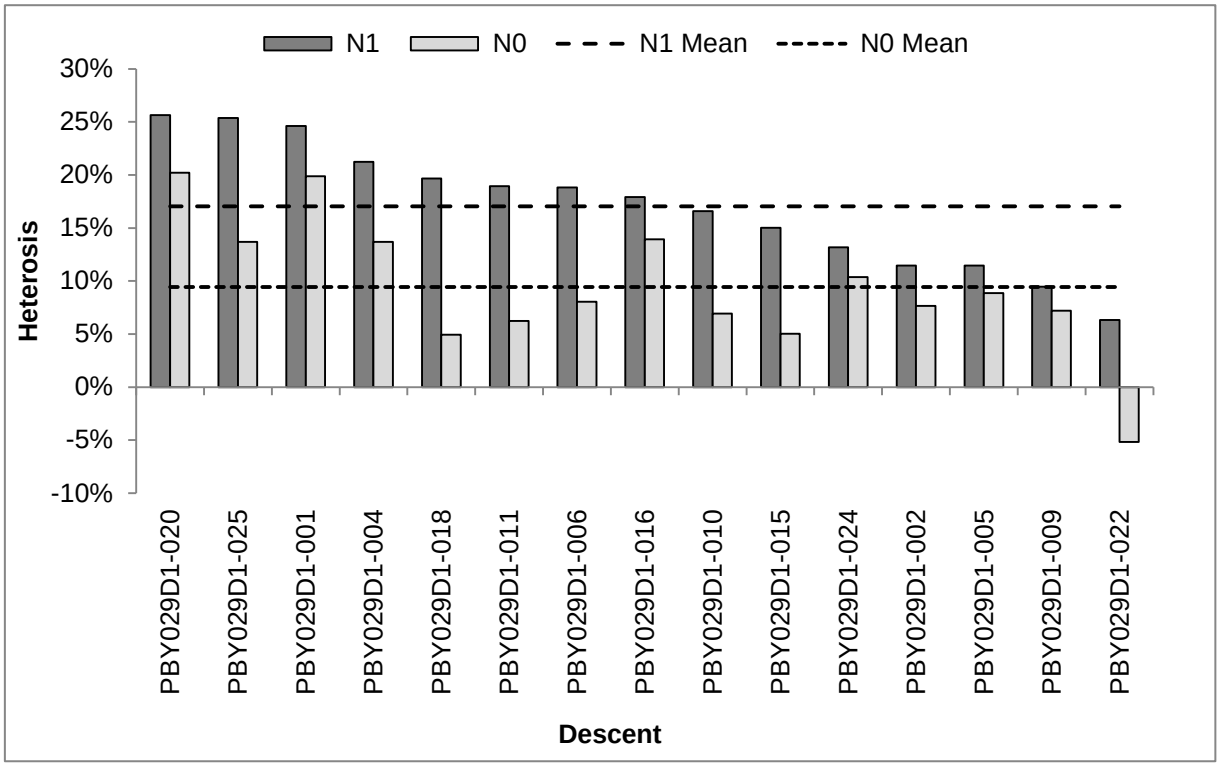

Fig. A 30: Heterosis for Seed 9% of Pop029
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

Nup_{MAT}

Nup_{MAT} was significantly affected by descent and interaction between descent and variety type. Nitrogen level, variety type and interactions between variety type and nitrogen level and between descent and variety type had no significant effect. Heritability was 0.82 (Tab. A 24). Nup_{MAT} of DH lines at N1 ranged from 1.37 dt ha^{-1} to 1.90 dt ha^{-1} and from 1.28 dt ha^{-1} to 1.94 dt ha^{-1} at N0. Some DH lines fell below the lower parent at N1 and N0. There were also some that exceeded the better DH parent (Fig. A 31). Nup_{MAT} of test hybrids ranged from 1.79 dt ha^{-1} to 2.07 dt ha^{-1} at N1 and from 1.25 dt ha^{-1} to 1.45 dt ha^{-1} at N0. Test hybrids did not exceed commercial ones (Fig. A 31).

Heterosis for Nup_{MAT} was positive at N1 and negative at N0. It ranged from 1 % to 18 % at N1 and from -28 % to -6 % at N0 (Fig. A 32).

Tab. A 24: ANOVA for Nup_{MAT} of Pop029

Source	DF	MS	Var.cp	F	
E	2	7.16	0.0574	26.40	*
R:E	3	0.27	-0.0008	0.85	*ns*
N	1	10.15	0.0331	2.42	*ns*
EN	2	4.19	0.0645	13.09	*
RN:E	3	0.32	0.0096	9.54	**
T	1	0.01	-0.0003	0.18	*ns*
ET	2	0.06	0.0005	1.85	*ns*
NT	1	6.74	0.0221	1.42	*ns*
ENT	2	4.75	0.1574	141.65	**
RNT:E	7	0.03	0.0010	1.86	*ns*
D	14	0.18	0.0055	4.18	**
ED	28	0.04	0.0030	2.33	**
ND	14	0.02	-0.0001	0.93	*ns*
TD	14	0.14	0.0102	9.16	**
END	28	0.02	0.0013	1.29	*ns*
ETD	28	0.02	-0.0007	0.83	*ns*
NTD	14	0.01	-0.0017	0.44	*ns*
ENTD	28	0.02	0.0000	1.00	*ns*
RNTD:E	167	0.02	0.0180		
Total	359				
h^2			0.64 - **0.82** - 0.90		

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, N nitrogen level, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval

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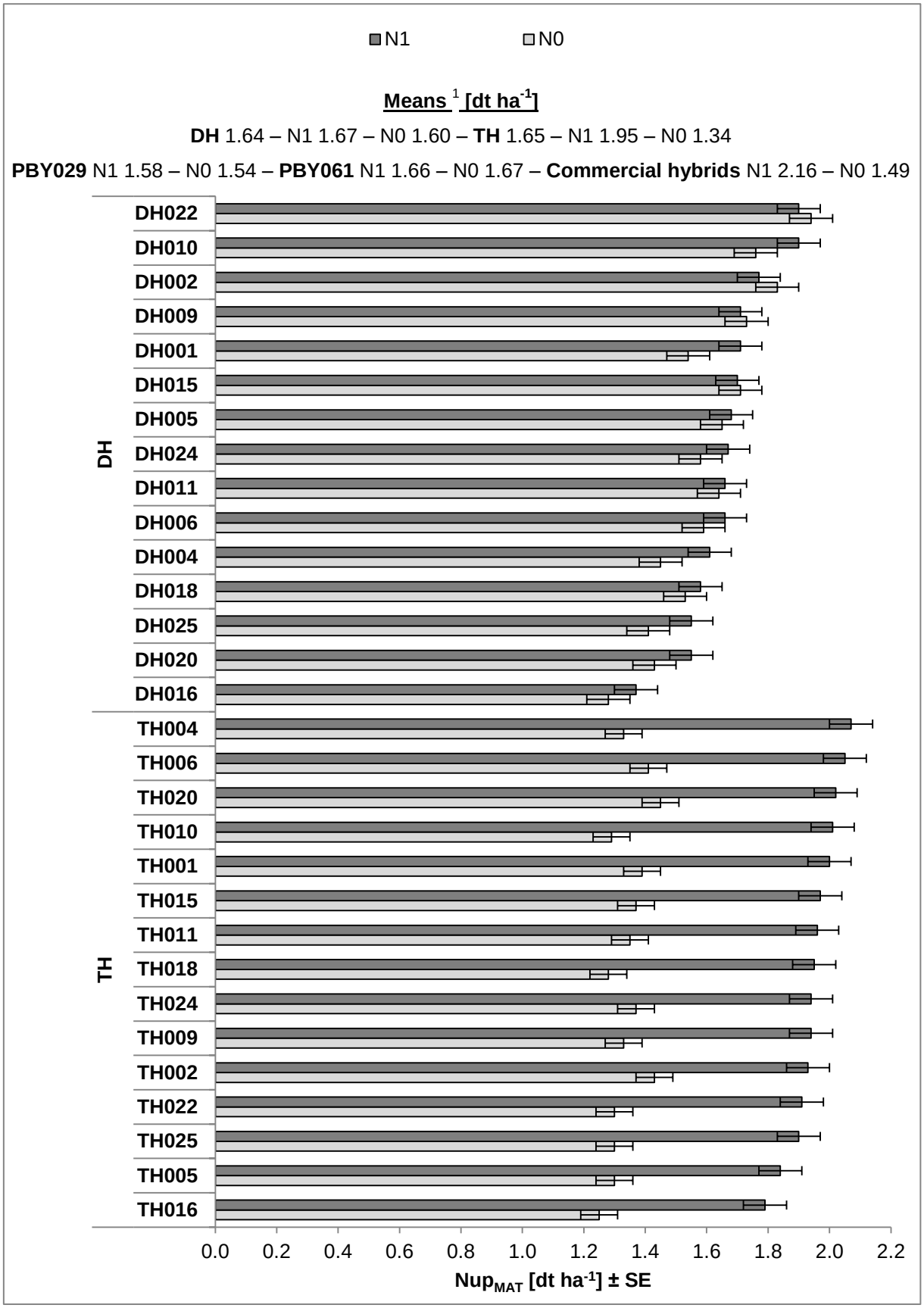

Fig. A 31: Nup_{MAT} of Pop029
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, [1] Means for DH and TH across both nitrogen levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0

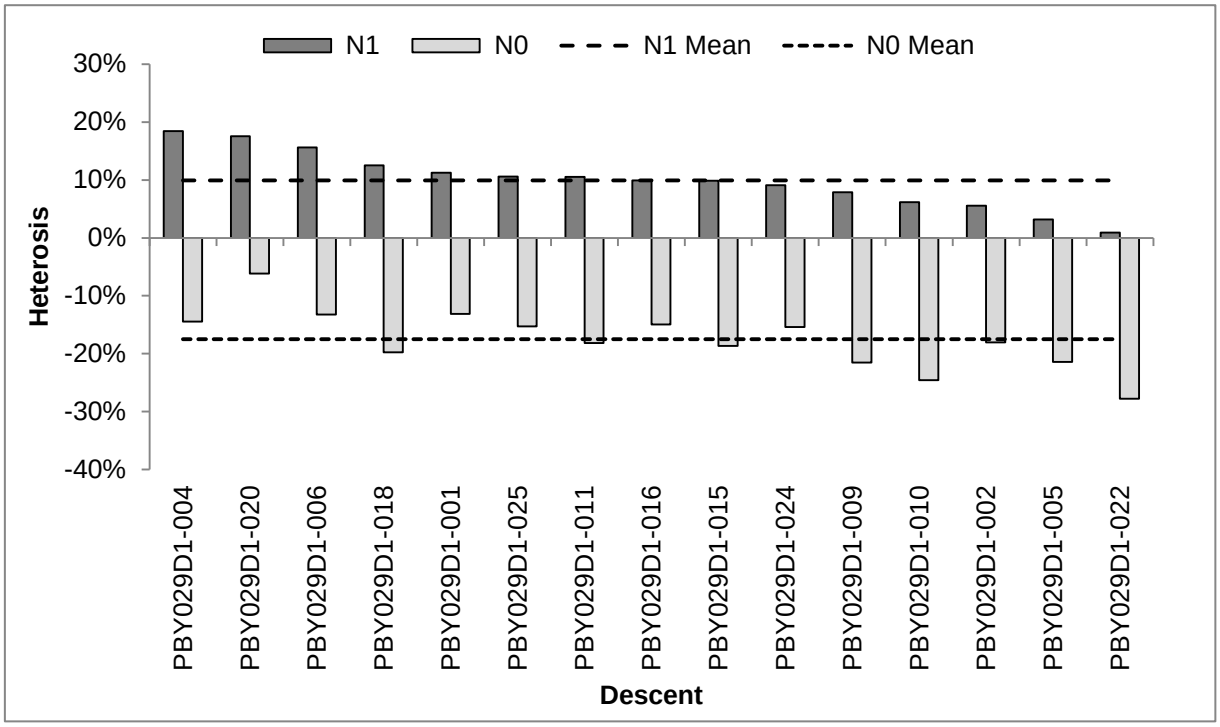

Fig. A 32: Heterosis for Nup_{MAT} of Pop029
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

$NupEff_{MAT}$

NupEff was significantly affected by descent and interaction between descent and variety type. Nitrogen level, variety type and the interactions between variety type and nitrogen level and between descent and nitrogen level had no significant effect on $NupEff_{MAT}$. Heritability was 0.80 (Tab. A 25). $NupEff_{MAT}$ of DH lines at N1 ranged from 0.37 to 0.51 and at N0 from 0.58 to 0.91. At N1 no DH lines exceeded the better parent. At N0 some DH lines showed superior $NupEff_{MAT}$. No DH lines fell below the lower parent (Fig. A 33). At N1 $NupEff_{MAT}$ of test hybrids ranged from 0.47 to 0.55 and at N0 from 0.59 to 0.69. Test hybrids did not exceed commercial hybrids (Fig. A 33).

Except for one test hybrid heterosis was positive at N1 and for all test hybrids negative at N0. It ranged from -2 % to 17 % at N1 and from -26 % to -6 % at N0 (Fig. A 34).

Tab. A 25: ANOVA for $NupEff_{MAT}$ of Pop029

Source	DF	MS	Var.cp	F	
E	2	0.3212	0.0022	5.63	*ns*
R:E	3	0.0570	0.0001	1.12	*ns*
N	1	4.2946	0.0223	15.67	*ns*
EN	2	0.2740	0.0037	5.39	*ns*
RN:E	3	0.0508	0.0014	6.76	*ns*
T	1	0.0389	0.0002	5.10	*ns*
ET	2	0.0076	0.0000	1.01	*ns*
NT	1	0.6743	0.0029	1.64	*ns*
ENT	2	0.4109	0.0134	54.70	**
RNT:E	7	0.0075	0.0003	2.73	*
D	14	0.0284	0.0009	3.63	**
ED	28	0.0078	0.0006	2.85	**
ND	14	0.0076	0.0002	1.58	*ns*
TD	14	0.0206	0.0015	9.35	**
END	28	0.0048	0.0005	1.75	*
ETD	28	0.0022	-0.0001	0.80	*ns*
NTD	14	0.0037	0.0002	1.57	*ns*
ENTD	28	0.0024	-0.0002	0.86	*ns*
RNTD:E	167	0.0027	0.0027		
Total	359				
h^2		0.59 - **0.80** - 0.89			

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, N nitrogen level, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval

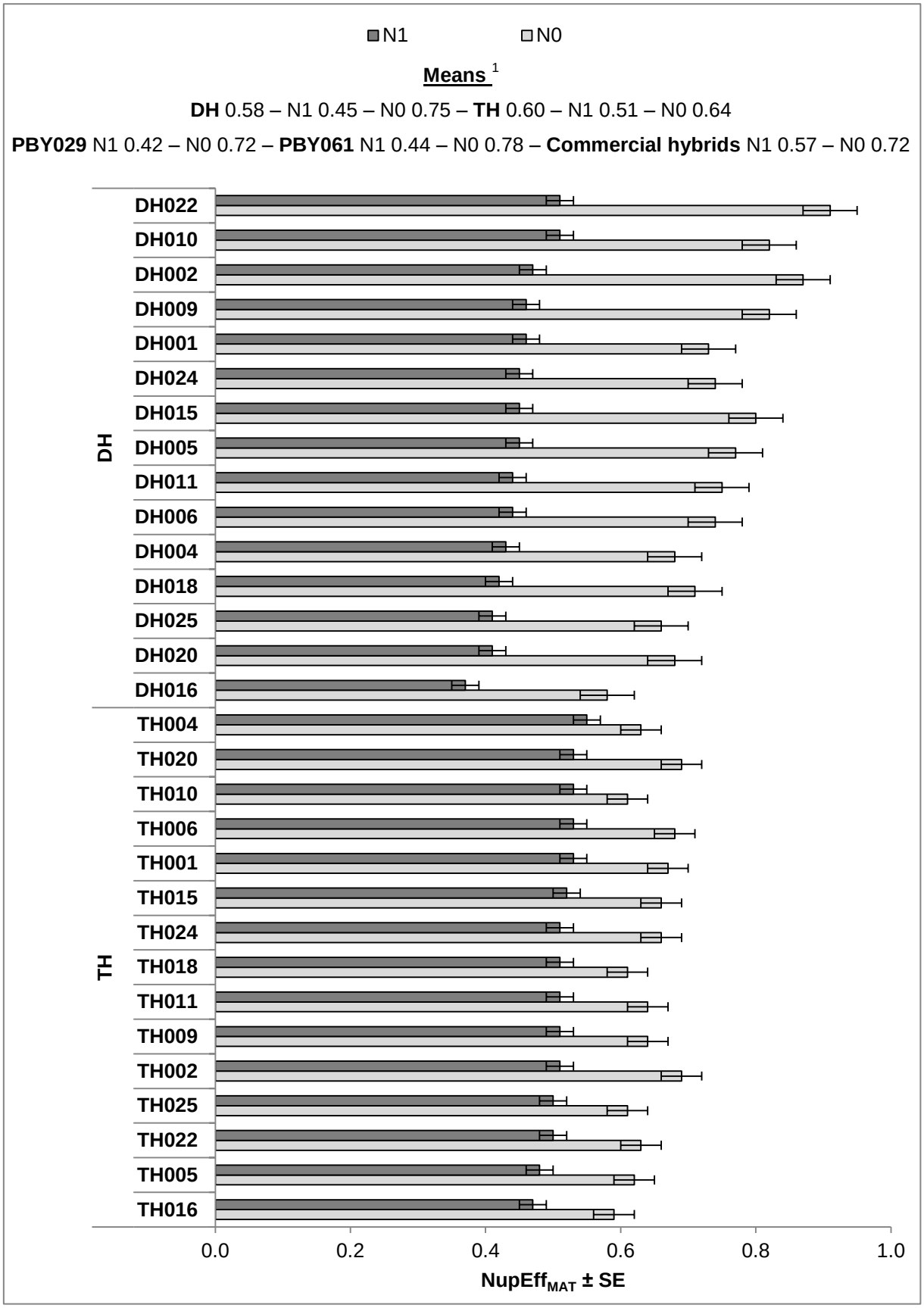

Fig. A 33: $NupEff_{MAT}$ of Pop029
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, [1] Means for DH and TH across both nitrogen levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0

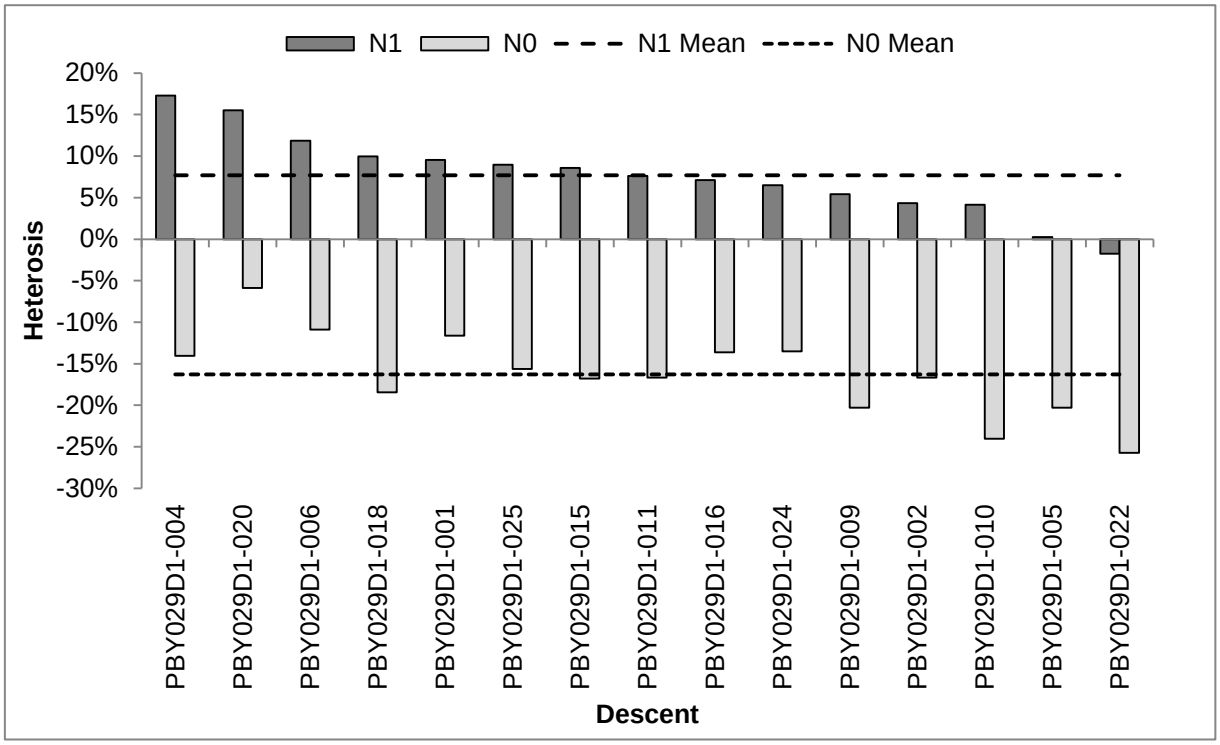

Fig. A 34: Heterosis for $NupEff_{MAT}$ of Pop029
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

NutEff

NutEff was significantly affected by descent and interaction between descent and variety type. Nitrogen level, variety type and the interactions between variety type and nitrogen level and between descent and nitrogen level did not significantly affect NutEff. Heritability was 0.69 (Tab. A 26). NutEff of DH lines at N1 and N0 ranged from 20 to 24. The better parent was exceeded by some DH lines at both nitrogen levels. No DH line fell below the lower DH parent (Fig. A 35). NutEff of test hybrids at N1 ranged from 20 to 21 and at N0 from 23 to 25. Test hybrids did not exceed commercial ones (Fig. A 35).

Except for one test hybrid at N1 heterosis was positive. It was lower at N1 than at N0. It ranged from -1 % to 12 % at N1 and from 20 % to 38 % at N0 (Fig. A 36).

Tab. A 26: ANOVA for NutEff of Pop029

Source	DF	MS	Var.cp	F	
E	2	283.21	2.101	9.10	*ns*
R:E	3	31.12	0.383	3.83	*ns*
N	1	339.15	0.951	2.02	*ns*
EN	2	167.94	2.664	20.69	*
RN:E	3	8.12	0.183	3.10	*ns*
T	1	0.03	-0.012	0.01	*ns*
ET	2	2.20	-0.007	0.84	*ns*
NT	1	418.87	0.537	1.13	*ns*
ENT	2	370.54	12.264	141.64	**
RNT:E	7	2.62	0.049	1.39	*ns*
D	14	7.07	0.222	4.05	**
ED	28	1.75	-0.018	0.93	*ns*
ND	14	1.65	0.024	1.21	*ns*
TD	14	5.96	0.310	2.66	*
END	28	1.36	-0.131	0.72	*ns*
ETD	28	2.24	0.089	1.19	*ns*
NTD	14	1.93	-0.071	0.82	*ns*
ENTD	28	2.35	0.233	1.25	*ns*
RNTD:E	167	1.89	1.887		
Total	359				
h^2		0.39 - **0.69** - 0.83			

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, N nitrogen level, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval

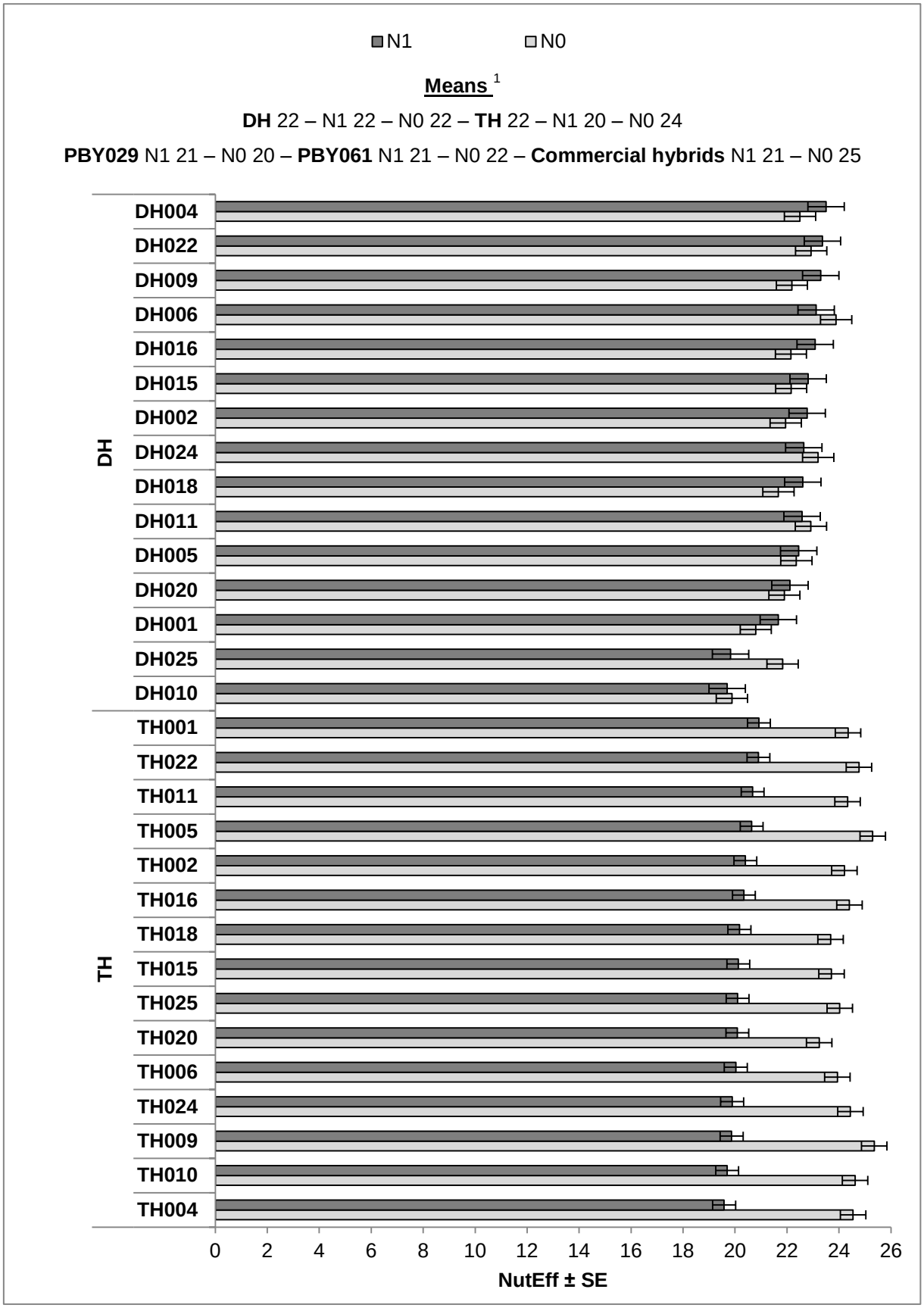

Fig. A 35: NutEff of Pop029
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, [1] Means for DH and TH across both nitrogen levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0

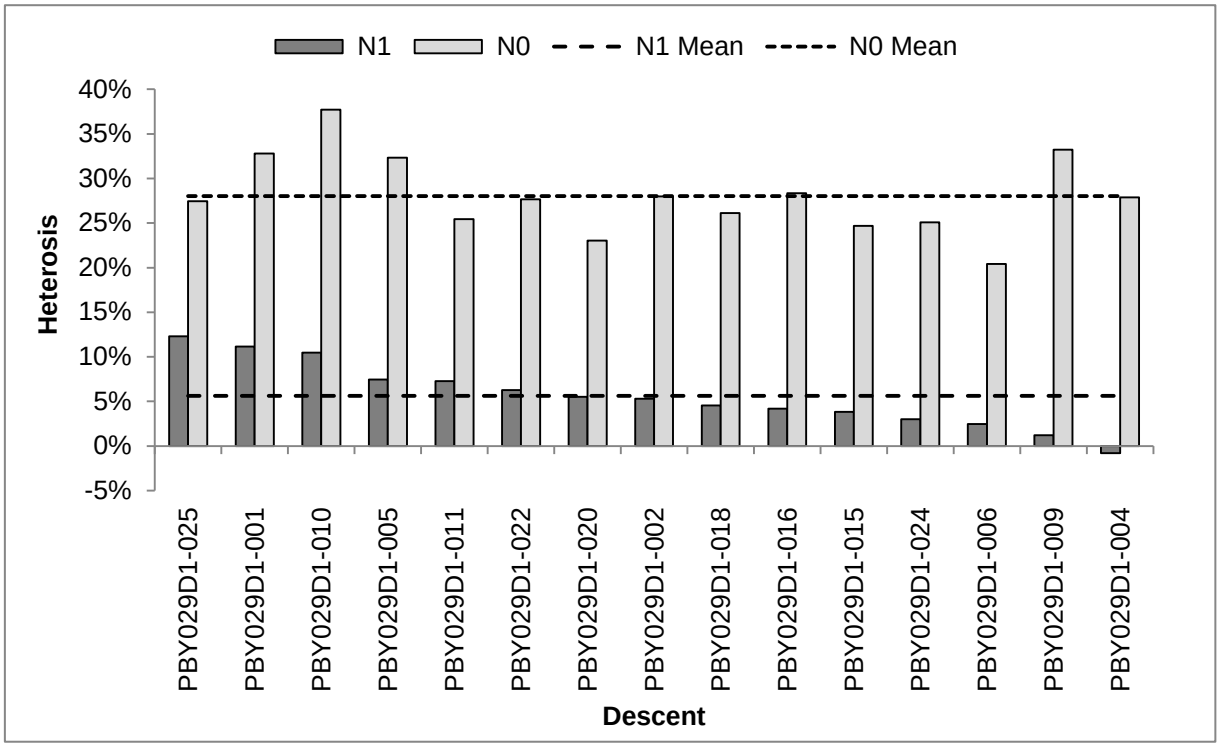

Fig. A 36: Heterosis for NutEff of Pop029
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

NUE

NUE was significantly affected by nitrogen level, descent and interaction between descent and variety type. Variety type and interactions between variety type and nitrogen level and between descent and nitrogen level had no significant effect on NUE. Heritability was 0.75 (Tab. A 27). NUE of DH lines ranged from 8 to 12 at N1 and from 13 to 21 at N0. At N1 nearly all DH lines exceeded the better parents. Also at N0 some DH lines outperformed the better parent. At N1 and some DH lines fell below the lower parent (Fig. A 37). NUE of test hybrids ranged from 10 to 11 at N1 and from 14 to 17 at N0. Test hybrids did not show higher NUE than commercial ones (Fig. A 37).

Heterosis was positive for all descents and nitrogen levels except one descent at N0. It was higher at N1 than at N0. At N1 it ranged from 5 % to 24 % and at N0 from -7 % to 18 % (Fig. A 38).

Tab. A 27: ANOVA for NUE of Pop029

Source	DF	MS	Var.cp	F	
E	2	150.89	1.19	18.72	*
R:E	3	8.06	-0.07	0.67	*ns*
N	1	3056.55	16.90	205.74	**
EN	2	14.86	0.05	1.23	*ns*
RN:E	3	12.09	0.28	3.26	*ns*
T	1	2.84	0.01	2.77	*ns*
ET	2	1.02	-0.04	0.28	*ns*
NT	1	50.31	0.39	3.38	*ns*
ENT	2	14.88	0.37	4.01	*ns*
RNT:E	7	3.71	0.17	3.05	**
D	14	18.64	0.54	3.31	**
ED	28	5.62	0.55	4.63	**
ND	14	4.75	0.15	1.61	*ns*
TD	14	9.75	0.68	6.15	**
END	28	2.94	0.43	2.42	**
ETD	28	1.59	0.09	1.31	*ns*
NTD	14	1.51	0.05	1.27	*ns*
ENTD	28	1.19	-0.01	0.98	*ns*
RNTD:E	167	1.21	1.21		
Total	359				
h^2		0.49 - **0.75** - 0.86			

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, N nitrogen level, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, ** significant for α =0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval

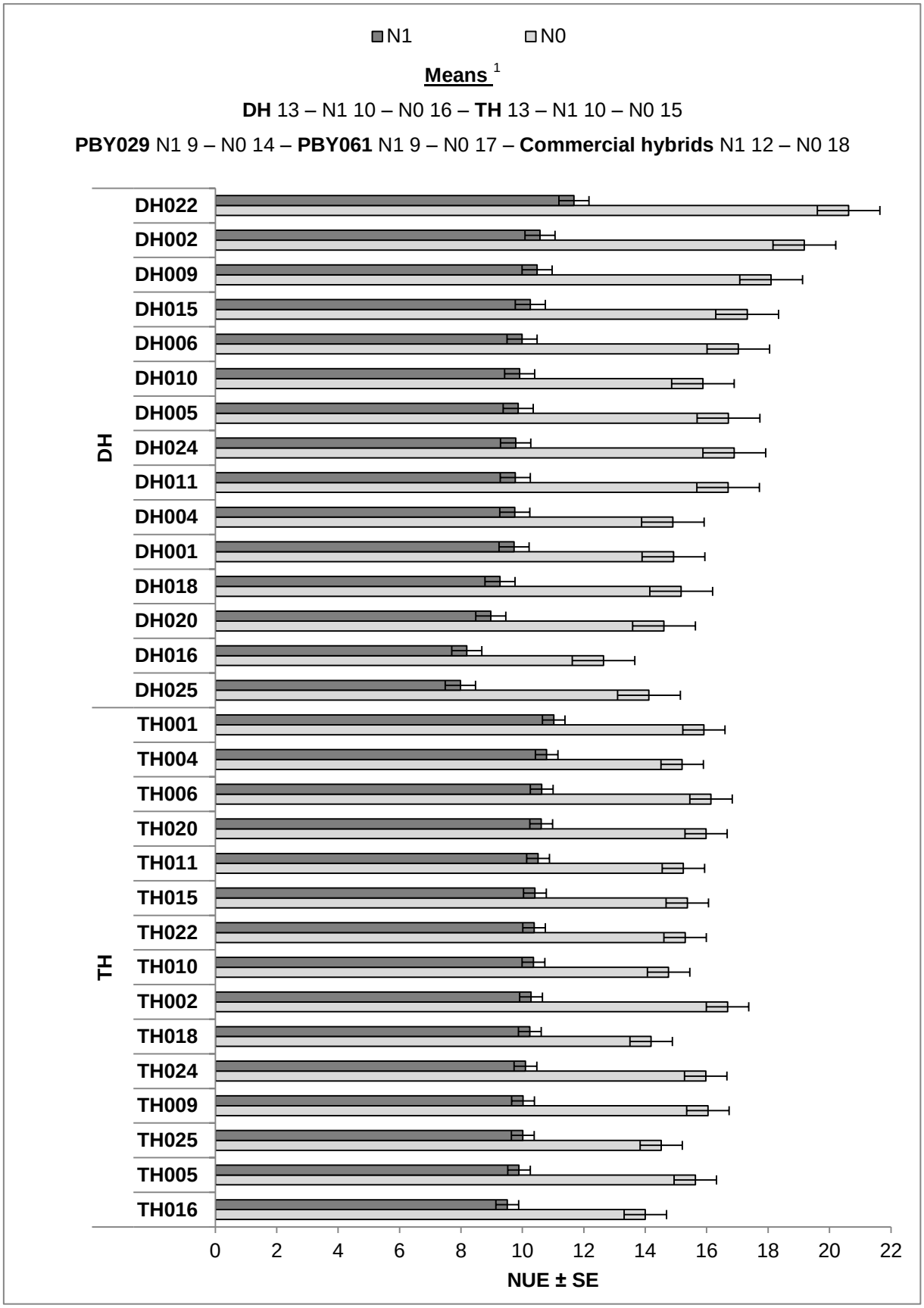

Fig. A 37: NUE of Pop029
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, [1] Means for DH and TH across both nitrogen levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0

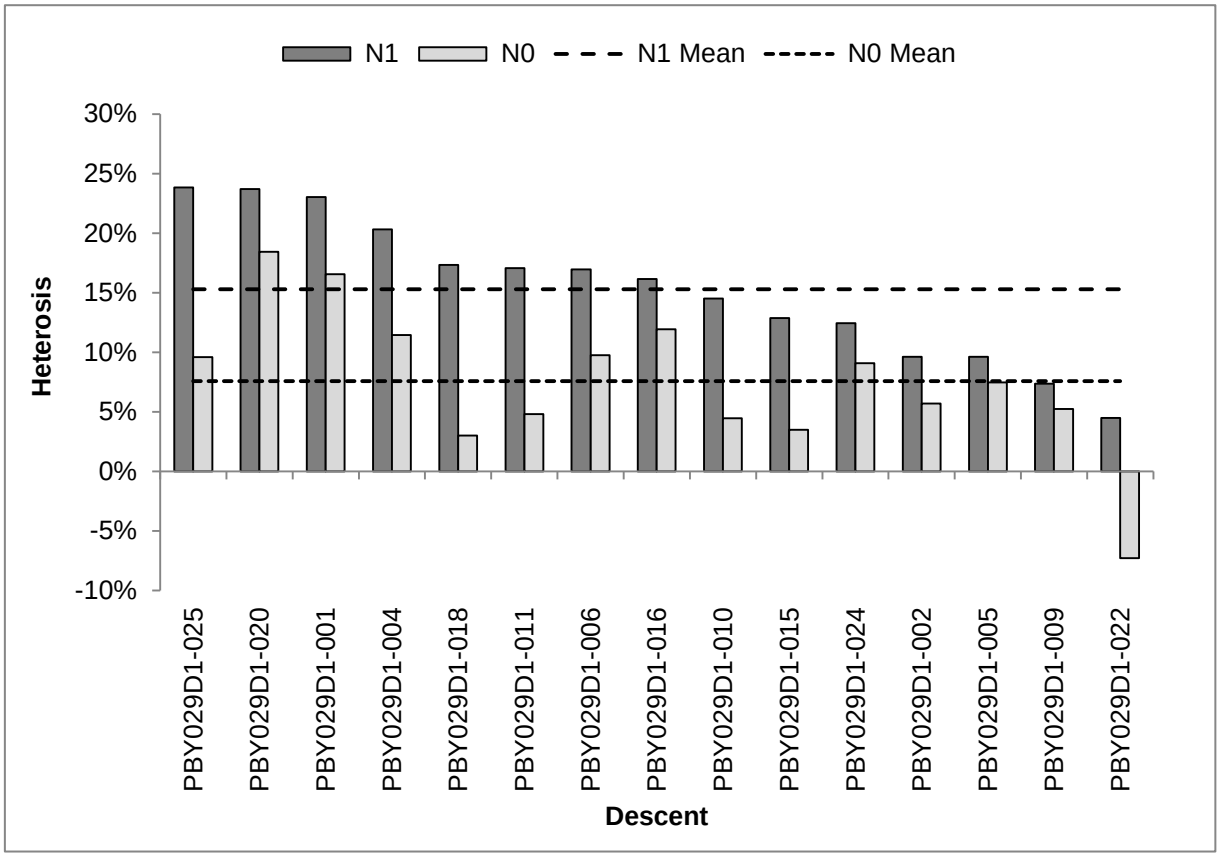

Fig. A 38: Heterosis for NUE of Pop029
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

NHI

Nitrogen level, variety type, interaction between variety type and nitrogen level, descent, interaction between descent and nitrogen level and interaction between descent and variety type did not significantly affect NHI. Heritability was 0.31 (Tab. A 28). NHI of DH lines at N1 ranged from 0.73 to 0.78 and at N0 from 0.74 to 0.79. DH lines showed similar NHI as their DH parents (Fig. A 39). NHI of test hybrids at N1 ranged from 0.72 to 0.77. At N0 it ranged from 0.76 to 0.82. Test hybrid did not exceed commercial ones but showed comparable NHI (Fig. A 39).

Positive heterosis was detected at N1 and N0. It was lower at N1 than at N0. Heterosis at N1 ranged from 2 % to 10 % and at N0 from 10 % to 19 % (Fig. A 40).

Tab. A 28: ANOVA for NHI of Pop029

Source	DF	MS	Var.cp	F	
E	2	0.082	0.0006	8.13	*ns*
R:E	3	0.010	0.0001	4.96	*ns*
N	1	0.057	0.0002	3.26	*ns*
EN	2	0.017	0.0003	8.62	*ns*
RN:E	3	0.002	0.0000	0.60	*ns*
T	1	0.002	0.0000	0.96	*ns*
ET	2	0.002	0.0000	0.53	*ns*
NT	1	0.026	0.0000	1.19	*ns*
ENT	2	0.022	0.0006	6.54	*
RNT:E	7	0.003	0.0001	2.77	**
D	14	0.002	0.0000	1.42	*ns*
ED	28	0.001	0.0000	0.97	*ns*
ND	14	0.001	-0.0001	0.60	*ns*
TD	14	0.002	0.0001	1.46	*ns*
END	28	0.002	0.0001	1.29	*ns*
ETD	28	0.001	0.0000	1.08	*ns*
NTD	14	0.001	-0.0001	0.65	*ns*
ENTD	28	0.002	0.0002	1.35	*ns*
RNTD:E	167	0.001	0.0012		
Total	359				
h^2		0.38 - **0.31** - 0.63			

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, N nitrogen level, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval

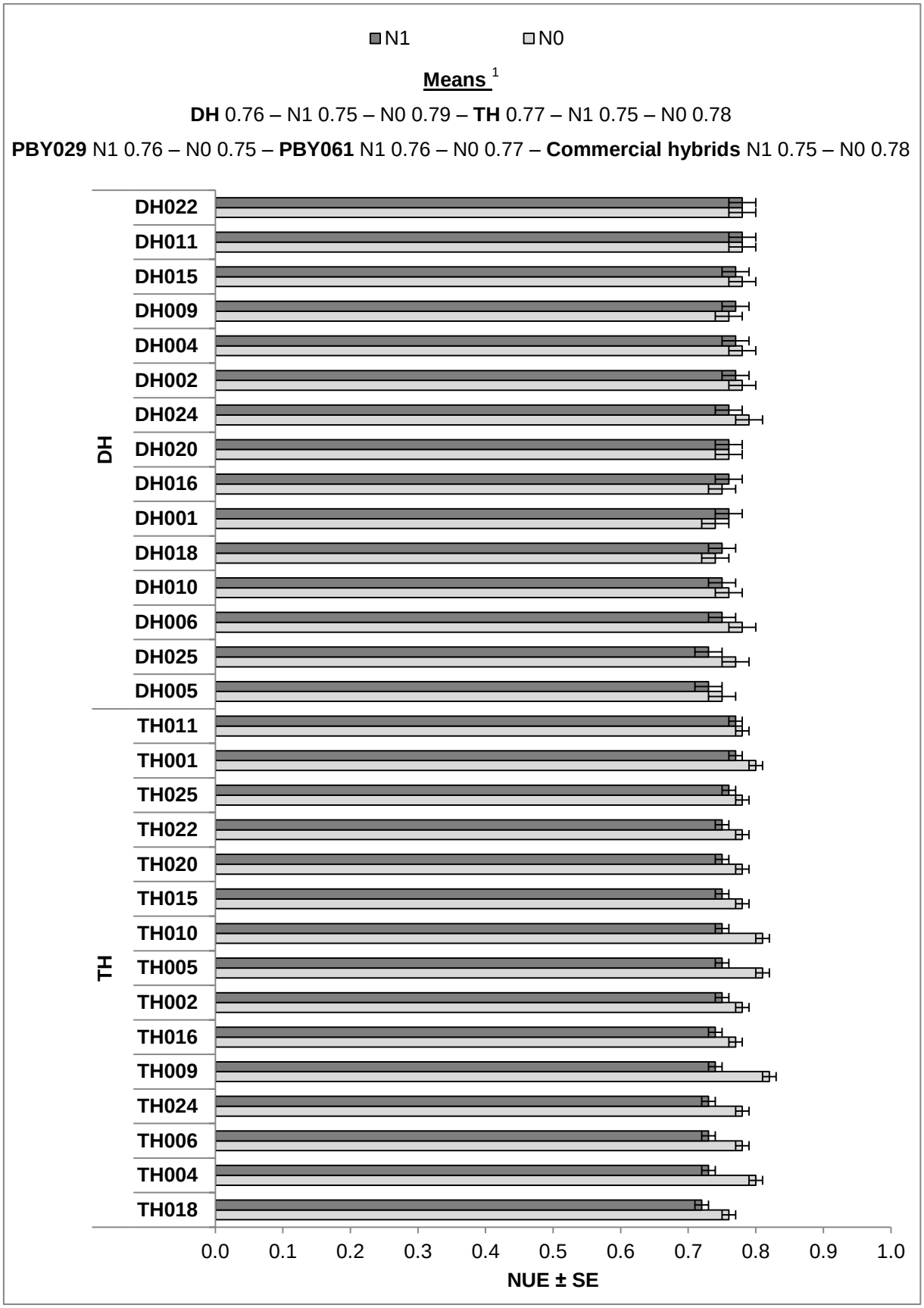

Fig. A 39: NHI of Pop029
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, [1] Means for DH and TH across both nitrogen levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0

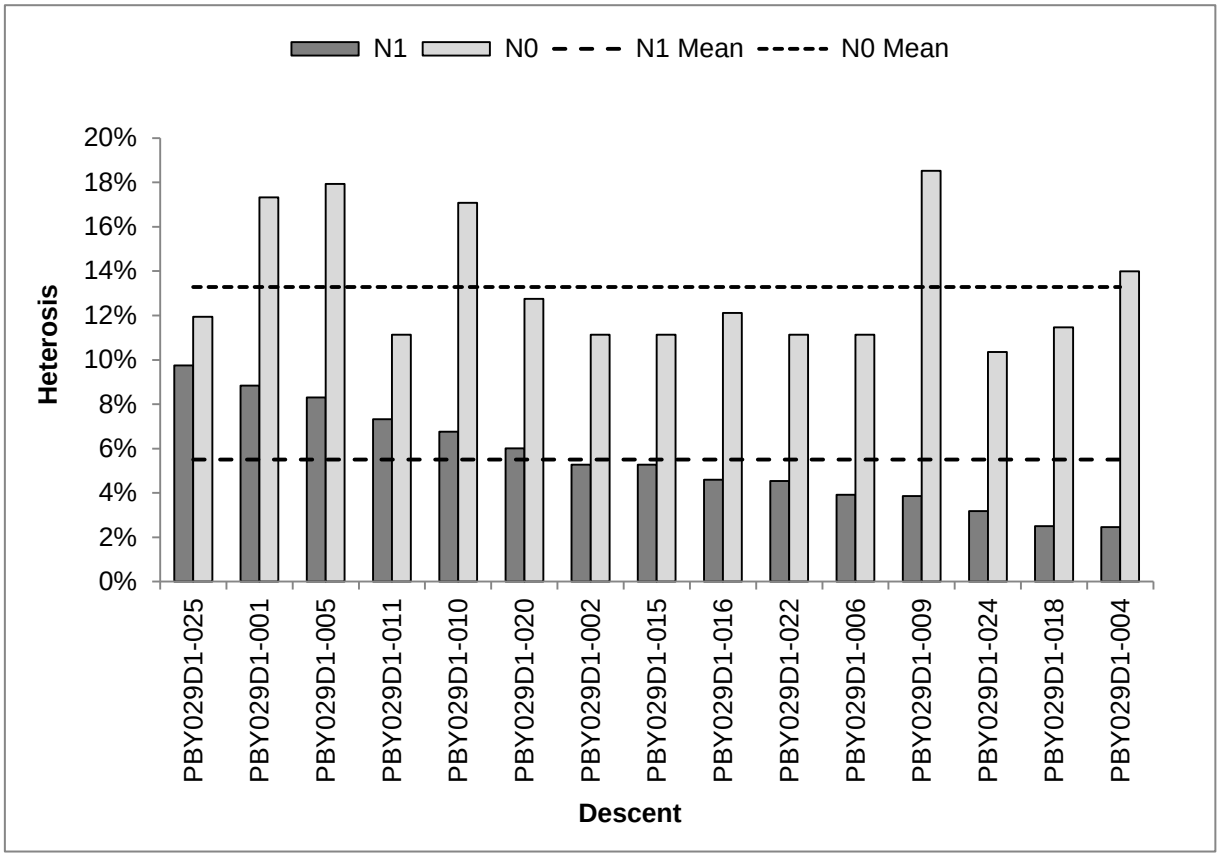

Fig. A 40: Heterosis for NHI of Pop029
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

Contribution of $NupEff_{MAT}$ and NutEff to NUE

For both variety types and at both nitrogen levels variance of $NupEff_{MAT}$ contributes to a higher portion to variance of NUE. This portion was higher at N0 and also higher for test hybrids than for DH lines (Fig. A 41).

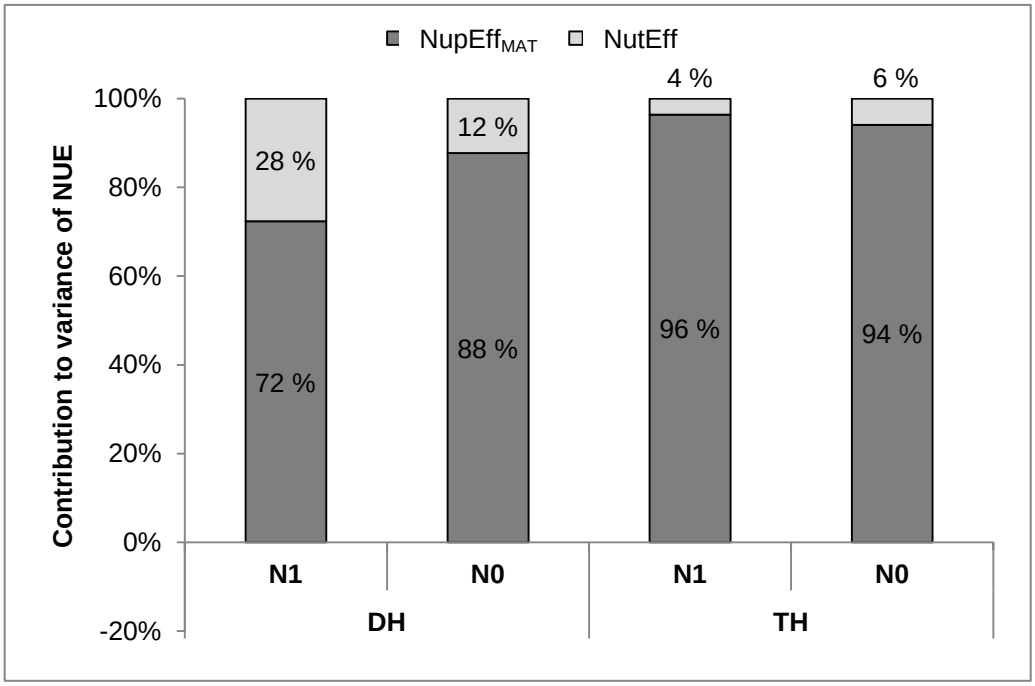

Fig. A 41: Contribution of variances of $NupEff_{MAT}$ and NutEff to variance of NUE of Pop029

Discussion

Diversity set

Significant genetic variation was observed for $Yield_{EOF}$, Nup_{EOF}, $NupEff_{EOF}$, Seed 9%, Nup_{MAT}, $NupEff_{MAT}$, NutEff, NUE, NHI and Delta Nup. All traits besides $NupEff_{MAT}$ and Delta Nup ($h^2 = 0.67$) showed heritabilities above 0.80. Except Delta Nup the traits were significantly affected by nitrogen level. $Yield_{EOF,}$ Nup_{EOF}, Seed 9% and Nup_{MAT} were higher at N1 while $NupEff_{EOF}$, $NupEff_{MAT}$, NutEff, NUE and NHI were higher at N0. Interactions between genotype and nitrogen level were significant for all traits except for $NupEff_{MAT}$. The significant genetic variation and high heritabilities enable successful selection for nitrogen efficiency and related parameters. The genotype by nitrogen level interaction for most traits suggests the selection of environments that resemble target environments especially with regards to nitrogen supply. The results of the current study are supported by previous studies that also showed significant genetic variation for seed yield and nitrogen efficiency parameters and their dependence on genotype by nitrogen level interactions when genotypes were tested without and with high nitrogen fertilisation (Berry et al. 2010, Kessel et al. 2012, Nyikako et al. 2014). But also when a third, medium nitrogen level was included, a significant interaction between genotype and nitrogen level was observed (Möllers et al. 2000, Schulte auf'm Erley et al. 2011).

A significant genotype by nitrogen level interaction means that a genotype which performed well at one nitrogen level did not necessarily performed well at another one. This indicates that to some extent different loci are responsible for trait expression at different nitrogen levels. This is supported by studies that analysed quantitative trait loci (QTL) of oilseed rape at different levels of nitrogen supply. Gül (2003) analysed QTL for pod length, number of seed per pod and thousand kernel weight at two contrasting levels of nitrogen supply in a DH population with 142 lines. For pod length no QTL were identified at low nitrogen supply while three were detected at high nitrogen supply. One QTL for number of seeds per pod was detected at both nitrogen levels while one appeared only at high and another one only at low nitrogen supply. For thousand kernel weight three QTL were found at both

nitrogen levels and one solely at high and another one solely at low nitrogen supply. Bouchet et al. (2014) examined two mapping populations at two levels of nitrogen supply to determine genomic regions associated with oil yield. In total 191 QTL were reported among them 96 identified at high and 77 at low nitrogen supply.

As in the current study higher NHIs at lower nitrogen supply were observed by Behrens (2002) and Schulte auf'm Erley et al. (2011). An increased remobilisation from shoot nitrogen to pods and seeds with decreasing nitrogen supply as reported by Ulas et al. (2013) is a possible explanation for higher NHI at low nitrogen levels. A high NHI is of special interest with regards to EU nitrate directive as this means that more nitrogen is removed from fields with harvested seeds and less nitrogen is left with straw and silique debris. In the current study genotypes were detected with high NHIs at both nitrogen levels, e.g. PBY028.

In the current study nitrogen accumulation between end of flowering and maturity was described by Delta Nup. At N1 a slight nitrogen loss was observed across all genotypes. But next to genotypes that lost up to 30 kg N ha^{-1} there were ones that showed a positive Delta Nup of maximum 24.5 kg N ha^{-1} (Fig. A 12). At N0 Delta Nup was positive across all genotypes i.e. nitrogen was taken up between end of flowering and maturity. Similar results were reported by other authors (Aufhammer et al. 1994, Schjoerring et al. 1995, Schulte auf'm Erley et al. 2011). In contrast to other traits total variance of Delta Nup was to a high degree explained by genotype and interaction between genotype by nitrogen level and only little by nitrogen level (Tab. A 16). A prolonged nitrogen uptake might increase recovering of fertiliser nitrogen by the crop. This combined with a high NHI could help to reduce the amount of nitrogen that remains on the field after harvest.

Concerning the reduction of nitrogen fertiliser input and thereby reduction of greenhouse gas emissions genotypes with high NUE may be interesting as they produce the high seed yields at a given nitrogen level. Especially at N0 some outstanding genotypes could be identified, e.g. PBY023, PBY061, PBY029, PBY015.

With respect to seed yield genotypes that show high performance at one and/or the other nitrogen level are of interest for rapeseed breeders. Interesting genotypes of the current study might be PBY023 or PBY015 which produced high seed yields N1 and N0.

Variance of nitrogen use efficiency was mainly affected by variance of nitrogen utilisation efficiency at both N1 and N0. This is in contrast to other studies that found nitrogen uptake efficiency to be more important particularly at N0. Importance of nitrogen utilisation efficiency increased at higher nitrogen levels and became more important within some environments (Kessel et al. 2012, Nyikako et al. 2014). The contradicting results may result from different genetic background used in different studies. Kessel et al. (2012) tested hybrids, old and new lines and resyntheses while mainly line varieties were tested in the current study.

DH lines and test hybrids

Both populations showed similar results concerning analyses of variance. Seed 9%, Nup_{MAT}, $NupEff_{MAT}$, NutEff and NUE showed significant variation among descents (pairs of DH line and descending test hybrid) and significant interaction between descent and variety type. Heritabilities ranged from 0.66 to 0.82. NHI was not significantly affected by descent and interaction between descent and variety type. It revealed lowest heritabilities in both populations – h^2 0.46 for Pop007 and h^2 0.31 for Pop029 (Tab. A 22, Tab. A 28). Most traits were not affected by nitrogen level or variety type. Only $NupEff_{MAT}$ of Pop007 and NUE of both populations were significantly higher at N0 than at N1. Significant differences between DH lines and test hybrids were observed only for NutEff and NUE in Pop007 – both higher for test hybrids than for DH lines. Interactions between nitrogen level and variety type and between nitrogen level and descent were not significant for any trait.

It was unexpected that variety type did not have a significant effect on most traits as hybrids are expected to outperform pure lines as observed for nitrogen utilisation efficiency and nitrogen use efficiency of Population 007. Leon (1991) found F1 hybrids producing 15 % higher seed yields than line varieties. Friedt et al (2003) tested line varieties, hybrids, DH lines and semi-synthetics at three nitrogen levels. They observed higher seed yield for hybrids at all nitrogen levels. But the difference between hybrids and line varieties decreased with decreasing nitrogen supply. Budewig & Leon (2003) also reported hybrids to outperform line varieties in seed and oil yield in official variety trials in Germany. Furthermore, they reacted stronger to favourable conditions. Gehringer et al. (2007) examined seed yield of test hybrids and parental DH lines in two contrasting environments. In the unfavourable

environment all test hybrids outperformed their parents while in the favourable environment this was not the case for each test hybrid. Nitrogen efficiency of hybrids, lines and semi-dwarfs was analysed at two nitrogen levels by Koeslin-Findeklee et al. (2014). Grain yield and nitrogen utilisation efficiency were higher for hybrids at both nitrogen levels. But hybrids showed higher nitrogen uptake and higher NHI only at N0.

Heterosis was examined to test the advantage of hybrids over their parents. Positive mid-parent heterosis at both nitrogen levels was detected for seed yield, nitrogen utilisation efficiency, nitrogen use efficiency and nitrogen harvest index. Hybrids exceeded parental mean of nitrogen uptake and nitrogen uptake efficiency at N1 but at N0 the heterosis was negative i.e. hybrids performed worse than parental mean. Gehringer et al. (2007) also observed individual hybrids performing worse than the parental mean with regards to seed yield.

When comparing N1 and N0, there was no general pattern of heterosis. For seed yield, nitrogen uptake, nitrogen uptake efficiency and nitrogen use efficiency heterosis was higher at N1 than at N0. But for nitrogen utilisation efficiency and nitrogen harvest index higher heterosis was expressed at N0.

The heterosis might have been biased by the usage of the male sterile form of the hybrid mother when calculating mid-parent heterosis. Thus, incomplete pollination should be considered. This is supported by the lower seed yield of the sterile mother compared to the DH lines. It is also possible that the hybrid mother performes generally worse than the DH lines – independently from its ability to produce fertile pollen.

Although variety type and nitrogen level were not significant seed yield was higher for test hybrids and higher at N1 than at N0. The difference between N1 and N0 was higher for test hybrids. This is in accordance to the results of Budewig & Leon (2003) and Friedt et al. (2003) who found decreasing differences in seed and/or oil yield between lines and hybrids with decreasing nitrogen supply and stronger reactions of hybrids to changing levels of nitrogen supply.

In both populations the variance of nitrogen uptake efficiency contributes to a higher portion to variance of nitrogen use efficiency than nitrogen utilisation efficiency. At N0 nitrogen uptake efficiency was more important than at N1. Nitrogen uptake efficiency

contributed to a higher portion to variance of nitrogen use efficiency of test hybrids than to that of DH lines. The importance of nitrogen uptake efficiency particularly at N0 is in accordance with findings that reported nitrogen uptake efficiency contributed to higher portion to variance of nitrogen use efficiency than nitrogen utilisation efficiency particularly at low nitrogen supply. Importance of nitrogen utilisation efficiency increased at higher nitrogen levels (Kessel et al. 2012, Nyikako et al. 2014). Nevertheless, the very high proportion of variance of nitrogen uptake efficiency of test hybrids (Fig. A 28, Fig. A 41) must be substantiated by further testing.

DH lines and test hybrids were only tested in one season which was characterised by a warm winter and early spring. That may have resulted in a shorter growth pause and continuous nitrogen uptake during autumn and winter but also in an earlier start of vegetative growth after winter pause and enhanced nitrogen uptake in spring. Therefore, the results are only preliminary and require further confirmation.

Conclusion

The significant genetic variation and high heritabilities observed in experiments with the diversity set support the conclusion that nitrogen efficiency of winter oilseed rape can be improved by breeding. Genotype by nitrogen level interactions affected nearly all traits, thus selection environments should resemble target environment especially with regards to nitrogen supply.

The current study did not reveal significant differences between DH lines and test hybrids. Nonetheless, positive heterosis was detected for nearly all traits but nitrogen uptake and nitrogen uptake efficiency at N0. As the season in which DH lines and test hybrids were grown was characterised by an unusual warm winter and early spring the current results are only preliminary and need to be confirmed in further trials.

CHAPTER B - HYPERSPECTRAL CANOPY REFLECTANCE AS PREDICTION TOOL FOR NITROGEN EFFICIENCY PARAMETERS OF WINTER OILSEED RAPE

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Introduction

Oilseed rape is the third most important oilcrop worldwide (USDA 2015). But it suffers from low nitrogen efficiency (Sylvester-Bradley & Kindred 2009). Legislative regulations have moved nitrogen efficiency of winter oilseed rape into focus of plant breeders. But this is a difficult trait to assess. Seeds and straw need to be harvested and analysed for nitrogen content. This is laborious and time consuming. Indirect selection methods would facilitate selection for nitrogen efficiency and allow its implementation in breeding programs. Nitrogen efficiency is directly related to nitrogen uptake and seed yield. Different definitions of available nitrogen lead to different results for nitrogen uptake efficiency, nitrogen utilisation efficiency and nitrogen use efficiency. Therefore, nitrogen uptake and seed yield rather than nitrogen efficiency should be predicted by hyperspectral canopy reflectance.

Electromagnetic radiation

Hyperspectral canopy reflectance measures electromagnetic radiation. Therefore, some information about electromagnetic radiation and its interaction with atmosphere and vegetation will be given in the following.

Electromagnetic spectrum

Different types of electromagnetic waves can be distinguished according to their wavelengths – gamma rays about 0.01 nm, X-radiation 0.01 nm to 10 nm, ultraviolet light (UV) 10 nm to 400 nm, visible light (VIS) 400 nm to 700 nm, infrared radiation (IR) 700 nm to 1,000,000 nm, microwaves 1,000,000 nm to 1,000,000,000 nm and radio waves from 1,000,000,000 nm to more than 10,000,000,000 nm. Within the UV range UV-B ranges from about 280 nm to 325 nm and UV-A from 325 nm to 400 nm. The human eye is sensitive to the VIS range which can be further divided into violet (400 nm to 450 nm), blue (450 nm to 500 nm), green (500 nm to 550 nm), yellow (550 nm to 600 nm), orange (600 nm to 650 nm) and red light (650 nm to 700 nm). Within the IR range near-infrared (700 nm to 1,000 nm), mid-infrared (1,000 nm to 4,000 nm) and far-infrared (4,000 nm to 1,000,000 nm) are distinguished. Of special

interest for the current study are the VIS and NIR range. If not stated otherwise the following paragraphs concern these ranges.

Radiation and matter

When radiation encounters a boundary it can pass the body/substance (transmittance) or it can be absorbed or reflected (Albertz 2001, Jones & Vaughan 2010 a). The proportions of energy that are transmitted, absorbed or reflected depend on the wavelength and on properties of matter. Absorbance describes the retention of electromagnetic energy. Reflection appears when radiation is redirected. The way reflectance takes place depends on surface properties. A surface is smooth when irregularities do not exceed one eighth of the wavelength of incoming radiation. It is rough when irregularities exceed one eighth of the wavelength. Specular reflectance appears on smooth surfaces. Radiation is reflected in a beam. The angle in which the radiation is reflected is the same as the angle of incidence. When the encountered surface is rough radiation is scattered (diffuse reflectance). Each irregularity of the surface presents a different angle to incoming radiation so that reflection appears in a cone of angles. Most natural surfaces do not scatter radiation equally in all directions. Instead reflection is enhanced at some places and reduced at others. The portion of light which is reflected (or emitted) can be captured by a sensor. Radiation that leaves a body/substance contains information about it.

Radiation and atmosphere

On its way from source to target and from target to sensor radiation passes the atmosphere and interacts with it (Albertz 2001, Jones &Vaughan 2010 a). Radiation can be absorbed or scattered by atmospheric aerosols or gases or reflected by clouds. Atmosphere attenuates radiation. The extent depends on wavelength, concentration, size and properties of gases and aerosols. Main absorbers in the atmosphere are carbon dioxide, water vapour, oxygen and ozone. But not each wavelength is absorbed to the same extent (Tab. B 1).

Tab. B 1: Atmospheric absorption wavelengths in the visible to mid-infrared range

Wavelengths	Absorbed by	Extent
200 - 300 nm	O_2, O_3	Completely
600 - 700 nm	O_2,O_3	Attenuated
800 nm	H_2O, O_2, O_3	Attenuated
950 nm	H_2O	Attenuated
1100 - 1200 nm	H_2O	Attenuated
1400 - 1500 nm	H_2O, CO_2	Completely
1800 nm	H_2O, CO_2	Completely
2700 nm	H_2O, CO_2	Completely

Completely wavelengths are completely absorbed, Attenuated wavelengths are not completely absorbed but only attenuated, According to Jones & Vaughan (2010 a)

Wavelengths in the VIS and NIR range are scattered when they meet smaller atmospheric molecules like oxygen, ozone or nitrogen but also when they encounter vapour or dust. The scattered portion can be added back to radiation before or after it meets the target. Two consequences can be drawn from the knowledge about atmospheric scattering – cloudy conditions are disadvantageous and shorter wavelengths should be avoided. But the signal-to-noise ratio is better for shorter than for longer wavelength and therefore, shorter wavelengths are to be preferred.

Radiation and characteristics of leaves and canopies

The interaction of radiation and leaves is determined by radiation and leaf characteristics (Gausman 1974, Albertz 2001, Sims & Gamon 2002, Gitelson et al. 2003, Jones & Vaughan 2010 a, Jones & Vaughan 2010 b). Structural and chemical characteristics as chemical compounds, leaf age, thickness, structure and water content interact differently with different wavelengths. Spectral properties of leaves are also determined by density of individual tissues, epidermal waxes, internal air spaces and pigments. All these are not stable characteristics but are affected by plant growth, development and environmental conditions. In general reflectance and transmission are low in VIS but high in NIR range.

Effects of chemical composition of leaves

Spectral properties of VIS range are affected by chlorophyll, carotenoids and anthocyanins. Properties of NIR are mainly determined by water, nitrogen, proteins, lignin, cellulose and oil (Tab. B 2) (Albertz 2001, Sims & Gamon 2002, Gitelson et al. 2003, Jones & Vaughan 2010 b).

Tab. B 2: Absorption of visible to mid-infrared wavelengths by chemical leaf compounds

Compound	Absorbed wavelengths
Chlorophylls	430 nm, 460 nm, 640 nm, 660 nm
Carotenoids	400 - 500 nm
Xanthophylls	460 - 550 nm
Water	970 nm, 1200 nm, 1450 nm, 1950 nm, 2500 nm
Nitrogen and Proteins	1510 nm, 2180 nm, 910 nm, 1020 nm, 1690 nm, 1940 nm, 1980 nm, 2060 nm, 2130 nm, 2240 nm, 2300 nm, 2350 nm
Lignin	1690 nm, 1120 nm, 1420 nm, 1940 nm
Cellulose	1780 nm
Oil	2310 nm, 930 nm, 1020 nm

Underlined wavelengths are strongly absorbed, According to Jones & Vaughan (2010 b)

Effects of leaf and canopy structure

Most wavelengths of NIR range are not affected by chemical leaf composition but by internal leaf structure. The leaf structure of dicotyledons is characterised by a dense palisade layer on the upper surface followed by a porous spongy-mesophyll tissue. Particularly the latter contains not only cells but also intercellular air spaces. Radiation can be reflected or scattered by the leaf surface – depending on its smoothness/roughness. Wavelengths that enter the leaf can be absorbed by leaf compounds as described above or they can be scattered or transmitted. Scattering takes place at boundaries where structural components have different refractive indices (n) – air n = 1.00, water n = 1.33, hydrated cell walls n = 1.40. Such boundaries are present at the surface of the leaf and at interfaces between cells and intercellular spaces (Gausman 1974, Jones & Vaughan 2010 b).

Reflectance and scattering not only depends on structure of individual leaves but also on canopy structure and architecture. The processes in canopies are similar to those within the leaf. Radiation can be directly reflected back to the atmosphere or be involved in secondary, tertiary or higher reflections where soil may be involved to some extent (Jones & Vaughan 2010 b).

Radiation which is not transmitted or absorbed by leaves and/or canopy is reflected and can be captured by optical sensors. The captured radiation delivers chemical and structural information about the canopy but is also affected by atmospheric scattering and absorption on its way from the target to the sensor.

Prediction of leaf and canopy properties by reflectance

Many studies were conducted that examined the relation between leaf and canopy properties to reflectance. Among the examined properties of leaves and canopy were pigment concentrations and leaf structure, but also nitrogen status of plants, yield and reaction to abiotic stress.

Gausman (1974) reported the effect of leaf structure on reflectance of wavelengths from 750 nm to 1350 nm. Structure was related to age, stress and species. Young and mature leaves and stressed and non-stressed plants were compared within a species as well as leaves of different species differing in structure. Mesophyll of young citrus leaves is compact with few air spaces while mesophyll of mature leaves contains many air spaces and thereby, more cell wall/air interfaces. Higher reflectance was observed for mature than for younger leaves, i.e. for structures with many cell wall/air interfaces than for compact structures. Leaves of salinity stressed cotton plants show a more stunted and compact appearance and delayed growth. When comparing stressed and non-stressed leaves sampled at the same day after planting stressed leaves showed higher reflectance than non-stressed ones. When the chronological age was taken into consideration stressed plant showed lower reflectance because of their stunted and compact structure.

The effect of structure was also confirmed by the comparison of corn leaves characterised by compact mesophyll with maple leaves characterised by more porous mesophyll. The first showed low reflectance and high transmittance while reflectance was higher and transmittance lower for the latter. Sims & Gamon (2002) examined leaf pigment contents across species, leaf structures and developmental stages and their relation to reflectance from 350 nm to 1100 nm. They found leaf chlorophyll content best correlated to reflectance of 705 nm and only weak correlated to reflectance of 680 nm and 800 nm. Gitelson et al. (2003) analysed leaf chlorophyll content and spectral reflectance from 400 nm to 800 nm of three tree species and vine. Reflectance from 400 nm to 500 nm was affected by chlorophyll and carotenoid content. With increasing chlorophyll content the reciprocal reflectance of 530 nm and about 700 nm also increased. Coefficients of determination (R^2) for the relation

between chlorophyll content and reciprocal reflectance were minimum for 400 nm to 500 nm and 680 nm. This was explained by the non-linearity of the relationship. The wavelengths were sensitive at chlorophyll concentrations below 150 µmol m^{-2} but above 150 µmol m^{-2} a saturation of sensitivity was observed. A linear relationship between chlorophyll content and reciprocal reflectance was detected for 510 nm to 620 nm and near 700 nm with R^2 above 0.90.

Thenkabail et al. (2000) analysed hyperspectral canopy reflectance under field conditions from 350 nm to 1050 nm of cotton, potato, soybean, corn and sunflower and its relation to crop variables like fresh biomass and yield. Depending on wavelength and crop correlation coefficients from -0.75 (cotton, around 680 nm) to 0.83 (soybean, 825 nm) were found when single wavebands were used for prediction. For the relation between reflectance and cotton yield coefficients of determination from 0.52 (954 nm) to 0.77 (combination of 525 nm, 582 nm, 668 nm and 968 nm) were found, depending on the wavelengths and number of wavelengths used for prediction. Crop variables showed strong relationship to reflectance of 500 nm to 550 nm, 650 nm to 700 nm, 720 nm, 845 nm and 900 nm to 940 nm. Read et al. (2002) examined the relation of nitrogen status of cotton to reflectance from 350 nm to 950 nm on leaf and canopy level. Higher R^2 were identified on canopy level than on leaf level. For total leaf chlorophyll content a maximum R^2 of 0.75 was found when reflectance of 415 nm and 695 nm was used for prediction. Total leaf nitrogen concentration could be predicted best when reflectance of 415 nm and 710 nm was used (R^2 0.70). This is due to the close relation between chlorophyll and nitrogen content. Ferrio et al. (2005) developed calibrations to predict yield of durum wheat by means of canopy reflectance from 400 nm to 1000 nm. Durum wheat was grown at low, medium and high nitrogen supply. Reflectance was measured at anthesis and milk-grain stage. The authors observed R^2 from 0.20 to 0.81 for calibration and from 0.16 to 0.74 for prediction. Calibration and prediction worked better at low and medium nitrogen supply than at high nitrogen supply. Canopy reflectance and properties of oilseed rape and barley were examined by Behrens et al. (2006) in three years field experiment with one variety per species at low and high nitrogen supply. In oilseed rape correlation between reflectance and shoot nitrogen uptake was highest when reflectance of 858 nm and 1240 nm were used (r = 0.63). In barley the usage of reflectance of 850 nm resulted in the highest correlation coefficient (r = 0.85). Shoot nitrogen content of oilseed rape and its predictability by

canopy reflectance was also examined by Müller et al. (2008). Highest R^2 were detected when reflectance of 780nm, 750 nm and 740 nm were used (R^2 = 0.82). Erdle et al. (2011) analysed biomass and nitrogen status of wheat and its relation to canopy reflectance of 400 nm to 1000 nm at different growth stages across six varieties. For grain yield significant correlations were observed when reflectance of 670 nm, 700 nm, 740 nm and 780 nm were combined (r = 0.63, r = 0.73).

Vegetation indices or multivariate regression

Reflectance of a crop stand can be used in several ways to predict its agronomic characteristics. On the one hand, one can use few wavelengths combined in so-called vegetation indices for prediction, e.g. reflectance of single wavelengths, simple ratio where reflectance of one wavelength is divided by reflectance of another one, normalized indices where the difference between reflectance of two wavelengths is divided by their sum. On the other hand, one can use all spectral information captured. Thenkabail et al. (2000) mostly found better predictions for fresh biomass and yield with stepwise regression than with combinations of two wavelengths (R^2 0.80 vs. 0.76, corn R^2 0.78 vs. 0.71, yield: cotton R^2 0.77 vs. 0.64). Read et al. (2002) reported increasing R^2 for the prediction of leaf nitrogen concentration with increasing number of wavelengths used for prediction – from R^2 0.36 with one wavelength to R^2 0.92 with seven wavelengths. Li et al. (2014) compared vegetation indices with multivariate regression to predict nitrogen content in wheat. Higher R^2 were reported for multivariate regression (R^2 0.75 – 0.90) than for vegetation indices (R^2 0.24 – 0.69).

Therefore, the current study applied multivariate regression for prediction.

Multivariate regression

Multivariate regression aims to model the relationship between several independent variables and dependent variables (Kessler 2007, Esbensen 2012). In a classical approach the independent reference values (x_i) and the dependent measured values (y_i, e.g. spectra) are used to develop the calibration model. The error of reference values is assumed to be close to zero. This is not true for multivariate data. Both, x

and y values, contain errors. Therefore, the calibration function is computed inverse, i.e. measured values (spectral data) are defined as independent X matrix and reference values (physiological/agronomic traits) as dependent Y matrix. The difference between the classical and the inverse approach lies in the way the error (or residual) is minimised. The error is always minimised in direction of the dependent variable. In the classical approach this is spectral data whereas it is the physiological/agronomic trait in the inverse approach. In the current study physiological/agronomic traits were considered as dependent y-variable and spectral data as independent x-variable. Multivariate regression consists of calibration and validation.

Calibration by partial least squares regression (PLSR)

Calibration is the step in which a model is developed that is to be used for prediction (Kessler 2007, Esbensen 2012). A calibration dataset is used to develop a regression model. It consists of a X matrix with independent variables and a corresponding Y matrix with dependent variables. Two problems arise when spectra are used for prediction. They may contain more than thousand wavelengths and neighboured wavelengths within a spectrum are correlated. **P**artial **L**east **S**quares **R**egression (PLSR) reduces the multiple independent variables of the X matrix to few PLSR components. At the same time it also considers eventual relations between independent x variables and dependent y variables. PLS can be conducted with one (PLS1) or more (PLS2) y variables. Two simultaneous principal component analyses are conducted simultaneously but not independent from each other (Fig. B 1). The Y matrix is decomposed in scores matrix (U) and loadings matrix (C). The X matrix is decomposed in scores matrix (T) and loadings matrix (P). The P matrix is not computed directly but by means of an intermediate W matrix. This W matrix forms the connection to y data and contains weighted loadings. The PLSR components are computed in a way that information of X and Y matrix are exchanged.

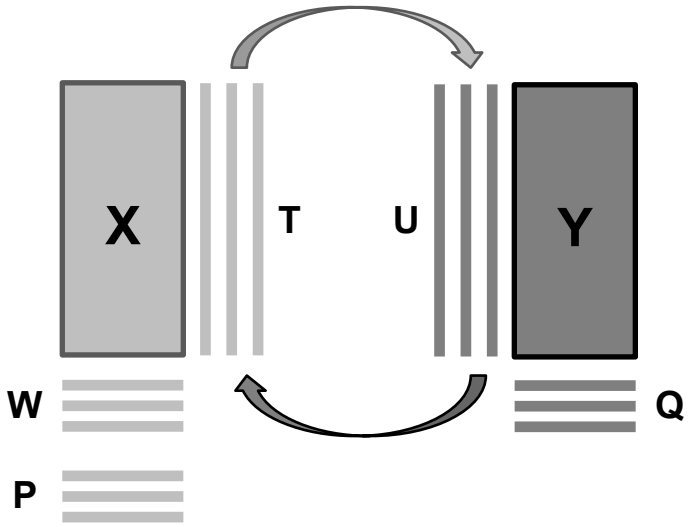

Fig. B 1: Principle of Partial Least Square Regression with more than one y variable (PLSR2) and matrices
X matrix of independent variables, T scores matrix of X, W loading weights matrix of X, P loadings matrix of X, Y matrix of dependent variables, U scores matrix of Y, Q loadings matrix of Y, arrows represent exchange of information when computing PLSR components (Kessler 2007)

The PLSR components are computed with the **N**onlinear **I**terative **PA**rtial **L**east **S**quare algorithm (NIPALS). NIPALS is an iterative process which computes PLSR components one by one (Kessler 2007, Esbensen 2012). For each component it starts with a random solution which is improved until a given threshold of improvement is achieved. In a first step variables are mean centred. NIPALS then starts with one vector of the X matrix (or of the Y matrix in case of PLSR) – preferably the one with highest variance. This is assumed as the first scores vector. Its corresponding loadings vector is estimated. To improve the estimation of the first scores vector a second scores vector is computed by means of the loading vector. The first and the second scores vectors are com-pared. If the difference between second and first vector is less than the convergence criterion scores and loadings vector are accepted to describe the first component. If the difference is larger than the convergence criterion a new iteration starts with the estimation of a new loadings vector. When the first component is defined, its information is removed from data before the next component is computed as described above.

In the following only details for PLS1 are given as this was the method used in the current study. It can be seen as special case of PLS2 (Kessler 2007, Esbensen 2012). PLS1 models one y variable. Hence the Y matrix (Fig. B 1) is reduced to a y vector. Instead of using many u vectors this y vector is used to compute PLSR

components. It presents the starting point to decompose X data in PLSR components. The first PLSR component is indexed with c. The estimation of t_c scores of the X matrix bases on the y_c vector. For each component a local model is defined e.g. for the first component it is:

$$X_c = y_c w_c^T + E$$

The influence of the y vector may result in a change of direction of X loadings (P). Therefore the weighted loadings w are computed. They need to be orthogonal to each other. The weighted loadings explain the relation between X and y. The covariance between y_c and $X_c w_c$ is to be maximised, i.e. error E is minimised. Therefor the least squares criterion is applied. The least squares solution for w is:

$$w_c = (X_c^T y_c)(|X_c^T y_c|)^{-1}$$

Now t_c scores are computed by applying the least squares criterion to the local model. That results in:

$$t_c = X_c w_c$$

This is followed by calculation of p loadings:

$$p_c = (X_c^T t_c)(t_c^T t_c)^{-1}$$

Afterwards the q_c loadings vector of y is computed using the t_c vector of X:

$$q_c = (t_c^T y_c)(t_c^T t_c)^{-1}$$

Herewith the first PLSR component is known and must be removed from x and y data before computing the second component. After computing C_{max} components information remains that is not explained – residual variance of x and y variables. With the estimated loadings the regression coefficients (b, b_0) can be computed:

$$b = W(P^T W)^{-1} q \qquad \text{and} \qquad b_0 = y_{Mean} - x_{Mean}^T b$$

Unknown samples (y_i) can be predicted by means of corresponding measured values (x_i, e.g. spectra) with the regression coefficients:

$$y_i = b_0 + x_i^T b$$

The optimum number of PLSR components can be found by validation. It is the number which leads to minimum error in validation. Instead of having as many x variables as wavelengths in the spectra the x data space is reduced to a small number of PLSR components that explains most of the variance and leads to minimum error of validation.

Validation

Validation analyses the calibration model with regards to its ability to describe the relation between independent and dependent variables and with regards to its applicability to new, unknown data (Kessler 2007, Esbensen 2012). Calibrations can be validated internally or externally. In **leverage correction** the leverage describes the influence of a sample to the model. It is related to the distance of a sample from the centre of the model. Samples with high distance to the centre affect the model to a high extent whereas samples close to the centre only have little influence. The estimates for prediction errors of individual samples are corrected for this leverage before squaring and summing to the mean squared error. Errors for samples with high leverage are reduced to less extent than errors of samples with low leverage. In **cross validation** every sample is used for calibration and validation but not simultaneously. The calibration data set is divided into subsets (segments). One subset is removed from calibration. The others are used to develop a calibration model. In the following the removed subset is predicted with this model and residuals are computed. The procedure is repeated until all subsets have been removed from calibration development once, i.e. were used for validation once. For all predicted samples the difference between predicted and measured trait value is used to compute the residual and the root mean square error of validation. There are several ways to make up the segments. Number of segments (S) ranges from two to N where N is the total number of samples (S fold cross validation). Samples can be randomly or systematically assigned to segments. In **external validation** different data sets are used for calibration and validation. The validation set should represent the data space of the calibration set.

Evaluation of calibration and validation

To evaluate calibrations and validations following parameters can be used – coefficient of determination of calibration (R^2_{Cal}) and cross validation (R^2_{Val}), root mean square error of calibration ($RMSE_{Cal}$), cross validation ($RMSE_{Val}$) and external validation ($RMSE_{EV}$) and bias of calibration ($Bias_{Cal}$) (Kessler 2007, Esbensen 2012).

The **coefficient of determination R²** expresses the ratio between the proportion of variance explained by predicted values and total variance (variance of observed trait values):

$$\mathbf{R^2 = \sum(y_{P,i} - y_{P,M})^2 \, (\sum(y_{R,i} - y_{R,M})^2)^{-1}}$$

$y_{P,i}$ = Predicted trait value

$y_{P,M}$ = Mean of predicted trait values

$y_{R,i}$ = Observed (reference) trait value

$y_{R,M}$ = Mean of observed (reference) trait values

The coefficient of determination ranges from 0 to 1 and should be as high as possible. An R² of 1 means that the predicted values equal the reference values i.e. there is no unexplained variance and therefore no residuals.

The **root mean square error RMSE** is an expression of the modelling error in calibration or of the prediction error in validation. It is the average deviation of observed values from the regression line:

$$\mathbf{RMSE = [(\sum(y_{R,i} - y_{P,i})^2) \, n^{-1} \,]^{-1/2}}$$

$y_{R,i}$ = Observed (reference) trait value

$y_{P,i}$ = Predicted trait value

n = Number of samples used to develop calibration

RMSE is expressed in trait units and should be as low as possible.

The **bias** is a systematic difference between observed and predicted values. It is computed as the averaged difference between observed and predicted trait values, i.e. the mean of all residuals:

Bias = $(\sum(y_{R,i}-y_{P,i}))\ n^{-1}$

$y_{R,i}$ = Observed (reference) trait value

$y_{P,i}$ = Predicted trait value

n = Number of samples used to develop calibration

For calibrations it should be close to zero.

A good calibration shows a high R^2 in calibration and validation, a small RMSE for calibration and validation and a bias close to zero for calibration and a small bias for validation.

Pre-treatment of spectral data

Spectral data is not only affected by the measured target but also from interactions between radiation and surroundings (Albertz 1991, Jones & Vaughan 2010 a, Jones & Vaughan 2010 b). It also contains noise that derives from the spectrometer itself. In order to correct the spectral signal for these influences, several pre-treatment procedures are available (Kessler 2007, Esbensen 2012)**.** The ones applied in the current study are described in the following.

Baseline offset correction (Base)

Baseline offset correction corrects the spectrum for systematic deviations from the baseline. For the spectrum of each plot the absorption of the lowest point is subtracted from all other wavelengths in the spectrum:

f(x) = x – min X

x = Absorption of a certain wavelength

X = All absorptions of the spectrum

min = Minimum

The point with minimum absorption is set zero whereas all other wavelength show positive absorption.

Standard normal variate transformation (SNV)

SNV is applied to correct spectra for effects caused by multiplicative interferences of scatter and effects of particle size. Each spectrum is centred and scaled to its mean and standard deviation:

$$x_{i,SNV} = (x_i - x_M)\ (\sigma_x)^{-1}$$

x_i = Absorption of wavelength i

x_M = Mean absorption of all wavelength in spectrum

σ_x = Standard deviation of absorption in spectrum

Derivative transformations

Derivative transformations were applied to remove noise caused by the spectrometer. The 1st derivation highlights overlaying peaks and corrects the offset. Additionally the second derivation removes linear offsets (linear slopes). As derivations cause new noise smoothing is applied at the same time.

Norris gap derivative transformation (Norris)

Norris applies moving average smoothing to a spectrum before derivation is conducted. By changing the gap size the size of the smoothing interval is influenced. The higher the number of smoothing points the stronger is the smoothing.

Savitzky-Golay transformation (SaGo)

SaGo fits a polynomial to the spectral data before derivation is applied. In the current study polynomial of order 2 was used as this enables the fitting of peaks. The number of smoothing points defines the number of points to which the polynomial is fitted. The higher this number the stronger is the smoothing.

Baseline offset correction can be combined with SNV, Norris and SaGo. Therefor first baseline offset correction is conducted followed by one of the other transformations.

Objectives of the study

The current study wants to answer following questions.

1. Can hyperspectral canopy reflectance of winter oilseed rape under field conditions be used to predict nitrogen uptake at end of flowering (Nup_{EOF}) , nitrogen uptake at maturity (Nup_{MAT}) and/or seed yield dry matter (Seed DM)?
2. Is it necessary to develop separate calibration models for different nitrogen supplies?
3. Which date of measurement, i.e. which developmental stage, does result in better calibrations and validations?

Therefore, hyperspectral canopy reflectance was measured in nitrogen efficiency trials (chapter A) before flowering and during fruit development. Multivariate regression was performed to develop models. Predicting ability was tested in cross and external validation.

Materials and Methods

Genotypes

Calibration set

The diversity set described in chapter A was used for calibration and cross validation (Tab. A 1). In the following it is denoted as calibration set.

Validation data sets

For external validation two data sets were used – validation set 1 (Val-1) and validation set 2 (Val-2).

Validation set 1 (Val-1)

Two types of test hybrids were tested by Miersch (2015). The two types differed in growth type – semi-dwarf and normal type. They derived from a DH population of the cross Alesi-*bzh* x H30 whose DH lines were crossed to a male sterile tester. Alesi-*bzh* is a dwarf isogenic line that derived from the German line cultivar Alesi which was backcrossed to a *bzh* dwarf mutant (Foisset et al. 1995) for four generations. The tall resynthesis H30 originated from a cross between *Brassica rapa* ssp. *chinensis* with *Brassica napus* ssp. *napus* var. *pabularia* (Girke 2002). DH lines segregated into dwarf and tall growing genotypes. They were crossed to a male sterile tester of normal growth type. Thus, test hybrids segregated into semi-dwarf and normal growth type. Val-1 consisted of 54 normal type test hybrids.

Validation set 2 (Val-2)

Val-2 consisted of DH lines and test hybrids of Population 007 (Pop007) and Population 029 (Pop029) described in chapter A.

Field trials

Experimental set-up

Calibration set and Val-2

Experimental set-up of EOF and MAT trials conducted with the diversity set and MAT007 and MAT029 conducted with DH lines and test hybrids of Pop007 and Pop029 are described in chapter A.

Val-1

Genotypes were tested at two nitrogen levels (N1 and N0) in a trial which was harvested at maturity. The trials were designed as split plots with nitrogen level as whole plot factor and genotype as subplot factor. Genotypes were randomised in alpha lattice design.

Cultivation

Reference traits for the calibration set derived from EOF and MAT trials of the diversity set (EOF_{Cal} and MAT_{Cal}) described in chapter A. Validation set 1 (Val-1) was tested in MAT trials in three of the five environments which were described in chapter A (Tab. B 3). Val-1 was tested in MAT_{Val-1} under the same conditions as MAT_{Cal} particularly concerning nitrogen levels. Reference traits for validation set 2 derived from trials MAT007 and MAT029 of validation set 2 (MAT_{Val-2}). The trials were cultivated as described in chapter A.

Tab. B 3: Environments of field trials

Environment	Trials
EIN2012	EOF_{Cal}, EOF_{Val}
EIN2013	EOF_{Cal}, MAT_{Cal}, MAT_{Val}-1
EIN2014	MAT_{Val-2}
GIE2013	EOF_{Cal}, MAT_{Cal}
GIE2014	MAT_{Val-2}
GOE2012	EOF_{Cal}, MAT_{Cal}, EOF_{Val}, MAT_{Val-1}
GOE2013	EOF_{Cal}, MAT_{Cal}, MAT_{Val-1}
GOE2014	MAT_{Val-2}

Assessment of traits

State after winter and growth stage

State after winter was evaluated at beginning of vegetation in spring. It was rated on a scale from 1 – 9 (1 no or very little failings, 2 very little to little failings, 3 little failings, 4 little to medium failings, 5 medium failings, 6 medium to heavy failings, 7 heavy failings, 8 heavy to very heavy failings, 9 very heavy failings). Main shoot of one genotype of calibration set died off in winter. Therefore, this genotype was removed from analyses. To evaluate growth stage two methods were applied. Before flowering it was assessed according to Lancashire (1991). Begin of flowering was evaluated as days after January 1st when 10 % of plants had started to flower.

Agronomic traits and nitrogen uptake

Aboveground biomass at end of flowering, seed yield (Seed DM) and straw yield at maturity, dry matter content, nitrogen content of aboveground biomass end of flowering, of seeds and of straw, nitrogen uptake at end of flowering (Nup_{EOF}) and nitrogen uptake at maturity (Nup_{MAT}) in EOF_{Cal}, MAT_{Cal}, MAT_{Val-1} and MAT_{Val-2} were assessed as described in chapter A. The only exception was nitrogen content of seeds of MAT_{Val-1} which was measured by near-infrared reflectance of intact seeds (NIRS monochromator model 6500, NIR Systems, Inc., Silversprings, MD, USA, calibrations raps2012.eqa and raps2013.eqa provided by VDLUFA Qualitätssicherung NIRS GmbH). For calibration data sets the standard error of reference values SE_{Cal} was calculated as quotient of standard deviation s of measured trait values and square root of number of observations n ($SE_{Cal} = s * n^{-1/2}$).

Hyperspectral reflectance

Spectrometer

Hyperspectral reflectance was captured with a HandySpec® Field spectrometer (tec5, Oberursel/Germany). It consists of two sensors. MMS1 measures wavelengths from 305 nm to 950 nm, PGS-PGS2.2 wavelengths from 951 nm to 2215 nm. Sunlight is used as natural light source. To compensate for changing intensity of the sunlight a reference channel measures the incoming light (simultaneously for MMS1 signal and sequential for PGS-NIR2.2) whereas a second measuring channel

captures the radiation reflected radiation. Incoming and reflected light are not captured permanently but the channels are closed by shutters. If a measurement is triggered the shutters open for a certain time (integration time). It depends on the light intensity of incoming and reflected light and on threshold intensities which can be set by the user. If the intensity falls below the minimum threshold integration time is prolonged, if the maximum threshold is exceeded integration time is reduced until optimum intensity is achieved. Minimum was set 0.50, optimum 0.80 and maximum 0.95.

The system consists of two parts – a sensor head and a main unit (Fig. B 2). The sensor head (Fig. B 3) contains the receiving optics and a switch to trigger the measurement. The reference channel with a standard cosine receiver is angled 90 ° upwards. A fibre optics receiver measures the reflected radiation. It is angled 90 ° downwards with an aperture angle of 25 °. The probe is connected to the main unit by fibre optics which is covered by a flexible PVC tube. The main unit consists of the two sensors, the operation electronics and a rechargeable battery (NiMH 12 V, 9.5 Ah). The main unit is encased by a metal cover. It is mounted on a back frame with shelf and is carried on the back.

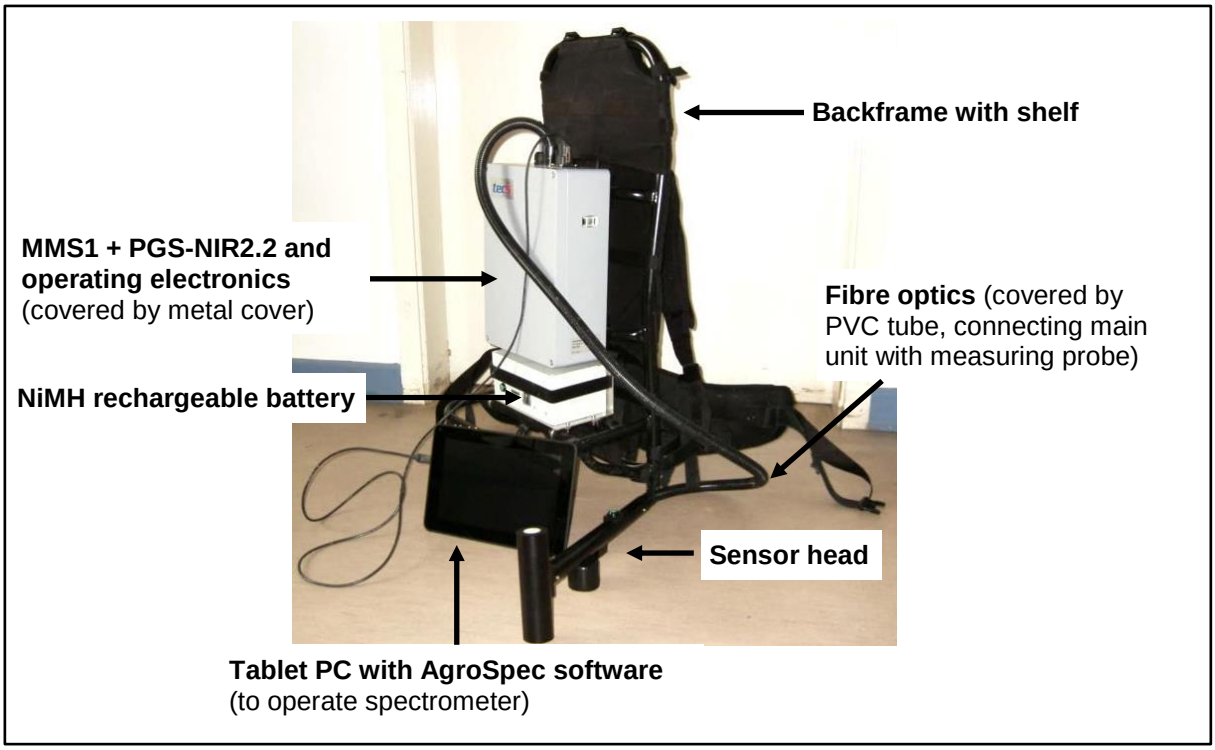

Fig. B 2: HandySpec® Field spectrometer
MMS1 + PGS-NIR2.2 (sensors), operating electronics and NiMH rechargeable battery form main unit, Total weight ~ 12 kg

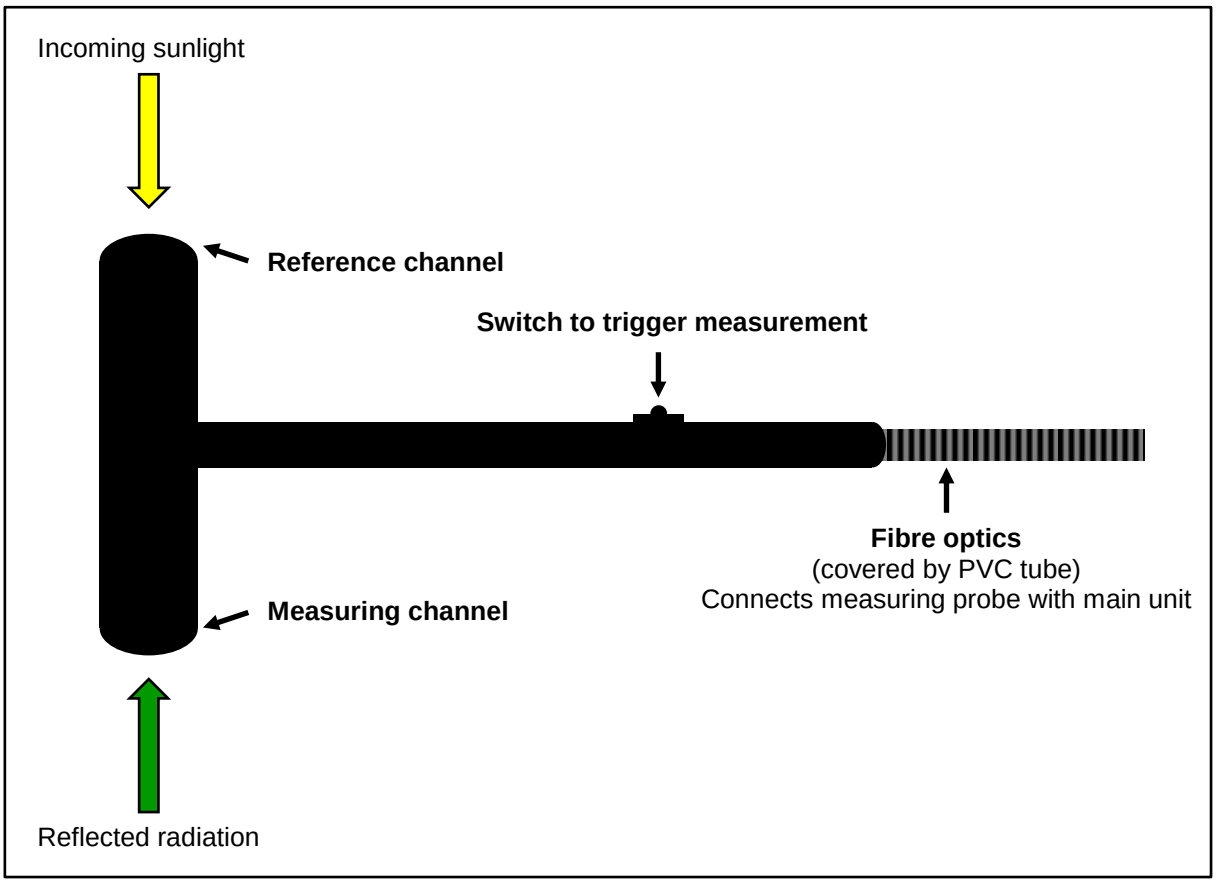

Fig. B 3: Sensor head of spectrometer

A Zenith Polymer® Diffuse Reflectance Standard 25 % (SphereOptics, Uhldingen/Germany) with a diameter of 50 mm was used as grey scale in order to adjust the two channels spectrally (internal calibration).

Measurements

In trial EOF_{Cal} reflectance was measured when most of the plots were in growth stages 53 to 57 (before flowering). In trials MAT_{Cal}, MAT_{Val-1} and MAT_{Val-2} reflectance of plots was measured before flowering and during fruit development. Measurements were conducted ± 2 h around sun's zenith. The grey scale was measured before each nitrogen level within a replication. The sensor head was placed perpendicular in 15 cm to 20 cm distance above the canopy halfway of the plot's width (between third and fourth row in EIN and GOE environments, between fifth and sixth row in GIE environments). Reflectance of ten measuring points per plot which were evenly distributed across the plot's length was captured. The first and last measurement per plot was taken about 25 cm from the respective front side. During measurements it was taken care that nothing shadowed the plot. Reflectance was expressed in percentage of incoming light for each wavelength. For Nup_{EOF} reflectance was

measured in EOF_{Cal} trials in four environments (Tab. B 4). For Nup_{MAT} and Seed DM reflectance before flowering and during fruit development was captured in four environments for the calibration set and in two and three environments, respectively for Val-1 and in three environments for Val-2 (Tab. B 4).

Tab. B 4: Date, trials and environments at which reflectance was captured for calibration and cross validation or external validation for respective traits

Date of measurement	Calibration + cross validation		External validation	
	Trial	Environment	Trial	Environment
		Nup_{EOF}		
Before flowering	EOF	EIN2012 EIN2013 GIE2013 GOE2013	No spectral data was captured	
		Nup_{MAT} and Seed DM		
Before flowering	MAT	EIN2013 GIE2013 GOE2012 GOE2013	MAT_{Val-1}	EIN2013 GOE2013
			MAT_{Val-2}	EIN2014 GIE2014 GOE2014
Fruit development	MAT	EIN2013 GIE2013 GOE2012 GOE2013	MAT_{Val-1}	EIN2013[1] GOE2012 GOE2013[1]
			MAT_{Val-2}	EIN2014 GIE2014[1] GOE2014[2]

[1] Replication 1, [2] Replication 1 and half of replication 2

Pre-handling of data

Only plots with state after winter from one to five were used in calibration and validation. Due to very low intensity of incoming light wavelengths with more than 100 % reflectance occurred. These were removed from spectral data. Afterwards the ten measurements per plot were checked for number of data points per wavelength. Wavelengths with less than seven data points were removed. Reflectance was then averaged across the seven to ten data points per wavelength and plot. This resulted in one reflectance spectrum per plot. The internal calibration with the grey scale did

not work for wavelengths which were filtered out by the atmosphere. These were not the same for every internal calibration. Respective wavelengths were labelled by the operating software in the internal calibration file of each grey scale measurement. Failed wavelengths were removed manually from plot spectra. Within trait and date of measurement plots and wavelengths with more than 5 % missing values were removed. Those procedures left the wavelength range from 305 nm to 1800 nm and 204 to 445 plots for calibration and cross validation (depending on nitrogen level) and 159 to 1288 plots for calibration and external validation (depending on nitrogen level and validation set) . Reflectance was divided by 100 and subsequently transformed to absorption by equation 5.

Equation 5

$$Abs = \log (R^{-1})$$

Abs = Absorption

R = Reflectance expressed in fractions between 0 and 1

Definition of wavelengths ranges

Spectra were divided into two wavelengths ranges according to the two sensors – range from 305 nm to 950 nm measured by sensor MMS1 (MMS1) and range from 951 nm to 1800 nm measured by sensor PGS-NIR2.2 (PGS_{all}). The latter contained two very noisy areas – one from 1351 nm to 1550 nm and another one above 1760 nm (Fig. B 4). Therefore, a third spectral range was defined which ranged from 951 nm to 1350 nm and from 1551 nm to 1760 nm (PGS_{red}). Five wavelengths ranges/combinations of ranges were tested in calibrations and cross validations – MMS1+PGS_{all}, MMS1+PGS_{red}, MMS1, PGS_{all} and PGS_{red}.

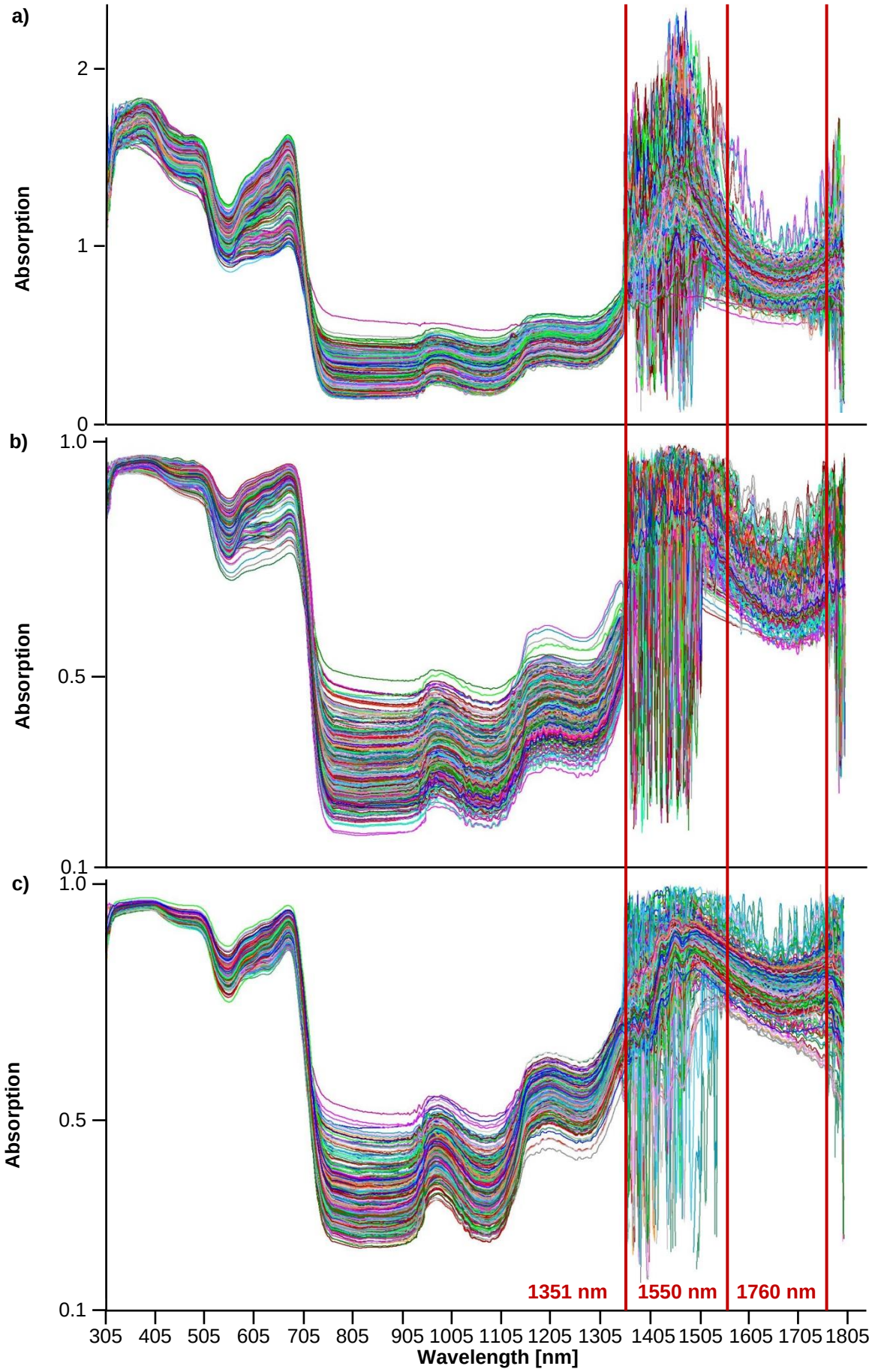

Fig. B 4: Absorption of EOF_{Cal} before flowering (a), MAT_{Cal} before flowering (b) and during fruit development (c)
Red vertical lines and numbers label noisy wavelengths ranges, each curve represents one plot

Spectral data space and influence of growth stage

Principal component analyses (PCA) were conducted with MMS1+PGS_{red} to compare the spectral data spaces of the different data sets and to test the influence of growth stages on spectral data. The analyses were computed with Unscrambler 10.3 (Camo®, Oslo/Norway). NIPALS algorithm was applied. Leverage correction was used for validation.

In order to compare spectral data spaces of the different datasets PCAs were computed with the wavelengths combination MMS1+PGS_{red} of calibration set and validation sets. One PCA was conducted for each measuring date.

The genetic material differed in growth stages, e.g. some genotypes had already started to flower while most others were still in growth stage 53 to 57 during the first measurement. PCAs were conducted to test influence of growth stage at the first and second measuring on spectral data. Growth stage at the first date was expressed according to Lancashire et al. (1991). At the second date it was expressed in days after begin of flowering. PCAs were computed with MMS1+PGS_{red} of plots which were used in calibration and cross validation.

Calibration and cross validation

Calibrations were developed with Unscrambler 10.3 (Camo®, Oslo/Norway) with the partial least squares regression method (PLSR) applying the non-linear iterative partial least squares algorithm (NIPALS, convergence criterion 10^{-6}). For all traits calibrations were developed for the combination of both nitrogen levels (N1+N0) as well as separate for N1 and N0. Reflectance in maturity trials was measured before flowering and during fruit development. Calibrations were developed for both growth stages separately to determine the best developmental stage to measure. Tenfold cross validations were conducted. Segments were made up randomly.

MMS1+PGS_{all}, MMS1+PGS_{red}, MMS1, PGS_{all} and PGS_{red} were tested to examine whether spectral ranges containing the noisy areas between 1350 nm and 1551 nm and above 1760 nm are useful for calibrations and to get a first idea which wavelengths ranges or combinations are best suited to predict the respective trait. In order to correct the spectral signal for noise, several pre-treatments were applied to MMS1 and PGS_{red} but not to their combinations. Pre-treatments that were used in the

current approach were baseline offset correction (Base), standard normal variate (SNV), 1st and 2nd derivations of Norris gap derivative transformations (Norris) and 1st and 2nd derivations of Savitzky-Golay derivative transformations of polynomial order 2 (SaGo). It was also tested whether the combination of baseline offset correction (computed first) with the other pre-treatments could improve calibration.

To evaluate calibrations the following parameters were examined: coefficient of determination of calibration (R^2_{Cal}) and cross validation (R^2_{CV}), root mean square error of calibration ($RMSE_{Cal}$) and cross validation ($RMSE_{CV}$) and Bias of calibration ($Bias_{Cal}$).

The best pre-treatments were selected within MMS1 and within PGS_{red} to be combined. The combined MMS1+PGS_{red} were again tested in calibrations. The best calibrations across and within nitrogen levels within the first and the second measuring date were selected for external validation.

Calibration and external validation

Calibrations and external validations were computed with Unscrambler 10.3 (Camo®, Oslo/Norway). It was conducted for Nup_{MAT} and for Seed DM. For Nup_{EOF} it was not possible due to lack of data. With the selected (pre-treated) wavelengths ranges/combinations PLS-R with NIPALS algorithm was conducted. External validation was conducted with the validation datasets. Val-1 and Val-2 were tested together (Val-1+Val-2) and separate. Val-2 was further divided into two subsets. Val-2 DH contained all DH lines and Val-2 TH all test hybrids of Val-2. The validation data sets were pre-treated in exactly the same way as the selected calibration data sets.

To evaluate calibrations and external validations the following parameters were examined: coefficient of determination of calibration (R^2_{Cal}) and external validation (R^2_{EV}), root mean square error of calibration ($RMSE_{Cal}$) and external validation ($RMSE_{EV}$) and Bias of calibration ($Bias_{Cal}$).

Prediction of genotypes

It was examined whether calibrations and cross validations resulted in the same ranking as the direct assessment of Nup_{EOF}, Nup_{MAT} and Seed DM. Therefore, predicted plot values of cross validations of selected models were used to compute

genetic means within nitrogen levels. The means were ranked from 1 (best) to 29 (worst) and compared to ranks that derived from genetic means within nitrogen levels shown in chapter A.

Results

Only a selection of calibrations is described in the following sections. An overview about further calibrations is given in appendix (Tab. VII to Tab. XXI).

Spectral data space

For spectral data captured at the first measuring date (before flowering) two groups could be clearly distinguished – calibration set and Val-1+Val-2. Within Val-1+Val-2 nor Val-1and Val-2 nor Val-2 DH or Val-2 TH could be distinguished at the first PCs (Fig. B 5 top). For spectral data captured at the second measuring date (during fruit development) the distinction between calibration and validation data sets is not that clear. But although the calibration set and the two validation sets overlapped they did not cover an identical data space (Fig. B 5 bottom).

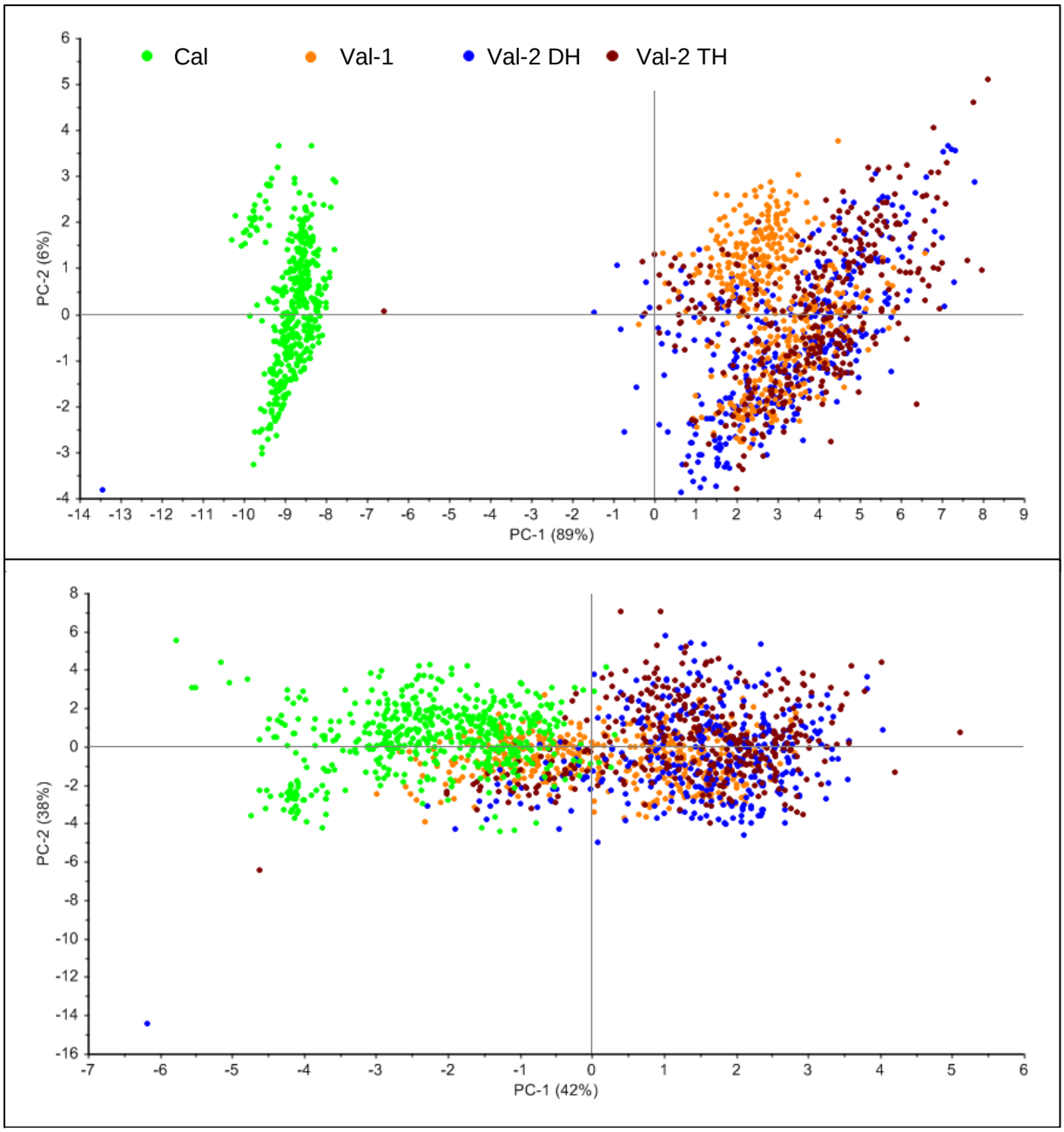

Fig. B 5: PCA of absorption before flowering (top) and during fruit development (bottom)
Colouring according to data set a plot belonged to (legend), Cal calibration data set used in calibration and cross validation, Val-1 validation dataset 1, Val-2 DH DH lines of validation data set 2, Val-2 TH test hybrids of validation dataset 2, Val-2 DH and Val-2 TH form validation set Val-2, Val-1 and Val-2 form Val-1+Val-2, all validation datasets are only used in external validation

Influence of growth stage

No sample grouping of spectral data according to developmental stage was detected at the first two PCs. This was true for measurements of EOF and MAT plots before flowering (Fig. B 6) as well as for measurements of MAT plots during fruit develop-

ment (Fig. B 7). Therefore no plot was excluded from calibration due to developmental stage.

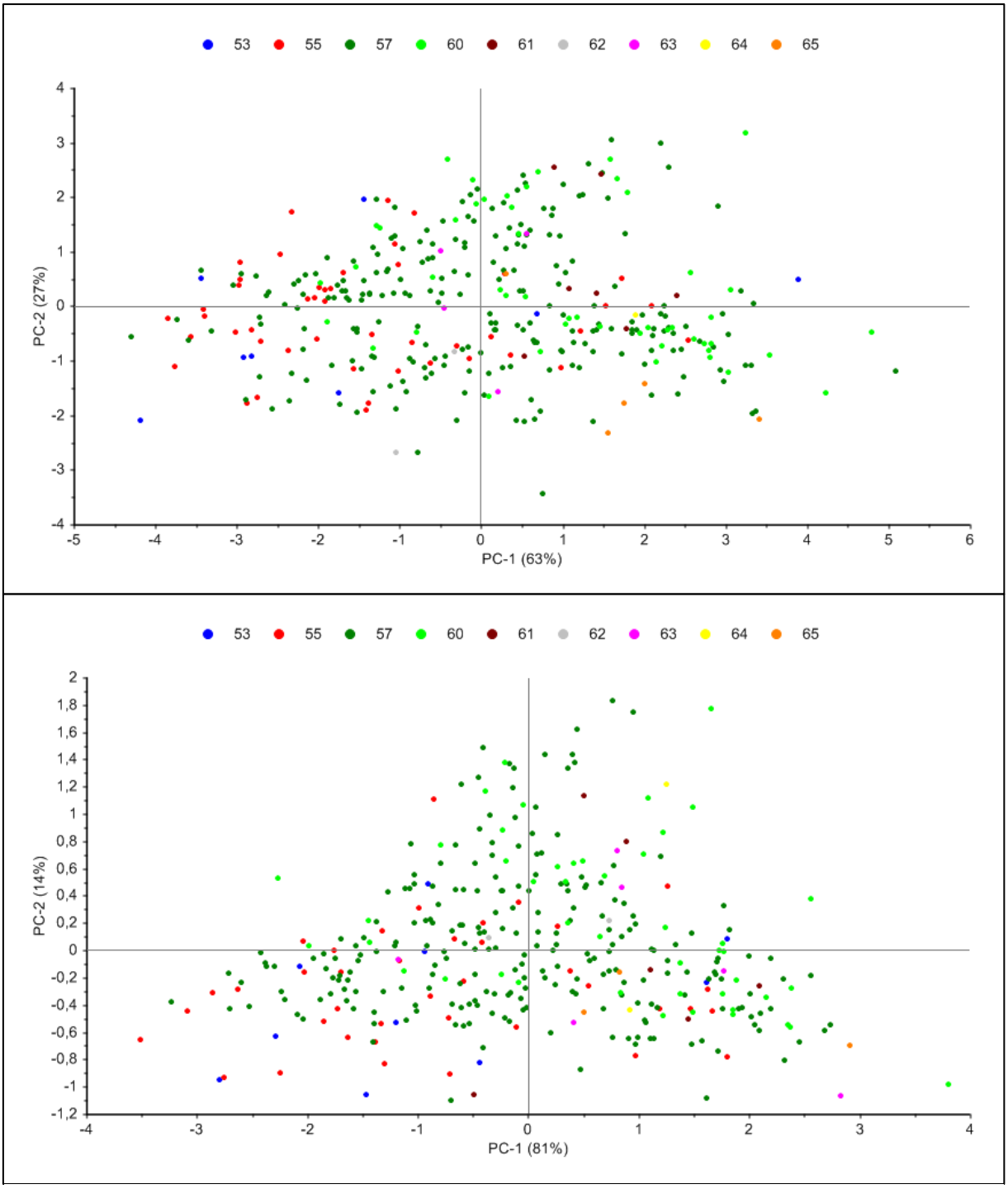

Fig. B 6: PCA of absorption of MMS1+PGS$_{red}$ of EOF plots (top) and MAT plots (bottom)
Spectral data captured end of flowering of N1 and N0 plots which were used in calibration for Nup$_{EOF}$ (top) and Nup$_{MAT}$ (bottom) and for which growth stage was evaluated, Colouring (legend) according to growth stage

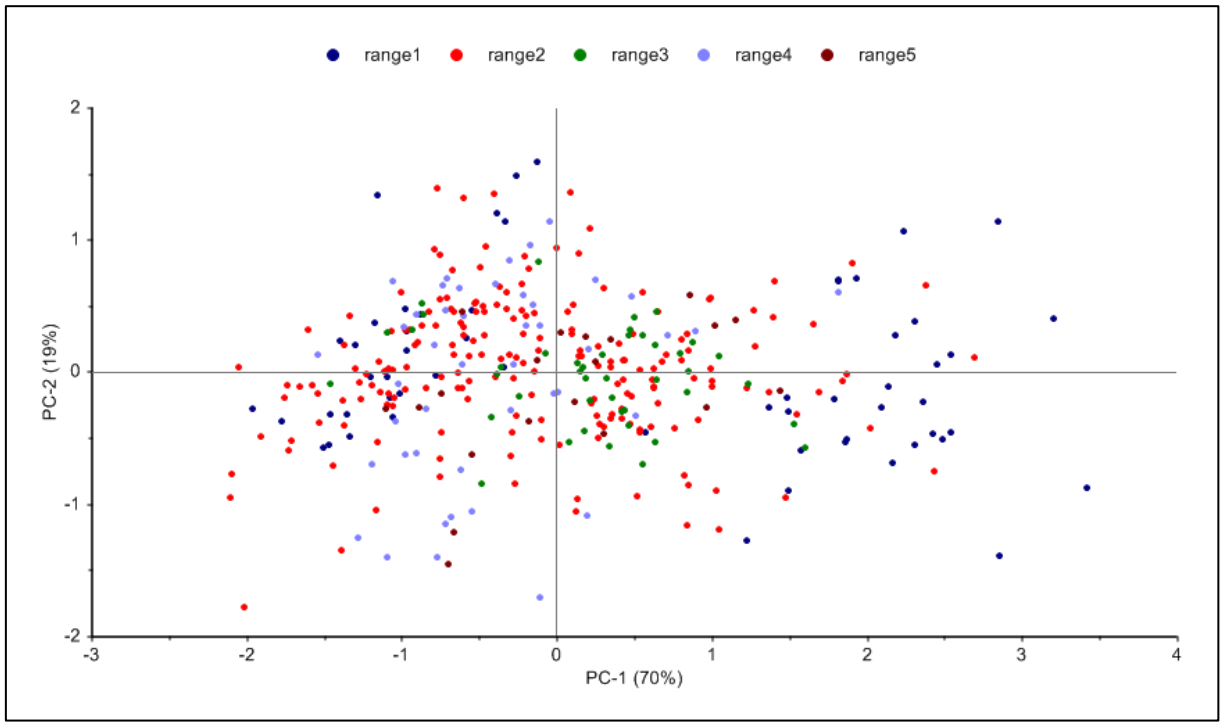

Fig. B 7: PCA of absorption of MMS1+PGS$_{red}$ of MAT plots
Spectral data captured during fruit development of N1 and N0 plots which were used in calibration for Nup$_{MAT}$ and Seed DM and for which begin of flowering was evaluated, Colouring (legend) according to date of measurement (calculated as days after begin of flowering), range 1 30 – 34 d, range 2 35 - 38 d, range 3 39 – 43 d, range 4 44 – 47 d, range 5 48 – 52 d

Nitrogen uptake at end of flowering (Nup_{EOF})

N1 + N0

Nup_{EOF}

Plot values of Nup_{EOF} across both nitrogen levels ranged from 0.2 dt ha^{-1} to 3.0 dt ha^{-1} with a mean of 1.2 dt ha^{-1} (Fig. B 8).

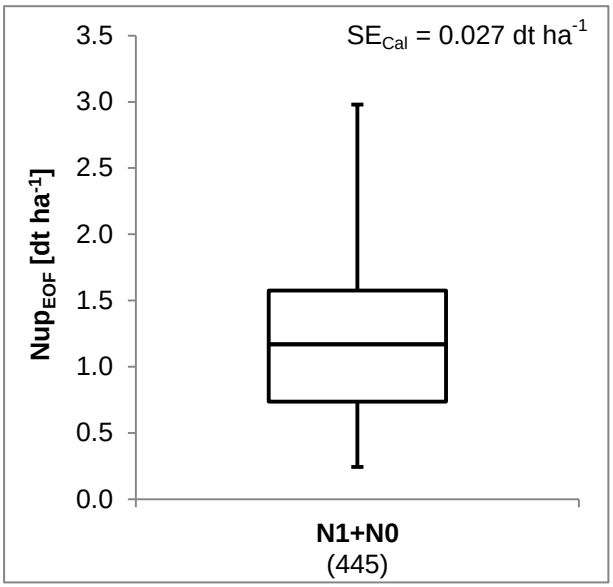

Fig. B 8: Boxplot of plot values of Nup_{EOF} of calibration dataset across N1 and N0
Numbers in brackets size of calibration + cross validation set, SE_{Cal} standard error of reference values in calibration dataset

Calibration and cross validation

The comparison of the untreated wavelengths ranges MMS1+PGS_{all} and MMS1+PGS_{red} as well as PGS_{all} and PGS_{red} revealed that the noisy wavelengths ranges between 1350 nm and 1551 nm and above 1760 nm deteriorated quality of calibration and cross validation. This particularly concerned bias of calibration which was too high. Therefore, PGS_{all} was excluded from further analyses. Wavelengths range MMS1 resulted in better calibrations than PGSred. Both were improved by pre-treatments. The combination of pre-treated MMS1 and PGSred did not outperform the best calibrations resulting from MMS1 (Tab. B 5). $RMSE_{Cal}$ and $RMSE_{CV}$ were about ten times higher than the standard error of the reference values (Fig. B 8, Tab. B 5).

Tab. B 5: Calibrations and cross validations for Nup_{EOF} across both N levels

Wavelengths range	Pre-treatment [number]		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1 + PGS_{all}	w/o		0.80	0.25	2.E-03	0.78	0.28	-2.E-04
MMS1 + PGS_{red}	w/o		0.85	0.22	6.E-08	0.82	0.24	-4.E-04
MMS1	w/o		0.85	0.22	2.E-07	0.82	0.24	-6.E-04
PGS_{all}	w/o		0.75	0.28	-3.E-04	0.72	0.30	2.E-03
PGS_{red}	w/o		0.80	0.25	6.E-08	0.76	0.28	2.E-03
MMS1	**Norris d1g9**	**[1]**	**0.87**	**0.20**	**4.E-09**	**0.85**	**0.22**	**-6.E-04**
MMS1	**Norris d1g15**	**[2]**	**0.87**	**0.20**	**2.E-08**	**0.85**	**0.22**	**4.E-04**
PGS_{red}	Base	[3]	0.85	0.22	-2.E-08	0.77	0.27	-4.E-04
PGS_{red}	SaGo d1s45	[4]	0.84	0.23	-4.E-08	0.79	0.26	1.E-03
MMS1 + PGS_{red}	MMS1 [1] + PGS_{red} [3]		0.87	0.21	1.E-08	0.79	0.26	1.E-03
MMS1 + PGS_{red}	MMS1 [1] + PGS_{red} [4]		0.85	0.22	4.E-08	0.82	0.24	-1.E-03
MMS1 + PGS_{red}	MMS1 [2] + PGS_{red} [3]		0.86	0.21	6.E-09	0.80	0.26	-8.E-04
MMS1 + PGS_{red}	MMS1 [2] + PGS_{red} [4]		0.82	0.24	4.E-08	0.79	0.26	5.E-04

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, plot values predicted by models resulting from underlined wavelengths range and pre-treatment were used to test prediction of genotypes

N1

Nup_{EOF}

Plot values of Nup_{EOF} within N1 ranged from 0.6 dt ha^{-1} to 3.0 dt ha^{-1} with a mean of 1.6 dt ha^{-1} (Fig. B 9).

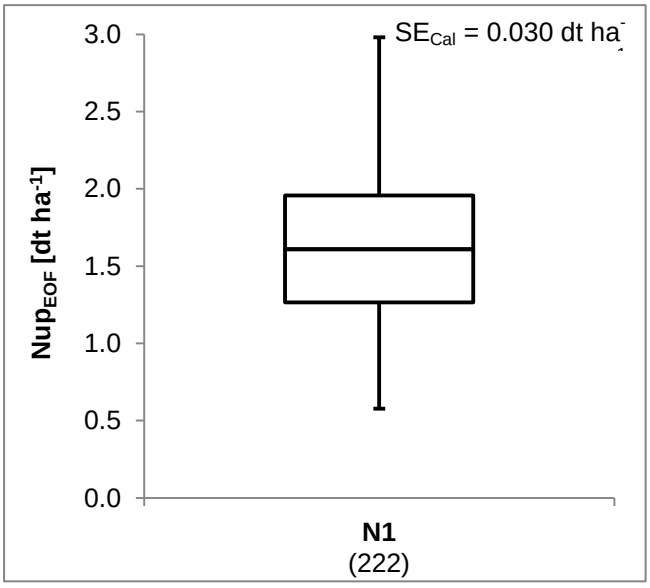

Fig. B 9: Boxplot of plot values of Nup_{EOF} of calibration dataset within N1
Numbers in brackets size of calibration + cross validation set, SE_{Cal} standard error of reference values in calibration dataset

Calibration and cross validation

Calibrations within N1 resulted in better calibrations when the noisy ranges between 1350 and 1551 nm and above 1760 nm were not used. Calibrations with wavelengths ranges that contained these areas like PGS_{all} showed a high bias for calibration. Therefore, PGS_{all} was not used in further analyses. PGS_{red} resulted in a better calibration than MMS1 as long as both remained untreated. After pre-treatment MMS1 calibrations were slightly better than PGS_{red} calibrations. The combination of pre-treated MMS1 and PGS_{red} did not improve calibration (Tab. B 6). $RMSE_{Cal}$ and $RMSE_{CV}$ were about seven to ten times higher than the standard error of the reference values (Fig. B 9, Tab. B 6)

Tab. B 6: Calibrations and cross validations for Nup_{EOF} within N1

Wavelengths range	Pre-treatment [number]		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1 + PGS_{all}	w/o		0.67	0.25	2.E-03	0.61	0.28	4.E-03
MMS1 + PGS_{red}	w/o		0.61	0.28	2.E-08	0.58	0.29	7.E-03
MMS1	w/o		0.58	0.29	-2.E-08	0.55	0.30	7.E-04
PGS_{all}	w/o		0.63	0.27	-9.E-04	0.52	0.31	5.E-03
PGS_{red}	w/o		0.74	0.23	1.E-07	0.60	0.28	1.E-03
MMS1	**Norris d1g43**	**[1]**	**0.77**	**0.21**	**2.E-07**	**0.66**	**0.26**	**-6.E-04**
MMS1	Base + Norris d2g17	[2]	0.77	0.21	6.E-08	0.65	0.26	5.E-03
MMS1	SaGo d1s17	[3]	0.76	0.21	-2.E-08	0.65	0.26	-2.E-03
PGSred	SaGo d1s41	[4]	0.76	0.22	7.E-08	0.65	0.26	-1.E-03
MMS1 +PGS_{red}	MMS1 [1] + PGS_{red} [4]		0.71	0.24	6.E-08	0.59	0.28	-2.E-03
MMS1 +PGS_{red}	MMS1 [2] + PGS_{red} [4]		0.75	0.22	5.E-08	0.65	0.26	1.E-03
MMS1 +PGS_{red}	MMS1 [3] + PGS_{red} [4]		0.59	0.28	3.E-08	0.55	0.30	8.E-06

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, plot values predicted by models resulting from underlined wavelengths range and pre-treatment were used to test prediction of genotypes

N0

Nup_{EOF}

Plot values of Nup_{EOF} within N0 ranged from 0.2 dt ha^{-1} to 1.3 dt ha^{-1} with a mean of 0.7 dt ha^{-1} (Fig. B 10).

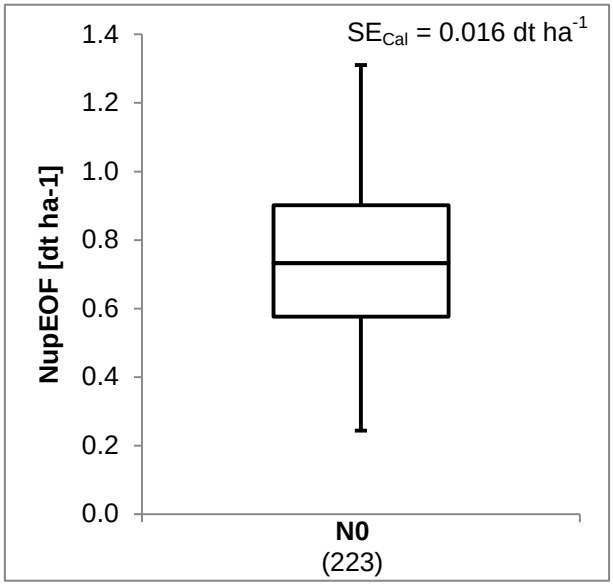

Fig. B 10: Boxplot of plot values of Nup_{EOF} of calibration dataset within N0
Numbers in brackets size of calibration + cross validation set, SE_{Cal} standard error of reference values in calibration dataset

Calibration and cross validation

Bias of calibration was very high when noisy areas between 1350 nm and 1551 nm and above 1760 nm were included in calibration. Therefore, PGS_{all} was not used for further computations. Untreated MMS1 and PGS_{red} resulted in calibrations and cross validations of same quality. Although R^2_{Cal} increased very slightly after pre-treatment for both wavelengths ranges there was a clear decrease of R^2_{CV} when using PGS_{red}. Pre-treated MMS1 resulted in an increased R^2_{CV}. The combination of pre-treated MMS1 and PGS_{red} led to the best calibration within N0 (Tab. B 7). $RMSE_{Cal}$ and $RMSE_{CV}$ were about eight times higher than the standard error of the reference values (Fig. B 10, Tab. B 7).

Tab. B 7: Calibrations and cross validations for Nup_{EOF} within N0

Wavelengths range	Pre-treatment [number]		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1 + PGS_{all}	w/o		0.80	0.11	3.E-04	0.77	0.12	1.E-03
MMS1 + PGS_{red}	w/o		0.79	0.11	3.E-08	0.76	0.12	9.E-04
MMS1	w/o		0.79	0.11	3.E-08	0.75	0.12	2.E-05
PGS_{all}	w/o		0.78	0.11	5.E-04	0.75	0.12	1.E-03
PGS_{red}	w/o	[1]	0.80	0.11	9.E-08	0.75	0.12	1.E-03
MMS1	Norris d2g9	[2]	0.81	0.10	3.E-08	0.77	0.12	4.E-04
MMS1	SaGo d1s3	[3]	0.82	0.10	3.E-08	0.77	0.12	1.E-03
MMS1	Base + SaGo d2s23	[4]	0.81	0.11	3.E-08	0.78	0.11	4.E-04
PGS_{red}	SaGo d1s13	[5]	0.81	0.11	3.E-08	0.73	0.13	4.E-04
MMS1 + PGS_{red}	MMS1 [2] + PGS_{red} [1]		0.78	0.11	7.E-08	0.73	0.13	7.E-04
MMS1 + PGS_{red}	**MMS1 [2] + PGS_{red} [5]**		**0.84**	**0.10**	**4.E-08**	**0.77**	**0.12**	**2.E-03**
MMS1 + PGS_{red}	MMS1 [3] + PGS_{red} [1]		0.81	0.10	8.E-08	0.74	0.12	6.E-04
MMS1 + PGS_{red}	MMS1 [3] + PGS_{red} [5]		0.77	0.12	3.E-08	0.74	0.12	2.E-04
MMS1 + PGS_{red}	MMS1 [4] + PGS_{red} [1]		0.80	0.11	9.E-08	0.75	0.12	2.E-03
MMS1 + PGS_{red}	MMS1 [4] + PGS_{red} [5]		0.81	0.11	3.E-08	0.74	0.13	3.E-03

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, plot values predicted by models resulting from underlined wavelengths range and pre-treatment were used to test prediction of genotypes

N1+N0 vs. N1 and N0

Best calibrations across both nitrogen levels showed higher R^2_{Cal} andR^2_{CV}. $RMSE_{Cal}$ and $RMSE_{Val}$ were slightly smaller across nitrogen levels than within N1. They decreased by half within N0. If RMSEs were expressed as percentage of mean of Nup_{EOF} in the respective nitrogen level this pattern changed – N1+N0 $RMSE_{Cal}$ = 15.7 %, $RMSE_{Val}$ = 17.3 %, N1 $RMSE_{Cal}$ = 13.0 %, $RMSE_{Val}$ = 16.1 % and N0 $RMSE_{Cal}$ = 13.7 %, $RMSE_{Val}$= 16.4 %. Within both nitrogen levels $RMSE_{Cal}$ and $RMSE_{Val}$ were relatively smaller than across nitrogen levels and smaller within N1 than within N0 (Tab. B 5, Tab. B 6, Tab. B 7).

Nitrogen uptake at maturity (Nup_{MAT})

N1 + N0

Nup_{MAT}

Plot values for Nup_{MAT} of the calibration set across both nitrogen levels ranged from 0.3 dt ha^{-1} to 2.6 dt ha^{-1} with a mean of 1.2 dt ha^{-1}. Val-1+Val-2 covered a broader range. Val-1 showed a lower mean while mean of Val-2 was higher (Fig. B 11).

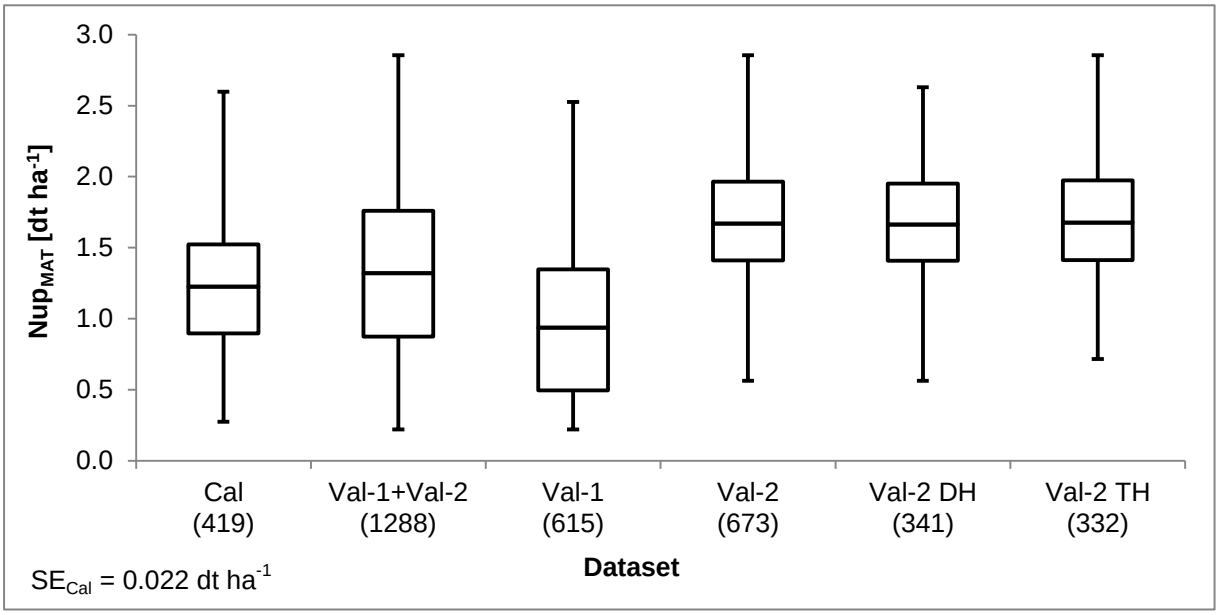

Fig. B 11: Boxplots of plot values of Nup_{MAT} across N1 and N0 for different data sets
Cal Calibration set, Val-1 validation set 1, Val-2 validation set 2, Val-2DH DH lines of Val-2, Val-2 TH test hybrids of Val-2, Numbers in brackets size of dataset, SE_{Cal} standard error of reference values in calibration dataset

Calibration and cross validation

For both measuring dates wavelengths ranges with noisy areas between 1350 nm and 1551 nm and above 1760 nm as in PGS_{all} caused a high bias of calibration (Tab. B 8, Tab. B 9). Therefore, PGS_{all} was excluded from further analyses. The best calibration for the first measuring date (before flowering) was accomplished with untreated MMS1+PGS_{red}. By pre-treatment calibrations with MMS1 or PGS_{red} were improved but the best calibration after pre-treatment was slightly better only in R^2_{CV} but not in other parameters. The combination of pre-treated MMS1 and PGS_{red} did not further improve calibration and cross validation

(Tab. B 8). $RMSE_{Cal}$ and $RMSE_{CV}$ were about ten times higher than the standard error of the reference values (Fig. B 11, Tab. B 8).

For the second measuring date (during fruit development) calibration and cross validation were improved by pre-treatment of MMS1 or PGS_{red} but their combination did not cause improvement. PGS_{red} pre-treated with Norris gap derivation (1^{st} derivation, gap size 3) and a combination of MMS1 and PGS were best in calibration while MMS1 pre-treated with Norris gap derivation (2^{nd} derivation, gap size 13) was best in cross validation (Tab. B 9). $RMSE_{Cal}$ and $RMSE_{CV}$ were more than ten times higher than the standard error of the reference values (Fig. B 11, Tab. B 9).

Spectral data of the first measuring date resulted in better calibrations and cross validations for Nup_{MAT} across nitrogen levels (Tab. B 8, Tab. B 9).

Tab. B 8: Calibrations and cross validations for Nup_{MAT} across both N levels with spectral data before flowering

Wavelengths range	Pre-treatment [number]		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
$MMS1+PGS_{all}$	w/o		0.79	0.21	-4.E-03	0.74	0.24	-7.E-03
$MMS1+PGS_{red}$	**w/o**		**0.84**	**0.19**	**-4.E-08**	**0.81**	**0.20**	**1.E-03**
MMS1	w/o		0.82	0.20	3.E-07	0.80	0.21	9.E-04
PGS_{all}	w/o		0.78	0.21	-5.E-05	0.71	0.25	2.E-04
PGS_{red}	w/o		0.78	0.22	-4.E-08	0.75	0.23	2.E-03
MMS1	**Base + SaGo d1s17**	**[1]**	**0.83**	**0.19**	**3.E-08**	**0.82**	**0.20**	**-5.E-04**
PGS_{red}	PGS_{red} SaGo d1s41	[2]	0.82	0.20	5.E-08	0.77	0.22	-6.E-04
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [2]		0.82	0.19	3.E-08	0.80	0.21	-7.E-05

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, Underlined wavelengths ranges/pre-treatments were also tested in calibration with external validation, plot values predicted by model resulting from underlined MMS1 range/pre-treatment were used to test prediction of genotypes

Tab. B 9: Calibrations and cross validations for Nup_{MAT} across both N levels with spectral data during fruit development

Wavelengths range	Pre-treatment [number]		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
$MMS1+PGS_{all}$	w/o		0.55	0.31	-1.E-03	0.54	0.32	-5.E-04
$MMS1+PGS_{red}$	w/o		0.70	0.25	1.E-07	0.64	0.28	-4.E-04
MMS1	w/o		0.59	0.30	9.E-08	0.58	0.30	-2.E-03
PGS_{all}	w/o		0.55	0.31	-2.E-03	0.51	0.33	-2.E-03
$PGSr_{ed}$	w/o		0.66	0.27	2.E-07	0.59	0.30	2.E-03
MMS1	**Norris d2g13**	[1]	0.70	0.26	-6.E-09	**0.66**	**0.27**	**1.E-03**
MMS1	SaGo d1s9	[2]	0.69	0.26	-6.E-08	0.65	0.28	8.E-04
PGS_{red}	**Norris d1g3**	**[3]**	**0.74**	**0.24**	**-2.E-08**	0.62	0.29	-3.E-03
PGS_{red}	Norris d2g41	[4]	0.71	0.25	1.E-07	0.62	0.29	-7.E-04
PGS_{red}	**Base + SaGo d1s5**	**[5]**	**0.74**	**0.24**	**-1.E-08**	0.60	0.30	-3.E-04
$MMS1+PGS_{red}$	**MMS1 [1] + PGS_{red} [3]**		**0.74**	**0.24**	**-1.E-08**	0.62	0.29	1.E-03
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [4]		0.68	0.26	-1.E-08	0.64	0.28	-1.E-04
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [5]		0.62	0.29	-2.E-08	0.59	0.30	3.E-03
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [3]		0.58	0.30	-2.E-08	0.56	0.31	-3.E-03
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [4]		0.69	0.26	-5.E-08	0.65	0.28	-2.E-03
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [5]		0.63	0.28	-2.E-08	0.60	0.29	-3.E-03

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations for MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, Underlined wavelengths ranges/pre-treatments were also tested in calibration with external validation, plot values predicted by models resulting from underlined wavelengths range/pre-treatment were used to test prediction of genotypes

Calibration and external validation

For both dates calibration with external validation resulted in decreased R^2_{Cal} and increased $RMSE_{Cal}$ compared to cross validation (Tab. B 8, Tab. B 9, Tab. B 10, Tab. B 11). For the first measuring date external validation with untreated $MMS1+PGS_{red}$ resulted in a low R^2_{EV} across both validation sets. For Val-2 R^2_{EV} was higher. Separating Val-2 in DH lines and test hybrids did not alter results for external validation. For Val-1 external validation failed. It also failed for all validation sets with pre-treated MMS1 (Tab. B 10).

For spectral data of the second date external validation failed for all validation sets (Tab. B 11).

Tab. B 10: Calibrations and external validations for Nup_{MAT} across both N levels with spectral data before flowering

Wavelengths range	Pre-treatment	Dataset for validation	Calibration			External validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1+PGS_{red}	w/o	Val-1+Val-2	0.58	0.30	4.E-08	0.35	0.46	7.E-02
		Val-1	0.58	0.30	4.E-08	Failed		
		Val-2	0.58	0.30	4.E-08	0.52	0.42	-1.E-01
		Val-2 DH	0.58	0.30	4.E-08	0.52	0.42	-6.E-02
		Val-2 TH	0.58	0.30	4.E-08	0.53	0.42	-2.E-01
MMS1	Base + SaGo d1s17	Val-1+Val-2	0.60	0.29	4.E-08			
		Val-1	0.60	0.29	4.E-08			
		Val-2	0.60	0.29	4.E-08	Failed		
		Val-2 DH	0.60	0.29	4.E-08			
		Val-2 TH	0.60	0.29	4.E-08			

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, g gap size, s number of smoothing points, Base baseline offset correction, w/o no pre-treatment, DH DH lines, TH test hybrids, Failed calibration model had no predictive ability (for the first PLSR component explained variance of validation was zero)

Tab. B 11: Calibrations and external validations for Nup_{MAT} across both N levels with spectral data during fruit development

Wavelengths range	Pre-treatment	Dataset for validation	Calibration			External validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	Norris d1g3	Val-1+Val-2	0.30	0.39	-2.E-08			
		Val-1	0.30	0.39	-2.E-08			
		Val-2	0.30	0.39	-2.E-08	Failed		
		Val-2 DH	0.30	0.39	-2.E-08			
		Val-2 TH	0.30	0.39	-2.E-08			

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, PGS_{red} 951 –1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, d derivation, g gap size, DH DH lines, TH test hybrids, Failed calibration model had no predictive ability (for the first PLSR component explained variance of validation was zero)

N1

Nup_{MAT}

Within N1 plot values of Nup_{MAT} of the calibration set ranged from 0.8 dt ha^{-1} to 2.6 dt ha^{-1} with a mean of 1.5 dt ha^{-1}. The data space covered by Val-1+Val-2 was broader with a lower mean for Val-1 and a higher mean for Val-2 (Fig. B 12).

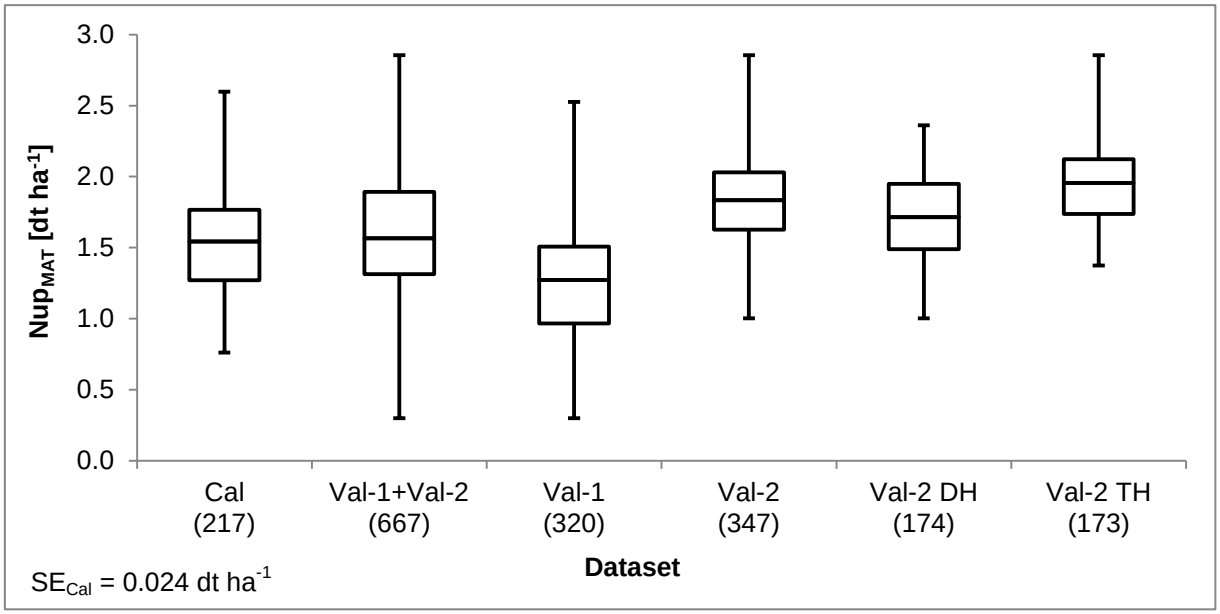

Fig. B 12: Boxplots of plot values for Nup_{MAT} within N1 for different datasets
Cal Calibration + cross validation set, Val-1 validation set 1, Val-2 validation set 2, Val-2DH DH lines of Val-2, Val-2 TH test hybrids of Val-2, Numbers in brackets size of dataset, SE_{Cal} standard error of reference values in calibration dataset

Calibration and cross validation

For both measuring dates a high bias of calibration was observed when noisy areas between 1350 nm and 1551 nm and above 1760 nm as in PGS_{all} were included (Tab. B 12, Tab. B 13). For the first date MMS1 lead to better results in calibration and cross validation than untreated PGS_{red}. Pre-treatment improved calibrations and cross validations with MMS1 and PGS_{red}. But their combination did not lead to further improvement. The best calibration and cross validation resulted from pre-treated MMS1 (Tab. B 12). $RMSE_{Cal}$ and $RMSE_{CV}$ were about ten times higher than the standard error of the reference values (Fig. B 12, Tab. B 12).

For the second date MMS1 resulted in better calibrations and cross validations than PGS_{red}. Pre-treatment of MMS1 only slightly increased R^2_{Cal} but lead to a clearly improved R^2_{Val}. No clear improvement was accomplished by pre-treatment of PGS_{red}.

The best calibration results were detected for a combination of pre-treated MMS1 and PGS_{red} but the best cross validation resulted from pre-treated MMS1 only (Tab. B 13). $RMSE_{Cal}$ and $RMSE_{CV}$ were eight to ten times higher than the standard error of the reference values (Fig. B 12, Tab. B 13).

Within N1 best results for calibration and cross validation did not clearly differ between the first and the second measurement date. But for the first date best results were found within one pre-treated wavelengths range whereas for the second date best calibration results derived from another pre-treated wavelengths range than best cross validation results (Tab. B 12, Tab. B 13).

Tab. B 12: Calibrations and cross validations for Nup_{MAT} within N1 with spectral data before flowering

Wavelengths range	Pre-treatment [number]		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
$MMS1+PGS_{all}$	w/o		0.59	0.22	-1.E-03	0.47	0.26	-8.E-03
$MMS1+PGS_{red}$	w/o		0.67	0.20	-6.E-09	0.59	0.23	-3.E-03
MMS1	w/o		0.63	0.21	2.E-07	0.57	0.23	1.E-03
PGS_{all}	w/o		0.65	0.21	-5.E-05	0.48	0.26	2.E-03
PGS_{red}	w/o		0.59	0.22	-5.E-08	0.55	0.24	-2.E-03
MMS1	**MMS1 Norris d1g41**	**[1]**	**0.72**	**0.19**	**-5.E-08**	**0.64**	**0.21**	**3.E-03**
PGS_{red}	PGS_{red} Norris d1g33	[2]	0.69	0.20	-4.E-08	0.57	0.23	-4.E-04
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [2]		0.65	0.21	-4.E-08	0.58	0.23	2.E-03

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, Underlined wavelengths ranges/pre-treatments were also tested in calibration with external validation, plot values predicted by models resulting from underlined wavelengths range/pre-treatment were used to test prediction of genotypes

Tab. B 13: Calibrations and cross validations for Nup_{MAT} within N1 with spectral data during fruit development

Wavelengths range	Pre-treatment		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
$MMS1+PGS_{all}$	w/o		0.53	0.24	-4.E-03	0.40	0.27	2.E-03
$MMS1+PGS_{red}$	w/o		0.61	0.21	3.E-07	0.40	0.27	-8.E-04
MMS1	w/o		0.66	0.20	-5.E-07	0.50	0.24	-4.E-03
PGS_{all}	w/o		0.53	0.23	-7.E-03	0.34	0.28	-3.E-03
PGS_{red}	w/o	[1]	0.62	0.21	3.E-07	0.45	0.26	3.E-03
MMS1	**Norris d2g9**	**[2]**	0.67	0.27	-2.E-08	**0.63**	**0.28**	**-5.E-04**
MMS1	SaGo d1s33	[3]	0.65	0.20	-6.E-08	0.53	0.24	4.E-03
PGS_{red}	Base+Norris d1g41	[4]	0.63	0.21	-9.E-08	0.45	0.26	-3.E-03
PGS_{red}	SaGo d2s41	[5]	0.65	0.20	4.E-09	0.41	0.26	3.E-03
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [1]		0.60	0.22	-2.E-07	0.41	0.26	4.E-03
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [4]		0.63	0.21	-7.E-08	0.47	0.25	-4.E-03
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [5]		0.61	0.21	-5.E-08	0.45	0.25	-2.E-03
$MMS1+PGS_{red}$	MMS1 [3] + PGS_{red} [1]		0.60	0.22	-2.E-07	0.42	0.26	-2.E-03
$MMS1+PGS_{red}$	**MMS1 [3] + PGS_{red} [4]**		**0.70**	**0.19**	**-7.E-08**	0.51	0.24	-1.E-03
$MMS1+PGS_{red}$	MMS1 [3] + PGS_{red} [5]		0.62	0.21	-6.E-08	0.49	0.25	-2.E-03

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, Underlined wavelengths ranges/pre-treatments were also tested in calibration with external validation, plot values predicted by models resulting from underlined wavelengths range/pre-treatment were used to test prediction of genotypes

Calibration and external validation

For both measuring dates calibration with external validation resulted in decreased R^2 and increased RMSE (Tab. B 12, Tab. B 13, Tab. B 14, Tab. B 15). For spectral data of the first date external validation failed (Tab. B 14).

With spectral data of the second date $RMSE_{Cal}$ was lower but external validation did not fail for all datasets although R^2_{EV} were low (Tab. B 15).

Tab. B 14: Calibrations and external validations for Nup_{MAT} within N1 with spectral data before flowering

Wavelengths range	Pre-treatment	Dataset for validation	Calibration			External validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Norris d1g41	Val-1+Val-2	0.31	0.29	-3.E-08	Failed		
		Val-1	0.31	0.29	-3.E-08			
		Val-2	0.31	0.29	-3.E-08			
		Val-2 DH	0.31	0.29	-3.E-08			
		Val-2 TH	0.31	0.29	-3.E-08			

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, Norris Norris gap derivative transformation, d derivation, g gap size, DH DH lines, TH test hybrids, Failed calibration model had no predictive ability (for the first PLSR component explained variance of validation was zero)

Tab. B 15: Calibrations and external validations for Nup_{MAT} within N1 with spectral data during fruit development

Wavelengths range	Pre-treatment	Dataset for validation	Calibration			External validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Norris d2g9	Val-1+Val-2	0.15	0.32	-4.E-08		Failed	
		Val-1	0.15	0.32	-4.E-08	0.26	0.45	-4.E-01
		Val-2	0.15	0.32	-4.E-08		Failed	
		Val-2 DH	0.15	0.32	-4.E-08		Failed	
		Val-2 TH	0.26	0.29	-4.E-08	0.42	0.33	8.E-02

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, Norris Norris gap derivative transformation, d derivation, g gap size, DH DH lines, TH test hybrids, Failed calibration model had no predictive ability (for the first PLSR component explained variance of validation was zero)

N0

Nup_{MAT}

Within N0 plot values of Nup_{MAT} of the calibration set ranged from 0.3 dt ha^{-1} to 1.6 dt ha^{-1} with a mean of 0.9 dt ha^{-1}. Val-1+Val-2 covered a broader range with lower mean for Val-1 and a higher mean for Val-2 (Fig. B 13).

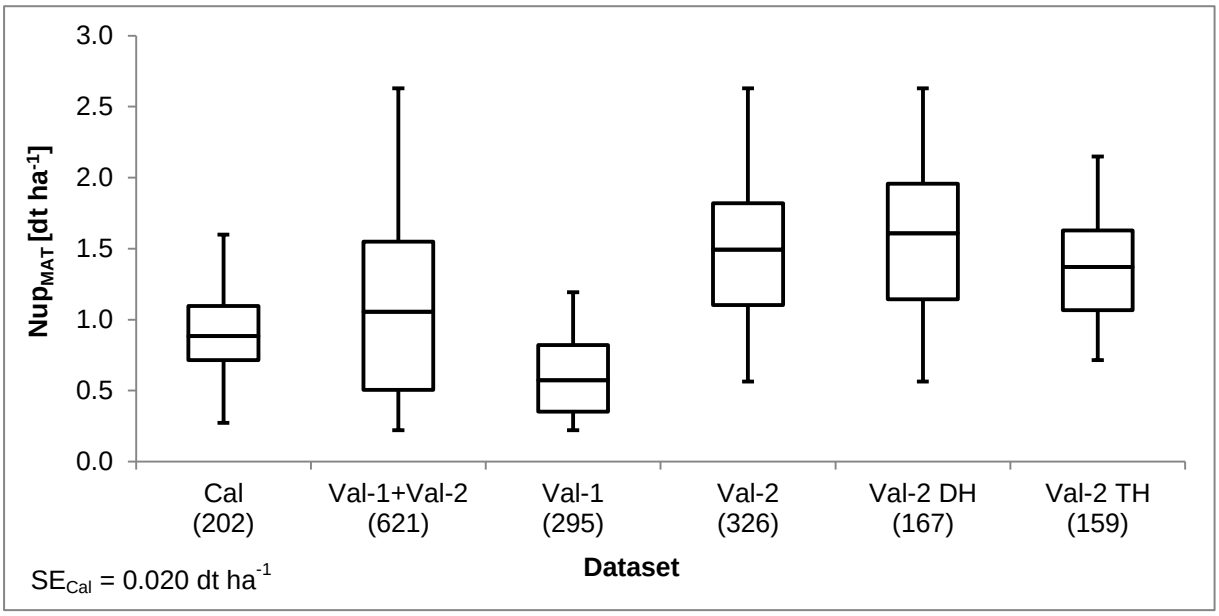

Fig. B 13: Boxplots of plot values of Nup_{MAT} within N0 for different datasets
Cal Calibration + cross validation set, Val-1 validation set 1, Val-2 validation set 2, Val-2 DH DH lines of Val-2, Val-2 TH test hybrids of Val-2, Numbers in brackets size of dataset, SE_{Cal} standard error of reference values in calibration dataset

Calibration and cross validation

For both measuring dates calibrations and cross validations that derived from wavelengths ranges with noisy areas between 1350 nm and 1551 nm and above 1760 nm showed high bias of calibration. Therefore, only MMS1 and PGS_{red} were used for further analyses (Tab. B 16, Tab. B 17). For the first measuring date highest R^2_{Cal} was detected for untreated MMS1+PGS_{red}. Compared to untreated MMS1 and PGS_{red} pre-treatment improved calibrations and cross validations but R^2_{Cal} of untreated MMS1+PGS_{red} was not exceeded. In case of pre-treated MMS1 R^2_{Cal} was only slightly smaller but R^2_{CV} was clearly higher. Combinations of pre-treated MMS1 and PGS_{red} did not further improve calibration and cross validation. The best calibration derived from pre-treated MMS1+PGSred, the best cross validation from pre-treated MMS1. But the difference between calibration results of both was only

little (Tab. B 16). $RMSE_{Cal}$ and $RMSE_{CV}$ were six to eight times higher than the standard error of the reference values (Fig. B 13, Tab. B 16).

For the second date MMS1 lead to better calibration and cross validation than PGS_{red}. This was true for untreated and pre-treated wavelengths ranges. Pre-treatment resulted in better results for calibration and cross validation for MMS1 as well as for PGS_{red}. Combination of MMS1 and PGS_{red} after pre-treatment did not further improve calibrations and cross validations. The best calibration and cross validation derived from pre-treated MMS1 (Tab. B 17). $RMSE_{Cal}$ and $RMSE_{CV}$ were six to eight times higher than the standard error of the reference values (Fig. B 13, Tab. B 17).

Calibration results did not differ between the first and the second date. But the best cross validation of the first date showed a higher R^2_{Val} than the best cross validation of the second date (Tab. B 16, Tab. B 17).

Tab. B 16: Calibrations and cross validations for Nup_{MAT} within N0 with spectral data before flowering

Wavelengths range	Pre-treatment [number]		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
$MMS1+PGS_{all}$	w/o		0.74	0.15	-6.E-05	0.70	0.16	-4.E-03
$MMS1+PGS_{red}$	**w/o**		**0.83**	**0.12**	**-2.E-08**	**0.75**	**0.14**	**-5.E-04**
MMS1	w/o		0.79	0.13	4.E-08	0.76	0.14	3.E-04
PGS_{all}	w/o		0.75	0.14	2.E-04	0.69	0.16	-6.E-04
PGS_{red}	w/o		0.76	0.14	-4.E-08	0.71	0.16	-2.E-03
MMS1	**Norris d1g13**	**[1]**	**0.82**	**0.12**	**-4.E-08**	**0.80**	**0.13**	**-4.E-04**
PGS	SaGo d1s33	[2]	0.77	0.14	-7.E-09	0.72	0.15	-1.E-03
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [2]		0.80	0.13	-2.E-08	0.76	0.14	-6.E-04

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, Underlined wavelengths ranges/pre-treatments were also tested in calibration with external validation, plot values predicted by models resulting from underlined wavelengths range/pre-treatment were used to test prediction of genotypes

Tab. B 17: Calibrations and cross validations for Nup_{MAT} within N0 with spectral data during fruit development

Wavelengths range	Pre-treatment [number]		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
$MMS1+PGS_{all}$	w/o		0.73	0.15	-2.E-04	0.72	0.16	4.E-03
$MMS1+PGS_{red}$	w/o		0.72	0.15	4.E-08	0.71	0.16	8.E-04
MMS1	w/o		0.77	0.14	9.E-09	0.73	0.15	-5.E-04
PGS_{all}	w/o		0.73	0.15	2.E-03	0.67	0.17	9.E-03
PGS_{red}	w/o		0.72	0.15	5.E-08	0.72	0.16	2.E-03
MMS1	**Norris d1g7**	**[1]**	**0.82**	**0.12**	**3.E-08**	**0.77**	**0.14**	**1.E-03**
MMS1	**Norris d1g9**	**[2]**	**0.82**	**0.12**	**2.E-08**	**0.77**	**0.14**	**3.E-04**
MMS1	**Base + Norris d1g9**	**[3]**	**0.82**	**0.12**	**7.E-09**	**0.77**	**0.14**	**-2.E-03**
PGS_{red}	Norris d1g43	[4]	0.79	0.13	1.E-08	0.74	0.15	-1.E-03
PGS_{red}	Base + Norris d1g41	[5]	0.79	0.13	8.E-09	0.73	0.15	7.E-04
PGS_{red}	Base + Norris d1g43	[6]	0.79	0.13	2.E-08	0.73	0.15	-5.E-04
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [4]		0.77	0.14	3.E-08	0.73	0.15	-1.E-03
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [5]		0.77	0.14	3.E-08	0.74	0.15	-1.E-03
$MMS1+PGSr_{ed}$	MMS1 [1] + PGS_{red} [6]		0.77	0.14	3.E-08	0.74	0.15	-1.E-03
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [4]		0.81	0.13	1.E-08	0.76	0.14	-3.E-03
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [5]		0.80	0.13	1.E-08	0.75	0.14	3.E-04
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [6]		0.81	0.13	1.E-08	0.75	0.14	-9.E-04
$MMS1+PGS_{red}$	MMS1 [3] + PGS_{red} [4]		0.76	0.14	-3.E-08	0.73	0.15	2.E-04
$MMS1+PGS_{red}$	MMS1 [3] + PGS_{red} [5]		0.76	0.14	-4.E-08	0.73	0.15	7.E-04
$MMS1+PGS_{red}$	MMS1 [3] + PGS_{red} [6]		0.76	0.14	-3.E-08	0.72	0.15	2.E-03

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, Underlined wavelengths ranges/pre-treatments were also tested in calibration with external validation, plot values predicted by models resulting from underlined wavelengths range/pre-treatment were used to test prediction of genotypes

Calibration and external validation

For both measuring dates R^2_{Cal} decreased and $RMSE_{Cal}$ increased compared to calibration with cross validation (Tab. B 16, Tab. B 17, Tab. B 18, Tab. B 19).

For spectral data of the first date external validation with Val-1 failed and with Val-1+Val-2 R^2_{EV} was low. But external validations with Val-2 resulted in R^2_{EV} close to $R^2_{CV.}$ With DH lines of data set Val-2 R^2_{EV} exceeded R^2_{CV} (Tab. B 16, Tab. B 18).

For spectral data of the second date no external validation failed. With Val-1 R^2_{Cal} was nearly as high as in calibration with cross validation whereas R^2_{EV} showed a clear decrease and RMSEs a clear increase (Tab. B 17, Tab. B 18).

In cases where external validation was successful spectral data of the first date lead to better results in calibration and external validation (Tab. B 18, Tab. B 19).

Tab. B 18: Calibrations and external validations for Nup_{MAT} within N0 with spectral data before flowering

Wavelengths range	Pre-treatment	Dataset for validation	Calibration			External validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Norris d1g13	Val-1+Val-2	0.70	0.16	-2.E-08	0.34	0.51	4.E-01
		Val-1	0.66	0.17	-2.E-08		Failed	
		Val-2	0.70	0.16	-2.E-08	0.75	0.38	3.E-01
		Val-2 DH	0.70	0.16	-2.E-08	0.82	0.39	2.E-01
		Val-2 TH	0.79	0.13	-3.E-08	0.68	0.33	2.E-01

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, Norris Norris gap derivative transformation, d derivation, g gap size, DH DH lines, TH test hybrids, Failed calibration model had no predictive ability (for the first PLSR component explained variance of validation was zero)

Tab. B 19: Calibrations and external validations for Nup_{MAT} within N0 with spectral data during fruit development

Wavelengths range	Pre-treatment	Dataset for validation	Calibration			External validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Norris d1g7	Val-1+Val-2	0.61	0.18	1.E-08	0.23	0.58	1.E-02
		Val-1	0.80	0.13	3.E-08	0.44	0.36	-2.E-01
		Val-2	0.61	0.18	1.E-08	0.56	0.51	-4.E-01
		Val-2 DH	0.61	0.18	1.E-08	0.62	0.55	-4.E-01
		Val-2 TH	0.61	0.18	1.E-08	0.43	0.46	-4.E-01

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, Norris Norris gap derivative transformation, d derivation, g gap size, DH DH lines, TH test hybrids

N1+N0 vs. N1 and N0

The best calibrations and cross validations across both nitrogen levels showed higher R^2_{Cal} and R^2_{CV} than calibrations and cross validations within in N1 while RMSEs were the same (Tab. B 8, Tab. B 12). Comparing best calibrations across both nitrogen levels with those within N0 revealed a different pattern. R^2_{Cal} were very similar while R^2_{CV} were lower within N0 than across both nitrogen levels. Within N0 absolute RMSEs were smaller than across both nitrogen levels and within N1 (Tab. B 8, Tab. B 12, Tab. B 16). If RMSEs are expressed as percentage of mean of Nup_{MAT} of the respective nitrogen level calibrations and cross validations within N1 were lowest ($RMSE_{Cal}$ = 12.3 %, $RMSE_{CV}$ = 13.6 %), followed by N0 ($RMSE_{Cal}$ = 13.6 %, $RMSE_{CV}$ = 15.9 %). Highest RMSEs were found for calibrations and cross validations across both nitrogen levels ($RMSE_{Cal}$ = 15.0 %, $RMSE_{CV}$ = 16.2 %).

Seed yield dry matter (Seed DM)

N1+N0

Seed DM

Plot values of Seed DM of the calibration set across nitrogen levels ranged from 5.5 dt ha^{-1} to 47.9 dt ha^{-1} with a mean of 25.0 dt ha$^{-1.}$ The range covered by Val-1+Val-2 was different with a similar mean and a broader range for Val 1 and a higher mean for Val-2 (Fig. B 14).

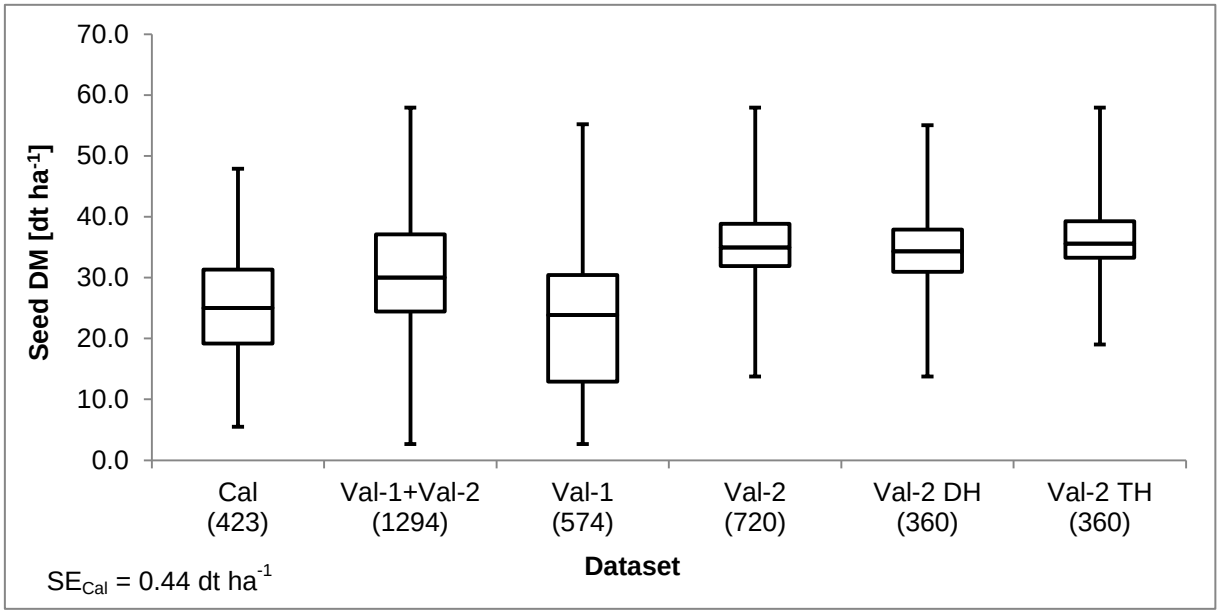

Fig. B 14: Boxplots of plot values of Seed DM across N1 and N0 for different datasets
Cal Calibration + cross validation set, Val-1 validation set 1, Val-2 validation set 2, Val-2DH DH lines of Val-2, Val-2 TH test hybrids of Val-2, Numbers in brackets size of dataset, SE_{Cal} standard error of reference values in calibration dataset

Calibration and cross validation

For spectral data of both measuring dates high bias of calibration was observed when noisy areas between 1350 and 1551 nm and above 1760 nm as in PGS_{all} were used in calibration (Tab. B 20, Tab. B 21). Therefore, PGS_{all} was not used in further analyses. For spectral data of the first date MMS1 resulted in better calibrations than PGS_{red}. Whereas calibrations and cross validations of MMS1 could be improved by pre-treatments this was not successful for PGS_{red}. Combination of pre-treated MMS1 and untreated PGS_{red} did not lead to better calibrations than pre-treated MMS1 alone

(Tab. B 20). $RMSE_{Cal}$ and $RMSE_{CV}$ were more ten times higher than the standard error of the reference values (Fig. B 14, Tab. B 20).

Calibrations and cross validations derived from spectral data of the second date were better with untreated MMS1 than with untreated PGS_{red}. After pre-treatment PGS_{red} calibrations were similar to those of MMS1 calibrations. But using pre-treated MMS1 resulted in better cross validations. Best calibrations and cross validations resulted from pre-treated MMS1. In one case combination of pre-treated MMS1 and PGS_{red} improved the calibration by decreasing $RMSE_{Cal}$ but quality of cross validation was not improved. Good calibrations were also found for PGS_{red} but their cross validations suffered from low R^2_{CV} and high $RMSE_{CV}$ (Tab. B 21). $RMSE_{Cal}$ and $RMSE_{CV}$ were more than ten times higher than the standard error of the reference values (Fig. B 14, Tab. B 21).

Better calibrations were found for spectral data of the first date than for spectral data of the second date (Tab. B 20, Tab. B 21).

Tab. B 20: Calibrations and cross validations for Seed DM across both N levels with spectral data before flowering

Wavelengths range	Pre-treatment [number]		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
$MMS1+PGS_{all}$	w/o		0.53	6.25	-2.E-01	0.46	6.73	-2.E-01
$MMS1+PGS_{red}$	w/o		0.61	5.71	-3.E-06	0.53	6.27	-2.E-02
MMS1	w/o		0.56	6.05	-4.E-06	0.54	6.24	7.E-03
PGS_{all}	w/o		0.48	6.61	-1.E-01	0.44	6.87	-9.E-02
PGS_{red}	w/o	[1]	0.54	6.19	5.E-07	0.47	6.70	1.E-02
MMS1	**SaGo d1s25**	**[2]**	**0.68**	**5.17**	**5.E-06**	**0.61**	**5.70**	**3.E-02**
MMS1	**SaGo d1s27**	**[3]**	**0.68**	**5.16**	**-3.E-06**	**0.61**	**5.72**	**1.E-01**
$MMS1 + PGS_{red}$	MMS1 [2] + PGS_{red} [1]		0.54	6.18	7.E-07	0.47	6.66	-8.E-04
$MMS1 + PGS_{red}$	MMS1 [3] + PGS_{red} [1]		0.48	6.60	2.E-07	0.45	6.82	-2.E-02

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, Underlined wavelengths ranges/pre-treatments were also tested in calibration with external validation, plot values predicted by models resulting from underlined wavelengths range/pre-treatment were used to test prediction of genotypes

Tab. B 21: Calibrations and cross validations for Seed DM across both N levels with spectral data during fruit development

Wavelengths range	Pre-treatment [number]		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
$MMS1+PGS_{all}$	w/o		0.53	6.26	-5.E-02	0.49	6.54	-2.E-02
$MMS1+PGS_{red}$	w/o		0.63	5.56	-2.E-06	0.57	5.99	-1.E-01
MMS1	w/o		0.56	3.05	-3.E-06	0.53	6.28	4.E-02
PGS_{all}	w/o		0.51	6.37	1.E-02	0.47	6.69	2.E-03
PGS_{red}	w/o		0.55	6.14	-2.E-06	0.51	6.41	2.E-02
MMS1	**Norris d2g17**	**[1]**	**0.65**	**5.42**	**8.E-07**	**0.57**	**6.00**	**-6.E-02**
MMS1	**Norris d2g41**	**[2]**	**0.64**	**5.47**	**3.E-06**	**0.58**	**5.96**	**5.E-02**
MMS1	**SaGo d1s7**	**[3]**	**0.64**	**5.49**	**-1.E-06**	**0.58**	**5.95**	**-3.E-02**
PGS_{red}	**SaGo d1s3**	**[4]**	**0.65**	**5.44**	**7.E-07**	0.53	6.26	-2.E-02
PGS_{red}	SaGo d1s25	[5]	0.62	5.65	8.E-07	0.55	6.16	8.E-02
PGS_{red}	**Base + SaGo d2s13**	**[6]**	**0.65**	**5.40**	**1.E-06**	0.53	6.30	-1.E-01
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [4]		0.62	5.61	8.E-07	0.52	6.37	4.E-03
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [5]		0.62	5.64	7.E-07	0.55	6.14	6.E-03
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [6]		0.63	5.54	1.E-06	0.30	7.67	3.E-01
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [4]		0.62	5.61	7.E-07	0.53	6.31	1.E-02
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [5]		0.50	6.45	7.E-07	0.48	6.61	-1.E-02
$MMS1+PGS_{red}$	**MMS1 [2] +PGS_{red} [6]**		**0.65**	**5.38**	**1.E-06**	0.54	6.23	2.E-02
$MMS1+PGS_{red}$	MMS1 [3] + PGS_{red} [4]		0.59	5.84	3.E-07	0.53	6.27	5.E-02
$MMS1+PGS_{red}$	MMS1 [3] + PGS_{red} [5]		0.60	5.77	6.E-07	0.55	6.10	4.E-02
$MMS1+PGS_{red}$	MMS1 [3] + PGS_{red} [6]		0.62	5.63	3.E-07	0.57	6.02	4.E-02

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, Underlined wavelengths ranges/pre-treatments were also tested in calibration with external validation, plot values predicted by models resulting from underlined wavelengths range/pre-treatment were used to test prediction of genotypes

Calibration and external validation

For spectral data of both measuring dates external validation decreased calibration quality compared to calibration and cross validation (Tab. B 20, Tab. B 21, Tab. B 22, Tab. B 23). All external validations with spectral data of the first date failed (Tab. B 22).

With spectral data during fruit development external validations were successful for all validation sets except for Val-1+Val-2. R^2_{EV} were as high as or higher than R^2_{CV}. The RMSE were higher in external validation than in cross validation (Tab. B 21, Tab. B 23).

Tab. B 22: Calibrations and external validations for Seed DM across both N levels with spectral data before flowering

Wavelengths range	Pre-treatment	Dataset for validation	Calibration			External validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	SaGo d1s25	Val-1 + Val-2	0.43	6.90	6.E-07	Failed		
		Val-1	0.43	6.90	6.E-07			
		Val-2	0.43	6.90	6.E-07			
		Val-2 DH	0.43	6.90	6.E-07			
		Val-2 TH	0.43	6.90	6.E-07			

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, SaGo Savitzky-Golay derivative transformation, d derivation, s number of smoothing points, DH DH lines, TH test hybrids, Failed calibration model had no predictive ability (for the first PLSR component explained variance of validation was zero)

Tab. B 23: Calibrations and external validations for Seed DM across both N levels with spectral data during fruit development

Wavelengths range	Pre-treatment	Dataset for validation	Calibration			External validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Norris d2g41	Val-1+Val-2	0.37	7.28	8.E-07	Failed		
		Val-1	0.37	7.28	8.E-07	0.56	6.65	5.E+00
		Val-2	0.37	7.23	8.E-07	0.68	6.59	-3.E+00
		Val-2 DH	0.37	7.23	8.E-07	0.70	6.01	-3.E-01
		Val-2 TH	0.37	7.23	8.E-07	0.66	7.12	-5.E+00

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, Norris Norris gap derivative transformation, d derivation, g gap size, DH DH lines, TH test hybrids, Failed calibration model had no predictive ability (for the first PLSR component explained variance of validation was zero)

N1

Seed DM

Plot values of Seed DM within N1 ranged from 9.5 dt ha^{-1} to 47.9 dt ha^{-1} with a mean of 28.8 dt ha^{-1}. Val-1+Val-2 covered a different range with a similar mean for Val-1 and a higher mean for Val-2 (Fig. B 15).

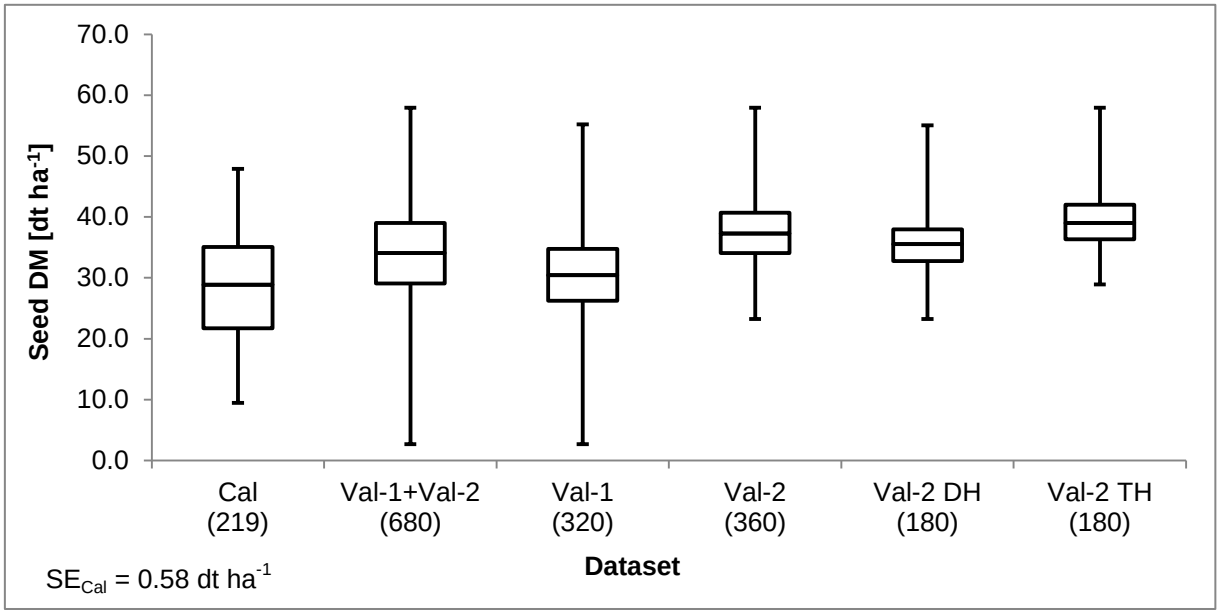

Fig. B 15: Boxplots of plot values of Seed DM within N1 for different datasets
Cal Calibration + cross validation set, Val-1 validation set 1, Val-2 validation set 2, Val-2DH DH lines of Val-2, Val-2 TH test hybrids of Val-2, Numbers in brackets size of dataset, SE_{Cal} standard error of reference values in calibration dataset

Calibration and cross validation

For spectral data of both measuring dates bias of calibrations with noisy areas between 1350 nm and 1551 nm and above 1760 nm was very high (Tab. B 24, Tab. B 25). Therefore PGS_{all} was excluded from further analyses. For spectral data of the first date untreated PGS_{red} resulted in better calibrations than untreated MMS1. By pre-treatment calibrations and cross validations with MMS1 were improved while no pre-treatment was found that improved PGS_{red} calibration and cross validation. Though $RMSE_{CV}$ was lowest for combination of pre-treated MMS1 and untreated PGS_{red} other parameters of calibration and cross validation could not be improved (Tab. 28). $RMSE_{Cal}$ and $RMSE_{CV}$ were more than ten times higher than the standard error of the reference values (Fig. B 15, Tab. B 24).

For spectral data of the second date untreated PGS_{red} resulted in better calibrations and cross validations than untreated MMS1. Pre-treatment improved MMS1 and PGS_{red} calibrations and cross validations. Calibrations and cross validations with pre-treated MMS1 outperformed those with pre-treated PGS_{red}. Calibrations and cross validations were not further improved by combination of pre-treated MMS1 and PGS_{red} (Tab. B 25). $RMSE_{Cal}$ and $RMSE_{CV}$ were more than ten times higher than the standard error of the reference values (Fig. B 15, Tab. B 25).

Calibrations and cross validations derived from spectral data of the first date had better quality than those derived from spectral data of the second date (Tab. B 24, Tab. B 25).

Tab. B 24: Calibrations and cross validations for Seed DM within N1 with spectral data before flowering

Wavelengths range	Pre-treatment [number]		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
$MMS1+PGS_{all}$	w/o		0.46	6.35	-7.E-02	0.26	7.47	-7.E-02
$MMS1+PGS_{red}$	w/o		0.52	6.01	2.E-06	0.36	6.94	1.E-03
MMS1	w/o		0.39	6.72	2.E-06	0.35	6.99	4.E-02
PGS_{all}	w/o		0.44	6.47	-3.E-01	0.28	7.35	-3.E-01
PGS_{red}	w/o	[1]	0.45	6.38	-1.E-06	0.31	7.21	-8.E-02
MMS1	**Norris d1g23**	**[2]**	**0.71**	**4.65**	**-3.E-06**	**0.51**	**6.12**	**2.E-01**
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [1]		0.38	6.78	-5.E-07	0.28	7.35	1.E-03

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, d derivation, g gap size, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, Underlined wavelengths ranges/pre-treatments were also tested in calibration with external validation, plot values predicted by models resulting from underlined wavelengths range/pre-treatment were used to test prediction of genotypes

Tab. B 25: Calibrations and cross validations for Seed DM within N1 with spectral data during fruit development

Wavelengths range	Pre-treatment [number]		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
$MMS1+PGS_{all}$	w/o		0.55	5.78	-6.E-02	0.37	6.89	-1.E-02
$MMS1+PGS_{red}$	w/o		0.58	5.57	-2.E-06	0.44	6.53	8.E-02
MMS1	w/o		0.41	6.62	4.E-07	0.37	6.92	-2.E-02
PGS_{all}	w/o		0.48	6.24	-2.E-01	0.26	7.45	-2.E-01
PGS_{red}	w/o		0.55	5.77	-1.E-06	0.41	6.69	2.E-02
MMS1	**Norris d1g17**	**[1]**	0.62	5.30	3.E-06	**0.47**	**6.30**	**-1.E-01**
MMS1	**Base + Norris d2g15**	**[2]**	**0.64**	**5.18**	**-6.E-06**	0.43	6.56	-6.E-03
MMS1	Base + Norris d2g41	[3]	0.61	5.39	8.E-07	0.46	6.36	-4.E-03
PGS_{red}	Base + SNV	[4]	0.57	5.68	-6.E-06	0.44	6.46	-4.E-02
$MMS1 + PGS_{red}$	MMS1 [1] + PGS_{red} [4]		0.51	6.05	-1.E-06	0.39	6.75	7.E-02
$MMS1 + PGS_{red}$	MMS1 [2] + PGS_{red} [4]		0.51	6.05	-1.E-06	0.42	6.64	1.E-01
$MMS1 + PGS_{red}$	MMS1 [3] + PGS_{red} [4]		0.51	6.05	-1.E-06	0.41	6.72	6.E-03

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, d derivation, g gap size, SNV standard normal variate transformation, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, Underlined wavelengths ranges/pre-treatments were also tested in calibration with external validation, plot values predicted by models resulting from underlined wavelengths range/pre-treatment were used to test prediction of genotypes

Calibration and external validation

Not only resulted calibrations with external validations in very low R^2_{Cal} and high $RMSE_{Cal}$ but also failed external validations for spectral data of both measuring dates and for all validation sets (Tab. B 26, Tab. B 27).

Tab. B 26: Calibrations and external validations for Seed DM within N1 with spectral data before flowering

Wavelengths range	Pre-treatment	Dataset for validation	Calibration			External validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Norris d1g23	Val-1+Val-2	0.17	7.86	-4.E-07	Failed		
		Val-1	0.17	7.86	-4.E-07			
		Val-2	0.17	7.86	-4.E-07			
		Val-2 DH	0.17	7.86	-4.E-07			
		Val-2 TH	0.17	7.86	-4.E-07			

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, Norris Norris gap derivative transformation, d derivation, g gap size, DH DH lines, TH test hybrids, Failed calibration model had no predictive ability (for the first PLSR component explained variance of validation was zero)

Tab. B 27: Calibrations and external validations for Seed DM within N1 with spectral data during fruit development

Wavelengths range	Pre-treatment	Dataset for validation	Calibration			External validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base + Norris d2g15	Val-1+Val-2	0.06	8.37	-4.E-07	Failed		
		Val-1	0.06	8.37	-4.E-07			
		Val-2	0.06	8.37	-4.E-07			
		Val-2 DH	0.06	8.37	-4.E-07			
		Val-2 TH	0.06	8.37	-4.E-07			

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, Base Baseline offset correction, Norris Norris gap derivative transformation, d derivation, g gap size, DH DH lines, TH test hybrids, Failed calibration model had no predictive ability (for the first PLSR component explained variance of validation was zero)

N0

Seed DM

Plot values of Seed DM of the calibration set within N0 ranged from 5.5 dt ha^{-1} to 40.3 dt ha^{-1} with a mean of 20.8 dt ha^{-1} (Fig. B 16). Val-1+Val-2 covered a broader range with a lower mean for Val-1 and a higher mean for Val-2 (Fig. B 16).

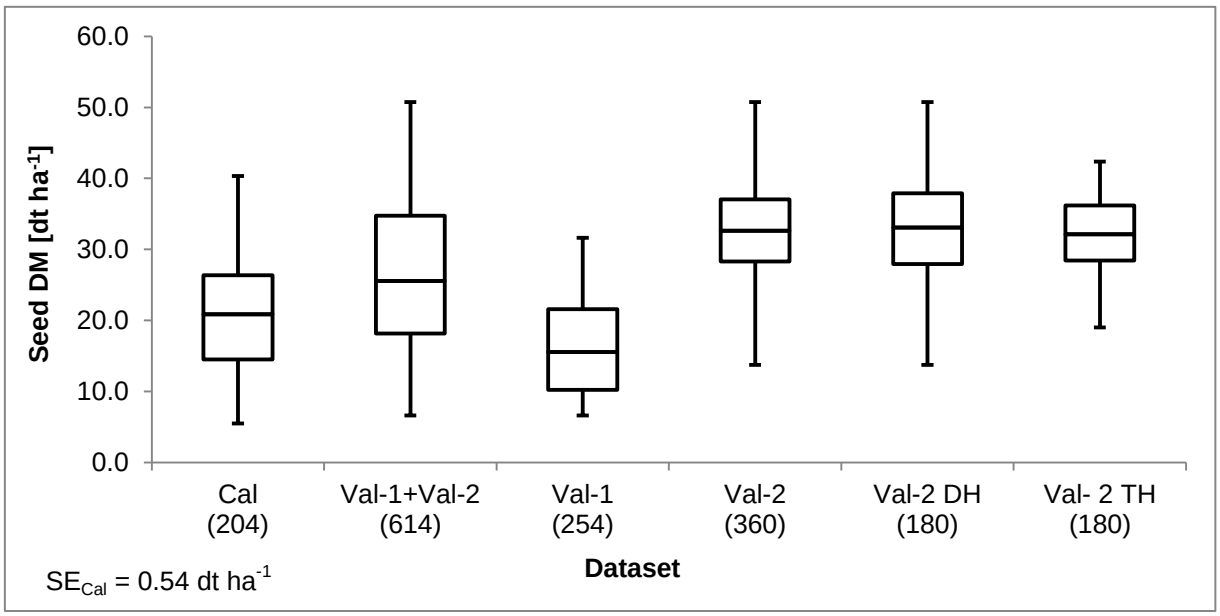

Fig. B 16: Boxplot of plot values of Seed DM within N0 for different datasets
Cal Calibration + cross validation set, Val-1 validation set 1, Val-2 validation set 2, Val-2DH DH lines of Val-2, Val-2 TH test hybrids of Val-2, Numbers in brackets size of dataset, SE_{Cal} standard error of reference values in calibration dataset

Calibration and cross validation

When noisy ranges between 1350 nm and 1551 nm and above 1760 nm were included in calibration this resulted in a high bias of calibration (Tab. B 28, Tab. B 29). Therefore, PGS_{all} was excluded from further analyses.

When spectral data of the first date was used untreated MMS1+PGS_{red} resulted in a better calibration than untreated MMS1 and PGS_{red} but untreated MMS1 resulted in better cross validation. Pre-treatment of MMS1 and PGS_{red} improved calibration and cross validation. Combination of pre-treated MMS1 and pre-treated PGS_{red} did not further improve calibration and cross validation. Hence, best calibrations and cross validations derived from pre-treated MMS1 (Tab. B 28). $RMSE_{Cal}$ and $RMSE_{CV}$ were

at least seven times higher than the standard error of the reference values (Fig. B 16, Tab. B 28).

For spectral data of the second date untreated MMS1 lead to a better calibration while untreated PGS_{red} resulted in better cross validation. Pre-treatment improved calibrations and cross validations with MMS1 and PGS_{red}. Combination of pre-treated MMS1 and pre-treated PGS_{red} did not further improved calibrations and cross validations. The best results derived from pre-treated MMS1 (Tab. B 29). $RMSE_{Cal}$ and $RMSE_{CV}$ were at least seven times higher than the standard error of the reference values (Fig. B 16, Tab. B 29).

There were no clear differences between best calibrations of first and second date. Though, best cross validation derived from spectral data of the first date was better than the best one derived from second date's spectra (Tab. B 28, Tab. B 29).

Tab. B 28: Calibrations and cross validations for Seed DM within N0 with spectral data before flowering

Wavelengths range	Pre-treatment		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
$MMS1+PGS_{all}$	w/o		0.55	5.20	3.E-03	0.49	5.54	-3.E-02
$MMS1+PGS_{red}$	w/o		0.67	4.44	-1.E-06	0.54	5.27	-3.E-02
MMS1	w/o		0.63	4.69	-5.E-07	0.58	5.00	-4.E-03
PGS_{all}	w/o		0.53	5.28	2.E-02	0.48	5.58	-5.E-02
PGS_{red}	w/o		0.53	5.30	-1.E-06	0.47	5.67	2.E-04
MMS1	**Norris d1g25**	**[1]**	**0.75**	**3.90**	**-6.E-07**	0.63	4.71	3.E-02
MMS1	**SaGo d1s29**	**[2]**	**0.74**	**3.93**	**2.E-06**	**0.66**	**4.53**	**4.E-02**
PGS_{red}	SNV	[3]	0.56	5.11	-3.E-07	0.45	5.73	-1.E-02
PGS_{red}	Norris d2g9	[4]	0.54	5.24	-7.E-07	0.50	5.49	3.E-03
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [3]		0.53	6.31	-4.E-07	0.43	5.85	-1.E-02
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [4]		0.66	4.50	-3.E-07	0.56	5.12	-3.E-02
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [3]		0.53	5.31	-5.E-07	0.44	5.82	4.E-02
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [4]		0.51	5.41	-6.E-07	0.47	5.64	-4.E-02

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, SNV standard normal variate transformation, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, Underlined wavelengths ranges/pre-treatments were also tested in calibration with external validation, plot values predicted by models resulting from underlined wavelengths range/pre-treatment were used to test prediction of genotypes

Tab. B 29: Calibrations and cross validations for Seed DM within N0 with spectral data during fruit development

Wavelengths range	Pre-treatment		Calibration			Cross validation		
			R^2	RMSE	Bias	R^2	RMSE	Bias
$MMS1+PGS_{all}$	w/o		0.61	4.83	-9.E-03	0.58	5.08	3.E-02
$MMS1+PGS_{red}$	w/o		0.59	4.93	-6.E-07	0.58	5.05	4.E-02
MMS1	w/o		0.62	4.79	-1.E-06	0.57	5.12	5.E-02
PGS_{all}	w/o		0.64	4.65	3.E-02	0.58	5.03	2.E-01
PGS_{red}	w/o		0.61	4.84	-9.E-07	0.60	4.97	1.E-02
MMS1	**Base**	**[1]**	**0.73**	**4.00**	**-1.E-06**	**0.63**	**4.69**	**9.E-02**
MMS1	Norris d1g41	[2]	0.72	4.12	-1.E-06	0.64	4.68	4.E-03
MMS1	**Norris d2g41**	**[3]**	**0.74**	**3.94**	**6.E-07**	**0.62**	**4.78**	**-3.E-02**
MMS1	Base + SaGo d1s7	[4]	0.73	4.00	9.E-07	0.63	4.73	2.E-03
PGS_{red}	Norris d1g41	[5]	0.71	4.19	-1.E-06	0.62	4.79	-3.E-02
PGS_{red}	Norris d1g43	[6]	0.72	4.12	-6.E-07	0.61	4.83	-9.E-02
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [5]		0.71	4.13	-2.E-06	0.63	4.71	1.E-02
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [5]		0.68	4.38	-7.E-07	0.63	4.76	4.E-02
$MMS1+PGS_{red}$	MMS1 [3] + PGS_{red} [5]		0.64	4.65	-8.E-07	0.59	4.99	-6.E-03
$MMS1+PGS_{red}$	MMS1 [4] + PGS_{red} [5]		0.67	4.47	-8.E-08	0.62	4.82	-1.E-02
$MMS1+PGS_{red}$	MMS1 [1] + PGS_{red} [6]		0.68	4.40	-4.E-06	0.63	4.71	-8.E-02
$MMS1+PGS_{red}$	MMS1 [2] + PGS_{red} [6]		0.67	4.46	-5.E-07	0.60	4.93	-1.E-01
$MMS1+PGS_{red}$	MMS1 [3] + PGS_{red} [6]		0.72	4.12	-5.E-07	0.62	4.77	4.E-02
$MMS1+PGS_{red}$	MMS1 [4] + PGS_{red} [6]		0.66	4.47	-3.E-07	0.61	4.84	-5.E-02

R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{all} 951 – 1800 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, Next to the untreated (w/o) five wavelengths ranges the best calibrations/cross validations for pre-treated MMS1 and PGS_{red} and calibrations resulting from their combinations are given, Best calibrations/cross validations marked bold, Underlined wavelengths ranges/pre-treatments were also tested in calibration with external validation, plot values predicted by models resulting from underlined wavelengths range/pre-treatment were used to test prediction of genotypes

Calibration and external validation

For spectral data of both measuring dates calibration with external validation resulted in lower R^2_{Cal} and decreased $RMSE_{Cal}$ than calibration and cross validation (Tab. B 28, Tab. B 29, Tab. B 30, Tab. B 31).

With spectral data of the first date external validation failed for Val-1. In external validation with test hybrids of Val-2 R^2_{EV} was higher than R^2_{CV} and $RMSE_{EV}$ similar to $RMSE_{CV}$ (Tab. B 28, Tab. B 30).

External validation failed when spectral data of the second date was used (Tab. B 31).

Tab. B 30: Calibrations and external validations for Seed DM within N0 with spectral data before flowering

Wavelengths range	Pre-treatment	Dataset for validation	Calibration			External validation		
			R²	RMSE	Bias	R²	RMSE	Bias
MMS1	SaGo d1s29	Val-1 + Val-2	0.50	5.45	-5.E-07	0.29	9.71	7.E+00
		Val-1	0.48	5.59	-6.E-07		Failed	
		Val-2	0.50	5.45	-5.E-07	0.63	8.15	6.E+00
		Val-2 DH	0.50	5.45	-5.E-07	0.45	10.44	8.E+00
		Val-2 TH	0.50	5.45	-5.E-07	0.85	4.93	4.E+00

R² coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, SaGo Savitzky-Golay derivative transformation, d derivation, s number of smoothing points, DH DH lines, TH test hybrids, Failed calibration model had no predictive ability (for the first PLSR component explained variance of validation was zero)

Tab. B 31: Calibrations and external validations for Seed DM within N0 with spectral data during fruit development

Wavelengths range	Pre-treatment	Dataset for validation	Calibration			External validation		
			R²	RMSE	Bias	R²	RMSE	Bias
MMS1	Base	Val-1+Val-2	0.42	5.87	-3.E-07			
		Val-1	0.42	5.87	-3.E-07			
		Val-2	0.42	5.87	-3.E-07		Failed	
		Val-2 DH	0.42	5.87	-3.E-07			
		Val-2 TH	0.42	5.87	-3.E-07			

R² coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, Base Baseline offset correction, DH DH lines, TH test hybrids, Failed calibration model had no predictive ability (for the first PLSR component explained variance of validation was zero)

N1+N0 vs. N1 and N0

Best calibrations and cross validations within N0 outperformed best calibrations and cross validations within N1 and across both nitrogen levels (Tab. B 20, Tab. B 24, Tab. B 28). When RMSEs are expressed as percentage of mean of Seed DM of respective nitrogen level lowest RMSEs were detected within N1 ($RMSE_{Cal}$ = 16.1 %, $RMSE_{CV}$ = 21.3 %), followed by N0 ($RMSE_{Cal}$ = 18.8 %, $RMSE_{CV}$ = 21.8 %). Highest RMSEs were observed for calibrations and cross validations across both nitrogen levels ($RMSE_{Cal}$ = 20.7 %, $RMSE_{CV}$ = 22.8 %).

Prediction of N uptake and seed yield on genotype level

It was tested whether calibrations and cross validations resulted in the same ranking as the direct assessment of Nup_{EOF}, Nup_{MAT} and Seed DM. Therefore, means calculated from predicted plot values were plotted against genetic means derived from reference plot values (genetic means shown in chapter A) according to their rank from 1 (best) to 29 (worst). The plots were divided into four quadrants. Genotypes in the bottom left quadrant performed well in field trials and were predicted to perform well. The upper right quadrant contains genotypes that performed badly in field trials and were predicted to perform badly. The upper left and bottom right quadrants present genotypes that were predicted contrary to their performance in field trials, i.e. well performing genotypes were predicted to perform badly and badly performing genotypes were predicted to perform well. Only selected plots are shown in the following. Further plots can be found in the appendix (Fig. I to Fig. XI). Depending on trait, nitrogen level and measuring date four to 20 genotypes were predicted contrary to their actual performance. The least wrong predicted genotypes were detected for Seed DM at N1. They were either predicted by a model developed across both nitrogen levels with spectral data captured during fruit development or within N1 with spectral data captured before flowering or during fruit development (Fig. B 17, Fig. B 18, Fig. B 19). Most genotypes were predicted wrong for nitrogen uptake at maturity at N1 with a model developed across both nitrogen levels with spectral data captured during fruit development (Fig. B 20).

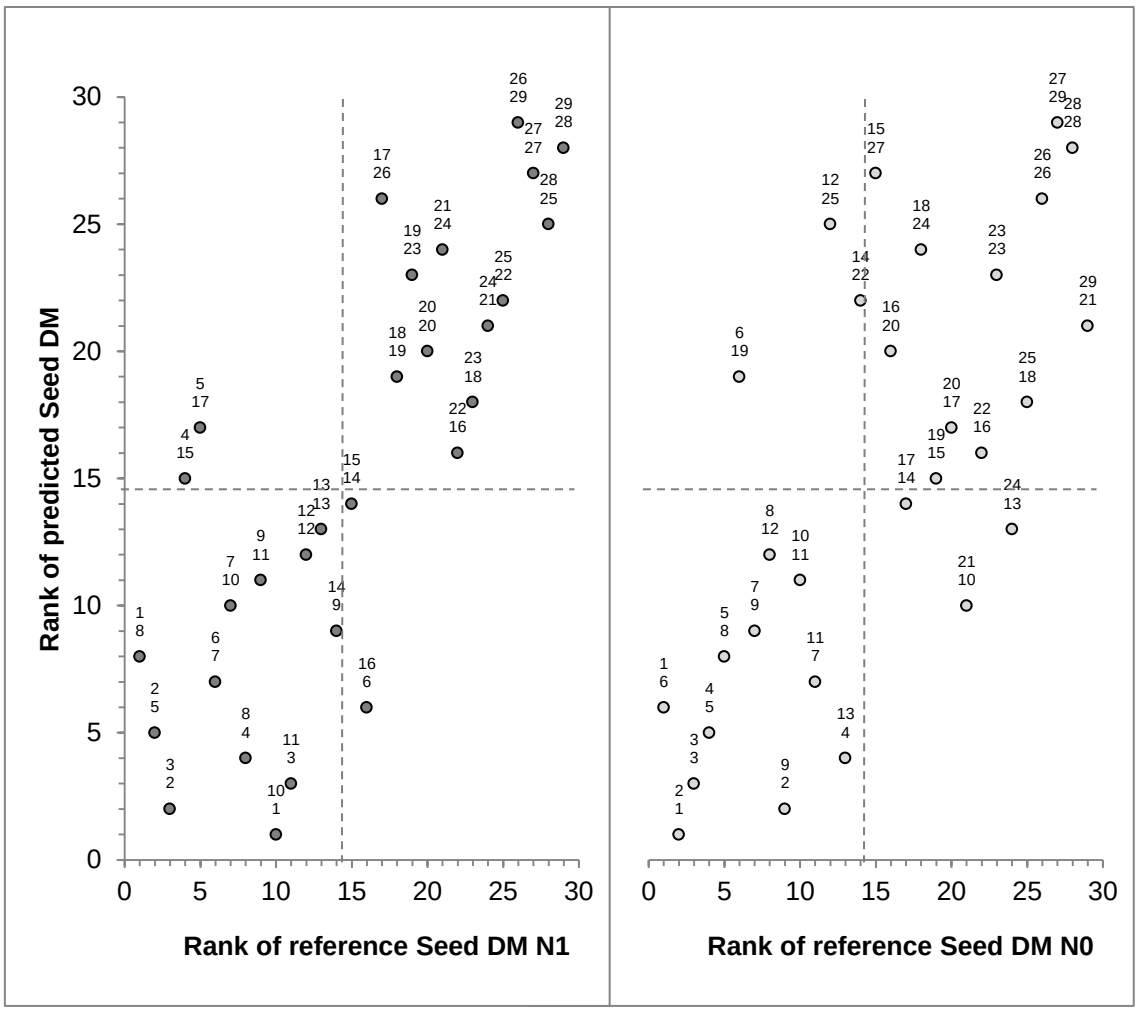

Fig. B 17: Seed DM Rank of genotypes for Seed DM – Ranks for N1 means (left) and N0 means (right), spectral data during fruit development across N1+N0

Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction across both N levels with MMS1 pre-treated with Norris gap 2nd derivative gap size 41, Ranks are plotted within N levels

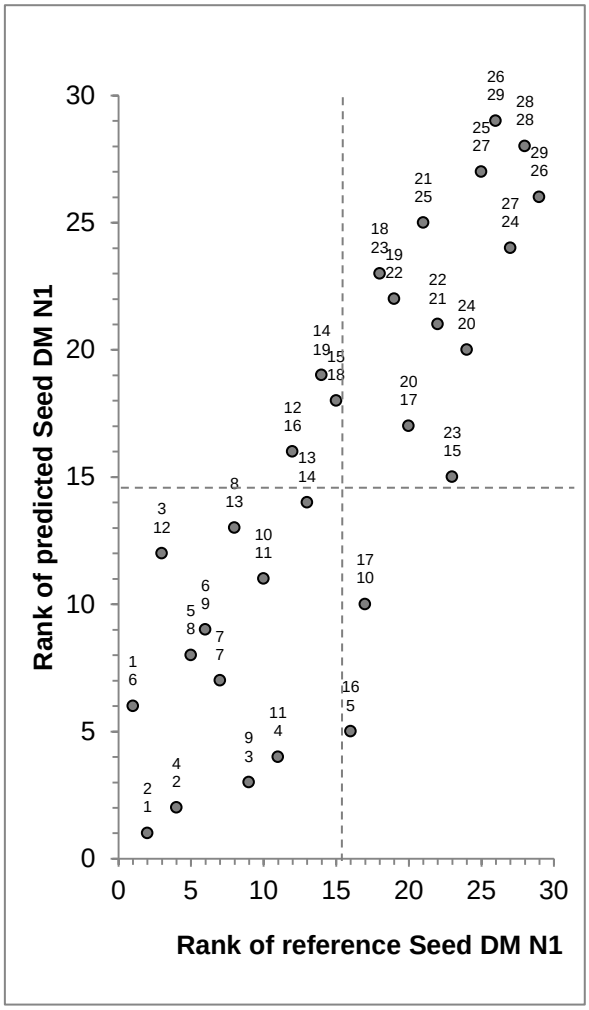

Fig. B 18: Seed DM Rank of genotypes for Seed DM at N1, spectral data before flowering at N1

Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction within N1 with MMS1 pre-treated with Norris gap 1st derivative gap size 23

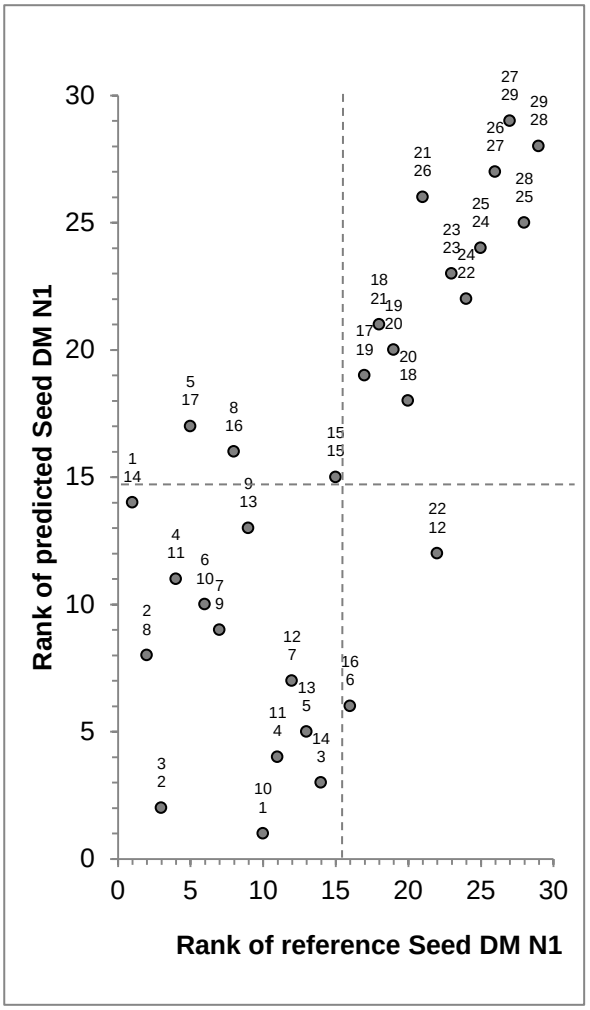

Fig. B 19: Seed DM Rank of genotypes for Seed DM at N1, spectral data during fruit development at N1

Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction within N1 with MMS1 pre-treated with baseline offset correction followed by Norris gap 2nd derivative gap size 15

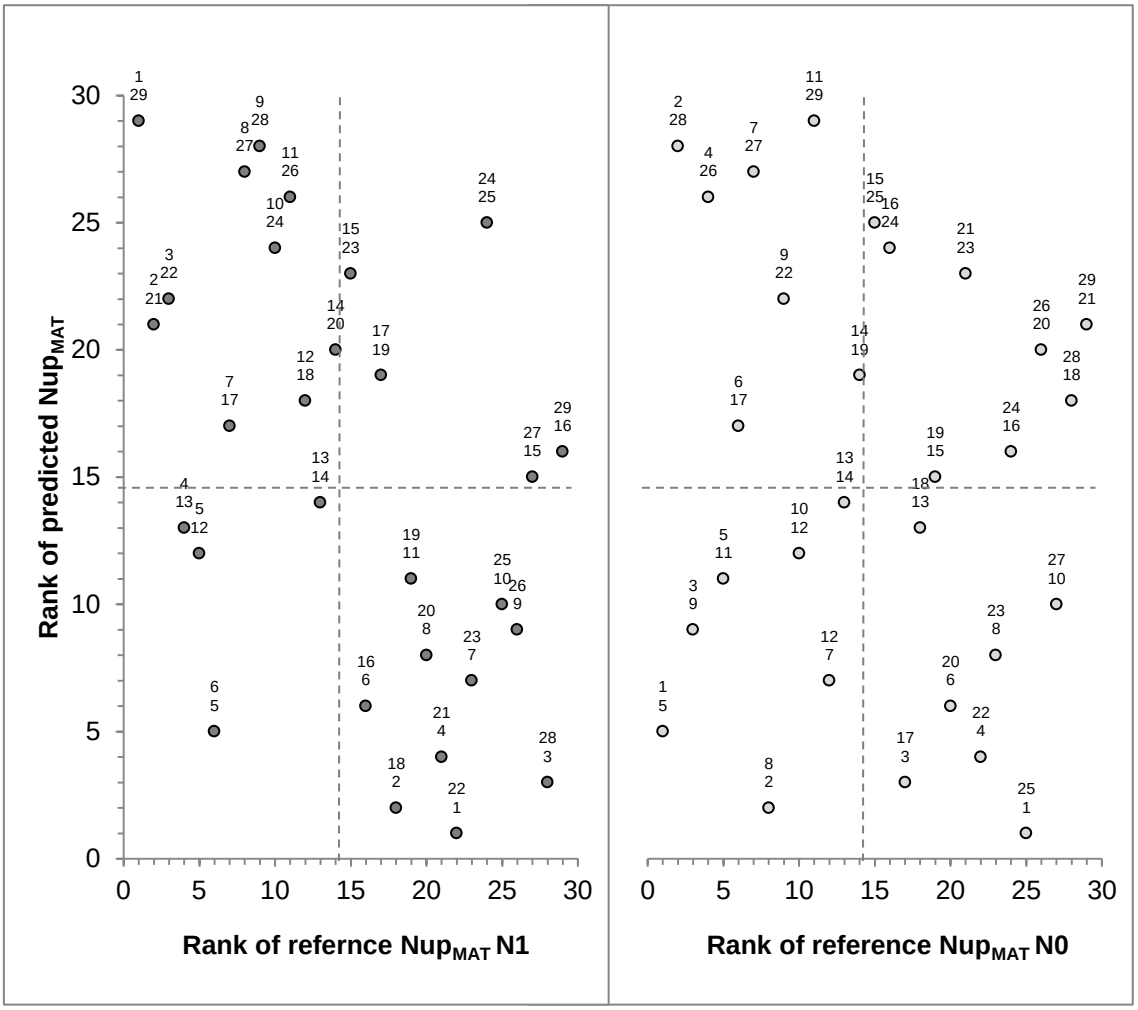

Fig. B 20: Nup$_{MAT}$ Ranks of genotypes for Nup$_{MAT}$ – Ranks for N1 means (left) and N0 means (right), spectral data during fruit development across N1+N0

Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction across both N levels with PGS$_{red}$ pre-treated with Norris gap 1st derivative gap size 3, Ranks are plotted within N levels

Discussion

Influence of growth stage

Behrens et al. (2006) measured reflectance of one variety of winter oilseed rape at several dates from start of regrowth in spring at different nitrogen levels. They reported a dependence of reflectance on growth stage. Especially at full flowering the yellow petals influenced the spectra. Mogensen et al. (1996) detected decreased reflection during flowering due to yellow petals. Therefore, PCAs were conducted with spectral data and sample grouping according to growth stage at time of measuring was tested. No grouping appeared according to the growth stages present in the set for calibration and cross validation. That seems to be contrary to results of Behrens et al. (2006). But in the current study at the first measuring date most of the genotypes were in growth stage 53 to 57 and only a few already had started to flower while no one was in full flowering. It is of advantage for applying hyperspectral reflectance in breeding programs that within a certain range the measurement is not sensitive to differences on growth stages as usually diverse genotypes are tested that may differ in developmental stages. Insensitivity to growth stages allows all plots/genotypes to be measured within one day instead of measuring all plots at a defined physiological age and thus measuring plots at different days.

Relation between reflectance and Nup_{EOF}, Nup_{MAT} and Seed DM

Leaves contain high amounts of nitrogen. It is mainly bound in light harvesting chlorophyll-protein complexes in thylakoids of chloroplasts and in ribulose-1,5-bisphosphate-carboxylase/-oxygenase (RUBISCO). But also other enzymes as well as free amino acids, soluble and structural proteins contribute to leaf nitrogen content. The level of nitrogen supply effects not only the chemical composition but also the internal structure of leaves. With decreasing nitrogen supply contents of light harvesting complexes, chlorophyll, RUBISCO, ATP synthase and amino acids decrease (Lawlor 2002). Particularly chlorophyll is a strong absorber of VIS

wavelengths (Jones & Vaughan 2010 b) and was reported to correlate strongly with reflectance of wavelengths around 500 nm, 620 nm and about 700 nm (Sims & Gamon 2002, Gitelson et al. 2003). Thus, changes in chlorophyll content change spectral properties of leaves. Decreasing nitrogen supply results in smaller and flatter chloroplasts that contain fewer thylakoid membranes. The size of structural components within chloroplasts ranges in dimension of VIS and NIR. Thus, particularly NIR wavelengths are scattered when they encounter chloroplasts (Gates et al. 1965). Therefore, changes in structure of chloroplasts influence spectral properties of leaves. Other structural changes related to decreased nitrogen supply appear such as smaller leaves, fewer cells with smaller volume and higher contents of structural proteins (Lawlor 2002). As reported by Gausman (1974) and described by Jones & Vaughan (2010 a, 2010 b) structural changes particularly alter scattering of NIR wavelengths. Accordingly correlations between reflectance and nitrogen concentration, biomass and/or nitrogen uptake were reported by several authors (Thenkabail et al. 2000, Behrens et al. 2006, Müller et al. 2008, Erdle et al. 2011, Bao et al. 2013, Erdle et al. 2011).

These findings were confirmed by high coefficients of determination in calibrations and cross validations detected for Nup_{EOF} and Nup_{MAT} (maximum R^2_{Cal} 0.87, maximum R^2_{Val} 0.85). Best calibrations and cross validations resulted when MMS1 range was used for calibration. That reflects the relations described above as MMS1 (305 nm to 950 nm) contains VIS and NIR wavelengths. Behrens et al. (2006) also reported correlations between canopy reflectance and nitrogen uptake. But they were weaker which may be due to the usage of only few wavelengths in correlations. Li et al. (2014) computed calibrations between hyperspectral canopy reflectance and canopy nitrogen content of winter wheat. The authors reported high R^2_{Cal} of 0.81 and R^2_{Val} of 0.90. In the current study better results were found with spectral data captured before flowering. Reflectance at this date mainly presents spectral properties of leaves while reflectance during fruit development can be ascribed to developing pods.

Strong relations were also found between reflectance and seed yield (maximum R^2_{Cal} 0.75, maximum R^2_{Val} 0.66). This is in accordance with findings of Ferrio et al. (2005) who observed similar R^2 for seed yield of durum wheat (maximum R^2_{Cal} 0.79, maximum R^2_{Val} 0.76). As observed for Nup_{EOF} and Nup_{MAT}, reflectance before flowering resulted in better predictions than reflectance during fruit development.

Prediction of Nup_{EOF}, Nup_{MAT} and Seed DM by hyperspectral reflectance

High R^2 for calibration and cross validation were detected for all traits. They were less for Seed DM than for Nup_{EOF} and Nup_{MAT}. Seed DM was used to compute Nup_{MAT} (equation A 2, equation A 4). Thus, it is also possible that the correlation between reflectance and Seed DM based on the relation between reflectance and Nup_{MAT}. Bias of calibration was sufficient low ($< 10^{-5}$). The high R^2 and low bias suggest the application of hyperspectral reflectance as indirect selection method for Nup_{EOF}, Nup_{MAT} and Seed DM. The method enables rapid estimation of Nup_{EOF}, Nup_{MAT} and Seed DM as it was possible to measure 250 to 300 plots within four hours. In the current study the ten measuring points within a plot were measured one by one. If installed on a frame which can be carried by a tractor or other vehicles the different measuring points within a plot can be measured at once. Thus, many more plots could be measured. It is also conceivable to install the optics on flying devices like multicopters which again would increase the throughput.

Calibration based on spectral data before flowering resulted in higher R^2_{Cal} and R^2_{CV} and lower $RMSE_{Cal}$ and $RMSE_{CV}$. Thus, hyperspectral reflectance before flowering is better suited to predict Nup_{EOF}, Nup_{MAT} and Seed DM. As a consequence, selection could be conducted before flowering. That offers many advantages. Unfavourable genotypes could be identified early in the season and only favourable genotypes need to be evaluated and grown until harvest. As this reduces workload particularly during harvest and post-harvest analyses more genotypes could be tested.

There is no general pattern when calibrations across nitrogen levels were compared with separate calibrations within nitrogen levels. For Nup_{EOF} the best calibrations across nitrogen levels outperformed best calibrations within nitrogen levels with regards to R^2_{Cal} and R^2_{CV} while N0 showed lowest RMSE for calibration and cross validation. When expressed in percentage of trait means calibrations within N1 showed lowest RMSEs. For Nup_{MAT} the best calibration across both nitrogen levels outperformed the best calibrations within nitrogen levels. Only when RMSEs are expressed as percentage of trait mean calibrations within nitrogen levels led to better results. For Seed DM best calibrations within N0 outperformed calibrations within N1

and across nitrogen levels. Further research is required to reveal whether it is more favourable to develop one model across both nitrogen levels or separate models within nitrogen levels. With regards to separate calibration models it may also be reasonable to consider the level of Nup_{EOF}, Nup_{MAT} or Seed DM instead of nitrogen level. Depending on environmental conditions a low nitrogen level at one environment might exceed a high nitrogen level at another environment with regards to reference values.

The high R^2_{Cal} and R^2_{CV} showed a strong relationship between reflectance and Nup_{EOF}, Nup_{EOF} and Seed DM. Nevertheless, the root mean square errors (RMSE) of calibration and cross validation were six to more than ten times higher than the standard error of reference values, i.e. an exact quantification of Nup_{EOF}, Nup_{MAT} and Seed DM was not possible. The existing models are not ready to be used. This became even more obvious in external validations. From 60 external validations tested 23 could to some extent predict new test sets. The most promising results in calibration and external validation were detected for Nup_{MAT} within N0 with maximum R^2_{Cal} of 0.80 and maximal R^2_{EV} 0.75 (Tab. B 18, Tab. B 19). Although $RMSE_{Cal}$ were lower than in calibration and cross validation $RMSE_{EV}$ were partly more than twice of $RMSE_{CV}$. For all other calibrations with external validations the results were not as good. In some cases R^2_{Cal} decreased to 0.15 and R^2_{EV} to 0.23 and 37 external validations failed at all. Datasets for calibration and samples that are to be predicted must cover the same data space. Spectral data spaces of calibration datasets and of datasets for external validation did not cover the same data space. MAT trials with Val-1 and calibration set were conducted in the same environments and under the same conditions but their genetic backgrounds were different. Val-2 on the other hand represented a genetic subsample of the calibration set as it consisted of DH lines derived from three genotypes of the calibration set and their test hybrids but it was tested in different environments than the calibration set. This might have caused the different data spaces covered by calibration and validation sets. The ranges of reference values which were covered by the different datasets were not exactly the same but they overlapped. Next to the models which require further improvement the different spectral data spaces may have caused the poor results of external validations.

To improve calibration models several approaches can be tested. Test sets used in external validation and in calibration can be combined to cover a broader data space.

Furthermore, reference values and spectra need to be assessed in further environments. One could also try whether sample selection can improve calibration and validation (Kessler 2007). Therefore, PCAs could be conducted with spectral data. Samples can be selected according to the distribution of their PCA scores along the different principal components. This should be done in a way that they are equally distributed along the different principal components. Besides this, cluster analysis can be applied to PCA scores. Subsequently samples can be selected according to their clusters, e.g. one sample per cluster (Zemroch 1986, Isaksson & Naes 1990).

Errors in calibration and cross validation ($RMSE_{Cal}$, $RMSE_{CV}$) were at least six times higher than the standard error of reference values. This prevents exact quantifications but in breeding it may be sufficient to rank genotypes. Some calibrations and cross validations were promising as they only predicted few genotypes wrong. The least wrong predicted genotypes (4) were detected for Seed DM at N1 predicted with a model developed across both nitrogen levels. But more often at least one fourth of the genotypes were predicted contrary to their performance in field trials. Most genotypes (20) were predicted wrong for Nup_{MAT} at N1 with a model developed across both nitrogen levels. As a consequence, one would go on with bad performers and thus, decrease gain in selection by reducing the average of the selected portion. Another consequence is the potential loss of superior genotypes which is also not desirable.

Conclusion

Hyperspectral reflectance can be used to predict Nup_{EOF}, Nup_{MAT} and Seed DM though, predictions for Nup_{EOF} and Nup_{MAT} worked better than ones for Seed DM. It can be clearly concluded that reflectance before flowering resulted in better calibrations and cross validations. Hyperspectral reflectance would enable selection among large numbers of genotypes before flowering.

Nevertheless, the existing models are not ready to be used. They require further improvement, e.g. by combining calibration and validation datasets or using reference values from further environments. Besides, one could try sample selection to improve calibrations and validations. Further research is required to reveal

whether it is more favourable to develop one model across high and low trait values or one model for high and another model for low trait values.

Chapter C - Electrical Capacitance and its Relationship to Nitrogen Efficiency and Root Characteristics of Winter Oilseed Rape

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Introduction

Roots and nitrogen uptake

Oilseed rape suffers from low nitrogen efficiency (Sylvester-Bradley & Kindred 2009). Legislative regulations have moved nitrogen efficiency of winter oilseed rape into focus of plant breeders (EU directive 2009/28/EG, EU nitrate directive). To assess nitrogen efficiency or related parameters seeds and straw need to be harvested and analysed. This is laborious and time consuming. Indirect selection methods would enable selection for nitrogen efficiency and allow its implementation in breeding programs. According to Moll et al. (1982) nitrogen use efficiency consists of two parameters – nitrogen uptake efficiency and nitrogen utilisation efficiency. Nitrogen uptake efficiency is defined as ratio between nitrogen uptake and available nitrogen. As reviewed by Miller & Cramer (2004) next to interactions between plant and rhizosphere, nitrate and ammonium transporters, nitrogen sensing by roots and root structure play an important role for nitrogen uptake and thus, for nitrogen uptake efficiency.

Root structure can be described by architectural features like root branching, mass, length and surface area of roots, distribution of roots that actively take up nitrogen, rooting depth, fine roots and root hairs. At nitrogen limitation root size increases while the ratio between shoot and root decreases. In that way the nitrogen uptake capacity of the plant is increased (Miller & Cramer 2004, Hawkesford et al. 2012). High rooting depths are favourable when nitrate leaching appears. Increasing numbers of fine roots and/or root hairs increase the root surface active in nutrient absorption. Roots react to spatial and temporal variation of available nitrogen in soil. When roots sense regions of high nitrogen content under nitrogen limiting conditions they show increased growth towards that direction. Particularly growth of lateral roots is enhanced. Not only root growth but also number and location of initiation sites of lateral roots are affected by nitrogen availability (Miller & Cramer 2004).

Phenotyping of roots

It is difficult to phenotype roots and root systems as they are hidden in the soil. They can be characterised by destructive or non-destructive methods (reviewed by Fiorani & Schurr 2013). Among destructive methods one can sample soil cores, samples can be taken from parts of the root system or plants can be uprooted in order to capture entire root systems. Destructive methods only allow isolated observations. Dynamics of roots cannot be assessed. Only limited number of samples can be taken which results in sampling errors. As destructive methods are laborious and time-consuming only a limited number of genotypes can be examined which limits their usefulness/application for breeding.

To circumvent these problems several non-destructive methods were developed. They allow not only the analysis of root traits like branching, length, width, lateral and fine roots but also the examination of root dynamics and responses of roots to varying environmental conditions. Mini-rhizotrons are (partly) transparent tubes that are driven in the soil, e.g. with an angle of 45 ° and equipped with a camera. Speed of root growth or rooting profile can be characterised without destroying roots but the observations are limited in spatial terms. Other methods are ground-penetrating radar, electrical resistance or impedance tomography. Recent developments involve the use of magnetic resonance imaging or X-ray computed tomography. Up to now these methods are expensive and require advanced technical equipment. They also underlie restrictions as for example magnetic resonance imaging is sensitive to iron.

Under controlled or semi-controlled conditions plants can be grown in transparent media or in a way that soil grown roots hit a transparent layer. Root characteristics can be assessed by images which then can be analysed automatically. These methods are limited in number of plants and in root system size that can be examined. Often plants are evaluated in seedling stage rather than during their whole life cycle.

Currently no method exists that facilitates quick and easy non-destructive phenotyping of a large number of plants and genotypes as required for breeding. One method discussed by Chloupek (1972) is electrical capacitance. In contrast to other methods which are limited in time, space and/or number of plants/genotypes

this method is highly flexible. It allows measuring of many plants/genotypes in many plots/crop stands in the field at any time (VanBeem et al. 1998).

Electrical capacitance of plants

Electrical capacitance describes the amount of charge that can be stored by a capacitor at a given voltage. Two conductive plates are separated by a dielectric which works as isolator. Therefore, charges are separated and stored at the conductive plates (Fig. C 1).

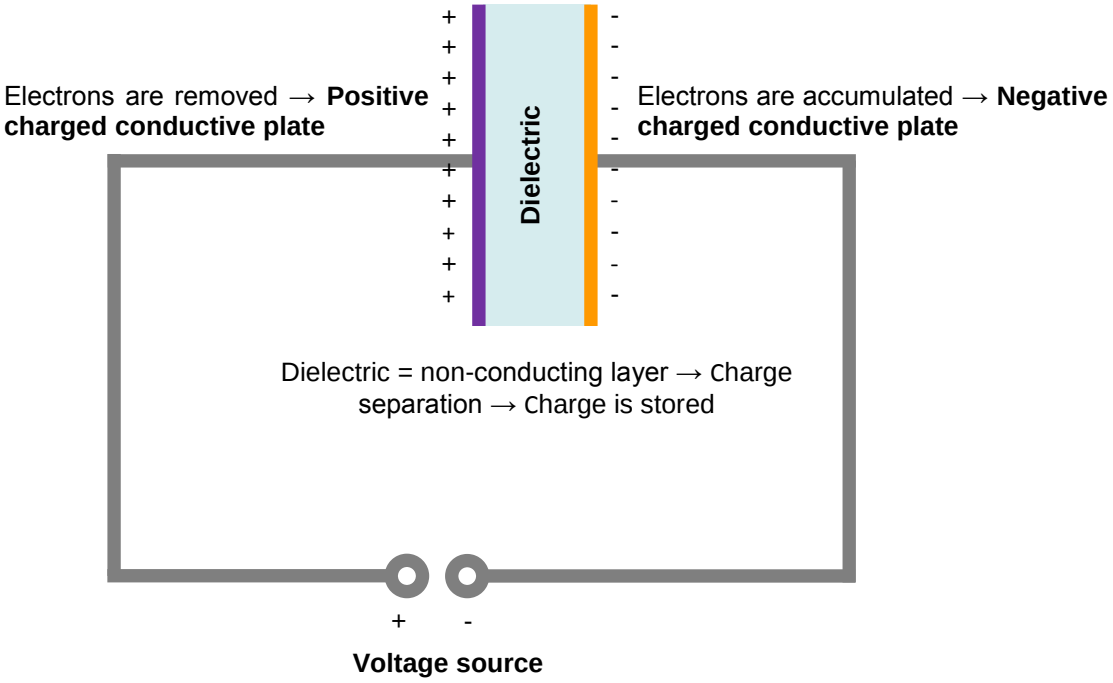

Fig. C 1: Capacitor with dielectric

To measure electrical capacitance of plants an electrode is attached to the plant (plant electrode) and another one is connected to the root medium (soil electrode) (Fig. C 2).

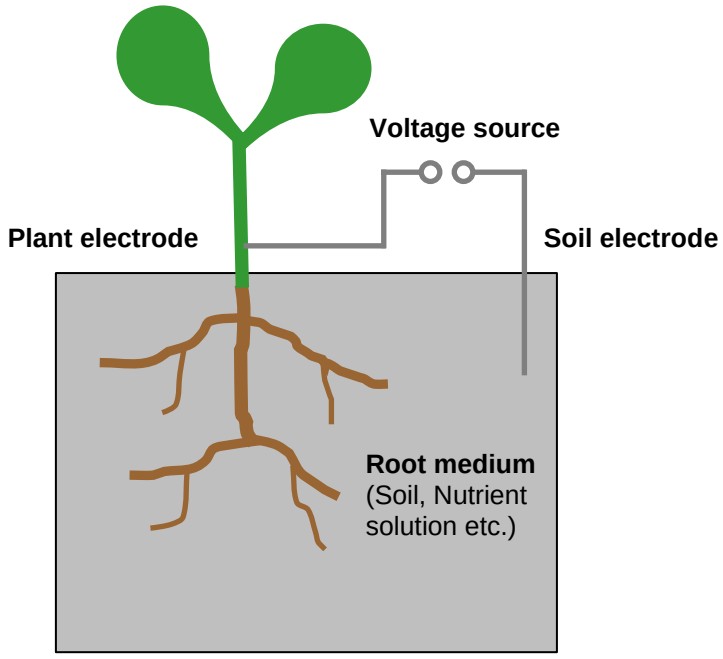

Fig. C 2: Measuring electrical capacitance of plants

Chloupek (1972) analysed root characteristics and measured electrical capacitance of roots of maize, sunflower, oats, onion and oilseed rape in quartz sand and clayey soil. Significant correlations with correlation coefficients between 0.66 and 0.96 were found between electrical capacitance and root fresh and dry weight for maize, sunflower, oats and onion but not for oilseed rape. That was ascribed to its root structure comprising a strong taproot and several lateral roots resulting in a high root mass and a relative small root surface. The relation of electrical capacitance and root volume as well as root surface area were analysed for maize and sunflower and maize and onion, respectively. Significant correlations with correlation coefficients from 0.73 to 0.96 were observed. The relationship between electrical capacitance and root characteristics was found to be significantly affected by substrate and plant species.

In a further study Chloupek (1977) proofed that electrical capacitance was affected by the measuring frequency, soil moisture content and voltage. The influence of distance between soil electrode and plant as well as the effect other plants between soil electrode and plant were tested. Both did not affect electrical capacitance

significantly. It was also shown that soils have their own capacitance but due to their great electrical conductance it was concluded not to contribute to capacitance of roots. Electrical capacitance rather depends on root surface and internal cell membranes.

Dalton (1995) suggested a model which explained electrical capacitance and its relationship to root characteristics. According to Dalton's model each root element (Fig. C 2) represents a cylindrical capacitor (Fig. C 3 a). The conducting xylem solution and its interface to root tissue form the inner cylinder with radius r_1 and surface area A_1. It is separated from the active root surface (surface area A_2) by the root tissue which works as dielectric. Root tissue and root surface form the outer cylinder which is surrounded by the conducting soil solution. The capacitance (C) depends on the radii of inner and outer cylinder and permittivity ε of the root tissue. It is also directly proportional to the surface area of the outer cylinder, i.e. the active root surface area (Fig. C 3 a). The xylem solution as well as the soil solution form low resistances. Single root segments can be understood as parallel resistance-capacitance circuits and the root system is described as a parallel circuit of them. The capacitance of the root system equals the sum of the capacitances of the single root elements (Fig. C 3 b - d).

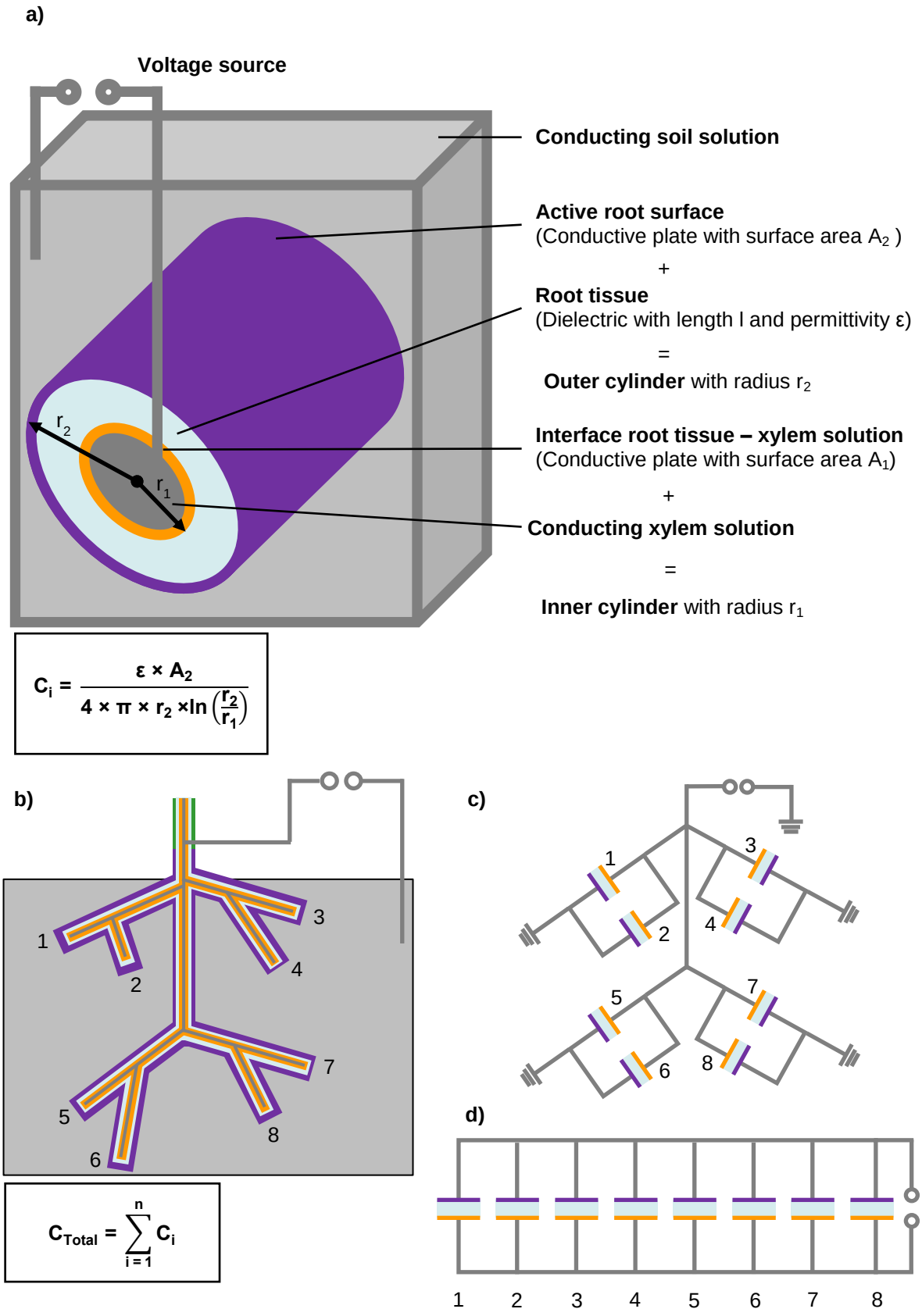

Fig. C 3: Root system as parallel circuit of cylindrical capacitors
a) Single root element as cylindrical capacitor with capacitance C_i, b) Root system as system of eight cylindrical capacitors, c) Root system as electrical network, and as d) resulting parallel circuit of cylindrical capacitors with capacitance C_{Total}, Colours according to Fig. C 1, Numbers according to root elements in Fig. C 2, according to Dalton (1995), for simplification resistances are not shown

Not only was the root system itself described as resistance-capacitance circuit but also the interfaces between soil electrode and soil and between plant electrode and plant as well as resistances of rooting medium and xylem solution. Among these only the capacitance of the root system was assumed to be correlated to variations in root extent. Electrical capacitance was assumed to measure active root area and root extent. Dalton admitted uncertainties within this model. Permittivity ε and also current paths within the plant which were not well understood and deviations from cylindrical root geometry were not considered.

The model was tested by Dalton (1995) in experiments with tomato plants grown under different salinity treatments resulting in different root system sizes. Electrical capacitance was measured and root mass was determined as it was assumed to be closely related to surface area. A significant correlation with a correlation coefficient of 0.77 was observed. Electrical capacitance and root mass were captured at six dates. While root mass increased with time electrical capacitance increased until the second last measuring date and then showed a steep decrease. This was explained by a reduction in active root surface area due to suberisation.

Next to developmental stage the influence of soil water content was tested (Dalton 1995). Electrical capacitance decreased with decreasing soil water content. That was explained by a reduced portion of root tissue which was in contact with soil solution. This relationship was not linear. When moisture saturation of soil decreased from 100 % to 85 % electrical capacitance decreased to 58 % of the value measured at 100 % moisture saturation. A further decrease in soil moisture saturation from 85 % to 35 % resulted in a slighter decrease of electrical capacitance from 58 % to 40 %. A 1:1 relationship between relative electrical capacitance and relative soil water content was observed when moisture saturation was further reduced from 35 % to 15 %.

With increasing distance between plant electrode and root crown resistance increased linear while electrical capacitance decreased hyperbolically. That was referred to resistance-capacitance elements in the shoot connected in series and not in parallel as in the root (Dalton 1995).

VanBeem et al. (1998) estimated root biomass of maize. Several genotypes were tested in greenhouse and field trials. Electrical capacitance and root fresh mass correlated significantly 35 d ($r = 0.85$) and 70 d ($r = 0.48$) after planting in the greenhouse trial. In the field trial significant correlations between electrical

capacitance and root fresh mass correlated significantly. Correlations depended on the position of the plant electrode. With the electrode placed at stem base the correlation coefficient was 0.63 while it was 0.73 with the electrode placed 6 cm above. In greenhouse and field trials ranking of genotypes according to electrical capacitance was identical to their ranking according to root fresh matter. It was concluded that electrical capacitance is not be understood as absolute measurement of a particular genotype but rather as relative measurement that is affected by soil conditions. The portability of the instrument and the large number of plants that can be measured within relative short time are advantages of the method.

The relationship between electrical capacitance and root mass of young poplar hybrids was examined in pot and field experiments by Preston et al. (2004). In the pot experiment significant correlations were observed between electrical capacitance and root fresh mass ($r = 0.93$) or root dry mass ($r = 0.95$) on single plant level. Three years old poplar hybrids were examined for electrical capacitance and root dry mass in a field trial. Across pot and field experiments electrical capacitance and root dry mass correlated significantly with a correlation coefficient of 0.88.

Electrical capacitance, root mass and root length of sunflower grown in sandy soil were analysed in pot experiments by Rajkaj et al. (2005). Traits were assessed at three growth stages. Two different plant electrodes were compared – needle and clamp electrode. The first was pricked into the stem while the latter attached to the surface of the stem which was covered by a conducting gel. Higher correlation coefficients were reported for the relationship of electrical capacitance to root mass than to root length. With the needle electrode correlation coefficients were 0.91 and 0.86, respectively while with the clamp electrode they were 0.96 and 0.73 respectively. As shown by Chloupek (1977) and Dalton (1995) soil moisture signify-cantly affected electrical capacitance. The correlation between electrical capacitance measured either with needle or with clamp was closest in saturated soil with a correlation coefficient of 0.97 but still high at field capacitance with a correlation coefficient of 0.94, i.e. both plant electrodes result in similar capacitance readings. In accordance with Chloupek (1977) frequency was reported to affect electrical capa-citance of plants with higher capacitance towards lower measuring frequencies and decreased capacitance at higher frequencies. The capacitance and resistance of root systems in soil were compared with that of root pieces and pure soil. At a measuring frequency of 1 kHz the capacitance of the soil was 16 nF while for root pieces it was

2.4 nF. For root system in soil a capacitance of 12.2 nF was reported. The highest resistance was reported for the root piece (R = 12.60 kΩ) followed by root system in soil (R = 1.54 kΩ) and pure soil (R = 0.11 kΩ). This was in contrast to Dalton (1995) who simplified the rooting medium as a simple resistor connected in series with soil electrode and root system. Instead Rajkaj et al. (2005) assumed the rooting medium as capacitor connected in series with soil electrode and root system.

A study with young willow cuttings in pots and mature individuals in the field electrical capacitance correlated significantly with root dry mass with a correlation coefficient of 0.90. Significant correlations were also observed between electrical capacitance and leave dry mass (r = 0.80), stem dry mass (r = 0.78), dry mass of cuttings (r = 0.82) and plant height (r = 0.71) (Pitre et al. 2010).

Aulen & Shipley (2012) tested the relationship between electrical capacitance and root mass within ten herbaceous species grown under controlled conditions in a mixture of humus, compost and agricultural soil. In a first experiment ten species were tested in 1.5 l pots each containing one plant. In a second experiment five species were tested in 1.5 l pots each containing two plants. In the first experiment linear regressions were computed for the relationship between electrical capacitance and root dry mass for each species. Different slope estimates were detected for different species, i.e. the relationship is species dependent. It ranged from 2.0 nF g^{-1} to 43.4 nF g^{-1}. For oilseed rape the slope was 7.8 nF g^{-1}. The second experiment examined the influence of sowing density on electrical capacitance. The highest and only significant increase of slope from 7.8 nF g^{-1} to 36.6 nF g^{-1} was observed for oilseed rape.

Electrical capacitance of barley grown in nutrient solution was examined by Dietrich et al. (2012). Different experiments were conducted. In one of them electrical capacitance and root mass of roots and root systems differing in age and size were measured. A significant correlation with a correlation coefficient of 0.93 was observed. For individual excised seminal and nodal roots tested in another experiment the relationship between capacitance and root mass was not significant. Instead capacitance correlated significantly with cross sectional area at the surface of nutrient solution with correlation coefficients of 0.90 for seminal and of 0.88 for nodal roots. In a further experiment parts of the submerged roots/root systems were cut off. This did not affect electrical capacitance. Furthermore the influence of submergence

depth of roots/root systems was examined. When the bottom parts of roots/root systems were submerged gradually a very slight increase of electrical capacitance was observed. Only when the upper parts of the root system were submerged additionally, a steep increase of electrical capacitance was detected. Hence, root tissues close to plant electrode contribute to a very high portion to electrical capacitance. Measurements of roots/root system in nutrient solution were compared to measurements in air, i.e. out of the nutrient solution. It was shown that root parts below the solution surface only little affected electrical capacitance, i.e. electrical capacitance only depends on material between plant electrode and solution surface. Only the significant correlation between electrical capacitance and root mass across different roots and root systems were in accordance with the model of Dalton (1995). Therefore, a new model was suggested with four central statements: 1) The nutrient solution has a greater capacitance than the plant tissue, 2) tissues along unbranched roots act as capacitors connected in series, 3) multiple unbranched roots (= root system) can be understood as capacitors connected in parallel and can be imagined as a single capacitor and 4) capacitance of individual roots are directly proportional to their cross sectional area. Resulting from the second statement the capacitance of a root element is dominated by the tissue with the least capacitance and thus, the direct relation to surface area does not longer hold true.

The validity of the new model was tested in a further study by Dietrich et al. (2013). Electrical capacitance of rootless compost and soil were measured at different water contents and at changing distances between the two electrodes. As reported by former studies electrical capacitance increased with increasing water content (Chloupek 1977, Dalton 1995). With increasing distance between the electrodes electrical capacitance of the substrate decreased. In a second experiment several wheat cultivars were grown in sand under controlled conditions. Electrical capacitance and root dry mass correlated significantly with a correlation coefficient of 0.87. In a further experiment barley plants were grown in compost under controlled conditions. The effect of different wetting regimes on electrical capacitance was tested. Either wetting took place from top to bottom or from bottom to top. When the top centimetres were wetted electrical capacitance was as high as in fully wetted compost. When the water was applied from the bottom the raise of the water table did affect electrical capacitance only little until it reached the top centimetres. It was concluded that it is necessary and sufficient that the substrate around the stem base

is wetted. At these circumstances electrical capacitance was linearly correlated to cross section area of the tissue at soil surface, i.e. electrical capacitance is mainly affected by dimensions of plant tissues close to soil surface. When electrical capacitance of excised shoots was measured between the original position of the plant electrode and compost surface it was almost identical to electrical capacitance before shoot excision. Thus, roots and soil only little contribute to electrical capacitance. The results were in accordance with the new model (Dietrich et al. 2012) that considers plant tissues above soil surface and the soil itself as individual components of a circuit which are connected in series.

Image-based analysis of root characteristics

Root characteristics can also be assessed by image-based analysis. Bucksch et al. (2014) developed a method that allows the estimation of root traits based on digital images taken under field conditions. The method was developed with roots of cowpea and maize. Roots or root systems are placed on a black background with diffuse reflectance properties. Furthermore, a circle of known diameter as well as the sample tag is freely positioned on the background. The circle acts as scale marker to calculate units. A digital camera mounted on a tripod is used to take pictures of roots/root systems, circle and tag. Image analysis is conducted in three steps. First the different objects on the background are detected. They are segmented into individual so-called “image-masks” of root crown, excised root, tag and scale marker. In a second step the structure of root crown and root is described. In mature root system interior and/or smaller roots are hidden by the outer root network. Due to excavation and washing procedures smaller roots are bound together. These problems are circumvented by computing the number of detectable root tips in the image. The structural information is given as number of root-tip paths (RTP). The third step uses the image masks and RTPs to compute architectural traits. Root angles, diameter, length, width and density are the bases for further traits. Image derived traits were found to significantly correlate with manually assessed traits in the field with Spearman correlation coefficients from -0.82 to 0.88.

Objectives of the study

Contradicting results were reported about the relation between electrical capacitance and root traits (e.g. Dalton 1995 vs. Dietrich et al. 2012). Despite these contradicting results electrical capacitance would enable phenotyping of large numbers of plants and genotypes in the field but also under controlled conditions at any time (VanBeem et al. 1998). Thus the method is interesting for breeders. Therefore, the current study wants to answer the following questions:

1. Is there genetic variation for electrical capacitance in winter oilseed rape and how stable is the trait expressed?

2. Is electrical capacitance correlated to nitrogen efficiency or related parameters of winter oilseed rape?

   To answer these questions nitrogen efficiency and related traits were assessed in field trials of chapter A. Electrical capacitance of the diversity set, DH lines and their test hybrids was measured in additional trials.

3. Is electrical capacitance related to directly assessed and image-based root characteristics assessed in the field and/or under controlled conditions?

   Therefore, ten genotypes of the diversity set (chapter A) differing in electrical capacitance were tested for electrical capacitance, root mass, image-based root characteristics and stem diameter in a field trial and under controlled conditions in the greenhouse.

Materials and Methods

Genotypes

Electrical capacitance and nitrogen efficiency

The same genotypes (Diversity set, Pop007, Pop029) as described in chapter A were used to analyse the relationship between electrical capacitance and nitrogen efficiency (Tab. A 1).

Electrical capacitance and root characteristics

Ten genotypes of the diversity set were selected for differences in electrical capacitance (Tab. A 1). They were tested in the field ($EC10_F$) and under controlled conditions ($EC10_C$).

Experimental design

Electrical capacitance and nitrogen efficiency

Diversity set

Agronomic traits and nitrogen efficiency were assessed in EOF and MAT trials described in chapter A. Electrical capacitance in GIE and GOE environments was measured in additional trials (EC). This was necessary as EOF and MAT trials were sown with a seed drill whereas in EC trials more uniform spacing for single plants was required. In GOE environments this was achieved by single seed sowing. In GIE environments EC trials were sown with a seed drill and thinned out in autumn. In EIN environments EOF and MAT trials were single seed sown. Therefore, additional trials for electrical capacitance were not necessary but electrical capacitance was measured in MAT trials.

As EOF and MAT trials EC trials were designed as two-factorial split plots with nitrogen level as whole plot factor and genotype as subplot factor. Genotypes were randomised in alpha lattice design except EC trials in GOE2012 which were

randomised in complete block design. Each trial was replicated twice. For similar neighbour effects between nitrogen levels the same two randomisations were used for both nitrogen levels of EC trials within one environment. They differed from the two randomisations used for replication 1 and 2 of EOF and MAT trials. In 2012/13 and 2013/14 the same two randomisations were used for all trials within one environment to realise the same neighbour effects in all trials and nitrogen levels.

DH lines and test hybrids

Agronomic traits and nitrogen efficiency were assessed in trials MAT007 and MAT029 described in chapter A. Electrical capacitance of Pop007 (EC007) and Pop029 (EC029) in GIE and GOE environments was examined in additional trials to allow more uniform spacing than in MAT trials. In EIN environment electrical capacitance could be captured in MAT007 and MAT029 trials which were sown with a single seed drill. Within environments the same randomisations which were used for MAT007 and MAT029 were applied to EC007 and EC029 for similar neighbour effects at different nitrogen levels.

Electrical capacitance and root characteristics

EC10 – Field trial ($EC10_F$)

Genotypes were tested in a completely randomised block design with four replications.

EC10 – Controlled conditions ($EC10_C$)

Genotypes were tested in the greenhouse in a completely randomised block design with ten replications.

Cultivation

Electrical capacitance and nitrogen efficiency

Experiments which were used for electrical capacitance were cultivated the same way as the corresponding EOF and MAT trials described in chapter A. Plot size in additional trials for electrical capacitance was 1.9 m². More information about plots and sowing is given in Tab. C 1. EC trials in GIE2014 were conducted at a different field than MAT007 and MAT029 (Tab. A 2).

Tab. C 1: Plots and sowing density for additional trials for electrical capacitance in GIE and GOE environments in seasons 2011/12, 2012/13 and 2013/14

Environment	Plot size (Length/width)	Number of rows	Distance between rows	Seeds m^{-2} at sowing
GIE	1.89 m² (3.0 m/0.63 m)	2	31 cm	60 thinned out to 30 plants m^{-2}
GOE	1.88 m² (2.5 m/0.75 m)	2	30 cm	26

GIE Fields of university Gießen/Germany, GOE Fields of university Göttingen/Germany

Electrical capacitance and root characteristics

EC10 – Field trial ($EC10_F$)

$EC10_F$ was conducted in GOE2014 and EIN2014 described in chapter A. Genotypes were tested in 4 row plots sown with a single seed drill. Plots had an area from 3.75 - 6 m² (Tab. C 2). Fertilisation and plant protection followed common practice.

Tab. C 2: Environments of $EC10_F$

Environment	Sowing date	Plot size (Length/width)	Number of rows	Between rows distance	Seed m^{-2} at sowing
EIN2014	04/09/2013	6 m² (4 m/1.5 m)	4	30 cm	50
GOE2014	26/08/2013	3.75 m² (2.5 m/1.5 m)	4	30 cm	26

EIN Fields of KWS Saat AG Einbeck/Germany, GOE Fields of university Göttingen/Germany

EC10 – Controlled conditions ($EC10_C$)

The experiment started end of March 2014. A heat sterilised, homogenous mixture of sand and top soil (volume ratio 3:1) was used as substrate. Plastic tubes (diameter 10.5 cm, height 80 cm) were filled with 8.47 kg of the substrate to a height of 78 cm (Fig. C 4). The substrate was allowed to settle for one day, then watered to 70 % field capacity (determined with a pressure plate extractor) and allowed to settle another day. Single vernalised plantlets were planted on April 3rd. Until mid of May plants were watered to 70 % field capacity and due to high evaporation to 90 % field capacity from mid of May until measuring electrical capacitance and root sampling. Therefore, once a week each pot was weighed and water was added until its weight at 70 %, 90 % or 100 % field capacity was reached. The other days one pot per replication was weighed. The difference between 70 %, 90 % or 100 % field capacity and the weight of this pot was then added to each pot of the replication.

Neither artificial lighting nor heating were applied. Depending on outside temperature the temperature in glasshouse ranged from 12 – 30 °C.

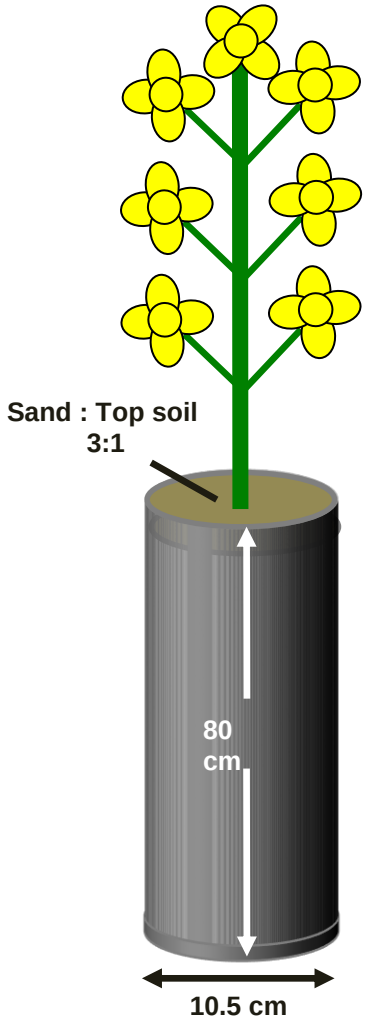

Fig. C 4: Cultivation of winter oilseed rape plant in pots in $EC10_C$

Assessment of traits

Experiments that examined the relation between electrical capacitance and root characteristics were conducted during two master theses at the Institute of Plant Breeding of Georg-August University Göttingen. Jan Oehlschläger supervised $EC10_F$ and Daniel Siebrecht $EC10_C$. The digital root images were analysed for root characteristics by Dr. Alexander Bucksch (Georgia Institute of Technology, School of Biology and School of Interactive Computing, Atlanta in Georgia/USA).

An overview about captured traits in all trials is given in Tab. C 3

Tab. C 3: Number of environments/replications traits were captured at in respective trials

Trait	Abbr.	EOF	MAT	EC	MAT007 MAT029	EC007 EC029	$EC10_F$	$EC10_C$
				End of flowering traits				
DM content of above-ground biomass	$DM\%_{EOF}$							
Aboveground biomass yield DM	$Yield_{EOF}$							
N content of above-ground biomass DM	$N\%_{EOF}$	5 env	ND	ND	ND	ND	ND	ND
N uptake of aboveground biomass DM	Nup_{EOF}							
N uptake efficiency	$NupEff_{EOF}$							
				Maturity traits				
DM content of seeds	$N\%_{Seed}$							
Seed yield DM	Seed DM							
Seed yield at 9% moisture	Seed 9%							
N content of seeds DM	$N\%_{Seed}$							
N uptake of seeds DM	Nup_{Seed}							
Oil content of seeds DM	Oil%							
Oil yield DM	Oil yield							
DM content of straw	$DM\%_{Straw}$							
Straw yield DM	Straw	ND	4 env	ND	3 env	3 env	ND	ND
N content of straw DM	$N\%_{Straw}$							
N uptake of straw DM	Nup_{Straw}							
N uptake of aboveground biomass	Nup_{MAT}							
N uptake efficiency	$NupEff_{MAT}$							
N utilisation efficiency	NutEff							
N use efficiency	NUE							
Harvest index	HI							
N harvest index	NHI							
N uptake after flowering[1]	Delta Nup	4 env		ND	ND	ND	ND	ND
Begin of flowering[2]	FL	4 env		ND	2 env	ND	ND	ND
Plant length[2]	PL	5 env		ND	2 env	ND	ND	ND
Stem diameter	StemDia	ND	ND	ND	ND	ND	2 env	10 rep

Abbr. Abbreviation, env Environment(s), ND Not determined, rep Replications, [1] EOF and MAT were necessary to capture the trait (see under „Nitrogen efficiency parameters“), [2] In 2011/12 and 2012/13 trait was captured in EOF or MAT, [3] For further definitions see Tab. C 7

Tab. C 3 (continued)

Trait	Abbr.	EOF	MAT	EC	MAT007 MAT029	EC007 EC029	$EC10_F$	$EC10_C$
Root characteristics in field trial								
Root mass in horizon 0-20 cm DM	RM_{0-20}							
Root mass in horizon 20-40 cm DM	RM_{20-40}	ND	ND	ND	ND	ND	2 env	ND
Root mass in horizon 40-60 cm DM	RM_{40-60}							
Root characteristics under controlled conditions								
Root system mass FM	RS_{FM}							
Taproot mass FM	Tap_{FM}							
Lateral root mass FM	Lat_{FM}							
Root diameter[3]	RootDia							
Projected root area[3]	RootArea							
Average root density[3]	$Dens_{Av}$							
Median width[3]	W_{Med}	ND	ND	ND	ND	ND	ND	5 rep
Maximal width[3]	W_{Max}							
Number of root tip paths[3]	RTP							
Maximal diameter at 90 % depth[3]	$DD90_{max}$							
Median tip diameter[3]	TD_{Med}							
Mean tip diameter[3]	TD_M							
Electrical capacitance								
Electrical capacitance	EC	ND	ND	ND	ND	ND	2 env	10 rep
Electrical capacitance end of flowering	EC_{EOF}	ND	1 env	4 env	1 env	2 env	ND	ND
Electrical capacitance during fruit development	EC_{FRUIT}	ND	1 env	4 env	1 env	2 env	ND	ND

Abbr. Abbreviation, env Environment(s), ND Not determined, rep Replications, [1] EOF and MAT were necessary to capture the trait (see under „Nitrogen efficiency parameters“), [2] In 2011/12 and 2012/13 trait was captured in EOF or MAT, [3] For further definitions see Tab. C 7

Electrical capacitance

Measuring set-up

Electrical capacitance was measured with battery driven handheld digital LCR meters (Escort ELC 132A and BK Precision 879B, both with the same specifications) at a frequency of 1 kHz. Two battery clamps were connected to the LCR meter. One was used as plant electrode which was tightly connected to the stem in order to cut it and get contact to xylem but without destroying the plant. The other one was connected to the top of a stainless steel rod (length 50 cm, diameter 5 mm) and worked as soil electrode (Fig. C 5).

Fig. C 5: Measuring set-up for electrical capacitance
LCR meter (Escort ELC 132A connected to two battery clamps, Red clamp is tightly connected to stem (Plant electrode), Black clamp is connected to the top of stainless steel rod with bar (Soil electrode), Steel rod is driven into soil to a depth of 40 cm

As shown by Chloupek (1977), Dalton (1995), VanBeem et al. (1998) and Rajkaj et al. (2005) measuring frequency, soil or substrate, soil moisture, the type and position of the plant electrode, plant species and developmental stage were reported to significantly affect electrical capacitance. Thus, results are only comparable when they are assessed at the same frequency, in the same soil/substrate, at sufficient soil moisture, with the same type of plant electrode in the same distance to soil surface and at the same developmental stage. These restrictions were considered in the current study. Electrical capacitance was always measured at a frequency of 1 kHz.

To ensure stable soil conditions measurements within one environment and measuring date were conducted within one day. For sufficient soil moisture capacitance was measured in wet soil in the field (if possible) and at field capacitance under controlled conditions. Clamp electrodes were always used as plant and soil electrode. It was taken care that the plant electrode was attached to the stem at constant distance to the soil surface.

Electrical capacitance and nitrogen efficiency

Electrical capacitance was measured in EC trials in GIE and GOE environments and in MAT trials in EIN environments. The measurements were conducted twice (Tab. C 4) – between full to end of flowering (growth stage 65 to 69, EC_{EOF}) and during fruit development (growth stage 75 to 79, EC_{FRUIT}). Halfway of plot length the rod of the soil electrode was driven into the ground to a depth of 40 cm between the two (outer) rows. The plant electrode was attached to the stem of a single plant 1 cm to 2 cm above soil surface. No leave, herb or other foreign matter was allowed to touch the plant electrode. After 5 s to 10 s a stable value could be captured. Ten plants per plot were measured and averaged. For the measurements the stand needed to be dry to prevent electrical bridges within and between plants. Soil conditions within one environment should be as uniform as possible. Therefore, measurements were conducted within one day if possible (Tab. C 4).

Electrical capacitance and root characteristics

Electrical capacitance in $EC10_F$ was measured between full and end of flowering (GS65 – GS69) following the same protocol as mentioned above. In GOE2014 electrical capacitance was measured twice (Tab. C 4), in EIN2014 once.

In $EC10_C$ electrical capacitance was measured between end of flowering (growth stage 69) and mid of fruit development (growth stage 75) (Tab. C 4). The date of measurement did not strictly follow growth stages but were temporally aligned with root and stem characterisation. One day before the measurements the pots were watered to 100 % field capacity. The soil electrode was driven 40 cm into the substrate halfway between plant and pot wall.

Tab. C 4: Dates of electrical capacitance measurements

Environment	EC_{EOF}	EC_{FRUIT}
Electrical capacitance and nitrogen efficiency		
2011/12 and 2012/13		
EIN2012	24/05/12	21/06/12
EIN2013	13/05/13	27/06/13
GIE2013	15/05/13	02/07/13
GOE2012	27/04/12[1], 07/04/12[2]	04/07/12
GOE2013	21/05/13	26/06/13
2013/14		
EIN2014	30/04/14	24/06/14
GIE2014	22/04/14	19/06/14
GOE2014	17/04/14	26/6/14[3], 27/6/14[4]
Electrical capacitance and root characteristics		
$EC10_F$		
EIN2014	05/05/14[5]	-
GOE2014	23/04/14[6], 05/05/14[7]	-
$EC10_C$*		
Rep 6-10	17/06/14	-
Rep 1 and 2	30/06/14	-
Rep 3 and 4	01/07/14	-
Rep 5	02/07/14	-

Rep replication, EC_{EOF} electrical capacitance measured at end of flowering, EC_{FRUIT} electrical capacitance measured during fruit development, Rep replication, [1]EC N0, [2]EC N1, [3]EC007 N0, EC007 N1 rep2, EC029 N0, EC029 rep2, [4]EC007 N1 rep1, EC029 N1 rep 1, [5]rep 1 und 2, [6]rep 3 and 4, [7]rep 1 and 2, - not measured, * In $EC10_C$ measurements of electrical capacitance were temporally aligned with measurements of stem diameter and root sampling

Agronomic traits and nitrogen efficiency

Begin of flowering and plant length, aboveground biomass at end of flowering ($Yield_{EOF}$), seed yield dry matter (Seed DM) and straw yield (Straw DM) at maturity, dry matter content of, oil content, nitrogen efficiency and nitrogen efficiency parameters were assessed as described in chapter A.

Root characteristics

EC10 – Field trial ($EC10_F$)

In $EC10_F$ next to electrical capacitance the stem diameter and root masses in different soil depths were determined. Stem diameter was assessed with a digital vernier calliper during capacitance measurements right underneath the plant electrode. Soil cores were taken to determine root mass in two replicates per environment one or three days after electrical capacitance was measured (Tab. C 5). Soil probes (length 60 cm, diameter 15 cm) were driven into soil with a pneumatic hammer at three measuring points per plot – two at the front sides about 50 cm distant from the plot borders and one in the plot centre. The samples were taken between the 2nd and 3rd row in order to take lateral roots only. The soil cores were about 60 cm in length. They were divided into three horizons – 0-20 cm, 20-40 cm and 40-60 cm. Samples were air dried to prevent microbiological processes, e.g. degradation of roots. Roots were washed out the soil cores and separated from foreign particles like straw and dead roots. Dry matter of roots was determined after drying at 60 °C for one day followed by 105 °C until constant weight.

Tab. C 5: Dates of assessment of traits in $EC10_F$

Combi Env+Date	Environment	Electrical capacitance Date	Stem diameter Date	Soil cores[1] Date	Replications
EIN_{May}	EIN2014	05/05/14	05/05/14	08/05/14	1 and 2
GOE_{April}	GOE2014	23/04/15	ND	24/04/14	1 and 2
GOE_{May}	GOE2014	05/05/14	05/05/14	ND	3 and 4

Combi Env+Date Combination of environment and measuring date, ND not detected, [1]Soil cores were taken to determine root masses in three horizons (0-20 cm, 20-40 cm, 40-60 cm)

EC10 – Controlled conditions ($EC10_C$)

In $EC10_C$ next to electrical capacitance stem diameter and several root characteristics were assessed. Stem diameter was measured with a vernier calliper during capacitance measurements (Tab. C 6) right underneath the plant electrode. Root diameter, root area, root density, root system width and root tips (Tab. C 7) were analysed on image base using a software package developed by Bucksch et al. (2014). To determine root mass and image-based traits root sampling took place right after capacitance measurements (Tab. C 6). Whole root systems were washed

out the substrate and carefully dried with paper towels. For the image-based analysis roots were placed on a black diffuse reflecting canvas (Fig. C 6). The root was spread as wide as possible without damaging the root. A white paper circle of a known diameter was freely placed on the canvas as scale. Pictures of root systems were taken with a digital camera (Finepix AX250, Fujifilm) which was placed perpendicular above the root system and in constant distant to the canvas. Each root system was weighed immediately after taking pictures. First the whole root system was weighed followed by separate determination of masses of taproot and lateral roots.

Tab. C 6: Dates of assessment of traits in $EC10_C$

Replication	Electrical capacitance	Stem diameter	Root sampling
1 and 2	30/06/14	30/06/14	30/06/14
3 and 4	01/07/14	01/07/14	01/07/14
5	02/07/14	02/07/14	02/07/14
6 – 10	17/06/14	17/06/14	-

Tab. C 7: Definitions of image-based traits (according to Bucksch et al. 2014)

Trait[1] (Abbreviation)	Unit	Definition
Root diameter[2] (RootDia)	mm	Diameter of the root at its first branching point
Projected root area (RootArea)		Number of foreground pixels[3] at the image
Average root density ($Dens_{Av}$)		Ratio of foreground[3] to background pixels[4]
Median root system width (W_{Med})	mm	Median of the calculated root system width
Maximal root system width (W_{Max})	mm	Maximum of the calculated root system width
Number of root tip paths (RTP)		Number of root tips
Maximal diameter at 90 % depth ($DD90_{max}$)	mm	Maximal tip diameter in last 10 % of the image
Median tip diameter (TD_{Med})	mm	Median diameter of all tips
Mean tip diameter (TD_M)	mm	Mean diameter of all tips

[1] Trait names as given in Bucksch et al. (2014) except [2] root diameter which is named stem diameter in Bucksch et al. (2014), [3] foreground pixels represent root, [4] background pixels represent canvas

Fig. C 6: Digital image used for image-based analysis of root traits
Whole root system is placed on a black diffuse reflecting canvas, White circle with known diameter is placed freely on the canvas as scale, photographed by Daniel Siebrecht

Statistical analysis

Plabstat (version 3A, Utz 2011, https://plant-breeding.uni-hohenheim.de/software.html) was used for analysis of variance and to estimate genetic correlations. Command “GENOT/1” was used to estimate genetic correlations. They were computed in a covariance analysis. As genetic correlations underlie estimation errors the relation between coefficient of genetic correlation (r-gen) and its standard error is given. Phenotypic correlations and their corresponding probabilities were estimated with JMP®11 (SAS Institute Inc.). Bonferroni-Holm correction was applied to phenotypic correlations.

Electrical capacitance and nitrogen efficiency

Diversity set

EC trials were analysed the same way as EOF and MAT trials described in chapter A (Model A 1 – A 4). Only that In GOE2012 lattice analysis was not applied as randomisation was in completely randomised block design. For EC was analysed in a split-plot ANOVA (model A 2) across the five environments of EOF trials and across the four environments MAT trials were available for (Tab. C 3). To prevent bias caused by nitrogen level correlations were estimated within nitrogen levels.

Genetic correlations within EC trial were estimated in model A 1. Genetic correlations between electrical capacitance and EOF traits, between electrical capacitance and

MAT traits and between electrical capacitance and Delta Nup based on genetic means within environment and nitrogen level. Means for EC, EOF and MAT derived from model A 2, means for Delta Nup from model A 3. Correlations between electrical capacitance and EOF traits based on means of five environments, correlations between electrical capacitance and MAT traits and electrical capacitance and Delta Nup on means of four environments. Genetic correlations were estimated in model A 4. Phenotypic correlations based on genetic means across environments within nitrogen levels. Means for electrical capacitance, EOF traits and MAT traits derived from model A 2, means for Delta Nup from model A 3. Means across five environments were used for correlations between electrical capacitance and EOF traits while for correlations between electrical capacitance and MAT traits and electrical capacitance and Delta Nup means across four environments were used.

DH lines and test hybrids

EC trials were analysed the same way as EOF and MAT trials described in chapter A (Model A 5 – A 8). To test variances within nitrogen levels and variety types ANOVA for EC, EOF and MAT trials was additionally computed with model C 1.

Model C 1

$$Y_{abc} = m + e_a + r_{b(a)} + g_c + (eg)_{ac} + (rg)_{bc(a)}$$

Y_{abc} = Observation of c^{th} genotype at a^{th} environment and b^{th} replication

m = Overall mean

e_a = Random effect of ^{ath} environment

$r_{b(a)}$ = Random effect of b^{th} replication within a^{th} environment

g_c = Fixed effect of c^{th} genotype

$(eg)_{ac}$ = Effect of interaction between a^{th} environment and c^{th} genotype

$(rg)_{bc(a)}$ = Error (Effect of interaction between b^{th} replication and c^{th} genotype within a^{th} environment)

To prevent bias caused by type or nitrogen level phenotypic and genetic correlations within EC007, MAT007, EC029 and MAT029 were estimated separate for DH lines and hybrids within nitrogen levels. Genetic correlations within EC trials were estimated in model C 1. Genetic correlations between electrical capacitance and MAT traits within Pop007 and Pop029 based on genetic means within environment,

nitrogen level, variety type and descent derived from model A 6. Correlations were estimated in model A 4. Phenotypic correlations between electrical capacitance and MAT traits based on genetic means within nitrogen level, variety type and descent across environments derived from analysis with model A 6. Phenotypic correlation coefficients were averaged across populations within variety type and nitrogen level. Probabilities and significances were adjusted with the Bonferroni-Holm method (equation C1).

Equation C 1

$$p_i = p \times (n - k_i + 1)^{-1}$$

p_i = Adjusted p-value for pair (of traits) i

p = Target p-value (here p = 0.05)

n = Number of pairs

k_i = Rank of pair i with regards to ascending order of unadjusted p-values

EC10 – Field trials ($EC10_F$)

ANOVA and heritabilities of electrical capacitance, stem diameter and root masses were analysed with model C 2. Electrical capacitance was analysed across EIN_{May}, GOE_{April} and GOE_{May} (Tab. C 5). Stem diameter and its relation to electrical capacitance were analysed across EIN_{May} and GOE_{May}. Root masses and their relation to electrical capacitance were examined across EIN_{May} and GOE_{April}. To explore the relation between electrical capacitance and root masses data from EIN_{May} and GOE_{April} were used. Genetic correlations were estimated in model C 2.

Model C 2

$$Y_{abc} = m + d_a + r_{b(a)} + g_c + (dg)_{ac} + (rg)_{bc(a)}$$

Y_{abc} = Observation of c^{th} genotype at a^{th} combination of environment and measuring date in b^{th} replication

m = Overall mean

d_a = Random effect of a^{th} combination of environment and measuring date

$r_{b(a)}$ = Random effect of b^{th} replication within a^{th} environment

g_c = Fixed effect of c^{th} genotype

$(dg)_{ac}$ = Effect of interaction between a^{th} combination of environment and measuring date and c^{th} genotype

$(rg)_{bc(a)}$ = Error (Effect of interaction between b^{th} replication and c^{th} genotype within a^{th} combination of environment and measuring date)

Phenotypic correlations of electrical capacitance to stem diameter and to root masses were estimated on genotype and on plot level. Correlations on genotype level based on genetic means derived from analysis with model C 2 (N = 10). Correlations on plot level based on observed plot values (N = 40). The correlation between electrical capacitance and stem diameter was also analysed on single plant level (N = 400).

EC10 – Controlled conditions ($EC10_C$)

ANOVA and heritabilities of electrical capacitance, stem diameter and root traits were analysed with model C 3. Electrical capacitance and stem diameter and their relation were analysed across ten replications. Root traits and their relation to electrical capacitance were analysed across five replications (Tab. C 6).

Model C 3

$$Y_{ab} = m + g_a + r_b + (gr)_{ab}$$

Y_{ab} = Observation of a^{th} genotype in b^{th} replication

g_a = Fixed effect of a^{th} genotype

r_b = Random effect of b^{th} replication

$(gr)_{ab}$ = Error (Effect of interaction between a^{th} genotype and b^{th} replication)

Phenotypic correlations were estimated on genotype and single plant level. On genotype level genetic means derived from analyses with model C 3 were used. Genetic correlations were estimated in model C 3.

Heterosis

Heterosis of test hybrids was computed for electrical capacitance within nitrogen levels. Simple mean was computed for the common tester PBY062 within nitrogen levels across all trials and environments. Means for DH lines across all environments within nitrogen levels derive from model A 6. The mean between the common tester and the respective DH line presented the mid-parent performance. Heterosis was calculated as relative difference between hybrid and mid-parent performance (equation A 13) and expressed in percentage.

Results

In the following section ANOVA and genetic means are only given for electrical capacitance. ANOVA and genetic means for root characteristics and stem diameter are given in appendix (Tab. XXII to Tab. XXV).

Electrical capacitance and nitrogen efficiency

Diversity set

Electrical capacitance (EC)

Electrical capacitance at end of flowering (EC_{EOF}) was significantly affected by nitrogen level, genotype and interaction between genotype and nitrogen level. Heritability was 0.81 (Tab. C 8). EC_{EOF} was higher at N1 (3.7 nF) than at N0 (2.4 nF). At N1 it ranged from 2.9 nF (PBY021) to 4.8 nF (PBY062). At N0 the range was 1.9 nF (PBY022) to 3.1 nF (PBY008) (Fig. C 7). Nitrogen level and genotype had significant effect on electrical capacitance during fruit development (EC_{FRUIT}). Interaction between genotype and nitrogen level was not significant. Heritability was 0.65 (Tab. C 8). Higher EC_{FRUIT} was observed at N1 (2.6 nF) than at N0 (1.9 nF). At N1 it ranged from 2.2 nF (PBY001) to 3.1 nF (PBY029) and at N0 from 1.4 nF (PBY022) to 2.4 nF (PBY020) (Fig. C 8). Significant genetic variation was also detected for EC_{EOF} and EC_{FRUIT} within nitrogen levels (Tab. C 9).

Tab. C 8: ANOVA for EC_{EOF} (left) and EC_{FRUIT} (right) of diversity set

Source	EC_{EOF}					EC_{FRUT}				
	DF	**MS**	**Var.cp**	**F**		**DF**	**MS**	**Var.cp**	**F**	
E	4	68.61	0.58	82.91	**	4	23.41	0.193	23.93	**
R:E	5	0.83	-0.02	0.48	*ns*	5	0.98	-0.003	0.86	*ns*
N	1	269.42	0.91	40.46	**	1	80.18	0.271	55.12	**
EN	4	6.66	0.09	3.86	*ns*	4	1.45	0.005	1.28	*ns*
RN:E	5	1.72	0.05	7.76	**	5	1.14	0.035	9.26	**
G	28	2.18	0.09	5.35	**	28	1.20	0.039	2.87	**
EG	112	0.41	0.05	1.84	**	112	0.42	0.074	3.40	**
NG	28	0.49	0.02	2.06	**	28	0.23	0.006	1.35	*ns*
ENG	112	0.24	0.01	1.06	*ns*	174	0.17	0.024	1.38	*
RNG:E	159	0.22	0.22			473	0.12	0.123		
Total	458									
h^2	0.64 – **0.81** – 0.89					0.33 – **0.65** – 0.80				

DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N nitrogen level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h^2 heritability (bold) with 0.95 confidence interval

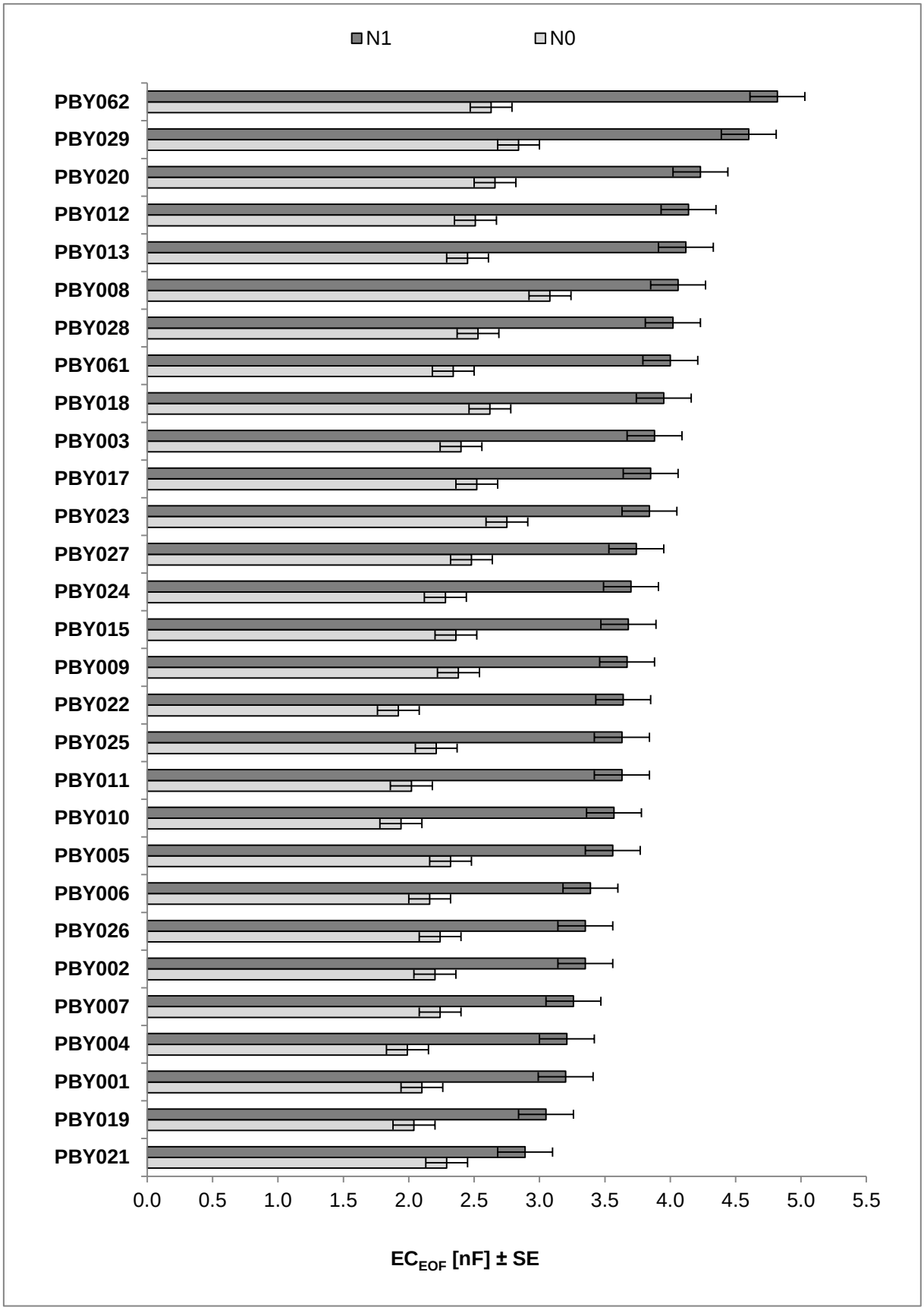

Fig. C 7: EC_{EOF} of diversity set
Means of genotypes across five environments for N1 and N0 with standard error SE

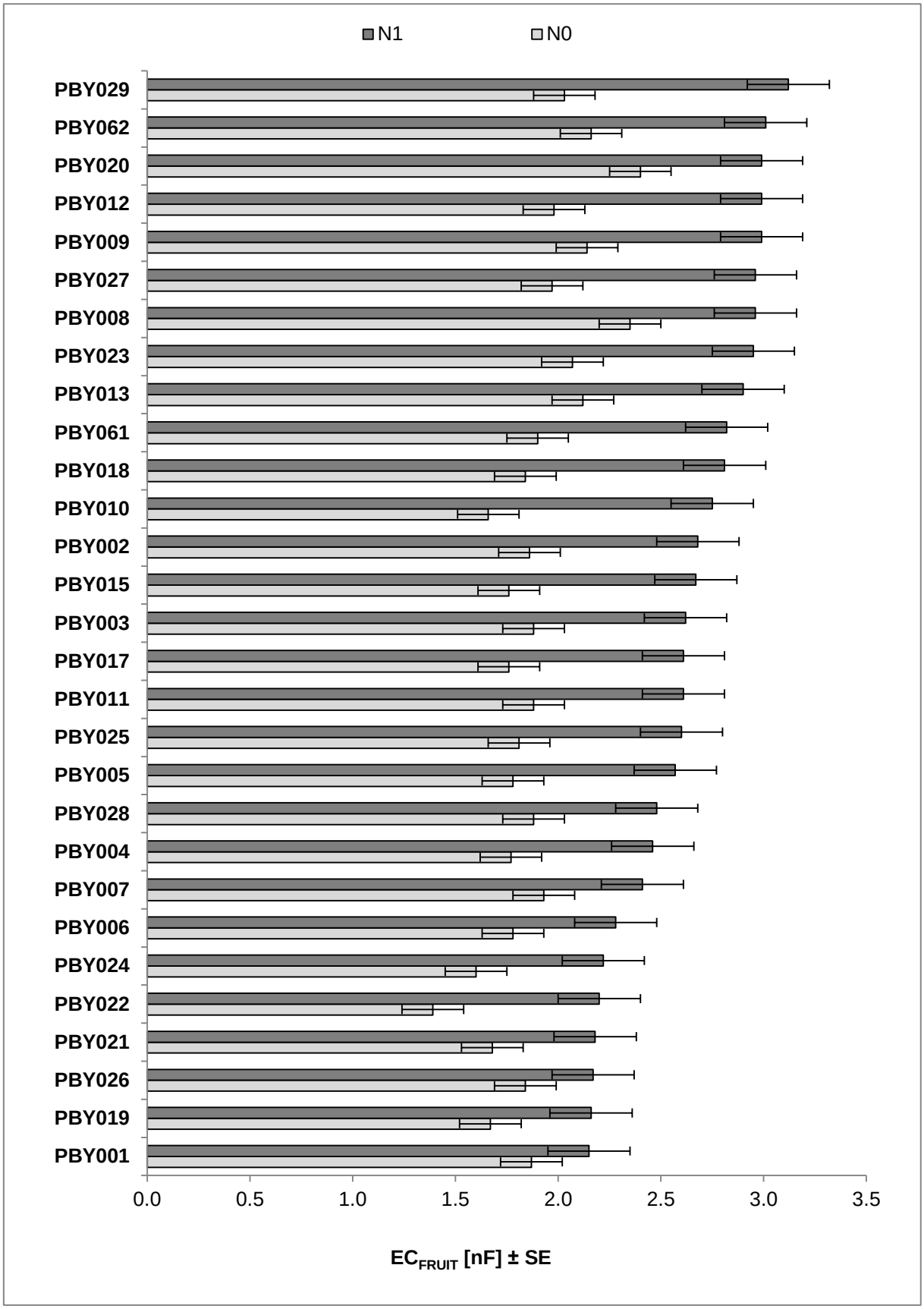

Fig. C 8: EC_{FRUIT} of diversity set
Means of genotypes across five environments for N1 and N0 with standard error SE

Tab. C 9: Genetic variation of EC_{EOF} and EC_{FRUIT} of diversity set within nitrogen levels

N level	Trait	Environments	G	h²	Min	Mean	Max
N1	EC1	5	**	0.76	2.89	3.73	4.82
		4	**	0.76	3.15	4.12	5.22
	EC2	5	**	0.59	2.15	2.63	3.12
		4	**	0.69	2.10	2.59	3.14
N0	EC1	5	**	0.68	1.92	2.36	3.08
		4	**	0.64	2.10	2.56	3.37
	EC2	5	**	0.48	1.39	1.89	2.40
		4	*	0.44	1.41	1.86	2.40

G Effect of genotype, h² Heritability, Min Minimum trait value, Mean Mean trait value, Max Maximum trait value, Min and Max represent the lowest and highest genetic mean across 4 or 5 environments, Mean bases on genetic means of 29 genotypes across 4 or 5 environments, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05

End of flowering traits (EOF traits)

For nearly all traits significant genetic variation was detected within both nitrogen levels. Only $N\%_{EOF}$ at N0 did not show significant genetic variation (Tab. C 10).

Tab. C 10: Genetic variation of EOF traits of diversity set within N levels

N level	Trait	G	h²	Min	Mean	Max
N1	$DM\%_{EOF}$ [%]	**	0.62	14.69	15.65	17.46
	$Yield_{EOF}$ [dt ha^{-1}]	**	0.78	35.40	57.03	63.74
	$N\%_{EOF}$ [%]	**	0.52	2.41	2.69	2.97
	Nup_{EOF} [dt ha^{-1}]	**	0.71	1.06	1.47	1.71
	$NupEff_{EOF}$	**	0.74	0.42	0.56	0.65
N0	$DM\%_{EOF}$ [%]	**	0.68	17.44	18.70	20.46
	$Yield_{EOF}$ [dt ha^{-1}]	**	0.83	26.97	40.25	48.73
	$N\%_{EOF}$ [%]	*ns*	0.32	1.45	1.62	1.84
	Nup_{EOF} [dt ha^{-1}]	**	0.78	0.48	0.63	0.79
	$NupEff_{EOF}$	**	0.72	0.60	0.74	0.88

G Effect of genotype, h² Heritability, Min Minimum trait value, Mean Mean trait value, Max Maximum trait value, Min and Max represent the lowest and highest genetic mean across 5 environments, Mean bases on genetic means of 29 genotypes across five environments, ** significant for α = 0.01, *ns* not significant for α = 0.05

Maturity traits (MAT traits)

Significant genetic variation was detected for all MAT traits within nitrogen levels (Tab. C 11).

Tab. C 11: Genetic variation for MAT traits of diversity set within N levels

N level	Trait	G	h²	Min	Mean	Max
N1	$DM\%_{Seed}$ [%]	*	0.43	94.03	95.01	95.49
	Seed DM [dt ha^{-1}]	**	0.90	16.58	31.07	39.35
	$N\%_{Seed}$ [%]	**	0.92	3.27	3.58	4.06
	Nup_{Seed} [dt ha^{-1}]	**	0.88	0.61	1.01	1.27
	$DM\%_{Straw}$ [%]	**	0.65	33.42	43.94	50.89
	Straw [dt ha^{-1}]	**	0.82	31.77	54.45	76.43
	$N\%_{Straw}$ [%]	**	0.62	0.80	0.98	1.23
	Nup_{Straw} [dt ha^{-1}]	**	0.72	0.37	0.53	0.75
	Nup_{MAT} [dt ha^{-1}]	**	0.83	0.97	1.53	1.88
	$NupEff_{MAT}$	**	0.82	0.36	0.54	0.66
	NutEff	**	0.88	12.91	18.35	22.33
	NUE	**	0.89	5.62	10.01	12.77
	HI	**	0.89	0.22	0.34	0.44
	NHI	**	0.83	0.51	0.65	0.76
	Oil%	**	0.95	41.68	46.30	49.12
	Oil yield [dt ha^{-1}]	**	0.90	6.76	13.14	16.85
N0	$DM\%_{Seed}$ [%]	**	0.53	93.51	94.80	95.46
	Seed DM [dt ha^{-1}]	**	0.85	9.38	21.31	27.27
	$N\%_{Seed}$ [%]	**	0.95	2.74	3.12	3.61
	Nup_{Seed} [dt ha^{-1}]	**	0.82	0.33	0.60	0.78
	$DM\%_{Straw}$ [%]	**	0.81	35.33	47.90	57.16
	Straw [dt ha^{-1}]	*	0.49	26.21	35.70	44.72
	$N\%_{Straw}$ [%]	**	0.52	0.54	0.65	0.82
	Nup_{Straw} [dt ha^{-1}]	**	0.67	0.18	0.24	0.34
	Nup_{MAT} [dt ha^{-1}]	**	0.67	0.62	0.83	0.99
	$NupEff_{MAT}$	**	0.55	0.60	0.76	0.90
	NutEff	**	0.91	15.27	23.20	27.84
	NUE	**	0.84	9.23	17.73	23.01
	HI	**	0.86	0.20	0.35	0.43
	NHI	**	0.83	0.55	0.72	0.80
	Oil%	**	0.95	43.21	49.00	52.50
	Oil yield [dt ha^{-1}]	**	0.86	3.42	9.54	12.59

G Effect of genotype, h² Heritability, Min Minimum trait value, Mean Mean trait value, Max Maximum trait value, Min and Max represent the lowest and highest genetic mean across four environments, Mean bases on genetic means of 29 genotypes across four environments, ** significant for α = 0.01, * significant for α = 0.05

Nitrogen uptake between end of flowering and maturity (Delta Nup)

Delta Nup describes nitrogen uptake between end flowering and maturity. The trait showed significant genetic variation at both nitrogen levels (Tab. C 12).

Tab. C 12: Genetic variation of DELTA Nup of diversity set within N levels

N level	Trait	G	h²	Min	Mean	Max
N1	Delta Nup [kg ha^{-1}]	**	0.59	-30.00	-0.77	24.50
N0	Delta Nup [kg ha^{-1}]	**	0.52	1.75	13.68	30.50

G Effect of genotype, h² Heritability, Min Minimum trait value, Mean Mean trait value, Max Maximum trait value, Min and Max represent the lowest and highest genetic mean across four environments, Mean bases on genetic means of 29 genotypes across four environments, ** significant for α = 0.01

Correlations

Across five environments EC_{EOF} and EC_{Fruit} showed significant phenotypic correlations at both nitrogen levels. Both at N1 and N0 high genetic correlations were detected which exceeded their twofold standard error (Tab. C 13). That was also true across the four environments data of MAT trials were available for (Tab. C 14).

EOF traits

Between EC_{EOF} and EOF traits a significant negative phenotypic correlation was only detected between EC_{EOF} and $DM\%_{EOF}$ at N1. EC_{EOF} correlated genetically to $DM\%_{EOF}$, Nup_{EOF} and $Yield_{EOF}$ at both nitrogen levels and to $NupEff_{EOF}$ at N0.

Tab. C 13: Correlations between EC_{EOF} and EOF traits of diversity set within N levels

Correlation of…	With…	N1				N0			
		r-phen		r-gen		r-phen		r-gen	
EC_{EOF}	EC_{FRUIT}	0.77	*	0.90	++	0.74	*	0.84	++
	$DM\%_{EOF}$	-0.70	*	-0.91	++	-0.45	*ns*	-0.61	++
	$N\%_{EOF}$	0.25	ns	0.19	-	-0.08	*ns*	-0.12	-
	$NupEff_{EOF}$	0.23	ns	-0.13	-	0.52	*ns*	0.69	++
	Nup_{EOF}	0.16	ns	0.25	+	0.46	*ns*	0.60	++
	$Yield_{EOF}$	-0.07	ns	0.27	+	0.42	*ns*	0.51	++

r-phen Pearson correlation coefficient based on genetic means across five environments, r-gen Genetic correlation across five environments, ** significant for α = 0.01, * significant for α = 0.05, *ns* significant for α = 0.05, ++ r-gen > 2fold standard error of r-gen, + r-gen > standard error of r-gen, - r-gen < standard error of r-gen

MAT traits

Within N1 significant positive phenotypic correlations were also detected to Nup_{MAT} and $NupEff_{MAT}$. Within N0 significant positive phenotypic correlations were observed between EC_{EOF} and Oil%. Genetic correlations were detected between electrical capacitance and MAT traits, e.g. between EC_{EOF} and $NupEff_{MAT}$ at N1 (r-gen= 0.64) and N0 (r-gen= 0.39) and between EC_{EOF} and $N\%_{Straw}$ at N1 (r-gen = -0.72) and N0 (r-gen = -0.66) (Tab. C 14).

Tab. C 14: Correlations between EC_{EOF} or EC_{FRUIT} and MAT traits and DELTA Nup in diversity set

Correlation of …	With …	N1				N0			
		r-phen		r-gen		r-phen		r-gen	
EC_{EOF}	EC_{FRUIT}	0.75	*	0.87	++	0.75	*	0.95	++
	$DM\%_{Straw}$	-0.06	*ns*	-0.06	-	-0.02	*ns*	-0.08	-
	Straw	0.19	*ns*	0.19	-	0.09	*ns*	-0.03	-
	$N\%_{Straw}$	-0.20	*ns*	-0.29	+	-0.47	*ns*	-0.72	++
	Nup_{Straw}	0.06	*ns*	0.05	-	-0.22	*ns*	-0.39	+
	$DM\%_{Seed}$	0.05	*ns*	0.06	-	0.35	*ns*	0.61	++
	Seed DM	0.50	*ns*	0.57	++	0.45	*ns*	0.54	++
	$N\%_{Seed}$	-0.45	*ns*	-0.54	++	-0.41	*ns*	-0.50	++
	Nup_{Seed}	0.48	*ns*	0.54	++	0.46	*ns*	0.58	++
	Nup_{MAT}	0.57	*	0.63	++	0.34	*ns*	0.42	+
	$NupEff_{MAT}$	0.57	*	0.64	++	0.37	*ns*	0.51	++
	NutEff	0.33	*ns*	0.40	++	0.40	*ns*	0.52	++
	NUE	0.50	*ns*	0.58	++	0.46	*ns*	0.56	++
	HI	0.27	*ns*	0.33	+	0.37	*ns*	0.51	++
	NHI	0.22	*ns*	0.26	+	0.37	*ns*	0.51	++
	Oil%	0.20	*ns*	0.25	+	0.57	*	0.72	++
	Oil yield	0.49	*ns*	0.56	++	0.49	*ns*	0.60	++
	Delta Nup	0.43	*ns*	0.63	++	0.01	*ns*	-0.08	-

r-phen Pearson correlation coefficient based on genetic means across five environments, r-gen Genetic correlation across four environments, * significant for $\alpha = 0.05$, *ns* for $\alpha = 0.05$, ++ r-gen > 2fold standard error of r-gen, + r-gen > standard error of r-gen, - r-gen < standard error of r-gen

Tab. C 14 (continued)

Correlation of …	With …	N1				N0			
		r-phen		r-gen		r-phen		r-gen	
	$DM\%_{Straw}$	-0.25	*ns*	-0.29	+	-0.35	*ns*	-0.66	++
	Straw	0.16	*ns*	0.15	-	0.23	*ns*	0.32	-
	$N\%_{Straw}$	0.06	*ns*	0.04	-	-0.08	*ns*	-0.07	-
	Nup_{Straw}	0.18	*ns*	0.18	-	0.17	*ns*	0.21	-
	$DM\%_{Seed}$	-0.15	*ns*	-0.24	-	-0.06	*ns*	-0.01	-
	Seed DM	0.22	*ns*	0.24	+	0.11	*ns*	0.18	-
	$N\%_{Seed}$	-0.21	*ns*	-0.27	+	0.06	*ns*	0.10	-
	Nup_{Seed}	0.21	*ns*	0.23	+	0.22	*ns*	0.39	+
EC_{FRUIT}	Nup_{MAT}	0.35	*ns*	0.36	+	0.27	*ns*	0.47	+
	$NupEff_{MAT}$	0.36	*ns*	0.39	+	0.35	*ns*	0.65	+
	NutEff	0.08	*ns*	0.12	-	-0.08	*ns*	-0.11	-
	NUE	0.22	*ns*	0.26	+	0.12	*ns*	0.19	-
	HI	0.07	*ns*	0.10	-	-0.01	*ns*	0.02	-
	NHI	0.01	*ns*	0.03	-	-0.05	*ns*	-0.02	-
	Oil%	0.15	*ns*	0.19	-	0.30	*ns*	0.45	+
	Oil yield	0.22	*ns*	0.26	+	0.14	*ns*	0.23	-
	Delta Nup	0.30	*ns*	0.35	+	0.14	*ns*	0.36	-

r-phen Pearson correlation coefficient based on genetic means across five environments, r-gen Genetic correlation across four environments, * significant for $\alpha = 0.05$, *ns* for $\alpha = 0.05$, ++ r-gen > 2fold standard error of r-gen, + r-gen > standard error of r-gen, - r-gen < standard error of r-gen

DH lines and test hybrids

Electrical capacitance of Population 007 (Pop007)

EC_{EOF} was not significantly affected by nitrogen level, variety type, interaction between variety type and nitrogen level, descent, interaction between descent and nitrogen level and interaction between descent and variety type. Heritability was 0.45 (Tab. C 15). EC_{EOF} of DH lines at N1 ranged from 3.1 nF to 4.5 nF and from 2.7 nF to 3.4 nF at N0. DH lines lay within the range of their parents (Fig. C 9). Test hybrids showed EC_{EOF} from 3.8 nF to 4.4 nF at N1 and from 2.8 nF to 3.9 nF at N0. Commercial hybrids had an EC_{EOF} of 4.0 nF at N1 and of 3.3 nF at N0 (Fig. C 9). EC_{FRUIT} was significantly affected by descent but nitrogen level, variety type, interaction between variety type and nitrogen level, interaction between descent and nitrogen level and interaction between descent and variety type had no significant

effect. Heritability was 0.54 (Tab. C 15). At N1 EC_{FRUIT} of DH lines ranged from 2.9 nF to 4.1 nF and at N0 from 2.5 nF to 3.1 nF. Most DH lines lay within the range of their parents. Only some fell below the lower one (Fig. C 10). EC_{FRUIT} of test hybrids ranged from 2.5 nF to 3.7 nF at N1 and from 2.7 nF to 3.3 nF at N0. For commercial hybrids at N1 an EC_{FRUIT} of 3.1 nF was detected, at N0 it was 2.9 nF (Fig. C 10).

Heterosis of EC_{EOF} was higher at N1 (2 %) than at N0 (-2 %). At N1 it ranged from -8 % to 13 % at N1 and from -16 % to 12 % at N0 (Fig. C 11). Heterosis of EC_{FRUIT} was mainly negative. The difference between N1 (-11 %) and N0 (-13 %) was only little. At N1 it ranged from -28 % to 6 % and at N0 from -21 % to -4 % (Fig. C 12).

Within nitrogen levels and variety types significant genetic variation was observed for EC_{EOF} of DH lines at N1 and for EC_{FRUIT} of DH lines and test hybrids at N1 (Tab. C 16).

Tab. C 15: ANOVA for EC_{EOF} (left) and EC_{FRUIT} (right) of Pop007

Source	EC_{EOF}					EC_{FRUIT}				
	DF	MS	Var.cp	F		DF	MS	Var.cp	F	
E	2	105.58	0.784	9.19	*ns*	2	145.27	1.203	163.58	**
R:E	3	11.49	0.071	1.58	*ns*	3	0.89	-0.021	0.41	*ns*
N	1	56.61	0.291	13.45	*ns*	1	12.78	0.002	1.03	*ns*
EN	2	4.21	-0.051	0.58	*ns*	2	12.35	0.170	5.76	*ns*
RN:E	3	7.26	0.231	22.70	**	3	2.14	0.046	2.75	*ns*
T	1	1.78	0.003	1.47	*ns*	1	0.15	-0.008	0.09	*ns*
ET	2	1.21	0.015	3.77	*ns*	2	1.62	0.014	2.08	*ns*
NT	1	0.02	-0.013	0.02	*ns*	1	1.30	-0.015	0.49	*ns*
ENT	2	1.21	0.030	3.80	*ns*	2	2.63	0.062	3.37	*ns*
RNT:E	7	0.32	0.006	1.35	*ns*	7	0.78	0.039	3.87	**
D	14	0.87	0.016	1.79	*ns*	14	0.70	0.016	2.28	*
ED	28	0.49	0.031	2.05	**	28	0.31	0.013	1.52	*ns*
ND	14	0.23	0.003	1.21	*ns*	14	0.18	0.002	1.15	*ns*
TD	14	0.38	0.015	1.89	*ns*	14	0.24	0.010	1.96	*ns*
END	28	0.19	-0.012	0.80	*ns*	28	0.16	-0.010	0.80	*ns*
ETD	28	0.20	-0.009	0.86	*ns*	28	0.12	-0.020	0.60	*ns*
NTD	14	0.20	0.007	1.26	*ns*	14	0.27	0.024	2.18	*
RNTD	28	0.16	-0.038	0.68	*ns*	28	0.12	-0.039	0.61	*ns*
RNTD:E	167	0.24	0.236			167	0.20	0.201		
Total	359					359				
h^2	-0.09 - **0.45** - 0.70					0.09 - **0.54** - 0.75				

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for $\alpha = 0.01$, * significant for $\alpha = 0.05$, *ns* not significant for $\alpha = 0.05$

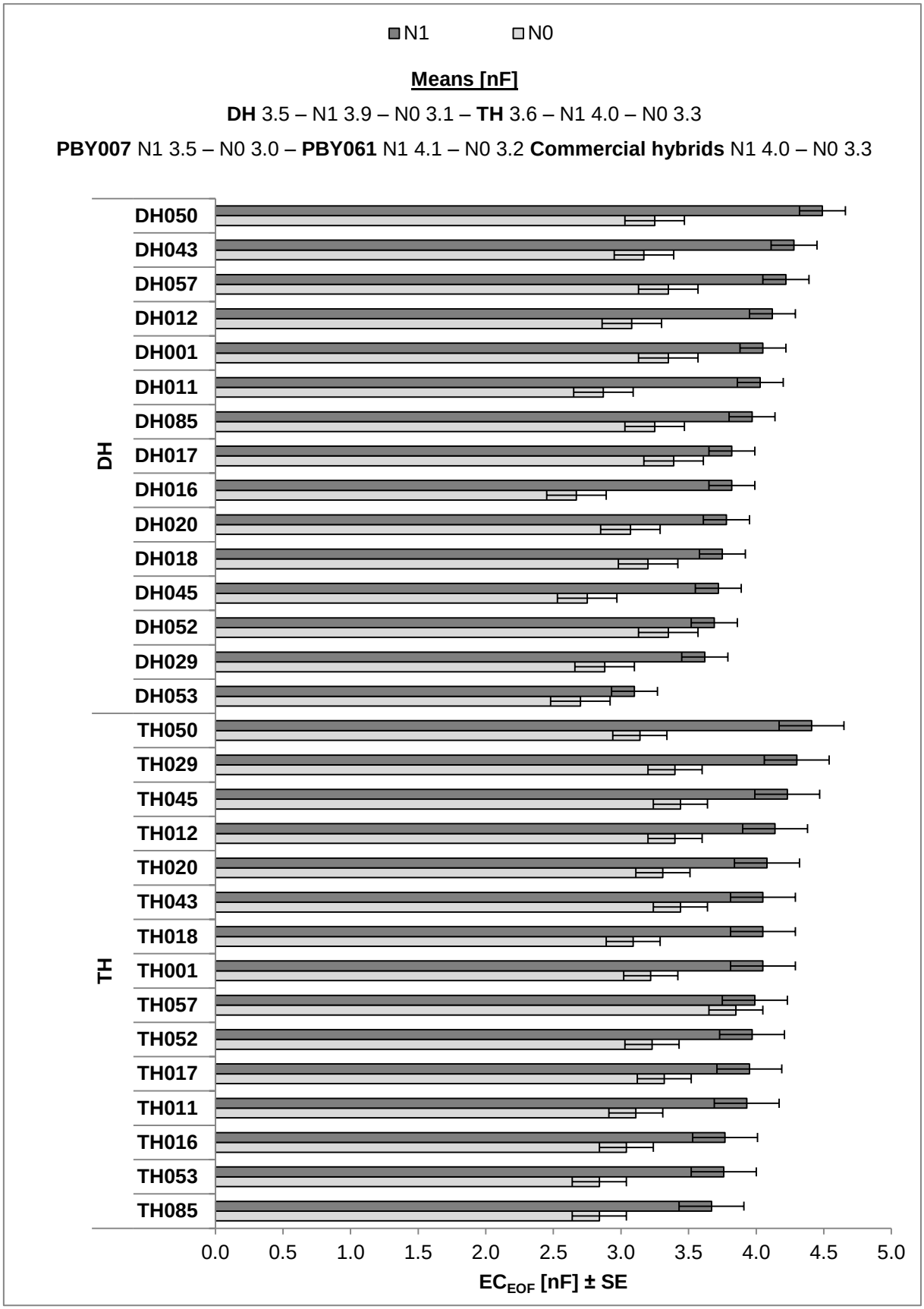

Fig. C 9: EC_{EOF} of Pop007
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, on top means for DH and TH across both N levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0 are given

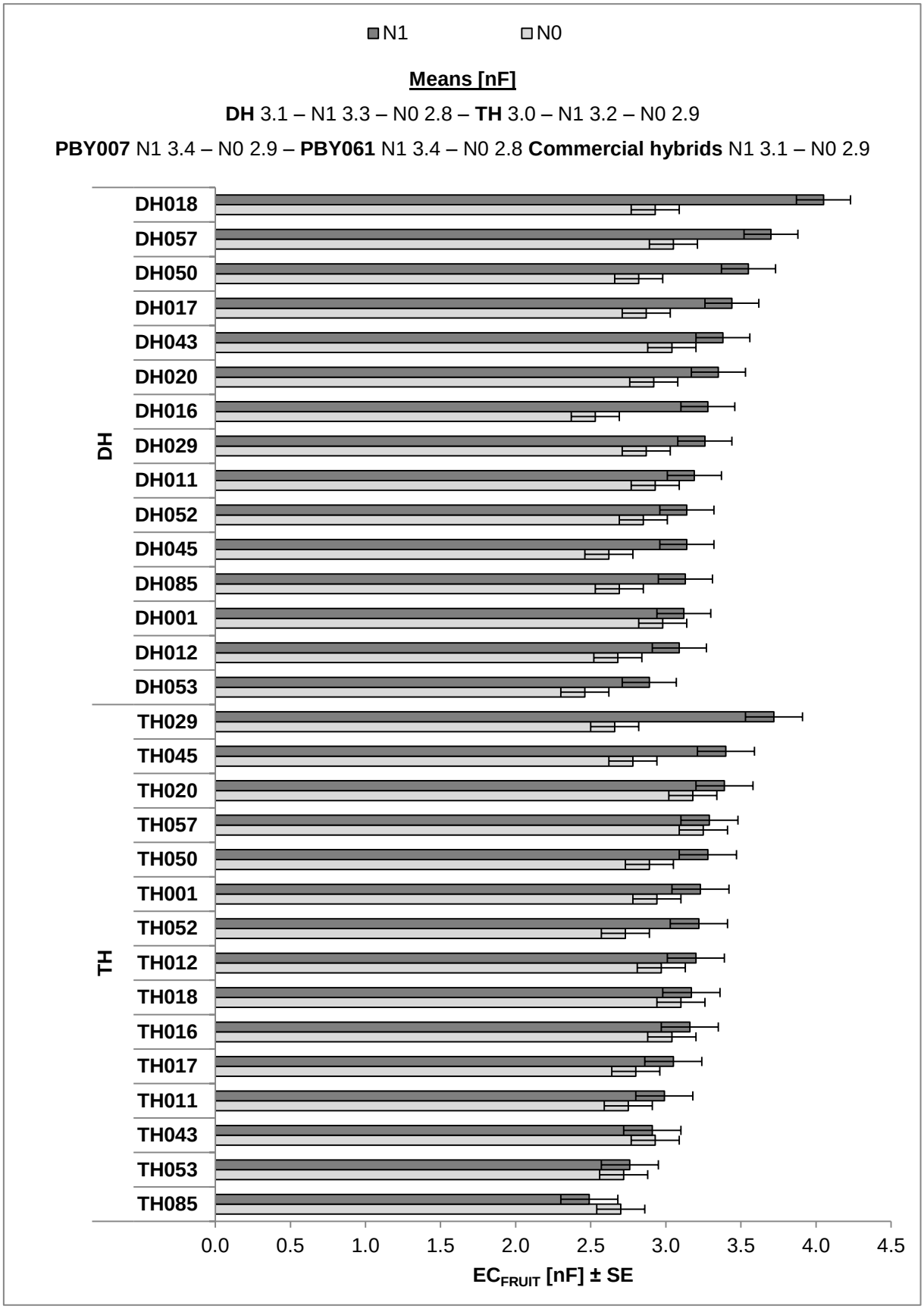

Fig. C 10: EC_{FRUIT} of Pop007
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, on top means for DH and TH across both N levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0 are given

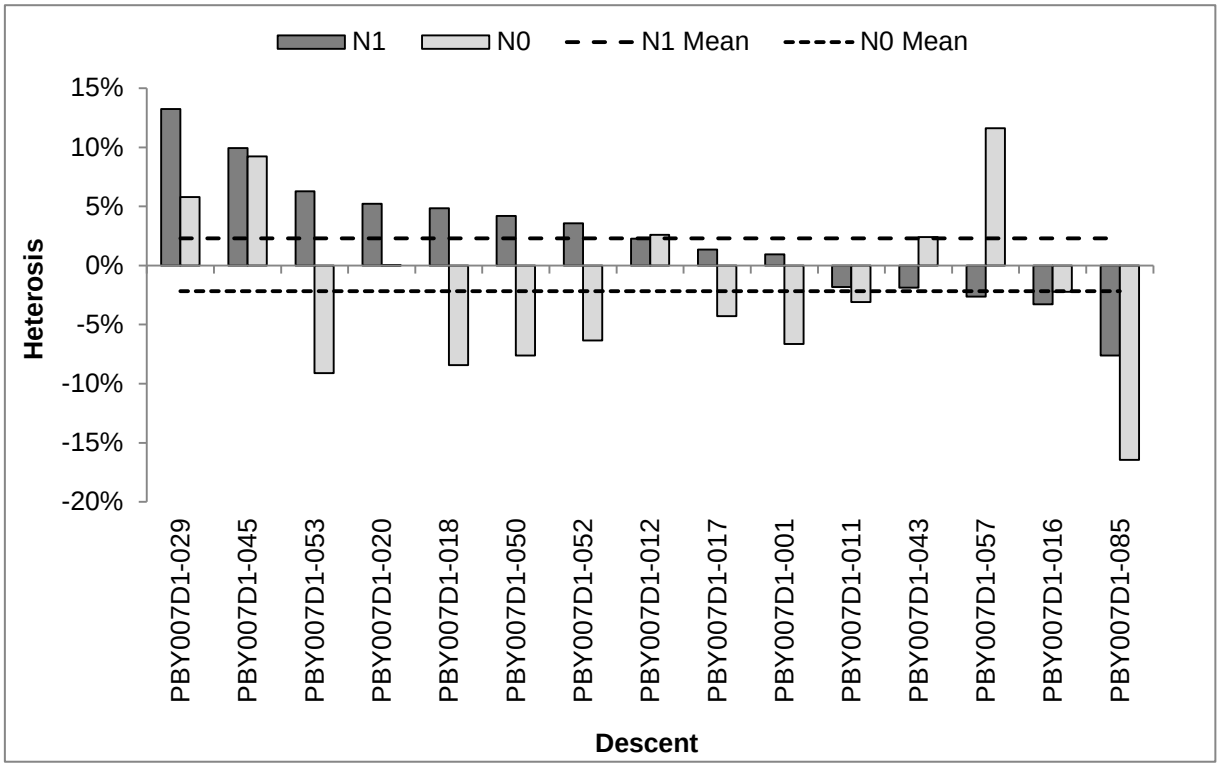

Fig. C 11: Heterosis for EC_{EOF} of Pop007
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

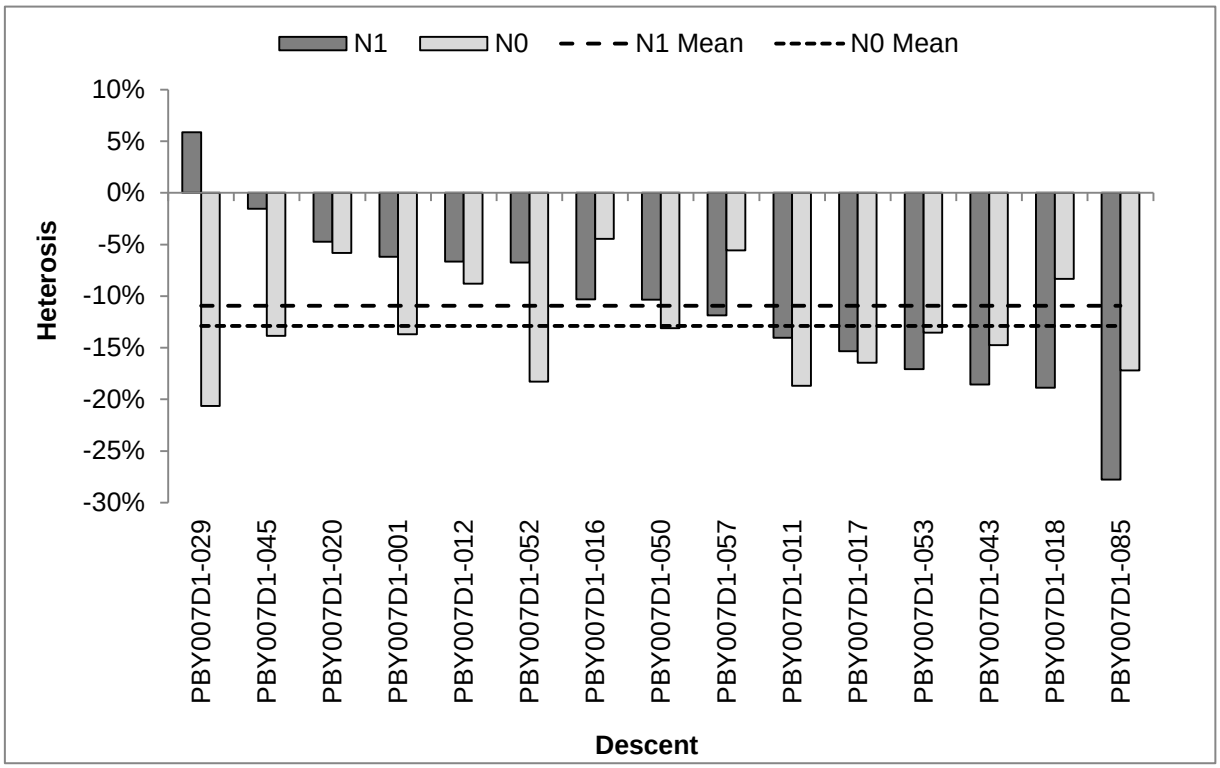

Fig. C 12: Heterosis for EC_{FRUIT} of Pop007
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

Tab. C 16: Genetic variation of EC_{EOF} and EC_{FRUIT} of Pop007 within N levels and variety types

N level	Trait	DH					TH				
		G	h²	Min	Mean	Max	G	h²	Min	Mean	Max
N1	EC_{EOF} [nF]	**	0.74	3.10	4.30	5.80	*ns*	0.00	3.00	3.43	3.64
	EC_{FRUIT} [nF]	*	0.62	2.89	3.54	4.84	*	0.56	2.80	3.19	3.91
N0	EC_{EOF} [nF]	*ns*	0.26	2.67	3.39	4.41	*ns*	0.42	3.00	3.43	3.64
	EC_{FRUIT} [nF]	*ns*	0.23	2.46	3.10	4.26	*ns*	0.28	2.80	3.19	3.91

DH DH lines, TH Test hybrids, G Effect of genotype, h² Heritability, Min Minimum trait value, Mean Mean trait value, Max Maximum trait value, Min and Max represent the lowest and highest genetic mean across three environments, Mean bases on genetic means of 15 genotypes across three environments, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.0

Electrical capacitance of Population 029 (Pop029)

EC_{EOF} was significantly affected by nitrogen level, descent and interaction between descent and variety type. Variety type and interactions between variety type and nitrogen level and between descent and nitrogen level had no significant effect on EC_{EOF}. Heritability was 0.70 (Tab. C 17). At N1 EC_{EOF} of DH lines ranged from 3.8 nF to 5.8 nF, at N0 from 3.0 nF to 4.4 nF. Their parents showed EC_{EOF} of 4.1 nF and 4.8 nF at N1 and of 3.2 nF and 4.2 nF at N0 (Fig. C 13). EC_{EOF} of test hybrids ranged from 3.9 nF to 4.7 nF at N1 and from 3.0 nF to 3.6 nF at N0. Commercial hybrids showed EC_{EOF} of 4.0 nF at N1 and of 3.3 nF at N0 (Fig. C 13). Descent and interaction between descent and variety type significantly influenced EC_{FRUIT}. Effects of nitrogen level, variety type and interactions between variety type and nitrogen level and between descent and nitrogen level were not significant. Heritability for EC_{FRUIT} was 0.75 (Tab. C 17). EC_{FRUIT} of DH lines ranged from 3.2 nF to 4.8 nF at N1 and from 2.7 nF to 4.3 nF at N0. The DH parents had an EC_{FRUIT} of 3.4 nF and 3.8 nF at N1 and of 2.8 nF and 3.7 nF at N0 (Fig. C 14). Test hybrids' EC_{FRUIT} ranged from 3.2 nF to 3.8 nF at N1 and from 2.8 nF to 3.9 nF at N0. Commercial hybrids showed an EC_{FRUIT} of 3.1 nF at N1 and of 2.9 nF at N0 (Fig. C 14). On average there was nearly no heterosis of EC_{EOF} at N1. It ranged from -9 % to 12 %. Heterosis at N0 was -5%. It ranged from -14 % to 7 % (Fig. C 15). Heterosis of EC_{FRUIT} was mainly negative. It was higher at N1 (-8 %) than at N0 (-12 %). It ranged from -20 % to 3 % at N1 and from -25 % to 7 % at N0 (Fig. C 16).

Within nitrogen levels and variety type significant genetic variation was detected for EC_{EOF} and EC_{FRUIT} of DH lines within both nitrogen levels, for EC_{EOF} of test hybrids at N1 and for EC_{FRUIT} of test hybrids at N0 (Tab. C 18).

Tab. C 17: ANOVA for EC_{EOF} and EC_{FRUIT} of Pop029

Source	EC_{EOF}					EC_{FRUIT}				
	DF	**MS**	**Var.cp**	**F**		**DF**	**MS**	**Var.cp**	**F**	
E	2	145.45	1.087	9.70	*	2	220.87	1.835	312.77	**
R:E	3	15.00	0.175	3.34	*ns*	3	0.71	-0.063	0.16	*ns*
N	1	81.94	0.446	51.16	*	1	9.22	-0.006	0.90	*ns*
EN	2	1.60	-0.048	0.36	*ns*	2	10.22	0.095	2.27	*ns*
RN:E	3	4.48	0.141	18.38	**	3	4.51	0.143	19.90	**
T	1	8.91	0.041	5.72	*ns*	1	5.48	0.029	17.05	*ns*
ET	2	1.56	0.022	6.38	*	2	0.32	0.002	1.42	*ns*
NT	1	0.25	-0.004	0.42	*ns*	1	0.21	-0.006	0.27	*ns*
ENT	2	0.60	0.012	2.47	*ns*	2	0.79	0.019	3.48	*ns*
RNT:E	7	0.24	-0.002	0.90	*ns*	7	0.23	-0.006	0.72	*ns*
D	14	2.14	0.059	2.98	**	14	2.14	0.067	3.92	**
ED	28	0.72	0.056	2.66	**	28	0.55	0.029	1.73	*
ND	14	0.22	0.005	1.36	*ns*	14	0.31	0.001	1.03	*ns*
TD	14	1.35	0.085	4.07	**	14	0.94	0.060	4.24	**
END	28	0.16	-0.027	0.60	*ns*	28	0.30	-0.003	0.97	*ns*
ETD	28	0.33	0.016	1.23	*ns*	28	0.22	-0.024	0.70	*ns*
NTD	14	0.15	-0.008	0.77	*ns*	14	0.32	0.026	1.95	*ns*
ENTD	28	0.20	-0.037	0.73	*ns*	28	0.16	-0.076	0.52	*ns*
RNTD:E	165	0.27	0.271			167	0.32	0.315		
Total	357					359				
h^2	0.40 - **0.70** - 0.84					0.50 - **0.75** - 0.87				

DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h^2 heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for $\alpha = 0.01$, * significant for $\alpha = 0.05$, *ns* not significant for $\alpha = 0.05$

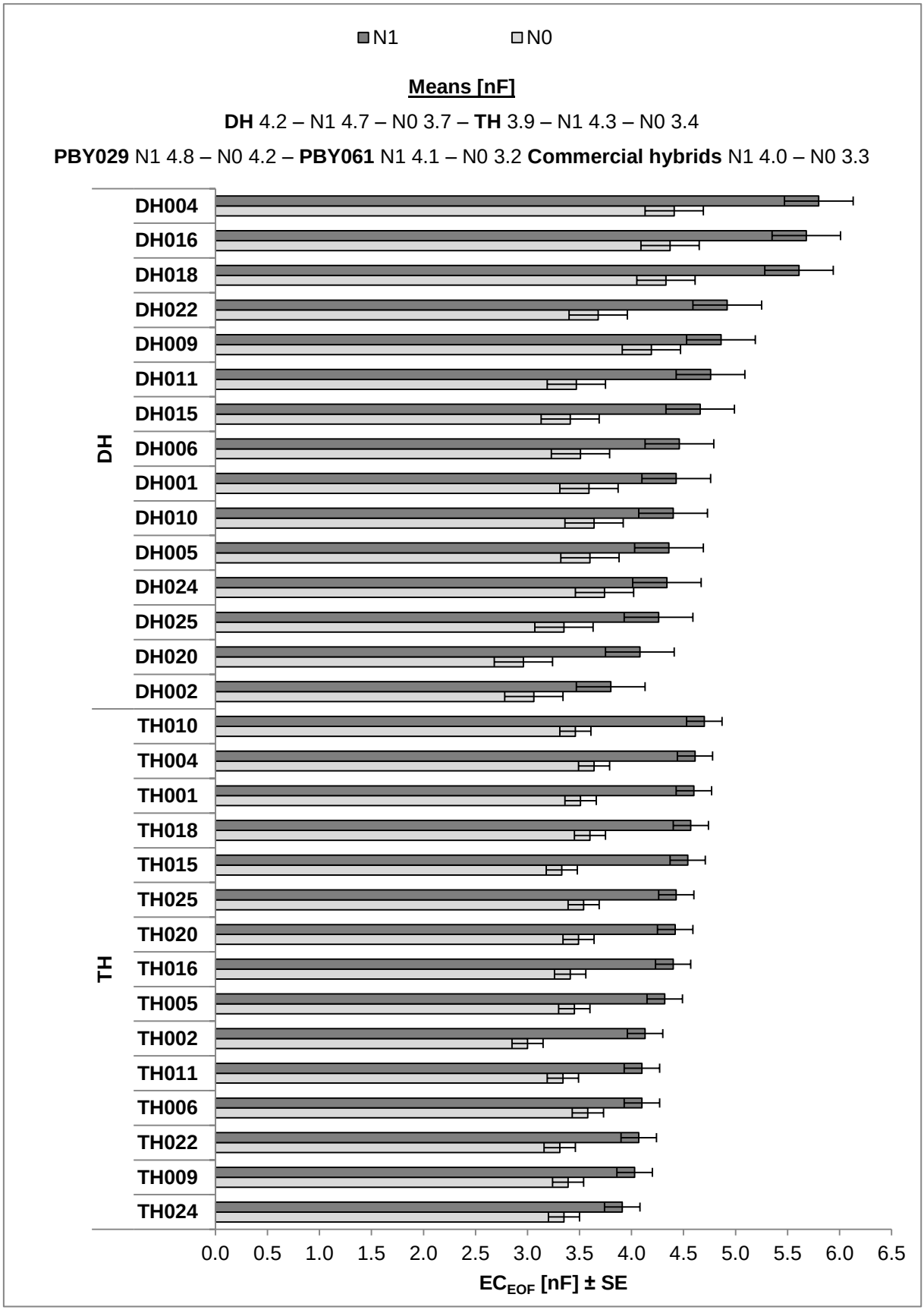

Fig. C 13: EC_{EOF} of Pop029
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, on top means for DH and TH across both N levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0 are given

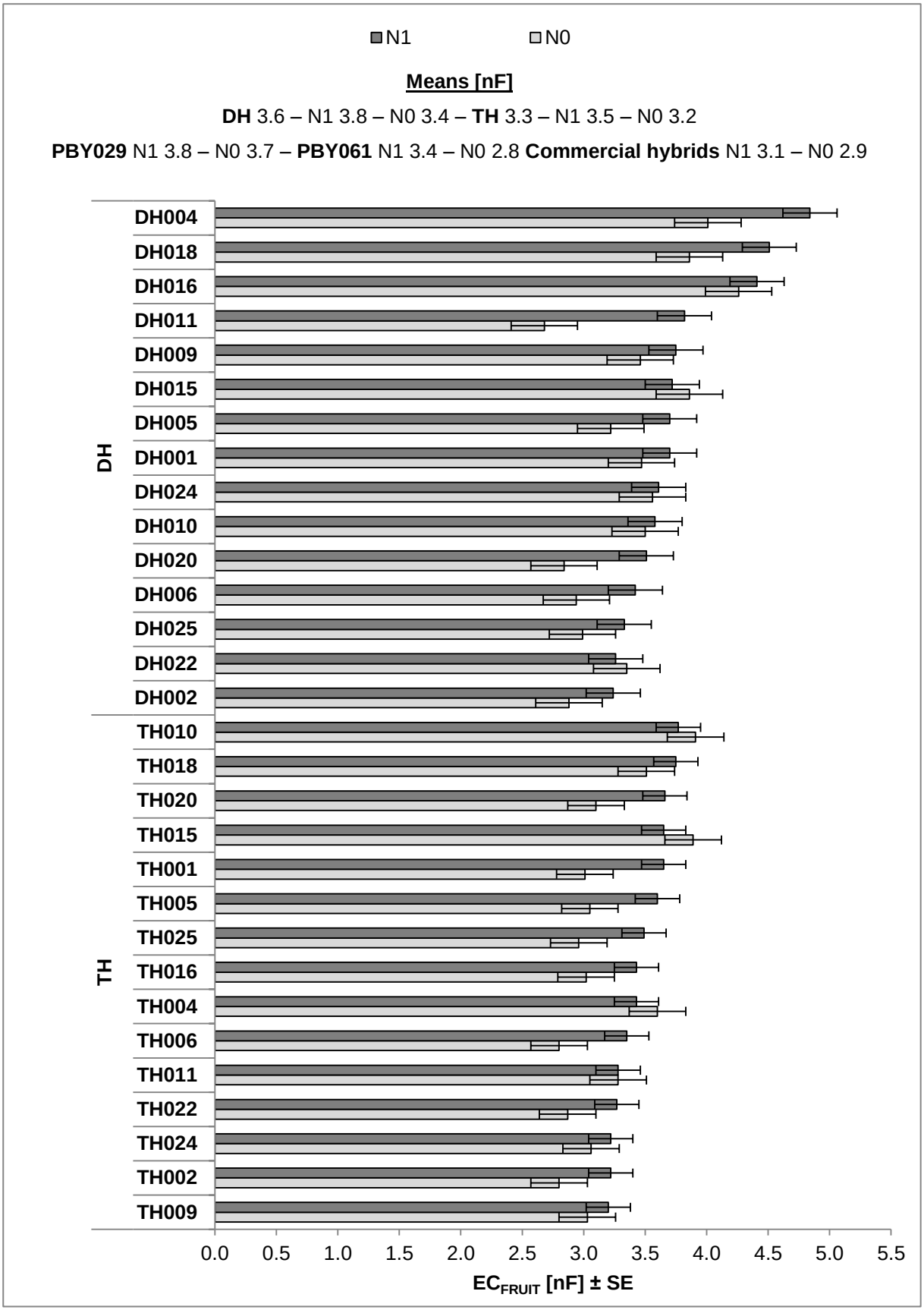

Fig. C 14: EC_{FRUIT} of Pop029
Means of genotypes across three environments at N1 and N0 with standard error SE, DH DH lines, TH test hybrids, on top means for DH and TH across both N levels and at N0 and N1, parental means for N1 and N0 and mean of three commercial hybrids at N1 and N0 are given

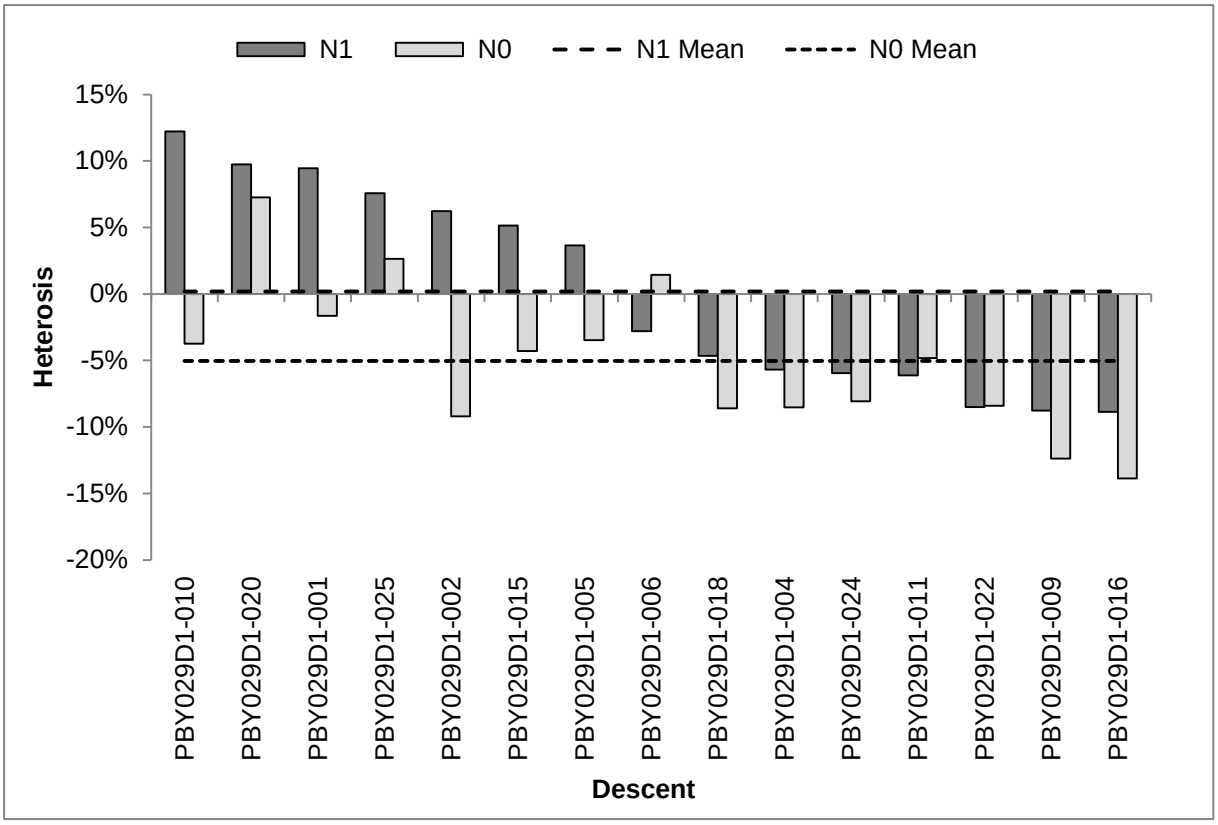

Fig. C 15: Pop029 Heterosis of EC_{EOF}
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

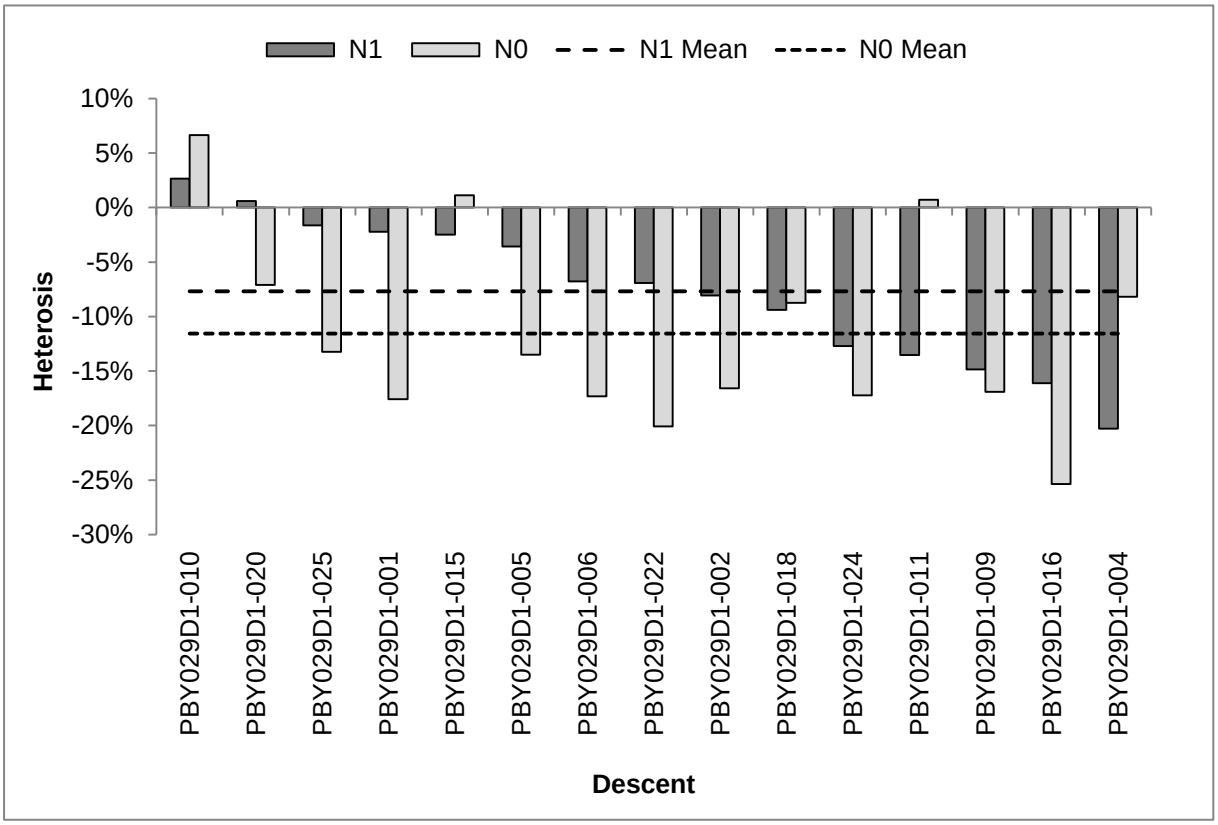

Fig. C 16: Heterosis for EC_{FRUIT} of Pop029
Difference between test hybrid of a descent and mean of DH line of this descent and hybrid mother PBY062

Tab. C 18: Genetic variation of EC_{EOF} and EC_{FRUIT} of Pop029 within N levels and variety types

N level	Trait	DH					TH				
		G	h²	Min	Mean	Max	G	h²	Min	Mean	Max
N1	EC_{EOF} [nF]	**	0.70	3.80	4.69	5.80	*	0.56	3.91	4.33	4.70
	EC_{FRUIT} [nF]	**	0.78	3.24	3.76	4.84	*ns*	0.23	3.20	3.46	3.77
N0	EC_{EOF} [nF]	*	0.62	2.96	3.69	4.41	*ns*	0.06	3.00	3.43	3.64
	EC_{FRUIT} [nF]	**	0.67	2.68	3.39	4.26	*	0.62	2.80	3.19	3.91

DH DH lines, TH Test hybrids, G Effect of genotype, h² Heritability, Min Minimum trait value, Mean Mean trait value, Max Maximum trait value, Min and Max represent the lowest and highest genetic mean across three environments, Mean bases on genetic means of 15 genotypes across three environments, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05

Maturity traits (MAT traits) of Pop007

Except $N\%_{Straw}$, Nup_{Straw}, and $DM\%_{Seed}$ at N1 and Straw, $N\%_{Straw}$, Nup_{Straw} and $DM\%_{Seed}$ at N0 MAT traits of DH lines showed significant genetic variation. Within test hybrids most traits revealed significant genetic variation within nitrogen levels (Tab. C 19).

Tab. C 19: Genetic variation of MAT traits of Pop007 within N levels and variety types

N level	Trait	DH					TH				
		G	h²	Min	Mean	Max	G	h²	Min	Mean	Max
N1	$DM\%_{Straw}$ [%]	**	0.79	32.11	52.37	69.01	**	0.69	38.90	49.88	59.33
	Straw [dt ha^{-1}]	*	0.59	36.39	51.99	59.93	*ns*	0.00	45.42	51.05	58.15
	$N\%_{Straw}$ [%]	*ns*	0.00	0.79	0.89	0.99	*ns*	0.00	0.94	1.00	1.17
	Nup_{Straw} [%]	*ns*	0.46	90.82	92.63	93.62	*ns*	0.00	92.30	92.74	93.32
	$DM\%_{Seed}$ [%]	*ns*	0.26	28.49	34.31	38.83	*ns*	0.34	34.78	38.85	45.22
	Seed DM [dt ha^{-1}]	**	0.65	3.48	3.73	4.12	*	0.57	3.60	3.76	3.90
	$N\%_{Seed}$ [%]	**	0.74	111.15	128.16	154.88	*ns*	0.48	131.52	146.35	172.12
	Nup_{Seed} [kg ha^{-1}]	**	0.65	152.71	174.73	207.49	**	0.69	185.40	197.71	239.36
	Nup_{MAT} [kg ha^{-1}]	*	0.62	0.41	0.47	0.55	*	0.63	0.49	0.52	0.63
	$NupEff_{MAT}$	*	0.59	16.73	19.94	22.15	*	0.61	18.54	19.85	21.02
	NutEff	**	0.75	7.58	9.12	10.40	*ns*	0.09	9.16	10.24	12.05
	NUE	*	0.60	0.33	0.40	0.48	*	0.52	0.39	0.44	0.47
	HI	**	0.83	0.69	0.74	0.79	*ns*	0.00	0.70	0.74	0.77
	NHI	*	0.58	46.63	49.85	52.28	*ns*	0.00	46.17	48.56	50.28
	Oil% [%]	**	0.89	13.51	17.10	19.21	**	0.82	17.15	18.84	21.66
	Oil yield [dt ha^{-1}]	**	0.65	32.11	52.37	69.01	*ns*	0.46	38.90	49.88	59.33
N0	$DM\%_{Straw}$ [%]	**	0.83	32.82	52.37	70.20	**	0.70	49.46	57.18	69.15
	Straw [dt ha^{-1}]	*ns*	0.40	43.37	54.19	62.77	*ns*	0.42	41.68	47.05	54.92
	$N\%_{Straw}$ [%]	*ns*	0.30	0.69	54.74	0.95	*ns*	0.12	0.65	0.70	0.76
	Nup_{Straw} [dt ha^{-1}]	*ns*	0.48	90.23	45.73	92.41	*ns*	0.00	90.84	91.77	92.51
	$DM\%_{Seed}$ [%]	*ns*	0.32	26.90	35.18	37.08	*ns*	0.05	30.47	32.33	34.49
	Seed DM [dt ha^{-1}]	**	0.79	3.48	32.01	4.08	*ns*	0.07	3.16	3.32	3.48
	$N\%_{Seed}$ [%]	**	0.93	104.36	3.78	141.62	**	0.76	99.88	107.86	119.97
	Nup_{Seed} [kg ha^{-1}]	**	0.77	146.85	122.59	199.25	*ns*	0.41	130.46	140.89	154.62
	Nup_{MAT} [kg ha^{-1}]	**	0.72	0.68	168.86	0.95	*ns*	0.39	0.63	0.68	0.74
	$NupEff_{MAT}$	**	0.65	17.12	0.79	23.03	*ns*	0.34	22.42	23.33	24.96
	NutEff	**	0.80	13.03	19.82	19.46	*ns*	0.51	14.57	15.61	16.79
	NUE	**	0.75	0.32	15.48	0.44	*ns*	0.02	0.39	0.41	0.43
	HI	*	0.59	0.69	0.37	0.81	*ns*	0.00	0.75	0.77	0.79
	NHI	*	0.58	46.47	0.74	52.47	*ns*	0.00	49.95	51.30	52.85
	Oil% [%]	**	0.93	12.81	49.66	18.24	**	0.73	15.47	16.51	17.64
	Oil yield [dt ha^{-1}]	**	0.78	32.82	52.37	70.20	*ns*	0.00	49.46	57.18	69.15

DH DH lines, TH Test hybrids, G Effect of genotype, h² Heritability, Min Minimum trait value, Mean Mean trait value, Max Maximum trait value, Min and Max represent the lowest and highest genetic mean across three environments, Mean bases on genetic means of 15 genotypes across three environments, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05

Maturity traits (MAT traits) of Pop029

DH lines at N1 showed significant genetic variation in nearly all MAT traits except $N\%_{Straw}$, $Nup_{Straw,}$ $DM\%_{Seed}$, HI and NHI. Within N0 $DM\%_{Seed}$, HI and NHI did not show significant genetic variation. Within test hybrids significant genetic variation was only detected for $DM\%_{Straw}$ within both nitrogen levels (Tab. C 20).

Tab. C 20: Genetic variation of MAT traits of Pop029 within N levels and variety types

N level	Trait	DH					TH				
		G	h²	Min	Mean	Max	G	h²	Min	Mean	Max
N1	$DM\%_{Straw}$ [%]	**	0.71	39.91	56.21	70.38	*	0.56	42.38	49.69	55.81
	Straw [dt ha^{-1}]	*	0.55	39.16	45.43	52.95	*ns*	0.20	42.69	49.70	57.30
	$N\%_{Straw}$ [%]	*ns*	0.42	0.80	0.89	1.02	*ns*	0.35	0.94	1.01	1.12
	Nup_{Straw} [%]	*ns*	0.00	92.27	92.78	93.71	*ns*	0.13	92.22	92.61	92.86
	$DM\%_{Seed}$ [%]	*ns*	0.07	31.05	36.79	43.92	*ns*	0.00	36.15	39.18	41.63
	Seed DM [dt ha^{-1}]	**	0.76	3.26	3.41	3.82	*ns*	0.02	3.58	3.70	3.81
	$N\%_{Seed}$ [%]	**	0.88	102.29	125.62	147.37	*ns*	0.40	131.86	145.09	153.75
	Nup_{Seed} [kg ha^{-1}]	**	0.73	137.18	166.72	190.49	*ns*	0.39	179.37	195.22	207.34
	Nup_{MAT} [kg ha^{-1}]	**	0.77	0.37	0.44	0.51	*ns*	0.19	0.47	0.51	0.55
	$NupEff_{MAT}$	**	0.76	19.70	22.37	23.50	*ns*	0.20	19.58	20.23	20.92
	NutEff	*	0.64	8.19	9.75	11.68	*ns*	0.00	9.51	10.32	11.02
	NUE	**	0.71	0.42	0.45	0.48	*ns*	0.06	0.42	0.44	0.49
	HI	*ns*	0.20	0.73	0.76	0.78	*ns*	0.37	0.72	0.74	0.77
	NHI	*ns*	0.00	47.64	48.64	50.43	*ns*	0.25	46.24	47.18	47.94
	Oil% [%]	**	0.67	14.97	17.90	21.38	*ns*	0.39	17.13	18.46	19.33
	Oil yield [dt ha^{-1}]	**	0.79	39.91	56.21	70.38	*ns*	0.00	42.38	49.69	55.81

DH DH lines, TH Test hybrids, G Effect of genotype, h² Heritability, Min Minimum trait value, Mean Mean trait value, Max Maximum trait value, Min and Max represent the lowest and highest genetic mean across three environments, Mean bases on genetic means of 15 genotypes across three environments, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05

Tab. C 20 (continued)

N level	Trait	DH					TH				
		G	h²	Min	Mean	Max	G	h²	Min	Mean	Max
N0	$DM\%_{Straw}$ [%]	*	0.61	43.78	57.76	71.37	*	0.55	49.29	59.64	67.35
	Straw [dt ha^{-1}]	*	0.52	36.80	45.72	53.61	*ns*	0.06	36.70	43.75	50.34
	$N\%_{Straw}$ [%]	*	0.52	0.69	0.83	0.96	*ns*	0.00	0.61	0.65	0.71
	Nup_{Straw} [%]	*	0.52	90.71	91.86	93.09	*ns*	0.15	91.07	91.87	92.93
	$DM\%_{Seed}$ [%]	*ns*	0.11	27.40	34.11	42.53	*ns*	0.18	29.57	31.98	34.22
	Seed DM [dt ha^{-1}]	**	0.83	3.31	3.51	3.87	*ns*	0.18	3.18	3.26	3.39
	$N\%_{Seed}$ [%]	**	0.82	97.47	122.05	149.12	*ns*	0.00	95.78	105.15	112.56
	Nup_{Seed} [kg ha^{-1}]	**	0.81	127.99	160.51	193.65	*ns*	0.13	125.09	134.25	144.73
	Nup_{MAT} [kg ha^{-1}]	**	0.85	0.58	0.75	0.91	*ns*	0.04	0.59	0.64	0.69
	$NupEff_{MAT}$	**	0.82	19.88	22.15	23.89	*ns*	0.09	23.24	24.33	25.36
	NutEff	*	0.61	12.64	16.32	20.62	*ns*	0.26	14.00	15.40	16.68
	NUE	**	0.75	0.40	0.43	0.45	*ns*	0.21	0.40	0.42	0.47
	HI	*ns*	0.00	0.74	0.77	0.79	*ns*	0.25	0.76	0.79	0.82
	NHI	*ns*	0.00	45.98	48.50	50.05	*ns*	0.42	48.75	49.55	50.41
	Oil% [%]	**	0.74	12.99	16.38	20.22	*ns*	0.36	14.56	15.76	17.09
	Oil yield [dt ha^{-1}]	**	0.82	43.78	57.76	71.37	*ns*	0.22	49.29	59.64	67.35

DH DH lines, TH Test hybrids, G Effect of genotype, h² Heritability, Min Minimum trait value, Mean Mean trait value, Max Maximum trait value, Min and Max represent the lowest and highest genetic mean across three environments, Mean bases on genetic means of 15 genotypes across three environments, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05

Correlations

Correlations are given as means within nitrogen level and variety type across the two populations.

Within DH significant phenotypic correlations between EC_{EOF} and EC_{FRUIT} were detected within N1 and N0. The respective genetic correlations were also high. No significant phenotypic correlation was detected between EC_{EOF} or EC_{FRUIT} and MAT traits. Within N1 the highest genetic correlation were detected for EC_{EOF} and $DM\%_{Seed}$, (r-gen = 1.40), $N\%_{Straw}$ (r-gen = -0.57) and $DM\%_{Seed}$ (r-gen = -0.45). All other genetic correlations were very low. Within N0 highest genetic correlations were observed for EC_{EOF} and $N\%_{Straw}$ (r-gen = -0.70) and Straw DM (r-gen = 0.43) (Tab. C 21).

Within test hybrids a significant phenotypic correlation was detected between EC_{EOF} and EC_{FRUIT} at N1. The respective genetic correlation was also very high. EC_{EOF} and EC_{Fruit} did not show significant phenotypic correlation to any MAT trait. Highest genetic correlation within N1 were observed between EC_{EOF} and $N\%_{Seed}$ (r-gen = 0.54) and between EC_{FRUIT} and Seed DM (r-gen = -0.82). Within N0 in some cases genetic correlations between were this high that it was considered as estimation error e.g. r-gen of -22.72 between EC_{EOF} and $NupEff_{MAT}$ or r-gen = -3.65 between EC_{FRUIT} and $NupEff_{MAT}$. High genetic correlations were observed between EC_{FRUIT} and $DM\%_{Straw}$ (r-gen = -1.00), $N\%_{Straw}$ (r-gen = 0.94) and $DM\%_{Seed}$ (r-gen = -0.90) (Tab. C 22).

Tab. C 21: Correlations between EC_{EOF} or EC_{FRUIT} and MAT traits within DH lines within N levels

Correlation of …	With …	N1			N0		
		r-phen		r-gen	r-phen		r-gen
EC_{EOF}	EC_{FRUIT}	0.62	*	0.74	0.73	*	1.05
	$DM\%_{Straw}$ [%]	-0.35	*ns*	-0.45	-0.18	*ns*	-0.34
	Straw [dt ha^{-1}]	0.19	*ns*	0.26	0.26	*ns*	0.43
	$N\%_{Straw}$ [%]	-0.31	*ns*	-0.57	-0.31	*ns*	-0.70
	Nup_{Straw} [%]	-0.03	*ns*	0.23	0.06	*ns*	0.08
	$DM\%_{Seed}$ [%]	-0.42	*ns*	-1.40	-0.09	*ns*	-0.09
	Seed DM [dt ha^{-1}]	0.07	*ns*	0.06	-0.06	*ns*	-0.11
	$N\%_{Seed}$ [%]	-0.10	*ns*	-0.08	0.07	*ns*	0.22
	Nup_{Seed} [dt ha^{-1}]	0.03	*ns*	0.03	0.01	*ns*	0.06
	Nup_{MAT} [dt ha^{-1}]	0.03	*ns*	0.00	0.06	*ns*	0.12
	$NupEff_{MAT}$	0.05	*ns*	0.04	0.04	*ns*	0.12
	NutEff	0.13	*ns*	0.25	-0.13	*ns*	-0.27
	NUE	0.08	*ns*	0.07	-0.06	*ns*	-0.12
	HI	-0.16	*ns*	-0.29	-0.41	*ns*	-0.27
	NHI	0.06	*ns*	-0.04	-0.18	*ns*	0.02
	Oil% [%]	0.17	*ns*	0.00	-0.02	*ns*	0.23
	Oil yield [dt ha^{-1}]	0.10	*ns*	0.14	-0.07	*ns*	-0.17
EC_{FRUIT}	$DM\%_{Straw}$ [%]	-0.11	*ns*	-0.25	-0.08	*ns*	-0.05
	Straw [dt ha^{-1}]	-0.05	*ns*	-0.09	0.16	*ns*	0.69
	$N\%_{Straw}$ [%]	-0.21	*ns*	-0.24	-0.18	*ns*	-0.84
	Nup_{Straw} [%]	-0.20	*ns*	0.12	0.00	*ns*	0.18
	$DM\%_{Seed}$ [%]	-0.12	*ns*	-0.67	-0.27	*ns*	-0.26
	Seed DM [dt ha^{-1}]	-0.04	*ns*	-0.05	-0.10	*ns*	-0.25
	$N\%_{Seed}$ [%]	-0.22	*ns*	-0.29	0.11	*ns*	0.23
	Nup_{Seed} [dt ha^{-1}]	-0.15	*ns*	-0.19	-0.05	*ns*	-0.12
	Nup_{MAT} [dt ha^{-1}]	-0.18	*ns*	-0.21	-0.03	*ns*	-0.03
	$NupEff_{MAT}$	-0.17	*ns*	-0.21	-0.05	*ns*	-0.13
	NutEff	0.22	*ns*	0.33	-0.15	*ns*	-0.37
	NUE	-0.04	*ns*	-0.05	-0.12	*ns*	-0.35
	HI	-0.05	*ns*	-0.01	-0.30	*ns*	-0.39
	NHI	0.06	*ns*	-0.05	-0.14	*ns*	-0.16
	Oil% [%]	0.04	*ns*	0.00	-0.01	*ns*	0.17
	Oil yield [dt ha^{-1}]	-0.02	*ns*	-0.02	-0.11	*ns*	-0.26

r-phen Pearson correlation coefficient based on means of 15 DH lines per DH population across three environments, r-gen Genetic correlation across three environments, * significant for $\alpha = 0.05$, *ns* significant for $\alpha = 0.05$, Correlation coefficients represent the mean within variety type DH line (DH) across the two populations

Tab. C 22: Correlations between EC_{EOF} or EC_{FRUIT} and MAT traits within test hybrids and N levels

Correlation of …	With …	N1			N0		
		r-phen		r-gen	r-phen		r-gen
EC_{EOF}	EC_{FRUIT}	0.82	*	1.12	0.35	*ns*	0.70
	$DM\%_{Straw}$ [%]	-0.01	*ns*	0.12	-0.31	*ns*	-1.68
	Straw [dt ha^{-1}]	0.23	*ns*	-0.05	0.11	*ns*	-2.30
	$N\%_{Straw}$ [%]	-0.06	*ns*	-0.12	-0.16	*ns*	-0.82
	Nup_{Straw} [%]	0.10	*ns*	-0.20	0.00	*ns*	-2.09
	$DM\%_{Seed}$ [%]	0.23	*ns*	0.00	-0.11	*ns*	-0.66
	Seed DM [dt ha^{-1}]	0.29	*ns*	0.37	-0.07	*ns*	-3.22
	$N\%_{Seed}$ [%]	0.15	*ns*	0.54	0.15	*ns*	0.04
	Nup_{Seed} [dt ha^{-1}]	0.31	*ns*	0.27	-0.05	*ns*	-3.18
	Nup_{MAT} [dt ha^{-1}]	0.29	*ns*	0.22	0.01	*ns*	-6.80
	$NupEff_{MAT}$	0.32	*ns*	0.25	-0.06	*ns*	-22.72
	NutEff	-0.09	*ns*	0.00	-0.07	*ns*	-0.61
	NUE	0.30	*ns*	0.23	-0.11	*ns*	-2.27
	HI	0.01	*ns*	0.05	-0.20	*ns*	-0.05
	NHI	0.03	*ns*	0.20	0.04	*ns*	0.10
	Oil% [%]	-0.01	*ns*	0.00	-0.24	*ns*	-2.10
	Oil yield [dt ha^{-1}]	0.26	*ns*	0.00	-0.19	*ns*	0.00
EC_{FRUIT}	$DM\%_{Straw}$ [%]	-0.04	*ns*	0.00	-0.41	*ns*	-1.00
	Straw [dt ha^{-1}]	0.12	*ns*	-0.41	0.07	*ns*	-0.61
	$N\%_{Straw}$ [%]	0.01	*ns*	0.31	0.28	*ns*	0.94
	Nup_{Straw} [%]	0.06	*ns*	-0.31	0.29	*ns*	-0.32
	$DM\%_{Seed}$ [%]	0.26	*ns*	-0.10	-0.23	*ns*	-0.90
	Seed DM [dt ha^{-1}]	0.38	*ns*	-0.82	-0.11	*ns*	-0.17
	$N\%_{Seed}$ [%]	0.05	*ns*	0.58	0.37	*ns*	0.45
	Nup_{Seed} [dt ha^{-1}]	0.36	*ns*	0.35	0.07	*ns*	0.16
	Nup_{MAT} [dt ha^{-1}]	0.31	*ns*	0.17	0.16	*ns*	-0.41
	$NupEff_{MAT}$	0.32	*ns*	0.19	0.11	*ns*	-3.65
	NutEff	0.07	*ns*	1.03	-0.37	*ns*	-0.78
	NUE	0.37	*ns*	-0.22	-0.11	*ns*	0.55
	HI	0.19	*ns*	0.22	-0.17	*ns*	0.14
	NHI	0.09	*ns*	0.13	-0.09	*ns*	0.14
	Oil% [%]	-0.10	*ns*	-0.41	0.07	*ns*	-0.07
	Oil yield [dt ha^{-1}]	0.32	*ns*	0.35	-0.08	*ns*	0.00

r-phen Pearson correlation coefficient based on means of 15 test hybrids per DH population across three environments, r-gen Genetic correlation across three environments, * significant for α = 0.05, *ns* significant for α = 0.05, Correlation coefficients represent the mean within variety test hybrid (TH) across the two populations

Electrical capacitance and root characteristics

Selection of genotypes

Based on electrical capacitance ten genotypes of the diversity set were selected for their differences in EC_{EOF} and EC_{FRUIT} at N1 and N0 (Fig. C 17).

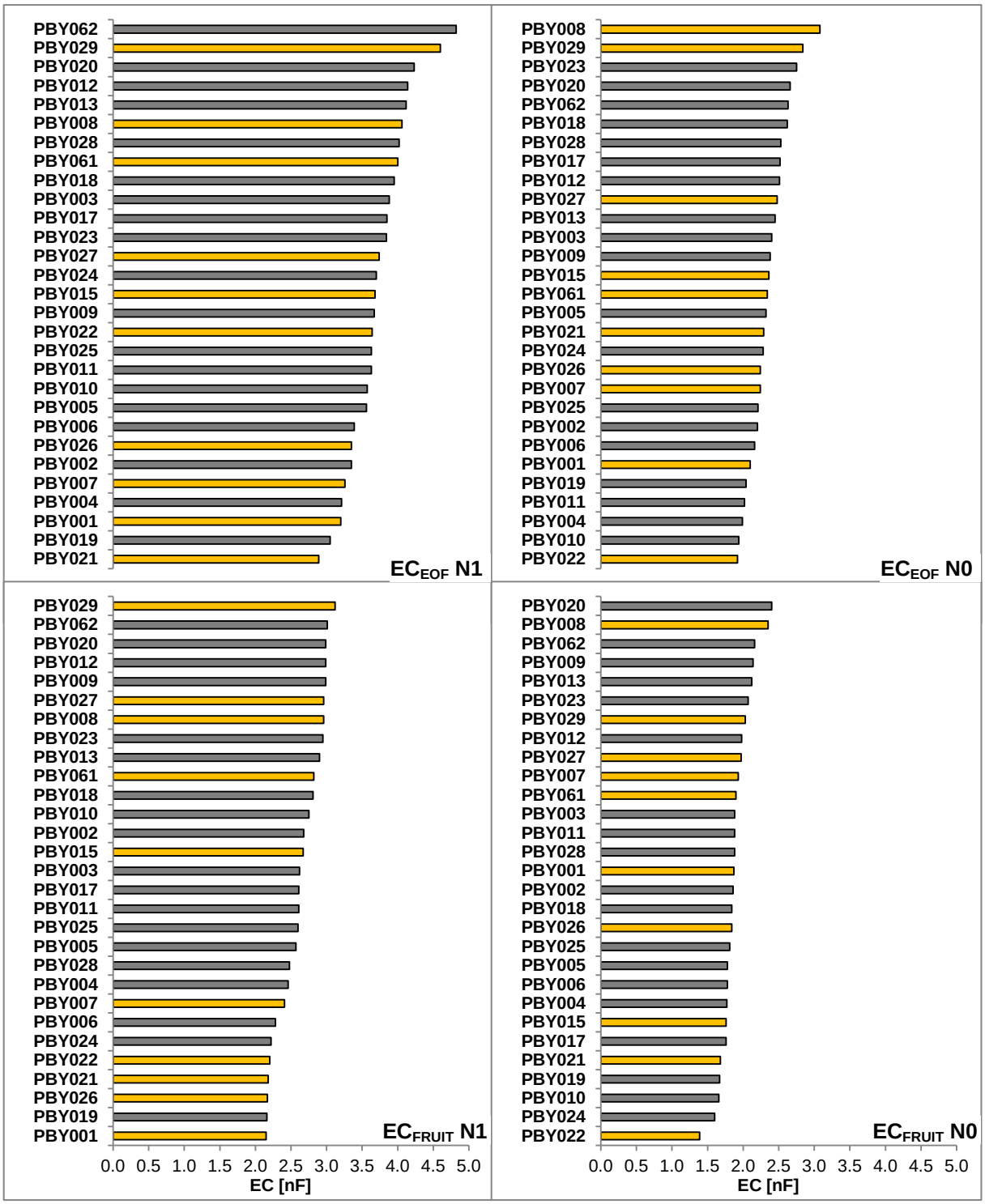

Fig. C 17: EC_{EOF} (top) and EC_{FRUIT} (bottom) within N levels of EC trials of diversity set
Genetic means across five environments, Orange bars present selected genotypes

EC10 - Field trial ($EC10_F$)

Electrical capacitance

Significant genetic variation and a high heritability of 0.91 were detected for electrical capacitance (Tab. C 23). It ranged from 3.5 nF (PBY001) to 6.2 nF (PBY029) (Fig. C 18). Significant genetic variation was also detected across combinations of environments and dates data for root mass and stem diameter was available for (Tab. C 24).

Tab. C 23: ANOVA for electrical capacitance of $EC10_F$

Source	DF	MS	Var.cp	F	
D	2	67.33	3.33	83.90	**
R:D	3	0.80	0.05	2.79	*ns*
G	9	3.48	0.53	10.90	**
DG	18	0.32	0.02	1.11	*ns*
RG:D	27	0.29	0.29		
Total	59				
h^2	0.66 - **0.91** - 0.97				

DF degrees of freedom, MS mean squares, Var.cp variance component, D combination of environment and measuring date, R: replication within D, G genotype, DG interaction, RG:D error, h^2 heritability (bold) with 0.95 confidence interval, ** significant for α = 0.01, *ns* not significant for α = 0.05

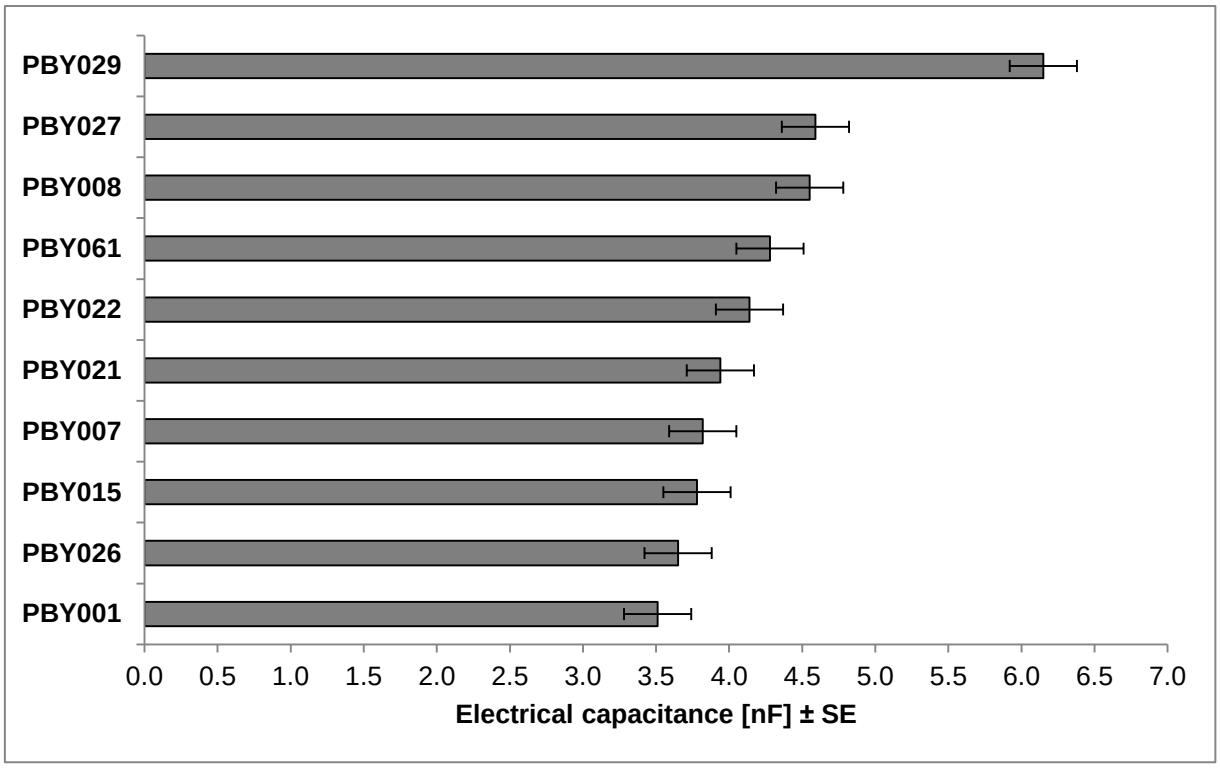

Fig. C 18: Electrical capacitance of $EC10_F$
Genetic means across three combinations of environment and measuring date ± standard error SE

Tab. C 24: Genetic variation of EC of $EC10_F$

Trait	Measured in	G	h²	Min	Mean	Max
EC [nF]	EIN_{May} + GOE_{April}	*	0.76	3.57	4.28	6.05
EC [nF]	EIN_{May} + GOE_{May}	**	0.92	2.77	3.30	5.31

G effect of genotype, h² heritability, Min minimum electrical capacitance, Mean Mean electrical capacitance, Max maximum electrical capacitance, Min and Max represent the lowest and highest genetic mean across two combinations of environment and measuring date, Mean bases on genetic means of 10 genotypes across two combinations of environment and measuring date, ** significant for α = 0.01, * significant for α = 0.05

Root masses at three horizons and stem diameter

No significant genetic variation was detected for root masses and stem diameter (Tab. C 25).

Tab. C 25: Genetic variation of root masses and stem diameter of $EC10_F$

Trait	Measured in	G	h²	Min	Mean	Max
RM_{0-20} [mg]	EIN_{May} + GOE_{April}	*ns*	0.00	48.3	71.1	105.4
RM_{20-40} [mg]	EIN_{May} + GOE_{April}	*ns*	0.00	12.9	20.2	29.2
RM_{40-60} [mg]	EIN_{May} + GOE_{April}	*ns*	0.00	6.2	9.4	13.5
StemDia [mm]	EIN_{May} + GOE_{May}	*ns*	0.14	13.9	14.9	16.7

G effect of genotype, h² heritability, Min minimum trait value, Mean Mean trait value, Max Maximum trait value, Min and Max represent the lowest and highest genetic mean across two combinations of environment and measuring date, Mean bases on genetic means of 10 genotypes across two combinations of environment and measuring date, *ns* not significant for α = 0.05

Correlations

No significant phenotypic correlation was detected on genotype level. Genetic correlations were observed between electrical capacitance and root mass in upper horizon (RM_{0-20}) and between electrical capacitance and stem diameter. But both were smaller than their standard error. On plot level significant phenotypic correlations were found between electrical capacitance and root masses in medium and bottom horizon (RM_{20-40}, RM_{40-60}) and between electrical capacitance and stem diameter. The latter was highest on plot level. On single plant level electrical capacitance and stem diameter also correlated significantly (Tab. C 26).

Tab. C 26: Correlations between electrical capacitance and root masses or stem diameter in $EC10_F$

Correlation of …	With …	r-phen	r-gen	r-plot	r-plant
EC	RM_{0-20}	-0.35 *ns*	-3.54 -	-0.08 *ns*	/
	RM_{20-40}	-0.49 *ns*	0.00 -	0.46 *	/
	RM_{40-60}	0.16 *ns*	0.00 -	0.34 *	/
	StemDia	0.51 *ns*	1.25 -	0.78 *	0.81 *

r-phen Pearson correlation coefficient based on genetic means across two combinations of environment and measuring date (N = 10), r-gen genetic correlation across two combinations of environment and measuring date, r-plot Pearson correlation coefficient based on plot means at two combinations of environment and measuring date (N = 40), r-plant Pearson correlation coefficient based on single plant values at two combinations of environment and measuring date (N=400), * significant for α = 0.05, ns not significant for α = 0.05, - r-gen < standard error of r-gen, / not tested

EC10 – Controlled conditions ($EC10_C$)

Electrical capacitance

Significant genetic variation and a high heritability of 0.95 were observed for electrical capacitance at controlled conditions (Tab. C 27). It ranged from 0.9 nF (PBY026) to 2.7 nF (PBY008) (Fig. C 19). Significant genetic correlation was also detected across the five environments root characteristics were assessed in (α = 0.01, h^2 0.89, minimum 0.9 nF, mean 1.5 nF, maximum 2.6 nF).

Tab. C 27: ANOVA for electrical capacitance of $EC10_C$

Source	DF	MS	Var.cp	F
G	9	3.58	0.34	18.91 **
R	9	0.72	0.05	3.80 **
RG	81	0.19	0.19	
Total	99			
h^2	0.82 - **0.95** - 0.98			

DF degrees of freedom, MS mean squares, Var.cp variance component, G genotype, R replication, RG interaction, h^2 heritability (bold) with 0.95 confidence interval, ** significant for α = 0.01

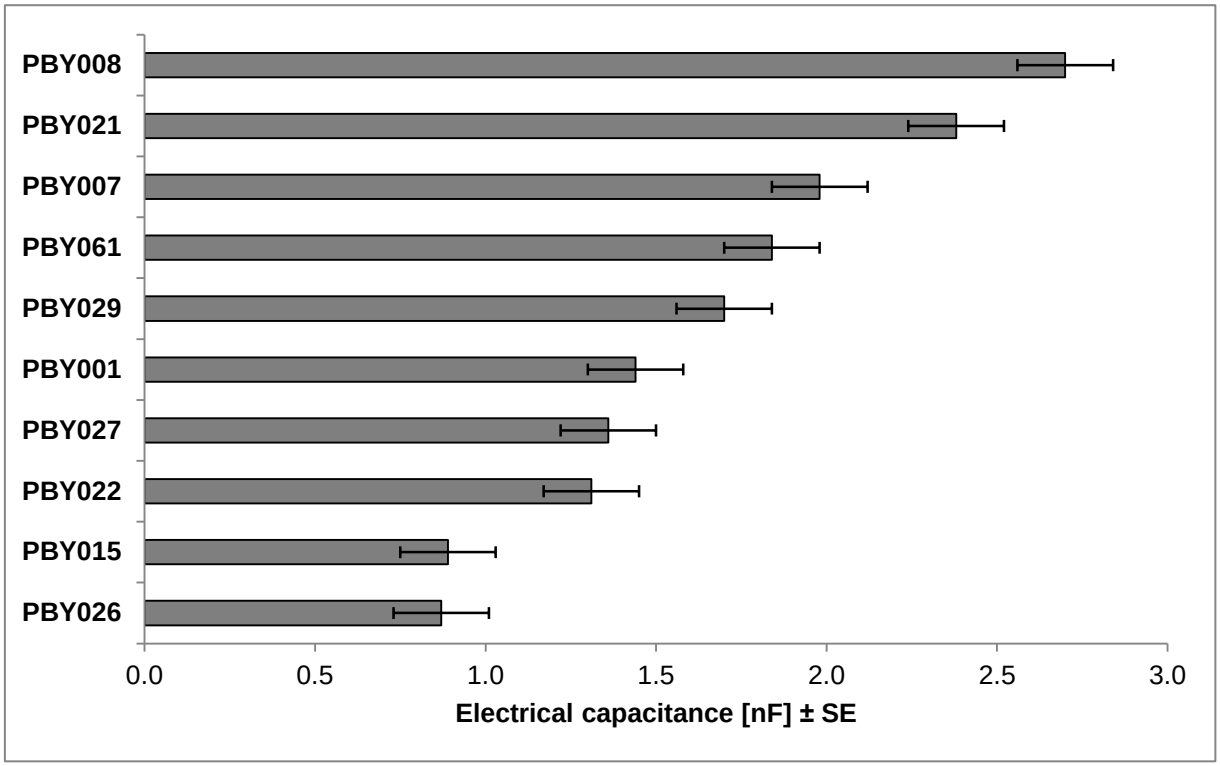

Fig. C 19: Electrical capacitance of $EC10_C$
Genetic means across ten replications ± standard error SE

Root characteristics and stem diameter

Significant genetic variation was found for fresh matter of root system (RS_{FM}), taproot (Tap_{FM}) and lateral roots (Lat_{FM}) as well as for projected root area (RootArea) and stem diameter (StemDia) (Tab. C 28). The latter was tested across the ten replications electrical capacitance was measured in and across the five replications root characteristics were determined in (Tab. C 28).

Tab. C 28: Genetic variation of root traits and stem diameter of $EC10_C$

Trait	G	h²	Min	Mean	Max
RS_{FM} [g]	**	0.72	13.8	17.0	23.9
Tap_{FM} [g]	*	0.61	8.0	6.3	15.5
Lat_{FM} [g]	**	0.72	5.0	10.7	8.4
RootDia [mm]	*ns*	0.44	16.0	18.0	19.8
RootArea	**	0.68	242.3	306.6	387.3
$Dens_{Av}$	*ns*	0.22	8.7	10.5	13.2
W_{Med} [mm]	*ns*	0.23	38.3	51.3	63.1
W_{Max} [mm]	*ns*	0.26	80.1	100.0	114.4
RTP	*ns*	0.00	177.5	230.6	286.8
TD_{Med} [mm]	*ns*	0.28	0.4	0.5	0.5
TD_{Mean} [mm]	*ns*	0.00	0.5	0.5	0.6
$DD90_{Max}$ [mm]	*ns*	0.00	1.0	1.2	1.4
StemDia [mm] (10)	**	0.92	8.0	9.8	11.6
StemDia [mm] (5)	**	0.76	8.3	9.8	11.5

G effect of genotype, h² heritability, Min minimum trait value, Mean Mean trait value, Max Maximum trait values, Min and Max represent the lowest and highest genetic mean across ten (10) or five (5) replications for stem diameter and across five replications for root characteristics, Mean bases on genetic means of 10 genotypes across ten (10) or five (5) replications for stem diameter and across five replications for root characteristics, ** significant for $\alpha = 0.01$, * significant for = 0.05, *ns* not significant for $\alpha = 0.05$

Correlations

On genotype level significant phenotypic correlation was only detected between electrical capacitance and stem diameter (StemDia, r-phen = 0.78). The respective genetic correlation was high (r-gen = 0.81). Electrical capacitance correlated genetically to some but not all root characteristics, e.g. to fresh matter of root system (RS_{FM}, r-gen = 0.55) and lateral roots (Lat_{FM}, r-gen = 0.67), to root diameter (RootDia, r-gen = 0.74), projected root area (RootArea, r-gen = 0.59) and median tip diameter (TD_{Med}, r-gen = 1.11). On single plant level electrical capacitance correlated significantly to RS_{FM}, Lat_{FM}, RootArea and StemDia (Tab. C 29). There was no significant phenotypic correlation between StemDia and root characteristics on genotype level. StemDia correlated genetically to root traits, e.g. to StemDia and RS_{FM} (r-gen = 0.63), to Lat_{FM} (r-gen = 0.70), to RootArea (r-gen = 0.78) and to TD_{Med} (r-gen = 1.68). On single plant level significant phenotypic correlations were found between StemDia and RS_{FM}, Lat_{FM}, RootArea and median root system width (W_{Med}) (Tab. C 29).

Tab. C 29: Correlations between electrical capacitance, root characteristics and stem diameter in $EC10_C$

Correlation of …	With …	r-phen		r-gen		r-plant	
EC	RS_{FM}	0.56	*ns*	0.55	++	0.47	*
	Tap_{FM}	0.20	*ns*	0.14	-	0.32	*ns*
	Lat_{FM}	0.64	*ns*	0.67	++	0.44	*
	RootDia	0.53	*ns*	0.74	+	0.32	*ns*
	RootArea	0.57	*ns*	0.59	++	0.48	*
	$Dens_{Av}$	0.34	*ns*	0.62	-	0.15	*ns*
	W_{Med}	0.28	*ns*	0.20	-	0.31	*ns*
	W_{Max}	0.26	*ns*	0.38	-	0.24	*ns*
	RTP	-0.20	*ns*	0.00	-	-0.02	*ns*
	TD_{Med}	0.64	*ns*	1.11	++	0.33	*ns*
	TD_{Mean}	0.45	*ns*	0.00	-	0.27	*ns*
	$DD90_{Max}$	0.35	*ns*	0.00	-	0.25	*ns*
	StemDia	0.78	*	0.81	++	0.57	*
StemDia	RS_{FM}	0.63	*ns*	0.63	++	0.54	*
	Tap_{FM}	0.35	*ns*	0.33	-	0.38	*ns*
	Lat_{FM}	0.68	*ns*	0.70	++	0.51	*
	RootDia	0.47	*ns*	0.31	-	0.41	*ns*
	RootArea	0.71	*ns*	0.78	++	0.57	*
	$Dens_{Av}$	0.36	*ns*	0.42	-	0.27	*ns*
	W_{Med}	0.47	*ns*	0.44	-	0.43	*
	W_{Max}	0.25	*ns*	0.02	-	0.38	*ns*
	RTP	-0.09	*ns*	0.00	-	0.04	*ns*
	TD_{Med}	0.85	*ns*	1.68	++	0.35	*ns*
	TD_{Mean}	0.66	*ns*	0.00	-	0.33	*ns*
	$DD90_{Max}$	0.73	*ns*	0.00	-	0.29	*ns*

r-phen Pearson correlation coefficient based on genetic means, r-gen genetic correlation, r-plant Pearson correlation coefficient based on single plant values, Correlations between EC and StemDia base on data of ten replications, Correlations between EC or StemDia and root characteristics based on data of five replications, * significant for $\alpha = 0.05$, *ns* not significant for $\alpha = 0.05$, ++ r-gen > 2fold standard error of r-gen, + r-gen > standard error of r-gen, - r-gen < standard error of r-gen

Correlations between electrical capacitance trials

Two significant correlations of electrical capacitances measured in different trials were detected. Electrical capacitance measured in $EC10_F$ correlated to EC_{EOF} within N1 and across N1 and N0 with correlation coefficients of 0.85 and 0.84, respectively (Fig. C 20).

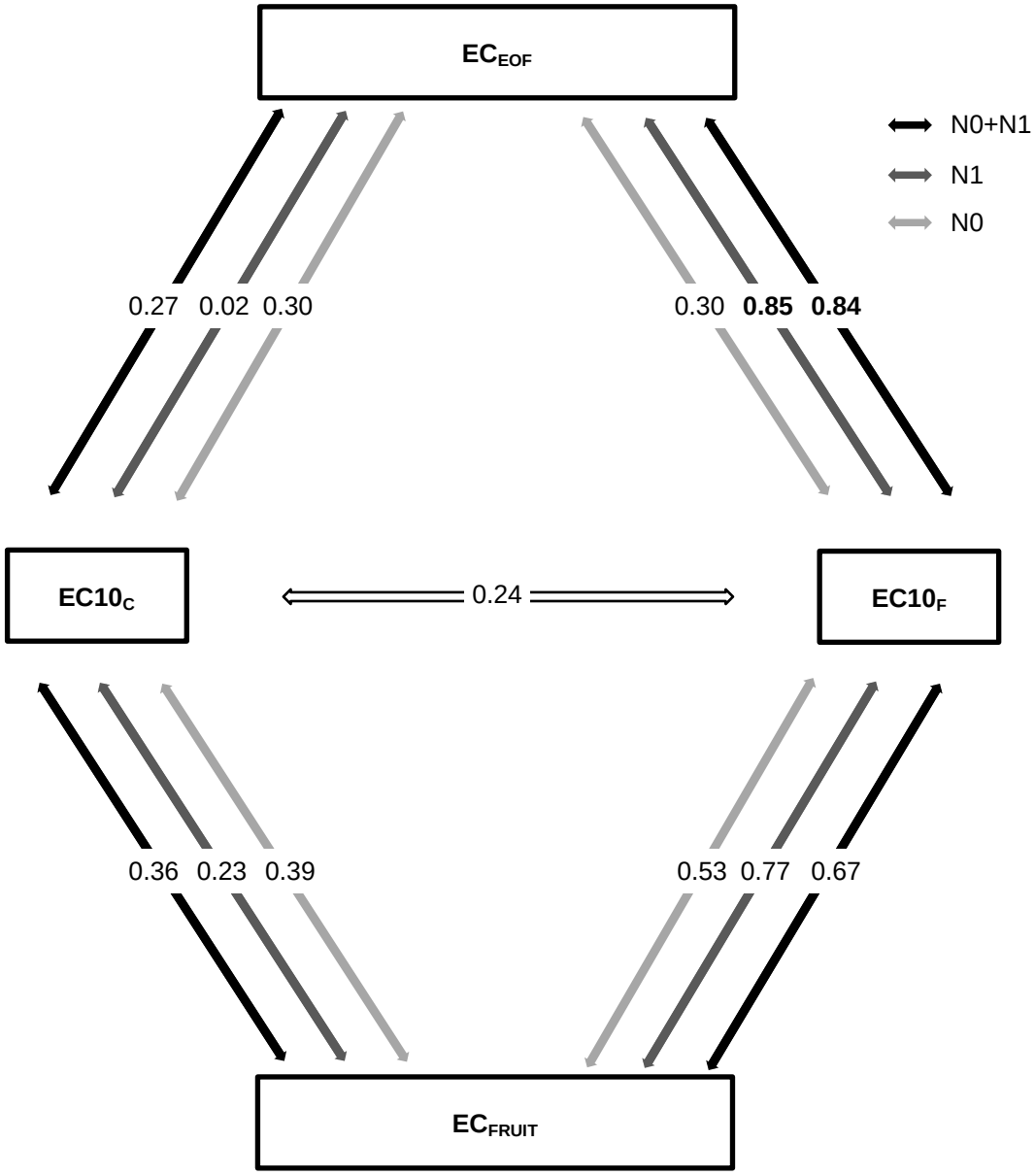

Fig. C 20: Correlations between electrical capacitances of the ten selected genotypes in different trials

Numbers along arrows represent Pearson correlation coefficients based on genetic means, Significant correlations (α = 0.05) are marked bold, N level at which electrical capacitance was measured in EC_{EOF} and EC_{FRUIT}, EC_{EOF} and EC_{FRUIT} genetic means across five environments within N1 and N0 and across both N levels (N1+N0), $EC10_f$ genetic means across three combinations of environment and measuring date, $EC10_c$ genetic means across ten replications

Discussion

Electrical capacitance as selection criterion

High heritabilities were detected for electrical capacitance in field trials with the diversity set and Pop029 and for the ten selected genotypes tested in field trials and under controlled conditions. This suggests that the measured electrical capacitance is a genetic characteristic of winter oilseed rape rather than a soil trait. This is in accordance with findings of Chloupek (1972 and 1977) and Dalton (1995) who reported electrical capacitance to be related with root characteristics. It is also in accordance with Dietrich et al. (2013) who reported that electrical capacitance is governed by the plant rather than by soil.

The significant genetic variation of electrical capacitance of the diversity set and its high heritability particularly at end of flowering (h^2 = 0.81, Tab. C 8) facilitate the use of electrical capacitance as selection criterion in breeding programs. This is supported by findings of Chloupek et al. (1999) who tested electrical capacitance in divergent selection of alfalfa. Progenies of plants with electrical capacitance below average showed lower electrical capacitance than progenies of plants selected for high electrical capacitance, i.e. electrical capacitance is an inheritable trait.

Field trials with the diversity set revealed a significant effect of nitrogen level with electrical capacitance being higher at N1 than at N0. That is in accordance with results of Worku et al. (2012) who tested maize hybrids tested at three different nitrogen levels in Zimbabwe and Kenya. Electrical capacitance was highest at highest nitrogen supply and lowest at lowest nitrogen supply. This study also reported hybrids to react differently to nitrogen stress.

For the diversity set a significant genotype by nitrogen level interaction was detected for electrical capacitance at end of flowering but not during fruit development. A significant genotype by nitrogen level interaction suggests selection environments that resemble target environments. Though, the interaction only contributes to a small portion to total variance.

There was no significant difference in electrical capacitance at end of flowering and during fruit development between DH lines and test hybrids in Pop007 and Pop029. Heterosis, if observed, for electrical capacitance at end of flowering was low. Electrical capacitance of hybrids during fruit development was less than that of the parental mean. DH lines and test hybrids were only tested in season 2013/14. This season was characterised by an extraordinary warm winter and an early and warm spring. Therefore, electrical capacitance of DH lines and test hybrids should be tested in further field trials.

Electrical capacitance and nitrogen efficiency

Significant genetic variation within nitrogen levels was detected for electrical capacitance at end of flowering and during fruit development as well as for all traits which were tested for their relationship to electrical capacitance except nitrogen content of aboveground biomass at end of flowering within N0. Thus, it should have been possible to detect correlations between electrical capacitance and nitrogen efficiency parameters if existing.

Only few significant phenotypic correlations were found. At N1 electrical capacitance at end of flowering correlated negatively with dry matter content of aboveground biomass at end of flowering ($Yield_{EOF}$) and positively with nitrogen uptake and nitrogen uptake efficiency at maturity (Nup_{MAT} and $NupEff_{MAT}$). At N0 electrical capacitance correlated positively with oil content (Oil%). In the current study correlations between electrical capacitance and several traits were tested. Among them were traits, e.g. harvest index that cannot be expected to be related to roots and thus, nitrogen efficiency. Bonferroni-Holm correction takes the number of computed correlations into account. Therefore, correlations between electrical capacitance and those traits led to decreased local p-values of correlations between electrical capacitance and more relevant traits like nitrogen uptake (efficiency), nitrogen use efficiency or nitrogen uptake between end of flowering and maturity. As a consequence, these correlations became non-significant although correlation coefficients were about 0.40 and 0.50 (Tab. C 14).

Correlations to nitrogen uptake and nitrogen uptake efficiency were promising as these traits are directly related to nitrogen efficiency. But although they were

significant they were not very strong (r-phen = 0.57, Tab. C 14). This was also true for the corresponding genetic correlation coefficients. If fewer correlations would have been tested, correlations between electrical capacitance and nitrogen use efficiency or nitrogen uptake between end of flowering and maturity would have become significant. Nevertheless, the correlation coefficients did not exceed 0.50 (Tab. C 14). The low to medium correlation coefficients were in accordance with findings of Worku et al. (2012). Electrical capacitance and grain yield or nitrogen uptake of maize hybrids correlated significantly. But with correlation coefficients of 0.32 for grain yield at medium nitrogen supply, of 0.56 at medium nitrogen supply and 0.48 at high nitrogen supply for nitrogen uptake of aboveground biomass the relations were not very strong.

Although phenotypic correlation was seldom significant genetic correlations between electrical capacitance at end of flowering and nitrogen efficiency parameters were detected which often exceeded their twofold standard error. When nitrogen efficiency parameters are to be selected by electrical capacitance correlated response to selection must be considered. Amongst others it depends on heritability of electrical capacitance and on genetic correlation between electrical capacitance and the nitrogen efficiency parameter (Bernardo 2010 b). Genetic correlations to seed yield, nitrogen uptake and nitrogen uptake efficiency at end of flowering and at maturity, nitrogen utilisation efficiency and nitrogen use efficiency were not very strong. The highest genetic correlation coefficient was found for nitrogen uptake efficiency at end of flowering at N0 (r-gen = 0.69, Tab. C 13). But most genetic correlation coefficients were below 0.60 (Tab. C 13, Tab. C 14). Heritability for electrical capacitance was high particularly at end of flowering (h^2 = 0.81, Tab. C 8). But genetic correlations not only were only medium but also underlie huge estimation errors (Bernardo 2010 b). Thus, electrical capacitance should not be suggested as selection criterion for nitrogen efficiency.

Electrical capacitance and root characteristics

In the field trial significant genetic variation was detected for electrical capacitance. This was not true for root masses and stem diameter. Thus, it was not unexpected that phenotypic correlations between electrical capacitance and root masses or stem diameter were not significant on genotype level. The lack of genetic variation might

be ascribed to sampling errors with regards to root masses as only three samples per plot were taken. Genetic correlations were detected to root mass in the upper horizon and stem diameter. But they were smaller than their standard error and thus, their estimation error was very large.

On plot level significant phenotypic correlations were detected to root masses of the lower horizons (20-40 cm and 40-60 cm) but they were weak. A significantly high positive correlation to stem diameter was detected on plot and single plant level.

Under controlled conditions significant genetic variation was detected for electrical capacitance, root system fresh mass, taproot fresh mass, lateral root fresh mass, root area and stem diameter. Thus, it should have been possible to detect correlations between electrical capacitance and the abovementioned traits if existing. But the only significant phenotypic correlation was observed between electrical capacitance and stem diameter. Genetic correlations that exceeded their twofold standard error were detected to root fresh mass, lateral root fresh mass, root area, median of tip diameter and stem diameter. They were highest for tip diameter, stem diameter and lateral root fresh mass. It cannot not be rejected that electrical capacitance can be used to select for root traits under the given conditions. But root traits were also and stronger genetically correlated to stem diameter. Hence, the observed genetic correlations between electrical capacitance and root traits may also result from the strong genetic correlations between stem diameter and root traits. A similar pattern was detected for phenotypic correlations on single plant level. Electrical capacitance correlated significant and strongest to stem diameter. Electrical capacitance correlated also to some root traits. Stem diameter correlated significantly to the same root traits but with higher correlation coefficients.

Significant correlations to root mass were also reported by Chloupek (1972), Dalton (1995), VanBeem et al. (1998), Rajkaj et al. (2005) and Aulen & Shipley (2012). They were stronger than the ones found in the current study. Chloupek (1972) and Aulen & Shipley (2012) reported the species dependence of the relation between electrical capacitance and root characteristics. As the current study examined winter oilseed rape while different species were addressed by the other studies e.g. tomato (Dalton 1995), maize (VanBeem et al. 1998) or sunflower (Rajkaj et al. 2005). This might explain the different range of correlation coefficient. It could also be explained by the fact that the previous studies examined the relation on single plant level while the

current study examined the relation on genotype and plot level. Furthermore experimental conditions were different in the current study, e.g. a clamp electrode was used while needle electrodes were used by Dalton (1995). Chloupek (1972) reported the relation between electrical capacitance and root mass to be not significant for oilseed rape due to the root morphology of oilseed rape which results in a high root mass and a relatively low root surface. Aulen & Shipley (2012) reported a significant but rather low relationship between electrical capacitance and root mass for oilseed rape grown in pots. The close relation between electrical capacitance and stem diameter is in accordance with Dietrich et al. (2012) who found cross section area which is directly related to perimeter and thus, to diameter to be highly related to electrical capacitance with a correlation coefficient of around 0.90 on single plant level.

Although it cannot be clearly rejected that electrical capacitance is related to root traits it rather appears that electrical capacitance is related to stem diameter. This again is stronger related to root traits than electrical capacitance and thus, stem diameter may mediate the relationship between electrical capacitance and root traits.

Nevertheless, the missing genetic variation for image-based root traits like $Dens_{Av}$ or W_{Max} (Tab. C. 28) suggests that image-based root analysis is not suited for pot experiments.

Findings of Kessel et al. (2012) and Nyikako et al. (2014) suggest that nitrogen uptake and nitrogen uptake efficiency are of particular importance at low nitrogen supply. Thus, one would expect that differences in root system that contribute to nitrogen uptake capacity are closely related to nitrogen efficiency parameters and that these relations would be stronger at low than at high nitrogen supply. In field trials with the diversity set and DH lines and test hybrids genetic as well as phenotypic correlations coefficients were not consistently higher at N0 than at N1. Hence, even if electrical capacitance captured root characteristics it can be concluded that these did not contribute to nitrogen efficiency parameters of winter oilseed rape.

Conclusion

Genetic variation existed for electrical capacitance and heritabilities were high. Regarding the question whether electrical capacitance captures nitrogen efficiency parameters it was shown that only few phenotypic correlations were significant. EC_{EOF} correlated significantly to $DM\%_{EOF}$, Nup_{MAT} and $NupEff_{MAT}$ within N1 and to Oil% within N0. For the relation between electrical capacitance and Nup_{MAT} or $NupEff_{MAT}$ correlation coefficients were only medium (r-phen = 0.57). Thus, electrical capacitance should not be suggested as selection tool for nitrogen efficiency or related parameters of winter oilseed rape

The question whether electrical capacitance is related to root characteristics like root mass, root surface area, root system density and width or root tips cannot be clearly answered. It rather appears that electrical capacitance is related to stem diameter.

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SUMMARY

Oilseed rape is the third most important oil crop worldwide. Under many conditions it is characterised by relatively low nitrogen efficiency. In Germany a nitrogen supply of 240 kg N ha^{-1} is aimed at which derives from soil mineral nitrogen and nitrogen fertiliser. Thus, large amounts of fertiliser are applied. But only about 50 % of fertilised nitrogen are recovered by the crop. Furthermore nitrogen losses appear with leaf shedding that starts during flowering. Only little amounts of nitrogen are taken up between end of flowering and maturity. With a nitrogen harvest index of 0.7 to 0.8 at least 20 % to 30 % of plant nitrogen remain on the field after harvest. As a result nitrogen surpluses of 90 kg N ha^{-1} to 100 kg N ha^{-1} were reported after cultivation of oilseed rape. EU legislative restrictions address greenhouse gas emissions in production of biodiesel made of oilseed rape (EU directive 2009/28/EG) and nitrogen surpluses in agricultural production (EU nitrate directive). These restrictions have moved nitrogen efficiency into focus of rapeseed breeders.

Nitrogen use efficiency can be defined as seed yield per unit available nitrogen. Nitrogen use efficiency is the product of nitrogen uptake efficiency, i.e. the amount of nitrogen which can be taken up per unit available nitrogen, and nitrogen utilisation efficiency measured as grain yield which is produced per unit nitrogen which was taken up. Nitrogen efficiency is a difficult trait to select for as seeds and straw need to be harvested and analysed for nitrogen content. This is laborious and time consuming. Indirect selection methods would facilitate selection. Reflectance of plants is reported to be related to chemical composition and structural features particularly of leaves. Also the nitrogen status of plants and crop stands were shown to be predicted by reflectance.

Roots are important for nitrogen uptake and thus, for nitrogen efficiency. Therefore, it may also be worth to consider the root when selecting for nitrogen efficiency. Phenotyping of roots is difficult, often destructive and only possible for a very limited number of genotypes. Electrical capacitance has been discussed for decades to be related to root characteristics like root surface area or root mass. If so, it may be also related to nitrogen uptake and thus nitrogen efficiency. In contrast to other methods for root phenotyping it is a flexible, non-destructive method that allows quick phenotyping of large numbers of genotypes in the field at any time and any place.

Field experiments were conducted to explore nitrogen efficiency of winter oilseed rape and its prediction by hyperspectral canopy reflectance and electrical capacitance in the field. A diversity set consisting of 29 genotypes was tested at five Central and Northern German environments in seasons 2011/12 and 2012/13. Genotypes were grown at high (160 kg N ha^{-1} to 180 kg N ha^{-1}) and without nitrogen supply. Two parallel trials were conducted – one was harvested at end of flowering, the other one at maturity. Aboveground biomass at end of flowering, nitrogen uptake at end of flowering, nitrogen uptake efficiency at end of flowering, seed yield, nitrogen uptake at maturity, nitrogen uptake efficiency at maturity, nitrogen utilisation efficiency, nitrogen use efficiency, nitrogen harvest index and nitrogen uptake between end of flowering and maturity were analysed for genetic variation and heritability. The genotype by nitrogen level interaction was examined to answer the question whether selection for nitrogen efficiency parameters should be conducted at different nitrogen levels.

Two populations of 15 DH lines each and their test hybrids were tested at three environments in season 2013/14. They were grown at high (N1) and without nitrogen (N0) fertilisation and harvested at maturity. Seed yield, nitrogen uptake at maturity, nitrogen uptake efficiency at maturity, nitrogen utilisation efficiency, nitrogen use efficiency and nitrogen harvest index were analysed to test variation, difference between DH lines and test hybrids, interactions between variety type and nitrogen level, heritability and mid-parent heterosis. For the diversity set and DH lines and test hybrids the contributions of variances of nitrogen uptake efficiency and nitrogen utilisation efficiency to nitrogen use efficiency were computed.

Hyperspectral canopy reflectance was measured with a portable field spectrometer in each plot before flowering and during fruit development. Reflectance from 305 nm to 1800 nm was used to develop calibrations for nitrogen uptake at end of flowering and at maturity and for seed yield. Calibrations were developed across and within nitrogen levels. Calibrations were validated in tenfold cross validations and external validations.

Electrical capacitance of the diversity set, DH lines and test hybrids was measured in the field at end of flowering and during fruit development. Its relation to nitrogen efficiency and agronomic parameters was tested. To examine the relationship between electrical capacitance and root characteristics ten genotypes of the diversity set selected for differences in electrical capacitance were tested in the field and

under controlled conditions. Next to electrical capacitance stem diameter and root masses in three horizons were determined in the field trials. Under controlled conditions single plants were grown in plastic tubes in the greenhouse. Electrical capacitance, stem diameter and fresh mass of whole root system, taproot and lateral roots were measured directly. Image-base analysis was used to analyse further root characteristics like root diameter, root area, root system width and root tips.

Field trials with the diversity set revealed high heritabilities from 0.67 to 0.92 for aboveground biomass at end of flowering, nitrogen uptake at end of flowering, nitrogen uptake efficiency at end of flowering, seed yield, nitrogen uptake at maturity, nitrogen uptake efficiency at maturity, nitrogen utilisation efficiency, nitrogen use efficiency, nitrogen harvest index and nitrogen uptake between end of flowering and maturity. Thus, these traits can be used as selection criteria for nitrogen efficiency. Except nitrogen uptake efficiency all traits were significantly affected by the interaction between genotype and nitrogen level. Therefore, selection environments should resemble nitrogen supply of target environments. At both nitrogen levels nitrogen utilisation efficiency contributed more to the variation in nitrogen use efficiency than nitrogen uptake efficiency.

All traits but nitrogen harvest index showed significant variation among pairs of DH line and descending test hybrid. Heritabilities ranged from 0.31 to 0.82. Most traits were not affected by nitrogen level. Only nitrogen uptake efficiency at maturity and nitrogen use efficiency were significantly higher at N0 than at N1. Significant differences between DH lines and test hybrids were observed only for nitrogen utilisation efficiency and nitrogen use efficiency – both higher for test hybrids than for DH lines. Interactions between nitrogen level and variety type and between nitrogen level and descent (describes the pair of a DH line and the test hybrid derived from this DH line) were not significant for any trait.

Mid-parent heterosis at both nitrogen levels was detected for seed yield, nitrogen utilisation efficiency, nitrogen use efficiency and nitrogen harvest index. Hybrids surpassed the parental mean for nitrogen uptake and nitrogen uptake efficiency at N1 but at N0 the heterosis was negative, i.e. hybrids performed worse than the parental mean. For seed yield, nitrogen uptake, nitrogen uptake efficiency at maturity and nitrogen use efficiency heterosis was higher at N1 than at N0. But for nitrogen utilisation efficiency and nitrogen harvest index higher heterosis was expressed at N0. In contrast to the diversity set nitrogen use efficiency of DH lines and test hybrids

was dominated by nitrogen uptake efficiency while nitrogen utilisation efficiency only contributed to a small portion to nitrogen use efficiency. DH lines and test hybrids were only grown in one season which was characterised by an extraordinary warm winter and early spring. Therefore, the findings for DH lines and test hybrids need to be confirmed in further field trials.

Best calibrations with hyperspectral reflectance showed coefficient of determinations up to 0.87 for calibration and up to 0.85 for cross validation though lower for seed yield than for nitrogen uptake. That suggests the application of hyperspectral reflectance as indirect selection method. Calibrations based on spectral data before flowering resulted in better predictions than calibrations based on spectral data during fruit development. There was no general pattern when calibrations across nitrogen levels were compared with separate calibrations within nitrogen levels. For nitrogen uptake best calibrations across nitrogen levels outperformed best calibrations within nitrogen levels. Best calibrations for seed yield within low nitrogen supply outperformed best calibrations within high nitrogen supply and across nitrogen levels.
Most calibrations lost their predictive ability when tested with external datasets. Thus, they need to be further improved before they can be applied in breeding programs.

Electrical capacitance revealed significant genetic variation and high heritabilities in the diversity set ($h^2 = 0.81$) and for the ten genotypes tested for root characteristics in the field ($h^2 = 0.91$) and under controlled conditions ($h^2 = 0.95$). Thus, electrical capacitance can in principal be used as selection criterion. But only few significant phenotypic correlations were found between electrical capacitance and nitrogen efficiency parameters in field trials with the diversity set. At N1 electrical capacitance at end of flowering correlated negatively with dry matter content of aboveground biomass at end of flowering ($r = -0.70$) and positively with nitrogen uptake ($r = 0.57$) and nitrogen uptake efficiency at maturity ($r = 0.57$). At N0 electrical capacitance at end of flowering correlated positively with oil content ($r = 0.57$). It cannot be suggested to employ electrical capacitance as selection criterion for nitrogen efficiency parameters. The ten selected genotypes did not show significant differences in root masses and stem diameter in the field trial. Accordingly, they did not reveal significant phenotypic correlations between electrical capacitance and root masses or stem diameter. On plot level electrical capacitance correlated weakly with root mass in the middle ($r = 0.46$) and bottom ($r = 0.34$) horizon and strongly with

stem diameter (r = 0.78). Under controlled conditions only the phenotypic correlation between electrical capacitance and stem diameter was significant (r = 0.78). Genetic correlations between electrical capacitance and root characteristics and stem diameter were detected. Correlation coefficients ranged from 0.55 for root fresh mass to 1.11 for root tip diameter. The same root traits that were related to electrical capacitance also correlated with stem diameter. Genetic correlation coefficients between stem diameter and root characteristics were higher than those between electrical capacitance and root characteristics. Although electrical capacitance might be related to root characteristics, stem diameter, which is much easier to measure, also correlates to root characteristics and often with higher correlation coefficients.

By the current study it could be shown that nitrogen efficiency and related parameters can be implemented as traits in plant breeding as they revealed high heritabilities. Selection should be conducted at nitrogen levels that resemble target nitrogen supply. Hyperspectral canopy reflectance measured before flowering can be applied to facilitate selection. Nevertheless, calibrations must be further improved. Electrical capacitance cannot be suggested as selection criterion for nitrogen efficiency parameters. It remained open which trait is captured by electrical capacitance. Yet, the high heritabilities confirm that it is a heritable trait.

Appendix

List of figures

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Tab. I: ANOVA for traits of diversity set

Trait	Source	DF	MS	Var.cp	F		h²
$DM\%_{EOF}$ [%]	E	4	149.208	1.2629	55.06	**	
	R:E	5	2.710	0.0252	2.17	*ns*	
	N	1	1353.808	4.3357	14.04	*	
	EN	4	96.455	1.6415	77.26	**	
	RN:E	5	1.248	0.0213	1.98	*ns*	
	G	28	6.496	0.2405	3.86	**	0.50 - **0.74** - 0.85
	EG	112	1.685	0.2637	2.67	**	
	NG	28	1.243	0.0476	1.62	*	
	ENG	112	0.767	0.0686	1.22	*ns*	
	RNG:E	138	0.630	0.6302			
	Total	437					
$N\%_{EOF}$ [%]	E	4	15.171	0.1302	238.10	**	
	R:E	5	0.064	-0.0026	0.30	*ns*	
	N	1	165.743	0.5481	24.39	**	
	EN	4	6.795	0.1135	31.82	**	
	RN:E	5	0.214	0.0059	5.19	**	
	G	28	0.200	0.0054	2.19	**	0.13 - **0.54** - 0.73
	EG	112	0.091	0.0125	2.22	**	
	NG	28	0.061	0.0023	1.61	*	
	ENG	112	0.038	-0.0017	0.92	*ns*	
	RNG:E	140	0.041	0.0411			
	Total	439					
$DM\%_{Seed}$ [%]	E	3	672.502	5.7670	190.43	**	
	R:E	4	3.532	-0.0113	0.84	*ns*	
	N	1	5.196	-0.0712	0.24	*ns*	
	EN	3	21.717	0.3023	5.19	*ns*	
	RN:E	4	4.185	0.1388	25.91	**	
	G	28	2.142	0.0716	2.15	**	0.10 - **0.53** - 0.74
	EG	84	0.996	0.2087	6.17	**	
	NG	28	0.309	0.0122	1.46	*ns*	
	ENG	84	0.212	0.0250	1.31	*ns*	
	RNG:E	131	0.162	0.1615			
	Total	370					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N N level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h² heritability (bold) with 0.95 confidence interval, An overview about trait abbreviations is given in Tab. A 5

Tab. I (continued)

Trait	Source	DF	MS	Var.cp	F		h²
$N\%_{Seed}$ [%]	E	3	0.457	0.0029	3.84	*ns*	
	R:E	4	0.119	0.0009	1.72	*ns*	
	N	1	24.312	0.1030	59.64	**	
	EN	3	0.408	0.0058	5.90	*ns*	
	RN:E	4	0.069	0.0019	4.92	**	
	G	28	0.889	0.0532	23.43	**	0.92 - **0.96** - 0.98
	EG	84	0.038	0.0060	2.70	**	
	NG	28	0.026	0.0010	1.47	*ns*	
	ENG	84	0.018	0.0018	1.25	*ns*	
	RNG:E	127	0.014	0.0140			
	Total	366					
Nup_{Seed} [dt ha^{-1}]	E	3	6.034	0.0509	45.66	**	
	R:E	4	0.132	0.0018	4.75	*ns*	
	N	1	19.145	0.0813	70.16	**	
	EN	3	0.273	0.0042	9.81	*	
	RN:E	4	0.028	0.0007	3.36	*	
	G	28	0.275	0.0154	9.93	**	0.80 - **0.90** - 0.94
	EG	84	0.028	0.0049	3.35	**	
	NG	28	0.057	0.0052	3.70	**	
	ENG	84	0.015	0.0035	1.85	**	
	RNG:E	127	0.008	0.0083			
	Total	366					
$DM\%_{Straw}$ [%]	E	3	736.509	5.8636	13.07	*	
	R:E	4	56.335	-2.5314	0.28	*ns*	
	N	1	1821.165	6.2827	5.01	*ns*	
	EN	3	363.585	2.7660	1.79	*ns*	
	RN:E	4	203.155	5.5310	4.75	**	
	G	28	378.379	20.0814	6.63	**	0.71 - **0.85** - 0.91
	EG	84	57.076	3.5799	1.33	*ns*	
	NG	28	70.795	3.5572	1.67	*	
	ENG	84	42.337	-0.2094	0.99	*ns*	
	RNG:E	161	42.756	42.7561			
	Total	400					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N N level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h² heritability (bold) with 0.95 confidence interval, An overview about trait abbreviations is given in Tab. A 5

Tab. I (continued)

Trait	Source	DF	MS	Var.cp	F		h²
Straw DM [dt ha^{-1}]	E	3	11842.885	97.4308	21.89	**	
	R:E	4	540.908	-16.6046	0.36	*ns*	
	N	1	40759.691	169.4037	27.96	*	
	EN	3	1458.040	-0.7920	0.97	*ns*	
	RN:E	4	1503.974	49.6120	23.06	**	
	G	28	692.310	35.4421	5.53	**	0.65 - **0.82** - 0.90
	EG	84	125.236	15.0028	1.92	**	
	NG	28	152.427	9.7625	2.05	**	
	ENG	84	74.327	4.5509	1.14	*ns*	
	RNG:E	114	65.225	65.2248			
	Total	353					
$N\%_{Straw}$ [%]	E	3	1.010	0.0081	13.76	*	
	R:E	4	0.073	-0.0008	0.62	*ns*	
	N	1	12.282	0.0518	45.30	**	
	EN	3	0.271	0.0026	2.29	*ns*	
	RN:E	4	0.119	0.0036	7.77	**	
	G	28	0.089	0.0038	3.12	**	0.38 - **0.68** - 0.82
	EG	84	0.029	0.0033	1.87	**	
	NG	28	0.021	0.0009	1.50	*ns*	
	ENG	84	0.014	-0.0007	0.90	*ns*	
	RNG:E	154	0.015	0.0153			
	Total	393					
Nup_{Straw} [dt ha^{-1}]	E	3	0.455	0.0031	4.93	*ns*	
	R:E	4	0.092	-0.0021	0.43	*ns*	
	N	1	9.857	0.0418	64.44	**	
	EN	3	0.153	-0.0011	0.71	*ns*	
	RN:E	4	0.215	0.0071	23.41	**	
	G	28	0.089	0.0045	4.95	**	0.61 - **0.80** - 0.89
	EG	84	0.018	0.0022	1.96	**	
	NG	28	0.026	0.0016	2.00	**	
	ENG	84	0.013	0.0020	1.43	*	
	RNG:E	124	0.009	0.0092			
	Total	363					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N N level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h² heritability (bold) with 0.95 confidence interval, An overview about trait abbreviations is given in Tab. A 5

Tab. I (continued)

Trait	Source	DF	MS	Var.cp	F		h²
HI	E	3	0.159	0.0013	14.95	*	0.85 - **0.92** - 0.96
	R:E	4	0.011	-0.0003	0.39	*ns*	
	N	1	0.010	-0.0001	0.45	*ns*	
	EN	3	0.022	-0.0001	0.80	*ns*	
	RN:E	4	0.027	0.0009	19.06	**	
	G	28	0.052	0.0030	12.87	**	
	EG	84	0.004	0.0006	2.82	**	
	NG	28	0.003	0.0001	1.44	*ns*	
	ENG	84	0.002	0.0004	1.57	*	
	RNG:E	114	0.001	0.0014			
	Total	353					
Oil% [%]	E	3	31.443	0.2052	4.11	*ns*	0.93 - **0.97** - 0.98
	R:E	4	7.644	0.0598	1.83	*ns*	
	N	1	849.235	3.6279	112.34	**	
	EN	3	7.559	0.0583	1.81	*ns*	
	RN:E	4	4.177	0.1265	8.20	**	
	G	28	55.647	3.3596	29.39	**	
	EG	84	1.893	0.3459	3.72	**	
	NG	28	1.041	0.0550	1.73	*	
	ENG	84	0.601	0.0458	1.18	*ns*	
	RNG:E	132	0.509	0.5094			
	Total	371					
Oil yield [dt ha^{-1}]	E	3	1171.890	-0.0823	61.08	**	0.84 - **0.92** - 0.95
	R:E	4	19.187	0.2649	5.02	*ns*	
	N	1	1498.612	6.1880	23.79	*	
	EN	3	62.990	1.0202	16.49	*	
	RN:E	4	3.820	0.0604	1.85	*ns*	
	G	28	110.221	6.3252	12.22	**	
	EG	84	9.017	1.7368	4.36	**	
	NG	28	9.635	0.7559	2.69	**	
	ENG	84	3.588	0.7592	1.73	**	
	RNG:E	128	2.070	2.0696			
	Total	367					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N N level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h² heritability (bold) with 0.95 confidence interval, An overview about trait abbreviations is given in Tab. A 5

Tab. I: continued

Trait	Source	DF	MS	Var.cp	F		h²
FL [d after January 1st]	E	3	8086.755	69.6996	5062.69	**	
	R:E	4	1.597	-0.0056	0.83	*ns*	
	N	1	9.951	-0.0468	0.48	*ns*	
	EN	3	20.814	0.3257	10.82	*	
	RN:E	4	1.924	0.0447	3.07	*	
	G	28	108.235	6.2089	12.17	**	0.84 - **0.92** - 0.95
	EG	84	8.893	2.0665	14.19	**	
	NG	28	1.973	0.1331	2.17	**	
	ENG	84	0.908	0.1408	1.45	*	
	RNG:E	141	0.627	0.6266			
	Total	380					
PL [cm]	E	4	33206.763	284.9839	223.42	**	
	R:E	5	148.626	0.7424	1.41	*ns*	
	N	1	11427.053	47.0378	22.22	**	
	EN	4	514.291	7.0469	4.87	*ns*	
	RN:E	5	105.568	2.7440	4.06	**	
	G	28	1206.142	65.7459	7.82	**	0.76 - **0.87** - 0.93
	EG	112	154.208	32.0542	5.93	**	
	NG	28	68.063	2.0325	1.31	*ns*	
	ENG	112	51.803	12.9063	1.99	**	
	RNG:E	155	25.991	25.9906			
	Total	454					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance component, E environment, R:E replication within E, N N level, RN:E whole plot error, G genotype, EN, EG, NG ENG interactions, RNG:E subplot error, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, h² heritability (bold) with 0.95 confidence interval, An overview about trait abbreviations is given in Tab. A 5

Tab. II: Means of genotypes within N levels for traits of diversity set

Genotype	$DM\%_{EOF}$ N1 [%]	$DM\%_{EOF}$ N0 [%]	$N\%_{EOF}$ N1 [%]	$N\%_{EOF}$ N0 [%]	$DM\%_{Seed}$ N1 [%]	$DM\%_{Seed}$ N0 [%]
PBY001	17.46	20.46	2.41	1.56	95.10	94.88
PBY002	15.32	18.31	2.53	1.49	94.43	94.38
PBY003	15.34	18.06	2.73	1.62	94.26	94.85
PBY004	16.45	19.30	2.59	1.61	94.84	94.59
PBY005	15.80	19.11	2.85	1.84	95.24	94.90
PBY006	15.46	18.16	2.86	1.66	95.13	94.98
PBY007	16.39	19.07	2.75	1.58	95.09	94.64
PBY008	15.21	17.44	2.53	1.45	94.66	94.69
PBY009	16.00	18.69	2.97	1.71	94.87	94.81
PBY010	16.28	18.61	2.50	1.60	94.05	94.11
PBY011	15.19	19.28	2.68	1.48	94.03	93.51
PBY012	15.49	18.82	2.71	1.47	95.15	94.72
PBY013	15.37	18.46	2.66	1.74	95.12	94.41
PBY015	15.96	18.77	2.66	1.70	94.81	94.93
PBY017	14.84	18.90	2.71	1.70	95.15	94.83
PBY018	15.28	18.50	2.78	1.64	95.43	95.30
PBY019	16.30	18.91	2.85	1.77	95.22	94.61
PBY020	14.81	17.82	2.88	1.72	95.26	95.15
PBY021	16.67	19.07	2.81	1.65	95.36	95.46
PBY022	15.28	17.91	2.74	1.62	95.22	94.90
PBY023	15.35	18.47	2.81	1.60	95.22	94.57
PBY024	15.48	19.36	2.55	1.64	95.21	94.89
PBY025	15.41	18.50	2.67	1.65	95.24	95.03
PBY026	16.33	19.64	2.55	1.50	95.39	95.00
PBY027	15.80	18.49	2.66	1.62	94.99	94.60
PBY028	14.96	18.92	2.80	1.65	95.26	95.03
PBY029	15.74	18.71	2.55	1.59	95.49	95.32
PBY061	15.07	18.66	2.66	1.58	95.41	95.18
PBY062	14.69	17.98	2.59	1.62	94.65	94.89

Means for traits that were not shown in chapter A, An overview about trait abbreviations is given in Tab. A 5

Tab. II (continued)

Genotype	$N\%_{Seed}$ N1 [%]	$N\%_{Seed}$ N0 [%]	Nup_{Seed} N1 [dt ha^{-1}]	Nup_{Seed} N0 [dt ha^{-1}]	$DM\%_{Straw}$ N1 [%]	$DM\%_{Straw}$ N0 [%]
PBY001	3.87	3.43	0.77	0.52	46.44	52.12
PBY002	3.76	3.40	0.83	0.59	39.13	35.82
PBY003	3.73	3.16	0.81	0.60	41.17	46.46
PBY004	3.72	3.40	0.93	0.60	44.51	50.92
PBY005	3.72	3.28	0.87	0.51	48.81	55.12
PBY006	3.58	3.13	0.95	0.51	41.61	46.79
PBY007	3.74	3.24	0.88	0.54	42.45	48.31
PBY008	3.71	3.31	0.87	0.49	37.88	36.78
PBY009	3.94	3.44	0.61	0.43	41.98	52.94
PBY010	4.06	3.58	0.68	0.56	33.42	44.56
PBY011	3.89	3.61	0.82	0.33	41.79	35.33
PBY012	3.27	2.95	1.05	0.59	42.14	43.87
PBY013	3.54	3.18	1.16	0.72	37.45	39.37
PBY015	3.42	2.77	1.09	0.67	49.78	52.33
PBY017	3.32	2.78	1.12	0.66	47.38	53.18
PBY018	3.28	2.83	1.13	0.65	48.85	50.99
PBY019	3.81	3.40	0.83	0.50	47.38	51.77
PBY020	3.55	3.11	1.17	0.75	46.05	46.61
PBY021	3.68	3.15	1.05	0.54	42.62	43.10
PBY022	3.33	2.89	1.17	0.60	50.89	53.85
PBY023	3.44	2.93	1.23	0.78	50.74	57.16
PBY024	3.29	2.74	1.01	0.63	44.46	51.65
PBY025	3.37	2.89	1.10	0.60	43.03	40.89
PBY026	3.38	2.95	1.23	0.65	46.39	54.90
PBY027	3.41	2.94	1.05	0.69	41.25	41.45
PBY028	3.65	3.17	1.27	0.71	45.91	54.00
PBY029	3.39	2.88	1.20	0.68	43.37	53.28
PBY061	3.34	2.83	1.18	0.69	45.63	50.94
PBY062	3.53	3.08	1.12	0.61	41.75	44.69

Means for traits that were not shown in chapter A, An overview about trait abbreviations is given in Tab. A 5

Tab. II (continued)

Genotype	Straw DM N1 [dt ha^{-1}]	Straw DM N0 [dt ha^{-1}]	N%$_{Straw}$ N1 [%]	N%$_{Straw}$ N0 [%]	Nup$_{Straw}$ N1 [dt ha-^{1}]	Nup$_{Straw}$ N0 [dt ha^{-1}]
PBY001	62.64	40.18	1.03	0.66	0.67	0.27
PBY002	68.76	42.38	1.07	0.73	0.75	0.29
PBY003	58.91	34.76	1.16	0.67	0.68	0.25
PBY004	50.26	34.10	0.96	0.67	0.49	0.23
PBY005	54.83	36.54	0.97	0.63	0.55	0.22
PBY006	53.96	32.01	1.01	0.66	0.50	0.21
PBY007	54.63	37.92	1.03	0.70	0.55	0.26
PBY008	60.84	35.27	0.95	0.66	0.58	0.23
PBY009	31.77	26.21	1.16	0.72	0.37	0.19
PBY010	52.87	27.17	1.23	0.82	0.68	0.30
PBY011	76.43	44.05	1.05	0.73	0.73	0.34
PBY012	58.10	44.72	0.90	0.63	0.53	0.27
PBY013	56.57	40.05	0.95	0.69	0.54	0.27
PBY015	56.65	39.03	0.86	0.63	0.49	0.23
PBY017	51.18	36.67	1.00	0.63	0.50	0.22
PBY018	58.01	34.30	0.97	0.54	0.49	0.19
PBY019	40.52	29.10	1.00	0.67	0.40	0.19
PBY020	54.62	33.69	0.95	0.69	0.55	0.23
PBY021	51.51	33.72	0.95	0.59	0.49	0.20
PBY022	48.35	35.76	0.82	0.67	0.39	0.24
PBY023	45.55	33.01	0.94	0.63	0.42	0.22
PBY024	51.70	37.10	0.89	0.55	0.41	0.20
PBY025	57.12	32.61	1.02	0.73	0.57	0.22
PBY026	50.06	34.02	0.80	0.59	0.39	0.20
PBY027	57.95	37.68	0.97	0.59	0.55	0.24
PBY028	49.10	31.66	0.81	0.56	0.39	0.18
PBY029	43.98	34.07	0.92	0.60	0.41	0.21
PBY061	47.73	32.97	0.93	0.59	0.44	0.20
PBY062	74.33	44.58	1.02	0.66	0.75	0.33

Means for traits that were not shown in chapter A, An overview about trait abbreviations is given in Tab. A 5

Tab. II (continued)

Genotype	HI N1	HI N0	Oil% N1 [%]	Oil% N0 [%]	Oil yield N1 [dt ha^{-1}]	Oil yield N0 [dt ha^{-1}]
PBY001	0.25	0.29	46.12	48.68	9.20	7.38
PBY002	0.23	0.29	46.82	49.45	9.86	8.70
PBY003	0.28	0.34	42.77	46.84	9.12	8.69
PBY004	0.33	0.36	44.19	46.68	10.90	8.55
PBY005	0.30	0.31	45.83	48.51	10.72	7.59
PBY006	0.33	0.32	46.11	49.01	12.36	7.88
PBY007	0.30	0.31	48.19	50.46	11.24	8.37
PBY008	0.29	0.30	49.12	51.97	11.42	7.73
PBY009	0.33	0.33	45.21	47.75	6.76	5.92
PBY010	0.25	0.30	44.24	47.17	7.48	6.90
PBY011	0.22	0.20	41.68	43.21	8.65	3.42
PBY012	0.34	0.30	47.62	49.53	14.36	10.22
PBY013	0.36	0.34	46.34	48.38	15.06	11.02
PBY015	0.36	0.41	45.17	48.37	14.57	11.87
PBY017	0.40	0.40	46.01	48.54	15.61	11.35
PBY018	0.38	0.39	48.29	51.41	16.54	11.76
PBY019	0.36	0.34	43.07	45.43	9.27	6.67
PBY020	0.38	0.42	46.85	49.76	15.58	11.85
PBY021	0.36	0.35	48.98	52.50	13.94	9.09
PBY022	0.42	0.37	45.67	48.17	15.73	10.03
PBY023	0.44	0.43	46.32	49.15	16.59	12.17
PBY024	0.36	0.38	47.22	50.09	14.72	11.58
PBY025	0.36	0.39	47.71	50.75	15.75	10.70
PBY026	0.42	0.40	47.41	49.78	16.61	11.20
PBY027	0.35	0.38	47.28	49.78	14.56	11.73
PBY028	0.42	0.43	45.88	48.34	15.89	10.77
PBY029	0.43	0.42	47.69	50.18	16.61	11.48
PBY061	0.42	0.43	47.85	51.45	16.85	12.59
PBY062	0.30	0.31	46.94	49.71	15.06	9.53

Means for traits that were not shown in chapter A, An overview about trait abbreviations is given in Tab. A 5

Tab. II (continued)

Genotype	FL N1 [d after January 1st]	FL N0 [d after January 1st]	PL N1 [cm]	PL N0 [cm]
PBY001	120	119	124	120
PBY002	121	120	128	121
PBY003	118	118	117	107
PBY004	117	116	123	116
PBY005	123	121	129	120
PBY006	124	123	133	120
PBY007	118	117	122	119
PBY008	119	119	132	120
PBY009	111	110	109	94
PBY010	117	117	109	105
PBY011	122	120	136	133
PBY012	116	116	126	118
PBY013	114	114	121	108
PBY015	117	117	126	116
PBY017	115	115	109	100
PBY018	116	117	128	122
PBY019	117	117	112	107
PBY020	117	116	128	116
PBY021	119	119	122	112
PBY022	120	120	131	120
PBY023	117	116	116	109
PBY024	116	116	131	119
PBY025	115	116	117	106
PBY026	116	116	115	107
PBY027	117	116	126	119
PBY028	117	117	116	110
PBY029	115	115	115	108
PBY061	114	115	114	106
PBY062	118	117	128	110

Means for traits that were not shown in chapter A, An overview about trait abbreviations is given in Tab. A 5

Tab. III: ANOVA for traits of Population 007

Trait	Source	DF	MS	Var.cp	F		h²
DM%$_{Seed}$ [%]	E	2	767.0012	6.3502	154.10	**	-0.42 - **0.29** - 0.61
	R:E	3	4.9772	0.0575	3.25	*ns*	
	N	1	104.8896	-0.0901	0.87	*ns*	
	EN	2	121.0989	1.9928	79.17	**	
	RN:E	3	1.5297	0.0288	2.30	*ns*	
	T	1	4.0111	0.0124	2.26	*ns*	
	ET	2	1.7774	0.0185	2.67	*ns*	
	NT	1	1.0390	-0.0322	0.26	*ns*	
	ENT	2	3.9338	0.1089	5.90	*	
	RNT:E	7	0.6662	0.0045	1.11	*ns*	
	D	14	3.2322	0.0497	1.59	*ns*	
	ED	28	2.0391	0.1800	3.40	**	
	ND	14	1.7308	0.0182	1.14	*ns*	
	TD	14	0.8793	-0.0015	0.98	*ns*	
	END	28	1.5121	0.2282	2.52	**	
	ETD	28	0.8971	0.0744	1.50	*ns*	
	NTD	14	0.4243	0.0257	1.57	*ns*	
	ENTD	28	0.2703	-0.1646	0.45	*ns*	
	RNTD:E	167	0.5995	0.5995			
	Total	359					
N%$_{Seed}$ [%]	E	2	2.7709	0.0212	12.36	*	0.70 - **0.85** - 0.92
	R:E	3	0.2241	-0.0059	0.39	*ns*	
	N	1	3.5027	0.0108	2.24	*ns*	
	EN	2	1.5618	0.0163	2.69	*ns*	
	RN:E	3	0.5808	0.0180	14.63	**	
	T	1	4.3450	0.0241	324.25	**	
	ET	2	0.0134	-0.0004	0.34	*ns*	
	NT	1	5.5131	-0.0132	0.82	*ns*	
	ENT	2	6.7027	0.2221	168.87	**	
	RNT:E	7	0.0397	0.0014	2.15	*	
	D	14	0.3133	0.0115	8.18	**	
	ED	28	0.0383	0.0025	2.08	**	
	ND	14	0.0281	0.0006	1.37	*ns*	
	TD	14	0.1153	0.0075	4.56	**	
	END	28	0.0205	0.0005	1.11	*ns*	
	ETD	28	0.0253	0.0017	1.37	*ns*	
	NTD	14	0.0111	-0.0007	0.72	*ns*	
	ENTD	28	0.0154	-0.0015	0.83	*ns*	
	RNTD:E	167	0.0184	0.0184			
	Total	359					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. A 5

Tab. III: (continued)

Trait	Source	DF	MS	Var.cp	F		h²
Nup_{Seed} [dt ha^{-1}]	E	2	1.9986	0.0161	30.40	**	0.57 - **0.79** - 0.88
	R:E	3	0.0657	-0.0015	0.43	*ns*	
	N	1	4.3913	0.0109	1.80	*ns*	
	EN	2	2.4380	0.0381	15.95	*	
	RN:E	3	0.1529	0.0029	2.34	*ns*	
	T	1	0.0277	-0.0001	0.52	*ns*	
	ET	2	0.0537	-0.0002	0.82	*ns*	
	NT	1	2.4338	0.0042	1.18	*ns*	
	ENT	2	2.0583	0.0664	31.52	**	
	RNT:E	7	0.0653	0.0034	4.66	**	
	D	14	0.1367	0.0046	5.33	**	
	ED	28	0.0257	0.0015	1.83	*	
	ND	14	0.0346	0.0011	1.65	*ns*	
	TD	14	0.0492	0.0029	3.49	**	
	END	28	0.0210	0.0018	1.50	*ns*	
	ETD	28	0.0141	0.0000	1.01	*ns*	
	NTD	14	0.0112	-0.0005	0.78	*ns*	
	ENTD	28	0.0143	0.0001	1.02	*ns*	
	RNTD:E	167	0.0140	0.0140			
	Total	359					
$DM\%_{Straw}$ [%]	E	2	13559.4145	109.608	33.36	**	0.73 - **0.86** - 0.93
	R:E	3	406.4569	5.5509	5.54	*ns*	
	N	1	1865.7738	2.0723	1.25	*ns*	
	EN	2	1492.7579	23.6559	20.34	*	
	RN:E	3	73.4056	-1.0113	0.71	*ns*	
	T	1	5.6550	-0.3839	0.08	*ns*	
	ET	2	74.7570	-0.4831	0.72	*ns*	
	NT	1	675.7936	4.3025	2.34	*ns*	
	ENT	2	288.5666	6.1608	2.78	*ns*	
	RNT:E	7	103.7441	2.8230	1.69	*ns*	
	D	14	1369.0895	49.9582	8.05	**	
	ED	28	170.0923	13.5866	2.77	**	
	ND	14	49.9508	-4.3464	0.49	*ns*	
	TD	14	302.4721	20.3771	5.22	**	
	END	28	102.1082	10.1772	1.66	*	
	ETD	28	57.9465	-0.8632	0.94	*ns*	
	NTD	14	53.9794	-1.2552	0.88	*ns*	
	ENTD	28	61.5106	0.0556	1.00	*ns*	
	RNTD:E	167	61.3995	61.3995			
	Total	359					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. A 5

Tab. III (continued)

Trait	Source	DF	MS	Var.cp	F		h²
Straw DM [dt ha^{-1}]	E	2	1494.1623	10.5166	6.44	*ns*	0.12 - **0.50** - 0.73
	R:E	3	232.1730	3.4531	9.29	*	
	N	1	34.7450	-1.8114	0.10	*ns*	
	EN	2	360.7977	5.5969	14.44	*	
	RN:E	3	24.9863	-3.1285	0.21	*ns*	
	T	1	1671.6766	6.3435	3.16	*ns*	
	ET	2	529.8429	6.8500	4.46	*ns*	
	NT	1	1026.8444	10.3250	10.52	*ns*	
	ENT	2	97.5944	-0.7083	0.82	*ns*	
	RNT:E	7	118.8422	2.5599	1.48	*ns*	
	D	14	352.4323	9.3348	2.74	*	
	ED	28	128.3959	5.9940	1.60	*	
	ND	14	50.9651	-5.6818	0.43	*ns*	
	TD	14	155.2707	2.4127	1.23	*ns*	
	END	28	119.1470	9.6758	1.48	*ns*	
	ETD	28	126.3186	11.4687	1.57	*	
	NTD	14	90.7626	4.4299	1.41	*ns*	
	ENTD	28	64.1835	-8.1302	0.80	*ns*	
	RNTD:E	167	80.4439	80.4439			
	Total	359					
$N\%_{Straw}$ [%]	E	2	3.4992	0.0277	19.63	*	-0.68 - **0.15** - 0.54
	R:E	3	0.1782	0.0028	24.22	*	
	N	1	3.1472	0.0149	6.64	*ns*	
	EN	2	0.4737	0.0078	64.37	**	
	RN:E	3	0.0074	-0.0001	0.65	*ns*	
	T	1	0.0035	-0.0002	0.07	*ns*	
	ET	2	0.0467	0.0006	4.14	*ns*	
	NT	1	1.2888	-0.0057	0.71	*ns*	
	ENT	2	1.8043	0.0598	159.8	**	
	RNT:E	7	0.0113	-0.0001	0.90	*ns*	
	D	14	0.0334	0.0001	1.08	*ns*	
	ED	28	0.0308	0.0023	2.44	**	
	ND	14	0.0151	-0.0001	0.95	*ns*	
	TD	14	0.0189	0.0005	1.41	*ns*	
	END	28	0.0158	0.0008	1.26	*ns*	
	ETD	28	0.0134	0.0002	1.06	*ns*	
	NTD	14	0.0083	-0.0004	0.79	*ns*	
	ENTD	28	0.0104	-0.0011	0.83	*ns*	
	RNTD:E	167	0.0126	0.0126			
	Total	359					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. A 5

Tab. III (continued)

Trait	Source	DF	MS	Var.cp	F		h²
Nup_{Straw} [dt ha^{-1}]	E	2	1.5350	0.0122	22.30	*	-0.16 - **0.42** - 0.69
	R:E	3	0.0688	0.0011	26.86	*	
	N	1	0.8294	0.0036	4.40	*ns*	
	EN	2	0.1884	0.0031	73.55	**	
	RN:E	3	0.0026	-0.0002	0.28	*ns*	
	T	1	0.1385	0.0003	1.63	*ns*	
	ET	2	0.0848	0.0013	9.18	*	
	NT	1	0.6882	0.0008	1.11	*ns*	
	ENT	2	0.6199	0.0204	67.13	**	
	RNT:E	7	0.0092	0.0000	0.99	*ns*	
	D	14	0.0295	0.0006	1.88	*ns*	
	ED	28	0.0157	0.0008	1.68	*	
	ND	14	0.0114	-0.0006	0.62	*ns*	
	TD	14	0.0128	0.0003	1.43	*ns*	
	END	28	0.0183	0.0022	1.96	**	
	ETD	28	0.0090	-0.0001	0.96	*ns*	
	NTD	14	0.0111	0.0007	1.55	*ns*	
	ENTD	28	0.0072	-0.0011	0.77	*ns*	
	RNTD:E	167	0.0093	0.0093			
	Total	359					
HI	E	2	0.0031	0.0000	0.99	*ns*	0.22 - **0.61** - 0.79
	R:E	3	0.0032	0.0000	2.16	*ns*	
	N	1	0.0714	0.0002	2.29	*ns*	
	EN	2	0.0312	0.0005	21.29	*	
	RN:E	3	0.0015	0.0000	1.10	*ns*	
	T	1	0.1057	0.0005	8.10	*ns*	
	ET	2	0.0131	0.0002	9.76	**	
	NT	1	0.0001	0.0000	0.02	*ns*	
	ENT	2	0.0028	0.0000	2.08	*ns*	
	RNT:E	7	0.0013	0.0000	0.81	*ns*	
	D	14	0.0087	0.0003	3.67	**	
	ED	28	0.0024	0.0001	1.45	*ns*	
	ND	14	0.0025	0.0000	1.08	*ns*	
	TD	14	0.0044	0.0001	1.59	*ns*	
	END	28	0.0023	0.0002	1.41	*ns*	
	ETD	28	0.0028	0.0003	1.68	*	
	NTD	14	0.0026	0.0002	1.90	*ns*	
	ENTD	28	0.0013	-0.0001	0.82	*ns*	
	RNTD:E	167	0.0016	0.0016			
	Total	359					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. A 5

Tab. III (continued)

Trait	Source	DF	MS	Var.cp	F		h²
Oil% [%]	E	2	314.3383	2.5658	48.81	**	-0.28 - **0.36** - 0.65
	R:E	3	6.4396	0.0235	1.28	*ns*	
	N	1	130.2368	0.2474	1.52	*ns*	
	EN	2	85.7089	1.3447	17.04	*	
	RN:E	3	5.0291	0.1504	9.75	**	
	T	1	0.6076	-0.0079	0.30	*ns*	
	ET	2	2.0265	0.0252	3.93	*ns*	
	NT	1	148.1608	-0.0801	0.95	*ns*	
	ENT	2	155.3700	5.1618	301.15	**	
	RNT:E	7	0.5159	-0.1569	0.18	*ns*	
	D	14	3.9014	0.0452	1.39	*ns*	
	ED	28	2.8156	-0.0067	0.98	*ns*	
	ND	14	1.4707	-0.0840	0.59	*ns*	
	TD	14	3.9889	0.1444	1.77	*ns*	
	END	28	2.4789	-0.0977	0.86	*ns*	
	ETD	28	2.2562	-0.1533	0.79	*ns*	
	NTD	14	3.1226	0.1678	1.48	*ns*	
	ENTD	28	2.1157	-0.3769	0.74	*ns*	
	RNTD:E	167	2.8695	2.8695			
	Total	359					
Oil yield [dt ha^{-1}]	E	2	52.9478	0.4006	10.85	*	0.47 - **0.73** - 0.86
	R:E	3	4.8803	-0.0186	0.81	*ns*	
	N	1	311.4198	0.4791	1.38	*ns*	
	EN	2	225.1797	3.6530	37.54	**	
	RN:E	3	5.9976	-0.0825	0.71	*ns*	
	T	1	119.7967	0.6240	16.02	*ns*	
	ET	2	7.4785	-0.0166	0.88	*ns*	
	NT	1	198.4851	0.9146	1.71	*ns*	
	ENT	2	116.1755	3.5901	13.71	**	
	RNT:E	7	8.4715	0.3526	2.66	*	
	D	14	23.9226	0.7473	4.00	**	
	ED	28	5.9868	0.3506	1.88	**	
	ND	14	5.8618	0.1489	1.44	*ns*	
	TD	14	7.4392	0.4223	3.14	**	
	END	28	4.0747	0.2231	1.28	*ns*	
	ETD	28	2.3722	-0.2025	0.75	*ns*	
	NTD	14	2.6778	0.0448	1.11	*ns*	
	ENTD	28	2.4088	-0.3867	0.76	*ns*	
	RNTD:E	167	3.1823	3.1823			
	Total	359					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. A 5

Tab. III (continued)

Trait	Source	DF	MS	Var.cp	F		h²
FL [d after January 1st]	E	1	3038.8167	25.2759	532.35	**	0.91 - **0.96** - 0.98
	R:E	2	5.7083	0.0928	40.29	*	
	N	1	198.0167	-0.2187	0.88	*ns*	
	EN	1	224.2667	3.7354	1583.06	**	
	RN:E	2	0.1417	-0.0497	0.09	*ns*	
	T	1	582.8167	4.7896	72.25	*ns*	
	ET	1	8.0667	0.1072	4.94	*ns*	
	NT	1	13.0667	0.0442	1.25	*ns*	
	ENT	1	10.4167	0.2928	6.38	*ns*	
	RNT:E	5	1.6333	0.0740	3.12	*	
	D	14	38.4613	2.3299	32.52	**	
	ED	14	1.1827	0.0824	2.26	**	
	ND	14	0.8292	0.0402	1.63	*ns*	
	TD	14	3.4327	0.3482	5.31	**	
	END	14	0.5077	-0.0040	0.97	*ns*	
	ETD	14	0.6470	0.0308	1.24	*ns*	
	NTD	14	0.4506	0.0464	1.70	*ns*	
	ENTD	14	0.2649	-0.1294	0.51	*ns*	
	RNTD:E	111	0.5237	0.5237			
	Total	239					
PL [cm]	E	1	35794.8375	296.6888	186.25	**	0.67 - **0.84** - 0.93
	R:E	2	192.1875	1.6822	2.11	*ns*	
	N	1	2822.2042	23.0431	49.48	*ns*	
	EN	1	57.0375	-0.5703	0.63	*ns*	
	RN:E	2	91.2542	0.5779	1.23	*ns*	
	T	1	870.2042	5.3014	3.72	*ns*	
	ET	1	234.0375	2.6687	3.17	*ns*	
	NT	1	116.2042	-2.5083	0.44	*ns*	
	ENT	1	266.7042	6.4263	3.61	*ns*	
	RNT:E	5	73.9158	2.2406	1.83	*ns*	
	D	14	984.6827	54.0216	8.18	**	
	ED	14	120.3375	10.0039	2.99	**	
	ND	14	36.2756	1.3824	1.44	*ns*	
	TD	14	120.5077	8.4271	2.27	*ns*	
	END	14	25.2161	-3.7726	0.63	*ns*	
	ETD	14	53.0911	3.1961	1.32	*ns*	
	NTD	14	22.9363	2.1518	1.60	*ns*	
	ENTD	14	14.3292	-12.9887	0.36	*ns*	
	RNTD:E	111	40.3066	40.3066			
	Total	239					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. A 5

Tab. IV: Means of genotypes within N levels for traits of Population 007

Variety type	Genotype	$DM\%_{Seed}$ N1 [%]	$DM\%_{Seed}$ N0 [%]	$N\%_{Seed}$ N1 [%]	$N\%_{Seed}$ N0 [%]	Nup_{Seed} N1 [dt ha^{-1}]	Nup_{Seed} N0 [dt ha^{-1}]
DH	DH001	92.21	90.23	3.92	3.96	1.38	1.31
	DH011	92.29	92.11	3.57	3.54	1.32	1.29
	DH012	92.21	91.65	3.81	3.87	1.31	1.28
	DH016	92.72	91.12	3.56	3.72	1.30	1.23
	DH017	93.37	92.41	3.66	3.76	1.23	1.14
	DH018	92.93	91.63	3.71	3.76	1.24	1.18
	DH020	92.55	91.11	4.00	4.02	1.55	1.38
	DH029	93.62	91.22	3.48	3.48	1.17	1.05
	DH043	90.82	90.85	4.12	4.08	1.18	1.11
	DH045	93.17	91.29	3.57	3.69	1.28	1.15
	DH050	92.22	92.00	3.82	3.75	1.48	1.42
	DH052	92.49	90.81	3.81	3.94	1.21	1.19
	DH053	93.14	92.19	3.80	3.82	1.18	1.13
	DH057	93.03	91.52	3.49	3.65	1.30	1.31
	DH085	92.75	91.56	3.70	3.73	1.11	1.24
TH	TH001	92.40	90.84	3.77	3.48	1.41	1.12
	TH011	92.68	92.14	3.69	3.21	1.43	1.08
	TH012	92.64	91.78	3.77	3.26	1.32	1.02
	TH016	92.78	91.18	3.79	3.46	1.54	1.20
	TH017	92.89	92.51	3.80	3.32	1.45	1.10
	TH018	92.57	91.53	3.76	3.28	1.41	1.05
	TH020	92.70	91.68	3.84	3.39	1.72	1.06
	TH029	93.08	91.86	3.60	3.16	1.44	1.02
	TH043	92.30	92.17	3.76	3.36	1.43	1.06
	TH045	92.91	91.44	3.65	3.25	1.49	1.08
	TH050	92.78	91.96	3.88	3.21	1.60	1.05
	TH052	92.65	91.45	3.90	3.42	1.55	1.10
	TH053	93.32	91.93	3.73	3.35	1.42	1.08
	TH057	92.56	92.16	3.74	3.35	1.46	1.16
	TH085	92.80	91.85	3.75	3.25	1.32	1.00

Means for traits that were not shown in chapter A, DH DH line, TH test hybrid, Numbers in genotype names mark descent, An overview about trait abbreviations is given in Tab. A 5

Tab. IV (continued)

Variety type	Genotype	$DM\%_{Straw}$ N1 [%]	$DM\%_{Straw}$ N0 [%]	Straw DM N1 [dt ha^{-1}]	Straw DM N0 [dt ha^{-1}]	$N\%_{Straw}$ N1 [%]	$N\%_{Straw}$ N0 [%]
DH	DH001	48.56	42.53	57.84	59.97	0.85	0.88
	DH011	69.01	63.60	53.31	49.85	0.89	0.69
	DH012	37.08	42.94	52.59	62.77	0.97	0.81
	DH016	43.29	47.67	49.31	52.15	0.91	0.79
	DH017	52.45	58.15	42.26	48.19	0.79	0.83
	DH018	58.81	61.53	54.80	59.84	0.90	0.79
	DH020	52.14	48.13	55.17	54.65	0.96	0.83
	DH029	63.15	70.20	36.39	43.37	0.99	0.95
	DH043	32.11	32.82	59.93	60.36	0.89	0.85
	DH045	53.49	53.66	48.61	51.95	0.92	0.92
	DH050	44.70	51.65	56.81	61.83	0.82	0.76
	DH052	55.61	67.36	48.56	59.01	0.84	0.74
	DH053	66.31	61.09	53.12	47.16	0.86	0.91
	DH057	46.50	50.47	58.60	60.57	0.85	0.78
	DH085	62.37	60.99	52.46	49.45	0.91	0.80
TH	TH001	45.10	49.83	50.91	46.36	0.98	0.71
	TH011	59.33	69.15	48.51	50.79	0.94	0.65
	TH012	55.40	59.98	58.15	43.97	1.04	0.69
	TH016	42.71	50.65	45.78	48.53	0.99	0.69
	TH017	52.23	62.01	48.91	48.49	0.96	0.67
	TH018	45.09	52.95	45.74	46.92	0.99	0.76
	TH020	46.18	50.21	56.82	45.81	1.17	0.73
	TH029	58.98	63.47	51.48	43.19	1.00	0.65
	TH043	38.90	49.46	51.97	46.91	0.98	0.71
	TH045	45.99	56.56	47.88	46.63	0.97	0.66
	TH050	48.79	55.26	54.56	48.88	0.98	0.71
	TH052	56.17	63.67	55.93	50.11	0.95	0.66
	TH053	52.77	61.92	45.42	42.61	1.01	0.75
	TH057	46.02	53.16	54.54	54.92	0.99	0.70
	TH085	54.58	59.35	49.18	41.68	1.08	0.74

Means for traits that were not shown in chapter A, DH DH line, TH test hybrid, Numbers in genotype names mark descent, An overview about trait abbreviations is given in Tab. A 5

Tab. IV (continued)

Variety type	Genotype	Nup_{Straw} N1 [dt ha^{-1}]	Nup_{Straw} N0 [dt ha^{-1}]	HI N1	HI N0	Oil% N1 [%]	Oil% N0 [%]
DH	DH001	0.50	0.54	0.38	0.36	47.16	50.11
	DH011	0.48	0.32	0.41	0.44	48.08	50.38
	DH012	0.51	0.53	0.40	0.34	49.02	50.37
	DH016	0.45	0.42	0.43	0.39	47.37	50.59
	DH017	0.34	0.42	0.45	0.39	48.70	50.07
	DH018	0.49	0.49	0.38	0.34	47.68	49.99
	DH020	0.53	0.45	0.42	0.38	48.55	50.46
	DH029	0.36	0.43	0.48	0.40	46.85	49.38
	DH043	0.55	0.54	0.33	0.32	48.54	50.11
	DH045	0.46	0.50	0.43	0.37	47.67	50.64
	DH050	0.45	0.48	0.41	0.39	47.33	50.69
	DH052	0.43	0.44	0.40	0.33	48.17	51.40
	DH053	0.46	0.43	0.37	0.38	46.91	49.04
	DH057	0.49	0.48	0.39	0.38	47.03	50.83
	DH085	0.50	0.40	0.37	0.40	47.68	49.96
TH	TH001	0.51	0.33	0.43	0.41	48.29	48.67
	TH011	0.45	0.33	0.45	0.40	48.65	49.71
	TH012	0.58	0.31	0.39	0.42	49.40	50.39
	TH016	0.45	0.33	0.47	0.42	49.05	49.10
	TH017	0.48	0.33	0.44	0.40	49.16	49.34
	TH018	0.47	0.36	0.46	0.40	49.26	48.99
	TH020	0.67	0.35	0.45	0.40	49.97	49.50
	TH029	0.51	0.28	0.45	0.43	47.80	49.41
	TH043	0.51	0.33	0.42	0.40	48.38	48.23
	TH045	0.46	0.32	0.46	0.41	48.89	48.81
	TH050	0.54	0.35	0.43	0.40	50.52	48.41
	TH052	0.54	0.34	0.42	0.39	47.09	47.68
	TH053	0.46	0.32	0.46	0.43	49.60	48.85
	TH057	0.55	0.38	0.42	0.39	49.27	47.68
	TH085	0.53	0.32	0.42	0.42	49.44	48.77

Means for traits that were not shown in chapter A, DH DH line, TH test hybrid, Numbers in genotype names mark descent, An overview about trait abbreviations is given in Tab. A 5

Tab. IV (continued)

Variety type	Genotype	Oil yield N1 [dt ha^{-1}]	Oil yield N0 [dt ha^{-1}]	FL N1 [d after January 1st]	FL N0 [d after January 1st]	PL N1 [cm]	PL N0 [cm]
DH	DH001	16.46	16.44	101	99	180	176
	DH011	17.75	18.01	99	97	152	143
	DH012	16.85	16.36	100	99	166	157
	DH016	17.26	16.58	104	103	169	157
	DH017	16.42	14.96	102	101	172	170
	DH018	15.96	15.32	100	99	170	165
	DH020	18.79	16.99	100	98	177	164
	DH029	15.62	14.47	100	98	154	146
	DH043	13.85	13.46	102	101	172	167
	DH045	17.03	15.44	98	98	171	161
	DH050	18.44	18.75	99	97	178	170
	DH052	15.33	15.18	103	103	180	169
	DH053	14.59	14.28	102	102	177	171
	DH057	17.50	18.06	101	99	186	176
	DH085	14.34	16.26	101	99	160	151
TH	TH001	17.92	15.57	97	95	164	164
	TH011	18.70	16.44	96	95	158	149
	TH012	17.20	15.59	99	96	163	156
	TH016	19.95	16.83	100	98	165	158
	TH017	18.84	16.05	99	96	174	165
	TH018	18.45	15.46	98	95	165	171
	TH020	22.69	15.18	98	96	163	158
	TH029	19.07	15.83	96	94	154	148
	TH043	18.34	15.10	100	98	170	164
	TH045	19.85	15.99	96	94	166	159
	TH050	20.82	15.76	98	95	172	159
	TH052	18.67	15.06	100	98	171	167
	TH053	18.72	15.71	100	98	167	161
	TH057	19.15	16.28	98	95	175	174
	TH085	17.39	14.74	97	94	161	153

Means for traits that were not shown in chapter A, DH DH line, TH test hybrid, Numbers in genotype names mark descent, An overview about trait abbreviations is given in Tab. A 5

Tab. V: ANOVA for traits of Population 029

Trait	Source	DF	MS	Var.cp	F		h²
DM%$_{Seed}$ [%]	E	2	536.4298	4.4149	80.72	**	-0.67 - **0.16** - 0.55
	R:E	3	6.6459	0.1090	63.25	**	
	N	1	61.7688	0.0089	1.03	*ns*	
	EN	2	60.1610	1.0009	572.54	**	
	RN:E	3	0.1051	-0.0026	0.58	*ns*	
	T	1	0.6300	0.0019	2.18	*ns*	
	ET	2	0.2884	0.0018	1.58	*ns*	
	NT	1	0.7272	-0.0287	0.22	*ns*	
	ENT	2	3.3132	0.1044	18.20	**	
	RNT:E	7	0.1820	-0.0520	0.19	*ns*	
	D	14	3.1699	0.0234	1.22	*ns*	
	ED	28	2.6077	0.2056	2.71	**	
	ND	14	2.1259	0.0054	1.03	*ns*	
	TD	14	0.5202	0.0020	1.05	*ns*	
	END	28	2.0610	0.2746	2.14	**	
	ETD	28	0.4967	-0.1165	0.52	*ns*	
	NTD	14	0.1174	-0.0215	0.48	*ns*	
	ENTD	28	0.2463	-0.3582	0.26	*ns*	
	RNTD:E	167	0.9626	0.9626			
	Total	359					
N%$_{Seed}$ [%]	E	2	2.8007	0.0213	11.33	*	0.72 - **0.86** - 0.92
	R:E	3	0.2472	-0.0011	0.79	*ns*	
	N	1	2.5688	-0.0017	0.90	*ns*	
	EN	2	2.8673	0.0426	9.18	*ns*	
	RN:E	3	0.3124	0.0088	6.64	*	
	T	1	0.0119	0.0000	1.71	*ns*	
	ET	2	0.0070	-0.0007	0.15	*ns*	
	NT	1	6.5044	0.0064	1.10	*ns*	
	ENT	2	5.9261	0.1960	125.96	**	
	RNT:E	7	0.0470	0.0018	2.32	*	
	D	14	0.1917	0.0072	9.70	**	
	ED	28	0.0198	-0.0001	0.97	*ns*	
	ND	14	0.0214	0.0004	1.31	*ns*	
	TD	14	0.0800	0.0051	4.33	**	
	END	28	0.0164	-0.0010	0.81	*ns*	
	ETD	28	0.0185	-0.0004	0.91	*ns*	
	NTD	14	0.0098	-0.0013	0.55	*ns*	
	ENTD	28	0.0178	-0.0012	0.88	*ns*	
	RNTD:E	167	0.0203	0.0203			
	Total	359					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. A 5

Tab. V (continued)

Trait	Source	DF	MS	Var.cp	F		h²
Nup_{Seed} [dt ha^{-1}]	E	2	3.3701	0.0274	42.40	**	0.61 - **0.80** - 0.92
	R:E	3	0.0795	-0.0026	0.34	*ns*	
	N	1	4.2576	0.0096	1.69	*ns*	
	EN	2	2.5235	0.0382	10.79	*	
	RN:E	3	0.2338	0.0060	4.24	*ns*	
	T	1	0.0148	-0.0001	0.40	*ns*	
	ET	2	0.0375	-0.0003	0.68	*ns*	
	NT	1	2.9612	0.0101	1.44	*ns*	
	ENT	2	2.0517	0.0666	37.18	**	
	RNT:E	7	0.0552	0.0029	4.69	**	
	D	14	0.1270	0.0040	3.97	**	
	ED	28	0.0320	0.0025	2.72	**	
	ND	14	0.0133	-0.0002	0.83	*ns*	
	TD	14	0.0834	0.0062	8.96	**	
	END	28	0.0160	0.0011	1.36	*ns*	
	ETD	28	0.0093	-0.0006	0.79	*ns*	
	NTD	14	0.0045	-0.0009	0.45	*ns*	
	ENTD	28	0.0100	-0.0009	0.85	*ns*	
	RNTD:E	167	0.0118	0.0118			
	Total	359					
$DM\%_{Straw}$ [%]	E	2	18792.2866	154.5587	76.63	**	0.49 - **0.75** - 0.86
	R:E	3	245.2431	3.8045	14.45	*	
	N	1	2971.1993	4.2953	1.35	*ns*	
	EN	2	2198.0438	36.3512	129.50	**	
	RN:E	3	16.9734	-1.5122	0.27	*ns*	
	T	1	483.4190	2.3535	8.09	*ns*	
	ET	2	59.7854	-0.0426	0.96	*ns*	
	NT	1	1589.2383	1.3164	1.08	*ns*	
	ENT	2	1470.7627	46.9474	23.59	**	
	RNT:E	7	62.3394	-2.0287	0.67	*ns*	
	D	14	704.4727	23.4340	4.96	**	
	ED	28	142.0572	6.1609	1.53	*ns*	
	ND	14	53.1434	-1.7596	0.72	*ns*	
	TD	14	232.3115	11.2955	2.40	*	
	END	28	74.2591	-4.6276	0.80	*ns*	
	ETD	28	96.7655	0.9990	1.04	*ns*	
	NTD	14	55.4474	-1.4709	0.86	*ns*	
	ENTD	28	64.2726	-14.2485	0.69	*ns*	
	RNTD:E	167	92.7696	92.7696			
	Total	359					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. A 5

Tab. V (continued)

Trait	Source	DF	MS	Var.cp	F		h²
Straw DM [dt ha^{-1}]	E	2	2164.3184	14.4184	4.99	*ns*	0.15 - **0.58** - 0.77
	R:E	3	434.1139	7.0515	39.38	**	
	N	1	719.8675	1.5580	1.64	*ns*	
	EN	2	439.428	7.1401	39.86	**	
	RN:E	3	11.0242	-0.3039	0.55	*ns*	
	T	1	118.9445	0.1037	1.19	*ns*	
	ET	2	100.2796	1.3356	4.98	*	
	NT	1	875.8777	8.2408	6.53	*ns*	
	ENT	2	134.2099	3.8023	6.66	*	
	RNT:E	7	20.1423	-2.4152	0.36	*ns*	
	D	14	161.8119	4.1223	2.57	*	
	ED	28	62.8778	0.8135	1.12	*ns*	
	ND	14	47.5850	-0.4210	0.90	*ns*	
	TD	14	161.676	7.2554	2.17	*	
	END	28	52.6371	-0.9332	0.93	*ns*	
	ETD	28	74.6107	4.5602	1.32	*ns*	
	NTD	14	59.7037	-3.2753	0.75	*ns*	
	ENTD	28	79.3554	11.4928	1.41	*ns*	
	RNTD:E	167	56.3698	56.3698			
	Total	359					
N%$_{Straw}$ [%]	E	2	2.0709	0.0154	9.39	*ns*	0.06 - **0.53** - 0.75
	R:E	3	0.2205	0.0033	8.65	*ns*	
	N	1	3.9774	0.0156	3.40	*ns*	
	EN	2	1.1711	0.0191	45.94	**	
	RN:E	3	0.0255	0.0000	0.98	*ns*	
	T	1	0.0700	0.0003	5.01	*ns*	
	ET	2	0.0140	-0.0002	0.54	*ns*	
	NT	1	1.9478	-0.0009	0.96	*ns*	
	ENT	2	2.0305	0.0668	78.39	**	
	RNT:E	7	0.0259	0.0011	2.61	*	
	D	14	0.0292	0.0007	2.41	*	
	ED	28	0.0121	0.0003	1.22	*ns*	
	ND	14	0.0158	0.0001	1.07	*ns*	
	TD	14	0.0171	0.0006	1.76	*ns*	
	END	28	0.0147	0.0012	1.48	*ns*	
	ETD	28	0.0097	0.0000	0.98	*ns*	
	NTD	14	0.0089	0.0002	1.12	*ns*	
	ENTD	28	0.0079	-0.0010	0.80	*ns*	
	RNTD:E	167	0.0099	0.0099			
	Total	359					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. A 5

Tab. V (continued)

Trait	Source	DF	MS	Var.cp	F		h²
Nup_{Straw} [dt ha^{-1}]	E	2	0.9300	0.0071	11.16	*	0.08 - **0.54** - 0.75
	R:E	3	0.0833	0.0012	6.80	*ns*	
	N	1	1.2650	0.0054	4.43	*ns*	
	EN	2	0.2854	0.0046	23.28	*	
	RN:E	3	0.0123	0.0001	1.48	*ns*	
	T	1	0.0007	-0.0001	0.05	*ns*	
	ET	2	0.0133	0.0001	1.60	*ns*	
	NT	1	0.7673	0.0023	1.37	*ns*	
	ENT	2	0.5597	0.0184	67.34	**	
	RNT:E	7	0.0083	0.0002	1.45	*ns*	
	D	14	0.0078	0.0001	1.70	*ns*	
	ED	28	0.0046	-0.0001	0.81	*ns*	
	ND	14	0.0054	-0.0001	0.85	*ns*	
	TD	14	0.0141	0.0007	2.53	*	
	END	28	0.0064	0.0002	1.12	*ns*	
	ETD	28	0.0056	0.0000	0.98	*ns*	
	NTD	14	0.0044	-0.0005	0.62	*ns*	
	ENTD	28	0.0071	0.0007	1.25	*ns*	
	RNTD:E	167	0.0057	0.0057			
	Total	359					
HI	E	2	0.0662	0.0005	14.62	*	-0.73 - **0.13** - 0.53
	R:E	3	0.0045	0.0000	2.42	*ns*	
	N	1	0.0412	0.0001	1.44	*ns*	
	EN	2	0.0286	0.0004	15.24	*	
	RN:E	3	0.0019	0.0000	1.70	*ns*	
	T	1	0.0021	0.0000	0.56	*ns*	
	ET	2	0.0038	0.0000	3.43	*ns*	
	NT	1	0.0004	0.0000	0.79	*ns*	
	ENT	2	0.0005	0.0000	0.44	*ns*	
	RNT:E	7	0.0011	0.0000	0.62	*ns*	
	D	14	0.0028	0.0000	1.03	*ns*	
	ED	28	0.0027	0.0001	1.49	*ns*	
	ND	14	0.0020	0.0000	1.21	*ns*	
	TD	14	0.0028	0.0001	1.30	*ns*	
	END	28	0.0016	0.0000	0.92	*ns*	
	ETD	28	0.0022	0.0001	1.22	*ns*	
	NTD	14	0.0017	-0.0002	0.65	*ns*	
	ENTD	28	0.0026	0.0004	1.44	*ns*	
	RNTD:E	167	0.0018	0.0018			
	Total	359					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. A 5

Tab. V (continued)

Trait	Source	DF	MS	Var.cp	F		h²
Oil% [%]	E	2	448.1234	3.6356	37.81	**	0 - **0** - 0
	R:E	3	11.8507	-0.3463	0.36	*ns*	
	N	1	136.7767	0.2290	1.43	*ns*	
	EN	2	95.5512	1.0487	2.93	*ns*	
	RN:E	3	32.6313	1.0376	21.71	**	
	T	1	0.0840	-0.0148	0.03	*ns*	
	ET	2	2.7552	0.0209	1.83	*ns*	
	NT	1	166.2465	0.2361	1.15	*ns*	
	ENT	2	144.9990	4.7832	96.47	**	
	RNT:E	7	1.5031	-0.1092	0.48	*ns*	
	D	14	2.3563	-0.0421	0.70	*ns*	
	ED	28	3.3669	0.0282	1.07	*ns*	
	ND	14	3.2749	0.0933	1.52	*ns*	
	TD	14	4.0238	0.0276	1.09	*ns*	
	END	28	2.1547	-0.2467	0.69	*ns*	
	ETD	28	3.6928	0.1378	1.18	*ns*	
	NTD	14	2.4186	-0.1786	0.69	*ns*	
	ENTD	28	3.4905	0.1744	1.11	*ns*	
	RNTD:E	167	3.1416	3.1416			
	Total	359					
Oil yield [dt ha^{-1}]	E	2	156.045	1.2330	19.31	*	0.54 - **0.77** - 0.87
	R:E	3	8.0809	-0.0095	0.93	*ns*	
	N	1	398.2872	1.1039	2.00	*ns*	
	EN	2	199.5829	3.1822	23.08	*	
	RN:E	3	8.6486	0.0335	1.13	*ns*	
	T	1	0.0745	-0.0179	0.02	*ns*	
	ET	2	3.2943	-0.0725	0.43	*ns*	
	NT	1	232.0991	1.1670	1.83	*ns*	
	ENT	2	127.0708	3.9809	16.62	**	
	RNT:E	7	7.6438	0.3324	2.88	**	
	D	14	28.9598	0.9015	3.95	**	
	ED	28	7.3231	0.5831	2.75	**	
	ND	14	3.5456	0.0030	1.01	*ns*	
	TD	14	14.359	0.9689	5.26	**	
	END	28	3.5102	0.2129	1.32	*ns*	
	ETD	28	2.7323	0.0184	1.03	*ns*	
	NTD	14	0.7709	-0.3341	0.28	*ns*	
	ENTD	28	2.7755	0.0585	1.04	*ns*	
	RNTD:E	167	2.6585	2.6585			
	Total	359					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. A 5

Tab. V (continued)

Trait	Source	DF	MS	Var.cp	F		h²
FL [d after January 1st]	E	1	2263.2042	18.8371	821.74	**	0.78 - **0.90** - 0.95
	R:E	2	2.7542	0.0303	2.94	*ns*	
	N	1	319.7042	0.6475	1.32	*ns*	
	EN	1	242.0042	4.0178	258.14	**	
	RN:E	2	0.9375	0.0152	1.94	*ns*	
	T	1	234.0375	1.9502	56169.00	*ns*	
	ET	1	0.0042	-0.0080	0.01	*ns*	
	NT	1	34.5042	0.3167	2.23	*ns*	
	ENT	1	15.5042	0.5007	32.13	**	
	RNT:E	5	0.4825	0.0041	1.15	*ns*	
	D	14	11.0238	0.6500	17.67	**	
	ED	14	0.6238	0.0254	1.48	*ns*	
	ND	14	0.6417	0.0429	2.15	*ns*	
	TD	14	4.2429	0.4149	4.59	**	
	END	14	0.2988	-0.0305	0.71	*ns*	
	ETD	14	0.9238	0.1258	2.20	*	
	NTD	14	0.2988	-0.0357	0.68	*ns*	
	ENTD	14	0.4417	0.0105	1.05	*ns*	
	RNTD:E	111	0.4208	0.4208			
	Total	239					
PL [cm]	E	1	22233.7500	180.4599	38.43	*	0.43 - **0.73** - 0.87
	R:E	2	578.5667	7.9314	5.63	*ns*	
	N	1	5645.4000	46.6694	125.27	*ns*	
	EN	1	45.0667	-0.9603	0.44	*ns*	
	RN:E	2	102.6833	-0.0677	0.98	*ns*	
	T	1	1135.3500	5.4944	2.39	*ns*	
	ET	1	476.0167	6.1884	4.55	*ns*	
	NT	1	11.2667	-1.7722	0.10	*ns*	
	ENT	1	117.6000	0.4296	1.12	*ns*	
	RNT:E	5	104.7133	4.6626	3.01	*	
	D	14	258.3542	12.4926	4.42	**	
	ED	14	58.4732	2.9624	1.68	*ns*	
	ND	14	18.1232	-0.4048	0.85	*ns*	
	TD	14	151.4482	12.4613	2.93	*	
	END	14	21.3613	-3.3532	0.61	*ns*	
	ETD	14	51.7577	4.2459	1.49	*ns*	
	NTD	14	21.8292	3.4167	2.67	*	
	ENTD	14	8.1625	-13.3058	0.23	*ns*	
	RNTD:E	111	34.7742	34.7742			
	Total	239					

ANOVA for traits that were not shown in chapter A, DF degrees of freedom, MS mean squares, Var.cp variance components, E environment, R:E replication within E, T variety type, D, descent, EN, ET, NT, ED, ND, TD, ENT, END, ETD, NTD, ENTD interactions, RN:E whole plot error, RNT:E subplot error, RNTD:E sub-subplot error, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. A 5

Tab. VI: Means of genotypes within N levels for traits of Population 029

Variety type	Genotype	$DM\%_{Seed}$ N1 [%]	$DM\%_{Seed}$ N0 [%]	$N\%_{Seed}$ N1 [%]	$N\%_{Seed}$ N0 [%]	Nup_{Seed} N1 [dt ha^{-1}]	Nup_{Seed} N0 [dt ha^{-1}]
DH	DH001	92.73	90.99	3.53	3.64	1.29	1.13
	DH002	93.25	92.18	3.38	3.60	1.35	1.41
	DH004	92.27	90.71	3.32	3.53	1.23	1.14
	DH005	93.71	92.52	3.27	3.40	1.22	1.21
	DH006	92.84	91.72	3.26	3.31	1.24	1.22
	DH009	92.47	92.00	3.32	3.45	1.31	1.30
	DH010	92.60	91.65	3.82	3.87	1.43	1.30
	DH011	92.72	93.09	3.48	3.48	1.29	1.28
	DH015	92.80	91.16	3.37	3.58	1.31	1.32
	DH016	93.04	92.96	3.30	3.44	1.02	0.97
	DH018	92.61	91.27	3.30	3.44	1.15	1.14
	DH020	92.69	91.31	3.44	3.48	1.16	1.07
	DH022	93.12	92.42	3.35	3.46	1.48	1.49
	DH024	92.48	92.06	3.39	3.44	1.25	1.24
	DH025	92.34	91.86	3.70	3.60	1.12	1.09
TH	TH001	92.86	91.26	3.70	3.29	1.54	1.10
	TH002	92.59	92.26	3.67	3.24	1.44	1.12
	TH004	92.75	91.38	3.72	3.28	1.50	1.05
	TH005	92.64	92.32	3.65	3.20	1.38	1.05
	TH006	92.59	91.44	3.67	3.28	1.49	1.08
	TH009	92.22	92.08	3.71	3.26	1.42	1.09
	TH010	92.76	91.85	3.81	3.30	1.50	1.03
	TH011	92.62	92.93	3.74	3.22	1.50	1.04
	TH015	92.43	91.07	3.74	3.30	1.48	1.06
	TH016	92.74	92.79	3.64	3.18	1.32	0.96
	TH018	92.84	91.49	3.60	3.25	1.41	0.97
	TH020	92.65	91.20	3.74	3.39	1.51	1.12
	TH022	92.69	92.03	3.58	3.19	1.42	1.02
	TH024	92.35	91.98	3.67	3.22	1.40	1.07
	TH025	92.35	91.92	3.79	3.26	1.44	1.02

Means for traits that were not shown in chapter A, DH DH line, TH test hybrid, Numbers in genotype names mark descent, An overview about trait abbreviations is given in Tab. A 5

Tab. VI (continued)

Variety type	Genotype	$DM\%_{Straw}$ N1 [%]	$DM\%_{Straw}$ N0 [%]	Straw DM N1 [dt ha^{-1}]	Straw DM N0 [dt ha^{-1}]	$N\%_{Straw}$ N1 [%]	$N\%_{Straw}$ N0 [%]
DH	DH001	39.91	43.78	40.33	42.14	1.02	0.96
	DH002	65.97	71.37	45.64	51.11	0.91	0.82
	DH004	48.35	51.20	42.74	45.23	0.87	0.69
	DH005	70.38	65.77	52.17	50.18	0.86	0.85
	DH006	46.27	46.87	44.45	43.45	0.95	0.81
	DH009	47.58	51.92	46.91	49.95	0.85	0.84
	DH010	59.26	62.73	51.67	50.98	0.92	0.85
	DH011	54.99	56.31	42.29	44.15	0.87	0.80
	DH015	65.73	62.62	46.12	45.16	0.83	0.86
	DH016	67.80	64.97	41.53	36.80	0.83	0.84
	DH018	56.00	56.12	45.17	46.72	0.90	0.86
	DH020	53.35	58.50	39.16	40.64	0.96	0.87
	DH022	54.92	58.48	52.95	53.61	0.80	0.83
	DH024	54.94	60.11	47.06	47.71	0.85	0.73
	DH025	57.74	55.60	43.25	37.99	1.00	0.83
TH	TH001	42.38	53.96	42.69	43.00	1.10	0.66
	TH002	55.21	67.35	51.11	49.30	0.95	0.64
	TH004	50.90	57.74	57.30	43.67	1.02	0.61
	TH005	46.74	53.01	44.24	40.19	1.04	0.63
	TH006	44.50	56.07	49.61	44.31	1.12	0.71
	TH009	49.19	49.29	53.14	39.11	0.97	0.62
	TH010	51.40	56.35	51.83	36.70	0.97	0.68
	TH011	42.99	62.24	45.10	44.58	1.00	0.67
	TH015	54.27	60.52	52.35	44.91	0.94	0.69
	TH016	53.79	66.45	44.64	44.28	1.07	0.64
	TH018	51.33	61.85	53.29	44.78	1.02	0.67
	TH020	50.56	65.40	49.92	50.34	1.02	0.64
	TH022	55.81	60.39	51.66	43.25	0.95	0.66
	TH024	50.15	63.09	52.01	45.45	1.06	0.65
	TH025	46.16	60.91	46.61	42.39	0.97	0.66

Means for traits that were not shown in chapter A, DH DH line, TH test hybrid, Numbers in genotype names mark descent, An overview about trait abbreviations is given in Tab. A 5

Tab. VI (continued)

Variety type	Genotype	Nup_{Straw} N1 [dt ha^{-1}]	Nup_{Straw} N0 [dt ha^{-1}]	HI N1	HI N0	Oil% N1 [%]	Oil% N0 [%]
DH	DH001	0.41	0.41	0.48	0.42	46.97	49.86
	DH002	0.42	0.42	0.47	0.43	47.49	50.28
	DH004	0.39	0.32	0.46	0.41	48.65	50.57
	DH005	0.46	0.43	0.42	0.41	47.61	51.67
	DH006	0.43	0.37	0.46	0.45	47.61	50.90
	DH009	0.40	0.43	0.46	0.43	47.72	49.67
	DH010	0.48	0.46	0.42	0.40	48.42	50.35
	DH011	0.37	0.37	0.47	0.44	48.47	50.02
	DH015	0.39	0.39	0.46	0.45	47.85	50.60
	DH016	0.35	0.31	0.43	0.42	46.70	49.86
	DH018	0.42	0.40	0.44	0.40	47.04	49.50
	DH020	0.38	0.36	0.47	0.43	46.73	51.12
	DH022	0.43	0.44	0.46	0.44	47.72	49.52
	DH024	0.41	0.35	0.45	0.43	48.17	49.27
	DH025	0.43	0.32	0.41	0.44	46.93	49.77
TH	TH001	0.46	0.29	0.49	0.44	49.42	47.85
	TH002	0.50	0.32	0.44	0.41	48.71	49.61
	TH004	0.57	0.27	0.42	0.42	48.66	48.67
	TH005	0.46	0.26	0.46	0.44	47.81	49.07
	TH006	0.56	0.30	0.45	0.43	49.11	48.30
	TH009	0.52	0.24	0.42	0.47	49.21	49.67
	TH010	0.50	0.25	0.44	0.46	48.93	48.75
	TH011	0.46	0.31	0.47	0.42	48.53	48.26
	TH015	0.49	0.31	0.43	0.42	49.12	50.05
	TH016	0.48	0.29	0.45	0.40	48.85	48.36
	TH018	0.54	0.31	0.43	0.40	50.31	49.92
	TH020	0.52	0.32	0.45	0.40	48.48	47.35
	TH022	0.49	0.28	0.43	0.43	48.85	49.64
	TH024	0.53	0.30	0.43	0.42	50.04	47.72
	TH025	0.46	0.29	0.45	0.42	47.97	48.88

Means for traits that were not shown in chapter A, DH DH line, TH test hybrid, Numbers in genotype names mark descent, An overview about trait abbreviations is given in Tab. A 5

Tab. VI (continued)

Variety type	Genotype	Oil yield N1 [dt ha^{-1}]	Oil yield N0 [dt ha^{-1}]	FL N1 [d after January 1st]	FL N0 [d after January 1st]	PL N1 [cm]	PL N0 [cm]
DH	DH001	17.19	15.29	102	100	158	150
	DH002	18.95	19.61	99	98	154	152
	DH004	17.90	15.84	104	103	174	162
	DH005	17.78	18.02	101	99	162	151
	DH006	18.00	18.25	101	99	160	152
	DH009	18.86	18.48	101	99	167	156
	DH010	18.11	16.54	101	100	162	146
	DH011	17.97	17.63	100	98	165	153
	DH015	18.42	18.22	101	100	155	145
	DH016	14.50	13.48	102	101	158	148
	DH018	16.47	15.86	102	101	170	160
	DH020	15.84	15.48	102	100	155	143
	DH022	21.06	20.91	100	98	174	165
	DH024	17.83	17.32	99	98	165	152
	DH025	14.24	14.71	100	98	155	147
TH	TH001	20.56	15.69	100	97	165	152
	TH002	19.04	16.88	99	97	169	157
	TH004	19.77	15.27	100	97	170	155
	TH005	17.99	15.75	100	97	165	160
	TH006	19.88	15.68	100	96	166	157
	TH009	18.82	16.37	99	96	170	160
	TH010	19.29	14.93	100	97	164	150
	TH011	19.44	15.18	100	96	168	162
	TH015	19.46	15.77	100	97	158	152
	TH016	17.63	14.06	100	98	172	161
	TH018	19.62	14.80	100	98	162	154
	TH020	19.53	15.49	100	97	164	157
	TH022	19.30	15.65	99	95	168	160
	TH024	19.05	15.61	100	96	167	161
	TH025	18.25	14.86	100	97	166	156

Means for traits that were not shown in chapter A, DH DH line, TH test hybrid, Numbers in genotype names mark descent, An overview about trait abbreviations is given in Tab. A 5

Tab. VII: Calibrations and cross validations for Nup_{EOF} across N levels with spectral data during fruit development

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.86	0.21	-9.E-08	0.82	0.24	-1.E-03
MMS1	SNV	0.83	0.23	-1.E-07	0.80	0.25	-1.E-03
MMS1	Norris d1g3	0.83	0.23	4.E-08	0.81	0.25	-6.E-04
MMS1	Norris d1g7	0.83	0.23	5.E-08	0.80	0.25	1.E-03
MMS1	Norris d1g11	0.87	0.21	1.E-07	0.84	0.23	3.E-03
MMS1	Norris d1g13	0.87	0.20	7.E-08	0.84	0.22	-2.E-03
MMS1	Norris d1g17	0.86	0.21	1.E-06	0.83	0.23	2.E-03
MMS1	Norris d1g25	0.86	0.21	7.E-08	0.84	0.23	-2.E-03
MMS1	Norris d1g41	0.86	0.21	7.E-08	0.83	0.24	4.E-03
MMS1	Norris d2g3	0.83	0.23	5.E-08	0.80	0.26	6.E-04
MMS1	Norris d2g9	0.82	0.24	6.E-08	0.80	0.25	-3.E-04
MMS1	Norris d2g15	0.85	0.22	7.E-08	0.82	0.24	4.E-03
MMS1	Norris d2g17	0.86	0.21	8.E-08	0.82	0.24	1.E-03
MMS1	Norris d2g19	0.86	0.21	4.E-08	0.83	0.23	3.E-03
MMS1	Norris d2g21	0.85	0.22	3.E-09	0.81	0.25	4.E-03
MMS1	Norris d2g25	0.85	0.22	7.E-08	0.82	0.24	4.E-04
MMS1	Norris d2g41	0.85	0.22	1.E-07	0.82	0.24	-1.E-03
MMS1	SaGo d1s3	0.83	0.23	5.E-08	0.80	0.25	4.E-04
MMS1	SaGo d1s9	0.84	0.23	4.E-08	0.82	0.24	-9.E-04
MMS1	SaGo d1s15	0.86	0.21	1.E-07	0.84	0.23	3.E-03
MMS1	SaGo d1s17	0.87	0.21	5.E-08	0.84	0.23	2.E-03
MMS1	SaGo d1s19	0.85	0.22	-8.E-08	0.83	0.24	2.E-03
MMS1	SaGo d1s25	0.85	0.22	-8.E-09	0.82	0.24	-5.E-04
MMS1	SaGo d1s41	0.83	0.23	2.E-06	0.80	0.25	-7.E-04
MMS1	SaGo d2s3	0.82	0.24	3.E-08	0.78	0.27	-2.E-03
MMS1	SaGo d2s9	0.84	0.23	4.E-08	0.81	0.25	2.E-03
MMS1	SaGo d2s11	0.86	0.21	5.E-08	0.82	0.24	2.E-03
MMS1	SaGo d2s13	0.86	0.21	5.E-08	0.83	0.24	-1.E-03
MMS1	SaGo d2s15	0.86	0.21	5.E-08	0.83	0.24	9.E-04
MMS1	SaGo d2s17	0.85	0.22	4.E-08	0.82	0.24	7.E-05
MMS1	SaGo d2s25	0.83	0.23	3.E-08	0.80	0.25	6.E-04
MMS1	SaGo d2s41	0.82	0.24	5.E-08	0.80	0.26	4.E-04
MMS1	Base + SNV	0.82	0.24	3.E-08	0.79	0.26	7.E-06
MMS1	Base + Norris d1g9	0.87	0.20	2.E-07	0.84	0.22	1.E-03
MMS1	Base + Norris d1g15	0.87	0.20	6.E-08	0.84	0.23	1.E-03
MMS1	Base + Norris d2g19	0.86	0.21	6.E-08	0.83	0.24	1.E-03
MMS1	Base+ SaGo d1s17	0.87	0.21	5.E-08	0.84	0.23	6.E-04
MMS1	Base + SaGo d2s13	0.86	0.21	4.E-08	0.82	0.24	3.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. VII (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	SNV	0.71	0.30	2.E-07	0.66	0.33	3.E-03
PGS_{red}	Norris d1g3	0.70	0.31	5.E-08	0.62	0.35	4.E-03
PGS_{red}	Norris d1g5	0.83	0.24	6.E-08	0.74	0.29	1.E-02
PGS_{red}	Norris d1g7	0.83	0.23	4.E-08	0.73	0.30	6.E-03
PGS_{red}	Norris d1g9	0.84	0.23	2.E-07	0.73	0.29	7.E-03
PGS_{red}	Norris d1g11	0.83	0.23	4.E-08	0.73	0.29	4.E-03
PGS_{red}	Norris d1g13	0.82	0.24	4.E-08	0.70	0.31	6.E-03
PGS_{red}	Norris d1g17	0.72	0.30	5.E-08	0.69	0.32	1.E-02
PGS_{red}	Norris d1g25	0.83	0.23	8.E-08	0.76	0.28	-1.E-03
PGS_{red}	Norris d1g37	0.82	0.24	6.E-08	0.73	0.29	4.E-03
PGS_{red}	Norris d1g39	0.84	0.23	7.E-08	0.74	0.29	5.E-03
PGS_{red}	Norris d1g41	0.84	0.23	1.E-07	0.73	0.29	-1.E-03
PGS_{red}	Norris d1g43	0.84	0.22	7.E-08	0.77	0.27	4.E-03
PGS_{red}	Norris d1g45	0.83	0.23	7.E-08	0.75	0.28	-2.E-04
PGS_{red}	Norris d2g3	0.62	0.35	4.E-08	0.56	0.38	-1.E-03
PGS_{red}	Norris d2g5	0.66	0.33	6.E-08	0.53	0.39	2.E-03
PGS_{red}	Norris d2g7	0.83	0.24	3.E-07	0.70	0.31	7.E-03
PGS_{red}	Norris d2g9	0.83	0.23	3.E-08	0.73	0.30	4.E-03
PGS_{red}	Norris d2g11	0.85	0.22	8.E-08	0.72	0.30	3.E-03
PGS_{red}	Norris d2g13	0.85	0.22	4.E-08	0.73	0.30	4.E-03
PGS_{red}	Norris d2g15	0.82	0.24	5.E-08	0.69	0.32	1.E-02
PGS_{red}	Norris d2g17	0.81	0.24	4.E-08	0.71	0.31	1.E-03
PGS_{red}	Norris d2g19	0.73	0.29	4.E-08	0.67	0.32	-8.E-04
PGS_{red}	Norris d2g21	0.83	0.23	5.E-08	0.73	0.29	3.E-03
PGS_{red}	Norris d2g23	0.82	0.24	6.E-08	0.76	0.28	8.E-04
PGS_{red}	Norris d2g25	0.83	0.24	5.E-08	0.74	0.29	7.E-03
PGS_{red}	Norris d2g27	0.81	0.24	4.E-08	0.73	0.29	3.E-03
PGS_{red}	Norris d2g29	0.83	0.24	3.E-07	0.74	0.29	4.E-04
PGS_{red}	Norris d2g31	0.80	0.25	5.E-08	0.72	0.30	-2.E-03
PGS_{red}	Norris d2g39	0.79	0.26	9.E-09	0.69	0.31	7.E-03
PGS_{red}	Norris d2g41	0.83	0.23	4.E-08	0.75	0.28	2.E-03
PGS_{red}	Norris d2g43	0.82	0.24	5.E-08	0.68	0.32	9.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. VII (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	SaGo d1s3	0.69	0.31	5.E-08	0.63	0.35	-1.E-03
PGS_{red}	SaGo d1s9	0.71	0.30	5.E-08	0.64	0.34	-2.E-07
PGS_{red}	SaGo d1s11	0.84	0.23	5.E-08	0.74	0.29	-2.E-03
PGS_{red}	SaGo d1s13	0.84	0.22	4.E-08	0.76	0.27	3.E-03
PGS_{red}	SaGo d1s15	0.84	0.23	2.E-07	0.76	0.28	7.E-03
PGS_{red}	SaGo d1s17	0.85	0.22	2.E-07	0.76	0.28	5.E-03
PGS_{red}	SaGo d1s19	0.81	0.24	1.E-07	0.73	0.29	2.E-03
PGS_{red}	SaGo d1s25	0.80	0.25	3.E-08	0.73	0.30	-5.E-03
PGS_{red}	SaGo d1s39	0.82	0.24	9.E-08	0.76	0.27	3.E-03
PGS_{red}	SaGo d1s41	0.83	0.23	7.E-09	0.78	0.27	3.E-03
PGS_{red}	SaGo d1s43	0.83	0.23	-3.E-07	0.78	0.27	-2.E-03
PGS_{red}	SaGo d1s47	0.84	0.23	-1.E-07	0.78	0.27	7.E-04
PGS_{red}	SaGo d1s49	0.83	0.23	-5.E-08	0.78	0.27	3.E-03
PGS_{red}	SaGo d2s3	0.61	0.35	5.E-08	0.52	0.39	-5.E-04
PGS_{red}	SaGo d2s9	0.66	0.33	4.E-08	0.56	0.38	-7.E-04
PGS_{red}	SaGo d2s17	0.83	0.23	4.E-08	0.74	0.29	7.E-03
PGS_{red}	SaGo d2s23	0.83	0.23	7.E-08	0.73	0.30	6.E-03
PGS_{red}	SaGo d2s25	0.84	0.22	6.E-08	0.73	0.29	5.E-03
PGS_{red}	SaGo d2s27	0.84	0.23	5.E-08	0.72	0.30	1.E-02
PGS_{red}	SaGo d2s29	0.83	0.23	6.E-08	0.73	0.29	-2.E-03
PGS_{red}	SaGo d2s31	0.82	0.24	3.E-07	0.71	0.30	-1.E-03
PGS_{red}	SaGo d2s41	0.83	0.23	1.E-06	0.75	0.29	2.E-03
PGS_{red}	Base + SNV	0.71	0.30	-2.E-07	0.64	0.34	-7.E-04
PGS_{red}	Base + Norris d1g43	0.83	0.23	4.E-08	0.75	0.28	3.E-03
PGS_{red}	Base + Norris d2g11	0.85	0.22	9.E-08	0.74	0.29	5.E-03
PGS_{red}	Base + Norris d2g13	0.85	0.22	3.E-07	0.71	0.31	6.E-03
PGS_{red}	Base + Norris d2g25	0.83	0.24	5.E-08	0.73	0.30	5.E-03
PGS_{red}	Base + SaGo d1s17	0.84	0.23	5.E+08	0.78	0.27	1.E-03
PGS_{red}	Base + SaGo d1s45	0.84	0.23	-2.E-07	0.79	0.26	-7.E-04
PGS_{red}	Base + SaGo d2s17	0.82	0.24	5.E-08	0.72	0.30	7.E-03
PGS_{red}	Base + SaGo d2s25	0.84	0.22	5.E-08	0.74	0.29	4.E-03
PGS_{red}	Base + SaGo d2s41	0.85	0.22	4.E-08	0.76	0.28	7.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. VIII: Calibrations and cross validations for Nup_{EOF} within N1 with spectral data during fruit development

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.60	0.28	1.E-07	0.56	0.30	1.E-03
MMS1	SNV	0.53	0.30	3.E-08	0.51	0.31	-3.E-04
MMS1	Norris d1g3	0.63	0.27	4.E-08	0.58	0.29	-8.E-04
MMS1	Norris d1g9	0.58	0.29	4.E-08	0.55	0.30	-4.E-04
MMS1	Norris d1g17	0.57	0.29	4.E-08	0.54	0.30	-2.E-03
MMS1	Norris d1g23	0.55	0.30	4.E-08	0.52	0.31	-4.E-04
MMS1	Norris d1g25	0.74	0.23	-2.E-08	0.60	0.28	-4.E-03
MMS1	Norris d1g27	0.74	0.23	2.E-07	0.62	0.27	3.E-03
MMS1	Norris d1g29	0.75	0.22	1.E-08	0.63	0.27	4.E-04
MMS1	Norris d1g31	0.62	0.27	7.E-08	0.56	0.30	-8.E-04
MMS1	Norris d1g39	0.74	0.23	2.E-08	0.64	0.27	2.E-03
MMS1	Norris d1g41	0.74	0.22	-2.E-08	0.65	0.27	-2.E-03
MMS1	Norris d1g45	0.75	0.22	5.E-08	0.64	0.27	-6.E-04
MMS1	Norris d1g47	0.75	0.22	-1.E-08	0.65	0.27	-1.E-03
MMS1	Norris d1g49	0.76	0.22	-1.E-07	0.66	0.26	9.E-04
MMS1	Norris d1g51	0.56	0.29	5.E-08	0.55	0.30	1.E-03
MMS1	Norris d2g3	0.66	0.26	4.E-08	0.60	0.28	-3.E-05
MMS1	Norris d2g9	0.59	0.29	5.E-08	0.56	0.29	4.E-04
MMS1	Norris d2g15	0.56	0.30	5.E-08	0.54	0.30	-2.E-04
MMS1	Norris d2g17	0.75	0.22	9.E-08	0.63	0.27	7.E-03
MMS1	Norris d2g19	0.55	0.30	4.E-08	0.53	0.30	1.E-05
MMS1	Norris d2g25	0.54	0.30	4.E-08	0.53	0.31	-7.E-04
MMS1	Norris d2g31	0.55	0.30	5.E-08	0.53	0.31	1.E-03
MMS1	Norris d2g33	0.73	0.23	5.E-09	0.63	0.27	-2.E-03
MMS1	Norris d2g35	0.74	0.23	-1.E-08	0.64	0.27	5.E-03
MMS1	Norris d2g37	0.74	0.22	-4.E-08	0.64	0.27	3.E-03
MMS1	Norris d2g39	0.73	0.23	8.E-08	0.65	0.27	2.E-03
MMS1	Norris d2g41	0.73	0.23	-2.E-08	0.63	0.27	-1.E-03
MMS1	Norris d2g43	0.74	0.23	-1.E-07	0.67	0.26	3.E-03
MMS1	Norris d2g45	0.56	0.29	4.E-08	0.53	0.31	2.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. VIII (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	SaGo d1s3	0.64	0.27	4.E-08	0.58	0.29	9.E-04
MMS1	SaGo d1s9	0.59	0.29	4.E-08	0.56	0.30	-9.E-04
MMS1	SaGo d1s13	0.56	0.29	4.E-08	0.52	0.31	-1.E-03
MMS1	SaGo d1s15	0.76	0.22	8.E-08	0.65	0.26	-6.E-04
MMS1	SaGo d1s19	0.75	0.22	1.E-07	0.64	0.27	9.E-04
MMS1	SaGo d1s21	0.58	0.29	3.E-08	0.56	0.30	-2.E-04
MMS1	SaGo d1s25	0.73	0.23	5.E-10	0.63	0.27	5.E-04
MMS1	SaGo d1s41	0.74	0.23	-7.E-08	0.65	0.26	-3.E-03
MMS1	SaGo d1s43	0.74	0.23	2.E-07	0.67	0.26	7.E-04
MMS1	SaGo d1s45	0.73	0.23	2.E-07	0.66	0.26	-3.E-03
MMS1	SaGo d1s47	0.73	0.23	-3.E-09	0.65	0.26	-2.E-03
MMS1	SaGo d1s49	0.73	0.23	-8.E-08	0.66	0.26	7.E-04
MMS1	SaGo d2s3	0.62	0.27	5.E-08	0.54	0.31	2.E-03
MMS1	SaGo d2s9	0.66	0.26	4.E-08	0.59	0.28	6.E-04
MMS1	SaGo d2s17	0.60	0.28	4.E-08	0.56	0.29	-2.E-03
MMS1	SaGo d2s25	0.56	0.29	4.E-08	0.53	0.30	-5.E-04
MMS1	SaGo d2s39	0.54	0.30	4.E-08	0.52	0.31	-4.E-04
MMS1	SaGo d2s41	0.74	0.23	3.E-08	0.63	0.27	-2.E-03
MMS1	SaGo d2s43	0.74	0.23	-3.E-08	0.63	0.27	8.E-03
MMS1	SaGo d2s45	0.54	0.30	6.E-08	0.52	0.31	2.E-03
MMS1	Base + SNV	0.53	0.30	4.E-08	0.51	0.31	-2.E-04
MMS1	Base + Norris d1g43	0.74	0.22	2.E-07	0.64	0.27	4.E-04
MMS1	Base + Norris d1g49	0.76	0.22	-3.E-08	0.66	0.26	2.E-03
MMS1	Base + Norris d2g43	0.74	0.23	-1.E-07	0.64	0.27	3.E-03
MMS1	Base + SaGo d1s17	0.76	0.21	-4.E-08	0.63	0.27	8.E-04
MMS1	Base + SaGo d1s43	0.73	0.23	1.E-07	0.65	0.26	-1.E-03
MMS1	Base + SaGo d2s41	0.73	0.23	9.E-09	0.61	0.28	4.E-03
MMS1	Base + SaGo d2s43	0.54	0.30	4.E-08	0.52	0.31	4.E-04
PGS_{red}	Base	0.70	0.24	9.E-08	0.58	0.29	7.E-03
PGS_{red}	SNV	0.64	0.27	2.E-08	0.55	0.30	-5.E-03
PGS_{red}	Norris d1g3	0.62	0.27	4.E-08	0.52	0.31	-9.E-04
PGS_{red}	Norris d1g9	0.56	0.30	4.E-08	0.44	0.33	-2.E-03
PGS_{red}	Norris d1g15	0.51	0.31	4.E-08	0.45	0.33	-5.E-03
PGS_{red}	Norris d1g17	0.75	0.22	8.E-08	0.56	0.30	-2.E-04
PGS_{red}	Norris d1g19	0.61	0.28	3.E-08	0.54	0.30	5.E-03
PGS_{red}	Norris d1g25	0.61	0.28	5.E-08	0.51	0.31	1.E-03
PGS_{red}	Norris d1g41	0.55	0.30	6.E-08	0.48	0.32	7.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. VIII (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	Norris d2g3	0.58	0.29	3.E-08	0.46	0.33	3.E-03
PGS_{red}	Norris d2g9	0.54	0.30	3.E-08	0.46	0.33	-3.E-03
PGS_{red}	Norris d2g17	0.57	0.29	4.E-08	0.47	0.32	1.E-03
PGS_{red}	Norris d2g23	0.66	0.26	6.E-08	0.53	0.30	6.E-03
PGS_{red}	Norris d2g25	0.71	0.24	2.E-08	0.59	0.29	-9.E-04
PGS_{red}	Norris d2g27	0.72	0.23	8.E-09	0.56	0.29	9.E-04
PGS_{red}	Norris d2g29	0.70	0.24	4.E-08	0.56	0.30	8.E-03
PGS_{red}	Norris d2g41	0.56	0.29	7.E-08	0.45	0.33	7.E-03
PGS_{red}	SaGo d1s3	0.52	0.31	3.E-08	0.47	0.32	-8.E-04
PGS_{red}	SaGo d1s9	0.65	0.26	5.E-08	0.53	0.30	2.E-03
PGS_{red}	SaGo d1s17	0.77	0.21	4.E-08	0.59	0.29	-2.E-03
PGS_{red}	SaGo d1s25	0.71	0.24	6.E-08	0.56	0.30	-6.E-03
PGS_{red}	SaGo d1s37	0.73	0.23	4.E-08	0.58	0.29	3.E-03
PGS_{red}	SaGo d1s39	0.75	0.22	6.E-08	0.62	0.27	-3.E-03
PGS_{red}	SaGo d1s43	0.74	0.23	1.E-07	0.61	0.28	-8.E-04
PGS_{red}	SaGo d2s3	0.60	0.28	5.E-07	0.46	0.33	4.E-03
PGS_{red}	SaGo d2s9	0.59	0.28	4.E-08	0.47	0.32	3.E-03
PGS_{red}	SaGo d2s17	0.66	0.26	4.E-08	0.53	0.30	-5.E-03
PGS_{red}	SaGo d2s23	0.67	0.25	7.E-08	0.53	0.31	5.E-03
PGS_{red}	SaGo d2s25	0.71	0.24	2.E-08	0.54	0.30	8.E-03
PGS_{red}	SaGo d2s27	0.72	0.24	3.E-08	0.53	0.30	1.E-02
PGS_{red}	SaGo d2s29	0.77	0.21	4.E-08	0.53	0.31	2.E-04
PGS_{red}	SaGo d2s31	0.75	0.22	6.E-08	0.55	0.30	8.E-03
PGS_{red}	SaGo d2s33	0.70	0.24	5.E-08	0.53	0.30	3.E-03
PGS_{red}	SaGo d2s41	0.55	0.30	3.E-08	0.48	0.32	7.E-03
PGS_{red}	Base + SNV	0.64	0.27	9.E-08	0.54	0.30	-6.E-03
PGS_{red}	Base + Norris d1g17	0.73	0.23	7.E-08	0.56	0.29	-7.E-03
PGS_{red}	Base + Norris d2g25	0.73	0.23	4.E-08	0.59	0.28	3.E-03
PGS_{red}	Base + Norris d2g27	0.72	0.23	5.E-08	0.57	0.29	4.E-03
PGS_{red}	Base + SaGo d1s17	0.78	0.21	3.E-08	0.59	0.29	5.E-03
PGS_{red}	Base + SaGo d1s41	0.76	0.22	8.E-08	0.63	0.27	-2.E-03
PGS_{red}	Base + SaGo d2s29	0.76	0.22	4.E-08	0.56	0.29	2.E-03
PGS_{red}	Base + SaGo d2s31	0.75	0.22	2.E-08	0.62	0.27	-2.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. IX: Calibrations and cross validations for Nup_{EOF} within N0 with spectral data during fruit development

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.79	0.11	-1.E-08	0.76	0.12	1.E-04
MMS1	SNV	0.79	0.11	4.E-08	0.76	0.12	6.E-04
MMS1	Norris d1g1	0.78	0.11	3.E-08	0.74	0.12	2.E-04
MMS1	Norris d1g3	0.81	0.11	4.E-08	0.76	0.12	-7.E-04
MMS1	Norris d1g5	0.80	0.11	3.E-08	0.75	0.12	2.E-04
MMS1	Norris d1g7	0.80	0.11	3.E-08	0.75	0.12	1.E-03
MMS1	Norris d1g9	0.79	0.11	4.E-08	0.75	0.12	7.E-04
MMS1	Norris d1g17	0.79	0.11	3.E-08	0.76	0.12	6.E-04
MMS1	Norris d1g25	0.79	0.11	3.E-08	0.76	0.12	-8.E-04
MMS1	Norris d1g41	0.77	0.12	2.E-08	0.75	0.12	-5.E-04
MMS1	Norris d2g0	0.77	0.12	3.E-08	0.64	0.14	3.E-03
MMS1	Norris d2g3	0.75	0.12	3.E-08	0.69	0.13	1.E-03
MMS1	Norris d2g5	0.72	0.13	3.E-08	0.69	0.14	2.E-04
MMS1	Norris d2g7	0.80	0.11	3.E-08	0.75	0.12	-5.E-04
MMS1	Norris d2g11	0.80	0.11	3.E-08	0.76	0.12	8.E-05
MMS1	Norris d2g13	0.77	0.12	2.E-08	0.74	0.12	7.E-04
MMS1	Norris d2g17	0.80	0.11	3.E-08	0.78	0.12	-9.E-04
MMS1	Norris d2g25	0.77	0.12	2.E-08	0.75	0.12	6.E-04
MMS1	Norris d2g41	0.75	0.12	3.E-08	0.74	0.12	-4.E-04
MMS1	SaGo d1s5	0.80	0.11	2.E-08	0.75	0.12	-3.E-03
MMS1	SaGo d1s7	0.81	0.11	4.E-08	0.76	0.12	3.E-04
MMS1	SaGo d1s9	0.79	0.11	3.E-08	0.76	0.12	4.E-04
MMS1	SaGo d1s17	0.78	0.11	3.E-08	0.75	0.12	8.E-04
MMS1	SaGo d1s25	0.77	0.12	2.E-08	0.76	0.12	-2.E-04
MMS1	SaGo d1s41	0.75	0.12	3.E-08	0.75	0.12	3.E-04

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. IX (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	SaGo d2s3	0.77	0.12	2.E-08	0.61	0.15	3.E-03
MMS1	SaGo d2s9	0.75	0.12	3.E-08	0.70	0.13	2.E-03
MMS1	SaGo d2s11	0.81	0.10	3.E-08	0.73	0.13	2.E-03
MMS1	SaGo d2s13	0.81	0.10	3.E-08	0.73	0.13	-2.E-03
MMS1	SaGo d2s15	0.80	0.11	3.E-08	0.73	0.13	9.E-04
MMS1	SaGo d2s17	0.78	0.11	3.E-08	0.73	0.13	-6.E-04
MMS1	SaGo d2s19	0.81	0.11	3.E-08	0.74	0.12	-5.E-04
MMS1	SaGo d2s21	0.80	0.11	3.E-08	0.76	0.12	4.E-04
MMS1	SaGo d2s23	0.81	0.11	2.E-08	0.76	0.12	-3.E-04
MMS1	SaGo d2s25	0.80	0.11	4.E-08	0.77	0.12	6.E-04
MMS1	SaGo d2s27	0.80	0.11	2.E-08	0.77	0.12	-2.E-04
MMS1	SaGo d2s29	0.78	0.11	3.E-08	0.76	0.12	4.E-04
MMS1	SaGo d2s31	0.78	0.11	3.E-08	0.75	0.12	-1.E-03
MMS1	SaGo d2s33	0.79	0.11	3.E-08	0.77	0.12	5.E-05
MMS1	SaGo d2s35	0.78	0.11	2.E-08	0.76	0.12	-1.E-03
MMS1	SaGo d2s37	0.79	0.11	4.E-08	0.76	0.12	1.E-03
MMS1	SaGo d2s39	0.79	0.11	3.E-08	0.77	0.12	5.E-04
MMS1	SaGo d2s41	0.78	0.11	4.E-08	0.77	0.12	-1.E-03
MMS1	SaGo d2s43	0.78	0.11	3.E-08	0.76	0.12	-1.E-04
MMS1	Base + SNV	0.79	0.11	2.E-08	0.76	0.12	9.E-04
MMS1	Base + Norris d1g3	0.78	0.11	3.E-08	0.75	0.12	-1.E-03
MMS1	Base + Norris d2g9	0.78	0.11	3.E-08	0.75	0.12	5.E-04
MMS1	Base + Norris d2g17	0.80	0.11	3.E-08	0.77	0.12	-9.E-04
MMS1	Base + SaGo d1s3	0.78	0.11	3.E-08	0.74	0.12	8.E-04
MMS1	Base + SaGo d2s19	0.81	0.11	3.E-08	0.76	0.12	1.E-03
MMS1	Base + SaGo d2s25	0.79	0.11	3.E-08	0.75	0.12	1.E-04
MMS1	Base + SaGo d2s27	0.79	0.11	3.E-08	0.76	0.12	4.E-04
PGS_{red}	Base	0.80	0.11	3.E-08	0.74	0.12	2.E-03
PGS_{red}	SNV	0.75	0.12	4.E-08	0.69	0.13	2.E-04
PGS_{red}	Norris d1g1	0.71	0.13	2.E-08	0.64	0.15	-3.E-04
PGS_{red}	Norris d1g3	0.72	0.13	4.E-08	0.67	0.14	-6.E-04
PGS_{red}	Norris d1g5	0.80	0.11	2.E-08	0.71	0.13	9.E-04
PGS_{red}	Norris d1g7	0.81	0.11	4.E-08	0.73	0.13	3.E-04
PGS_{red}	Norris d1g9	0.80	0.11	4.E-08	0.71	0.13	5.E-03
PGS_{red}	Norris d1g11	0.80	0.11	3.E-08	0.72	0.13	5.E-04
PGS_{red}	Norris d1g13	0.79	0.11	3.E-08	0.71	0.13	2.E-04
PGS_{red}	Norris d1g17	0.78	0.11	4.E-08	0.71	0.13	2.E-03
PGS_{red}	Norris d1g25	0.78	0.11	2.E-08	0.69	0.13	3.E-03
PGS_{red}	Norris d1g41	0.78	0.11	2.E-08	0.71	0.13	2.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. IX (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	Norris d2g5	0.72	0.13	3.E-08	0.66	0.14	-1.E-04
PGS_{red}	Norris d2g7	0.74	0.12	3.E-08	0.67	0.14	6.E-04
PGS_{red}	Norris d2g9	0.76	0.12	3.E-08	0.69	0.14	2.E-03
PGS_{red}	Norris d2g11	0.76	0.12	3.E-08	0.70	0.13	3.E-03
PGS_{red}	Norris d2g13	0.78	0.11	3.E-08	0.70	0.13	6.E-04
PGS_{red}	Norris d2g15	0.78	0.11	3.E-08	0.69	0.14	8.E-04
PGS_{red}	Norris d2g17	0.76	0.12	2.E-08	0.69	0.14	1.E-03
PGS_{red}	Norris d2g19	0.77	0.12	3.E-08	0.67	0.14	9.E-04
PGS_{red}	Norris d2g21	0.74	0.12	3.E-08	0.63	0.15	5.E-04
PGS_{red}	Norris d2g25	0.75	0.12	3.E-08	0.65	0.14	-3.E-04
PGS_{red}	Norris d2g37	0.76	0.12	3.E-08	0.68	0.14	2.E-03
PGS_{red}	Norris d2g39	0.78	0.11	3.E-08	0.71	0.13	7.E-04
PGS_{red}	Norris d2g41	0.76	0.12	3.E-08	0.69	0.13	6.E-04
PGS_{red}	Norris d2g43	0.77	0.12	3.E-08	0.71	0.13	3.E-04
PGS_{red}	Norris d2g45	0.78	0.11	3.E-08	0.70	0.13	1.E-03
PGS_{red}	Norris d2g47	0.78	0.11	3.E-08	0.70	0.13	3.E-03
PGS_{red}	Norris d2g49	0.79	0.11	3.E-08	0.71	0.13	4.E-03
PGS_{red}	Norris d2g51	0.79	0.11	3.E-08	0.71	0.13	2.E-04
PGS_{red}	Norris d2g53	0.78	0.11	4.E-08	0.71	0.13	1.E-03
PGS_{red}	Norris d2g55	0.76	0.12	4.E-08	0.70	0.13	2.E-03
PGS_{red}	SaGo d1s3	0.71	0.13	2.E-08	0.65	0.14	6.E-04
PGS_{red}	SaGo d1s7	0.73	0.13	3.E-08	0.67	0.14	-5.E-04
PGS_{red}	SaGo d1s9	0.78	0.11	3.E-08	0.71	0.13	2.E-03
PGS_{red}	SaGo d1s11	0.81	0.11	3.E-08	0.72	0.13	4.E-03
PGS_{red}	SaGo d1s13	0.81	0.11	3.E-08	0.73	0.13	4.E-04
PGS_{red}	SaGo d1s15	0.80	0.11	3.E-08	0.74	0.12	1.E-03
PGS_{red}	SaGo d1s17	0.78	0.11	3.E-08	0.71	0.13	3.E-03
PGS_{red}	SaGo d1s19	0.78	0.11	3.E-08	0.71	0.13	1.E-03
PGS_{red}	SaGo d1s21	0.78	0.11	4.E-08	0.73	0.13	2.E-03
PGS_{red}	SaGo d1s23	0.78	0.11	3.E-08	0.73	0.13	2.E-03
PGS_{red}	SaGo d1s25	0.79	0.11	2.E-08	0.72	0.13	1.E-03
PGS_{red}	SaGo d1s27	0.78	0.11	4.E-08	0.71	0.13	1.E-04
PGS_{red}	SaGo d1s29	0.78	0.11	4.E-08	0.68	0.14	1.E-03
PGS_{red}	SaGo d1s31	0.75	0.12	3.E-08	0.67	0.14	-3.E-04
PGS_{red}	SaGo d1s41	0.77	0.12	3.E-08	0.70	0.13	5.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. IX (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	SaGo d2s3	0.73	0.13	2.E-08	0.62	0.15	-7.E-04
PGS_{red}	SaGo d2s9	0.74	0.12	3.E-08	0.66	0.14	1.E-03
PGS_{red}	SaGo d2s15	0.73	0.13	3.E-08	0.67	0.14	-4.E-04
PGS_{red}	SaGo d2s17	0.77	0.12	3.E-08	0.69	0.13	4.E-03
PGS_{red}	SaGo d2s19	0.74	0.12	3.E-08	0.66	0.14	2.E-03
PGS_{red}	SaGo d2s23	0.76	0.12	3.E-08	0.68	0.14	3.E-03
PGS_{red}	SaGo d2s25	0.76	0.12	3.E-08	0.70	0.13	3.E-03
PGS_{red}	SaGo d2s27	0.76	0.12	2.E-08	0.67	0.14	3.E-03
PGS_{red}	SaGo d2s41	0.76	0.12	3.E-08	0.68	0.14	9.E-04
PGS_{red}	Base + SNV	0.75	0.12	3.E-08	0.70	0.13	1.E-03
PGS_{red}	Base + Norris d1g7	0.81	0.11	4.E-08	0.72	0.13	9.E-04
PGS_{red}	Base + Norris d2g49	0.79	0.11	2.E-08	0.74	0.13	2.E-04
PGS_{red}	Base + Norris d2g51	0.79	0.11	2.E-08	0.71	0.13	8.E-04
PGS_{red}	Base + SaGo d1s13	0.81	0.11	3.E-08	0.72	0.13	2.E-03
PGS_{red}	Base + SaGo d1s15	0.79	0.11	3.E-08	0.72	0.13	3.E-03
PGS_{red}	Base + SaGo d2s17	0.74	0.12	3.E-08	0.68	0.14	6.E-04
PGS_{red}	Base + SaGo d2s25	0.76	0.12	3.E-08	0.68	0.14	2.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. X: Calibrations and cross validations for Nup_{MAT} across N levels with spectral data before flowering

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.82	0.19	5.E-07	0.80	0.21	2.E-03
MMS1	SNV	0.79	0.21	-3.E-07	0.77	0.22	6.E-04
MMS1	Norris d1g3	0.78	0.22	3.E-08	0.76	0.23	2.E-03
MMS1	Norris d1g5	0.80	0.21	6.E-08	0.78	0.22	-1.E-03
MMS1	Norris d1g9	0.82	0.19	6.E-08	0.80	0.21	-8.E-04
MMS1	Norris d1g13	0.83	0.19	2.E-07	0.80	0.20	6.E-04
MMS1	Norris d1g17	0.82	0.20	4.E-08	0.80	0.21	2.E-03
MMS1	Norris d1g25	0.82	0.20	3.E-07	0.80	0.21	7.E-04
MMS1	Norris d1g33	0.81	0.20	7.E-08	0.80	0.21	2.E-03
MMS1	Norris d1g41	0.79	0.21	3.E-08	0.78	0.22	2.E-03
MMS1	Norris d2g3	0.82	0.20	4.E-08	0.79	0.21	-3.E-03
MMS1	Norris d2g5	0.80	0.21	3.E-08	0.78	0.22	5.E-04
MMS1	Norris d2g9	0.80	0.21	4.E-08	0.78	0.22	7.E-04
MMS1	Norris d2g13	0.82	0.19	5.E-08	0.80	0.21	2.E-03
MMS1	Norris d2g17	0.81	0.20	6.E-08	0.79	0.21	1.E-03
MMS1	SaGo d1s3	0.79	0.21	5.E-08	0.78	0.22	-1.E-03
MMS1	SaGo d1s5	0.78	0.21	4.E-08	0.77	0.22	3.E-03
MMS1	SaGo d1s9	0.80	0.21	5.E-08	0.78	0.21	3.E-03
MMS1	SaGo d1s13	0.82	0.20	5.E-08	0.80	0.21	7.E-04
MMS1	SaGo d1s17	0.83	0.19	4.E-08	0.81	0.20	3.E-03
MMS1	SaGo d1s25	0.82	0.19	5.E-08	0.80	0.21	1.E-03
MMS1	SaGo d1s33	0.83	0.19	2.E-07	0.81	0.20	2.E-03
MMS1	SaGo d1s41	0.81	0.20	6.E-08	0.79	0.21	5.E-04
MMS1	SaGo d2s3	0.81	0.20	4.E-08	0.78	0.22	-1.E-03
MMS1	SaGo d2s5	0.78	0.21	3.E-08	0.76	0.23	2.E-03
MMS1	SaGo d2s9	0.80	0.21	4.E-08	0.77	0.22	1.E-03
MMS1	SaGo d2s13	0.80	0.21	4.E-08	0.78	0.22	2.E-03
MMS1	SaGo d2s17	0.77	0.22	5.E-08	0.75	0.23	8.E-04
MMS1	Base + SaGo d1s33	0.82	0.20	1.E-08	0.80	0.21	2.E-03
PGS_{red}	Base	0.78	0.22	1.E-07	0.75	0.23	2.E-04
PGS_{red}	SNV	0.76	0.23	-1.E-08	0.72	0.24	1.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. X (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	Norris d1g3	0.78	0.22	5.E-08	0.71	0.25	2.E-03
PGS_{red}	Norris d1g5	0.80	0.21	3.E-08	0.73	0.24	4.E-03
PGS_{red}	Norris d1g9	0.79	0.21	4.E-08	0.74	0.24	2.E-03
PGS_{red}	Norris d1g13	0.75	0.23	5.E-08	0.70	0.25	7.E-04
PGS_{red}	Norris d1g17	0.81	0.20	5.E-08	0.76	0.23	3.E-03
PGS_{red}	Norris d1g19	0.79	0.21	-4.E-08	0.74	0.23	2.E-03
PGS_{red}	Norris d1g21	0.76	0.23	4.E-08	0.72	0.24	2.E-03
PGS_{red}	Norris d1g23	0.77	0.22	3.E-08	0.73	0.24	7.E-04
PGS_{red}	Norris d1g25	0.74	0.23	3.E-08	0.72	0.25	6.E-04
PGS_{red}	Norris d1g33	0.76	0.23	3.E-08	0.73	0.24	-1.E-03
PGS_{red}	Norris d1g41	0.76	0.23	4.E-08	0.72	0.24	-5.E-04
PGS_{red}	Norris d2g3	0.73	0.24	5.E-08	0.67	0.27	6.E-04
PGS_{red}	SaGo d1s3	0.81	0.20	3.E-10	0.74	0.24	2.E-03
PGS_{red}	SaGo d1s5	0.79	0.21	4.E-08	0.72	0.24	-1.E-03
PGS_{red}	SaGo d1s9	0.77	0.22	4.E-08	0.71	0.25	1.E-03
PGS_{red}	SaGo d1s13	0.80	0.21	-3.E-08	0.74	0.24	9.E-04
PGS_{red}	SaGo d1s17	0.79	0.21	3.E-08	0.73	0.24	3.E-04
PGS_{red}	SaGo d1s25	0.81	0.20	4.E-08	0.75	0.23	7.E-03
PGS_{red}	SaGo d1s33	0.81	0.20	4.E-08	0.75	0.23	1.E-03
PGS_{red}	SaGo d1s43	0.81	0.20	4.E-08	0.76	0.22	2.E-03
PGS_{red}	SaGo d1s45	0.81	0.20	7.E-08	0.76	0.22	2.E-06
PGS_{red}	SaGo d1s51	0.80	0.21	7.E-08	0.75	0.23	-2.E-04
PGS_{red}	SaGo d2s3	0.72	0.24	1.E-07	0.66	0.27	-2.E-03
PGS_{red}	Base + SaGo d1s41	0.82	0.20	5.E-08	0.76	0.23	-2.E-04

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XI: Calibrations and cross validation for Nup_{MAT} across both N levels with spectral data during fruit development

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.59	0.30	-6.E-08	0.58	0.30	-1.E-03
MMS1	SNV	0.67	0.27	-3.E-07	0.63	0.28	-2.E-03
MMS1	Norris d1g3	0.66	0.27	-3.E-08	0.62	0.29	2.E-05
MMS1	Norris d1g5	0.68	0.26	9.E-09	0.62	0.29	-2.E-03
MMS1	Norris d1g9	0.69	0.26	-3.E-08	0.63	0.28	-3.E-03
MMS1	Norris d1g13	0.68	0.26	-1.E-08	0.64	0.28	1.E-03
MMS1	Norris d1g17	0.68	0.26	-4.E-08	0.63	0.28	3.E-03
MMS1	Norris d1g25	0.63	0.28	-3.E-08	0.59	0.30	2.E-03
MMS1	Norris d1g33	0.67	0.27	5.E-09	0.61	0.29	-3.E-03
MMS1	Norris d1g41	0.70	0.28	1.E-08	0.65	0.28	2.E-04
MMS1	Norris d1g45	0.60	0.29	-2.E-08	0.58	0.30	6.E-04
MMS1	Norris d1g49	0.62	0.29	-2.E-08	0.59	0.30	2.E-03
MMS1	Norris d1g57	0.65	0.28	-5.E-08	0.61	0.29	-1.E-03
MMS1	Norris d2g3	0.65	0.28	-2.E-08	0.62	0.29	1.E-03
MMS1	Norris d2g5	0.66	0.27	-2.E-08	0.62	0.29	-2.E-05
MMS1	Norris d2g9	0.60	0.30	-2.E-08	0.59	0.30	-1.E-04
MMS1	Norris d2g17	0.70	0.26	-5.E-08	0.65	0.28	1.E-03
MMS1	Norris d2g25	0.69	0.26	-2.E-08	0.64	0.28	-3.E-04
MMS1	Norris d2g33	0.67	0.27	6.E-08	0.62	0.29	7.E-04
MMS1	Norris d2g41	0.69	0.26	-6.E-08	0.64	0.28	-9.E-04
MMS1	SaGo d1s3	0.66	0.27	-2.E-08	0.62	0.29	6.E-04
MMS1	SaGo d1s5	0.66	0.27	-2.E-08	0.61	0.29	2.E-03
MMS1	SaGo d1s13	0.69	0.26	9.E-09	0.65	0.28	2.E-03
MMS1	SaGo d1s17	0.68	0.26	-3.E-08	0.65	0.26	-3.E-03
MMS1	SaGo d1s25	0.66	0.27	-2.E-08	0.63	0.29	2.E-04
MMS1	SaGo d1s33	0.62	0.29	-4.E-08	0.59	0.30	-5.E-05
MMS1	SaGo d1s41	0.61	0.29	-1.E-08	0.58	0.30	1.E-03
MMS1	SaGo d2s3	0.68	0.26	-3.E-08	0.65	0.28	3.E-03
MMS1	SaGo d2s5	0.67	0.27	-2.E-08	0.64	0.28	-2.E-04
MMS1	SaGo d2s9	0.67	0.27	-3.E-08	0.63	0.29	-4.E-04
MMS1	SaGo d2s13	0.63	0.28	-2.E-08	0.60	0.29	-4.E-04
MMS1	SaGo d2s17	0.67	0.27	-3.E-08	0.63	0.28	2.E-03
MMS1	Base + SNV	0.65	0.28	-3.E-07	0.60	0.29	2.E-03
MMS1	Base + Norris d2g13	0.68	0.26	-1.E-08	0.65	0.28	-2.E-03
MMS1	Base + SaGo d1s9	0.70	0.26	-6.E-08	0.65	0.27	-8.E-04
MMS1	Base + SaGo d1s17	0.68	0.26	-7.E-08	0.65	0.28	-1.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XI (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	Base	0.68	0.26	3.E-07	0.60	0.29	-1.E-03
PGS_{red}	SNV	0.57	0.31	-1.E-07	0.50	0.33	8.E-04
PGS_{red}	Norris d1g5	0.58	0.30	-3.E-08	0.53	0.32	5.E-04
PGS_{red}	Norris d1g9	0.60	0.29	-2.E-08	0.55	0.32	3.E-03
PGS_{red}	Norris d1g13	0.71	0.25	-1.E-08	0.61	0.29	3.E-03
PGS_{red}	Norris d1g17	0.58	0.30	-3.E-08	0.55	0.32	2.E-03
PGS_{red}	Norris d1g25	0.70	0.25	3.E-08	0.61	0.29	-1.E-03
PGS_{red}	Norris d1g33	0.67	0.27	-3.E-09	0.62	0.29	6.E-04
PGS_{red}	Norris d1g41	0.67	0.27	6.E-09	0.60	0.29	-1.E-03
PGS_{red}	Norris d2g3	0.71	0.25	-3.E-08	0.56	0.31	2.E-03
PGS_{red}	Norris d2g5	0.73	0.24	-5.E-08	0.56	0.31	6.E-03
PGS_{red}	Norris d2g9	0.71	0.25	-2.E-09	0.61	0.29	-1.E-03
PGS_{red}	Norris d2g13	0.70	0.26	-4.E-09	0.59	0.30	-1.E-03
PGS_{red}	Norris d2g17	0.58	0.30	-2.E-08	0.55	0.31	7.E-03
PGS_{red}	Norris d2g25	0.55	0.31	-1.E-08	0.53	0.32	1.E-03
PGS_{red}	Norris d2g33	0.66	0.27	-2.E-08	0.60	0.30	1.E-03
PGS_{red}	SaGo d1s3	0.73	0.24	6.E-09	0.60	0.30	-8.E-03
PGS_{red}	SaGo d1s5	0.73	0.24	-2.E-08	0.59	0.30	4.E-03
PGS_{red}	SaGo d1s9	0.58	0.30	-2.E-08	0.53	0.32	3.E-03
PGS_{red}	SaGo d1s13	0.61	0.29	-3.E-08	0.55	0.31	2.E-03
PGS_{red}	SaGo d1s17	0.58	0.30	-3.E-08	0.54	0.32	4.E-03
PGS_{red}	SaGo d1s25	0.70	0.25	-6.E-08	0.59	0.30	4.E-04
PGS_{red}	SaGo d1s33	0.69	0.26	3.E-08	0.60	0.29	-5.E-03
PGS_{red}	SaGo d1s41	0.52	0.32	-2.E-08	0.50	0.33	-1.E-05
PGS_{red}	SaGo d2s3	0.66	0.27	2.E-07	0.46	0.34	1.E-02
PGS_{red}	SaGo d2s5	0.69	0.26	-9.E-08	0.52	0.32	8.E-03
PGS_{red}	SaGo d2s9	0.71	0.25	-6.E-08	0.58	0.30	5.E-03
PGS_{red}	SaGo d2s13	0.73	0.24	-6.E-08	0.55	0.31	4.E-03
PGS_{red}	SaGo d2s17	0.72	0.25	-2.E-08	0.56	0.31	2.E-03
PGS_{red}	SaGo d2s25	0.64	0.28	-2.E-08	0.57	0.31	5.E-03
PGS_{red}	SaGo d2s33	0.69	0.26	-4.E-08	0.62	0.29	-1.E-03
PGS_{red}	SaGo d2s41	0.70	0.25	-3.E-08	0.59	0.30	-2.E-03
PGS_{red}	SaGo d2s45	0.67	0.27	-9.E-09	0.58	0.30	3.E-04
PGS_{red}	Base + SNV	0.57	0.31	-2.E-08	0.49	0.33	9.E-04
PGS_{red}	Base + Norris d1g3	0.58	0.30	-2.E-08	0.50	0.33	3.E-03
PGS_{red}	Base + Norris d2g41	0.69	0.26	9.E-08	0.61	0.29	-4.E-03
PGS_{red}	Base + SaGo d1s3	0.73	0.24	2.E-08	0.60	0.29	7.E-06
PGS_{red}	Base + SaGo d2s33	0.69	0.26	-3.E-08	0.60	0.30	2.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XII:Calibrations and cross validations for Nup_{MAT} within N1 with spectral data before flowering

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.72	0.18	2.E-07	0.63	0.21	-1.E-03
MMS1	SNV	0.63	0.21	2.E-07	0.57	0.23	8.E-04
MMS1	Norris d1g3	0.63	0.21	-3.E-08	0.60	0.22	9.E-04
MMS1	Norris d1g5	0.64	0.21	-4.E-08	0.59	0.23	2.E-03
MMS1	Norris d1g9	0.71	0.19	-4.E-08	0.62	0.22	2.E-03
MMS1	Norris d1g13	0.71	0.19	-7.E-08	0.62	0.22	2.E-03
MMS1	Norris d1g17	0.69	0.20	-6.E-10	0.62	0.22	-2.E-04
MMS1	Norris d1g25	0.68	0.20	-2.E-08	0.61	0.22	2.E-03
MMS1	Norris d1g33	0.72	0.19	-1.E-07	0.64	0.21	3.E-03
MMS1	Norris d2g3	0.67	0.20	-3.E-08	0.58	0.23	-4.E-03
MMS1	Norris d2g5	0.66	0.21	-4.E-08	0.59	0.23	-8.E-05
MMS1	Norris d2g9	0.64	0.21	-5.E-08	0.58	0.23	-1.E-03
MMS1	Norris d2g13	0.65	0.20	-5.E-08	0.58	0.23	-7.E-04
MMS1	Norris d2g17	0.71	0.19	-4.E-08	0.64	0.21	-2.E-03
MMS1	SaGo d1s3	0.63	0.21	-4.E-08	0.60	0.22	1.E-03
MMS1	SaGo d1s5	0.63	0.21	-3.E-08	0.59	0.23	2.E-03
MMS1	SaGo d1s9	0.61	0.22	-2.E-08	0.58	0.23	3.E-04
MMS1	SaGo d1s13	0.71	0.19	-2.E-08	0.64	0.21	3.E-03
MMS1	SaGo d1s17	0.68	0.20	-5.E-08	0.59	0.22	3.E-03
MMS1	SaGo d1s25	0.65	0.21	-1.E-08	0.60	0.22	-4.E-03
MMS1	SaGo d1s33	0.64	0.21	-5.E-08	0.58	0.23	4.E-04
MMS1	SaGo d1s41	0.64	0.21	-5.E-08	0.57	0.23	-1.E-03
MMS1	SaGo d2s3	0.58	0.23	-4.E-08	0.49	0.25	6.E-04
MMS1	SaGo d2s5	0.59	0.22	-3.E-08	0.52	0.24	-2.E-03
MMS1	SaGo d2s9	0.67	0.20	-3.E-08	0.59	0.22	-9.E-04
MMS1	SaGo d2s13	0.67	0.20	-3.E-08	0.60	0.22	1.E-03
MMS1	SaGo d2s17	0.66	0.20	-3.E-08	0.59	0.23	-1.E-03
MMS1	Base + Norris d1g33	0.64	0.21	-4.E-08	0.58	0.23	-2.E-03
MMS1	Base + Norris d1g41	0.71	0.19	-6.E-08	0.62	0.22	-3.E-03
PGS_{red}	Base	0.60	0.22	3.E-08	0.55	0.24	-9.E-04
PGS_{red}	SNV	0.55	0.23	-2.E-08	0.51	0.25	1.E-04

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XII (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	Norris d1g3	0.63	0.21	-4.E-08	0.53	0.24	9.E-04
PGS_{red}	Norris d1g5	0.64	0.21	-3.E-08	0.53	0.24	-1.E-03
PGS_{red}	Norris d1g9	0.52	0.24	-3.E-08	0.50	0.25	-6.E-04
PGS_{red}	Norris d1g13	0.63	0.21	-4.E-08	0.55	0.24	1.E-04
PGS_{red}	Norris d1g17	0.58	0.23	-3.E-08	0.54	0.24	2.E-03
PGS_{red}	Norris d1g19	0.58	0.23	-4.E-08	0.53	0.24	2.E-04
PGS_{red}	Norris d1g21	0.58	0.23	-4.E-08	0.53	0.24	1.E-03
PGS_{red}	Norris d1g23	0.58	0.23	-5.E-08	0.53	0.24	-2.E-03
PGS_{red}	Norris d1g25	0.58	0.23	-4.E-08	0.55	0.24	-5.E-04
PGS_{red}	Norris d1g41	0.57	0.23	4.E-08	0.53	0.24	3.E-04
PGS_{red}	Norris d2g3	0.55	0.23	-4.E-08	0.48	0.25	-3.E-03
PGS_{red}	SaGo d1s3	0.61	0.22	-4.E-08	0.51	0.25	8.E-04
PGS_{red}	SaGo d1s5	0.63	0.21	3.E-08	0.53	0.24	4.E-04
PGS_{red}	SaGo d1s9	0.64	0.21	-4.E-08	0.53	0.24	-3.E-07
PGS_{red}	SaGo d1s13	0.52	0.24	-3.E-08	0.49	0.25	2.E-04
PGS_{red}	SaGo d1s17	0.55	0.23	-2.E-08	0.51	0.25	-3.E-04
PGS_{red}	SaGo d1s25	0.56	0.23	-3.E-08	0.53	0.24	3.E-03
PGS_{red}	SaGo d1s33	0.57	0.23	5.E-08	0.53	0.24	2.E-04
PGS_{red}	SaGo d1s41	0.66	0.21	-2.E-08	0.56	0.23	-5.E-03
PGS_{red}	SaGo d1s43	0.55	0.24	-5.E-08	0.50	0.25	2.E-03
PGS_{red}	SaGo d1s45	0.54	0.24	-5.E-08	0.50	0.25	1.E-03
PGS_{red}	SaGo d1s51	0.55	0.24	-4.E-08	0.52	0.25	1.E-03
PGS_{red}	SaGo d2s3	0.61	0.22	-7.E-08	0.50	0.25	4.E-03
PGS_{red}	PGS Base + Norris d1g33	0.57	0.23	-4.E-08	0.52	0.24	-7.E-04

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XIII: Calibrations and cross validations within N1 with spectral data during fruit development

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.62	0.21	8.E-07	0.47	0.25	-2.E-03
MMS1	SNV	0.61	0.21	4.E-08	0.46	0.25	5.E-04
MMS1	Norris d1g3	0.56	0.23	-5.E-08	0.46	0.25	2.E-04
MMS1	Norris d1g5	0.56	0.23	-3.E-08	0.47	0.25	-9.E-04
MMS1	Norris d1g9	0.58	0.22	-7.E-08	0.46	0.25	-1.E-03
MMS1	Norris d1g13	0.62	0.21	1.E-08	0.47	0.25	-6.E-03
MMS1	Norris d1g17	0.63	0.21	2.E-08	0.47	0.25	2.E-03
MMS1	Norris d1g25	0.64	0.20	-2.E-07	0.50	0.24	-8.E-04
MMS1	Norris d1g33	0.62	0.21	3.E-08	0.49	0.24	8.E-04
MMS1	Norris d1g41	0.64	0.20	2.E-08	0.47	0.25	-7.E-04
MMS1	Norris d1g45	0.56	0.23	3.E-08	0.39	0.27	9.E-03
MMS1	Norris d1g49	0.62	0.21	-1.E-07	0.45	0.25	-2.E-03
MMS1	Norris d1g57	0.60	0.22	-4.E-08	0.44	0.26	-1.E-04
MMS1	Norris d2g3	0.51	0.24	-5.E-08	0.45	0.26	-3.E-04
MMS1	Norris d2g5	0.57	0.22	3.E-08	0.48	0.25	5.E-04
MMS1	Norris d2g13	0.60	0.22	-3.E-08	0.46	0.25	3.E-03
MMS1	Norris d2g17	0.59	0.22	-4.E-09	0.45	0.26	1.E-03
MMS1	Norris d2g25	0.64	0.21	-2.E-10	0.48	0.25	6.E-03
MMS1	Norris d2g33	0.50	0.24	-5.E-08	0.43	0.26	-4.E-03
MMS1	Norris d2g41	0.61	0.21	2.E-09	0.47	0.25	6.E-03
MMS1	SaGo d1s3	0.56	0.23	-5.E-08	0.44	0.26	3.E-03
MMS1	SaGo d1s5	0.51	0.24	-5.E-08	0.43	0.26	3.E-03
MMS1	SaGo d1s9	0.59	0.22	-2.E-08	0.47	0.25	2.E-03
MMS1	SaGo d1s13	0.60	0.22	-9.E-08	0.46	0.25	4.E-03
MMS1	SaGo d1s17	0.62	0.21	0.E+00	0.47	0.25	4.E-03
MMS1	SaGo d1s25	0.63	0.21	2.E-08	0.50	0.24	-3.E-03
MMS1	SaGo d1s41	0.62	0.21	-7.E-08	0.50	0.24	-3.E-03
MMS1	SaGo d2s3	0.50	0.24	-4.E-08	0.43	0.26	5.E-05
MMS1	SaGo d2s5	0.51	0.24	-4.E-08	0.44	0.26	-2.E-03
MMS1	SaGo d2s9	0.57	0.23	-3.E-08	0.46	0.25	8.E-04
MMS1	SaGo d2s13	0.56	0.23	-4.E-08	0.45	0.26	-3.E-03
MMS1	SaGo d2s17	0.57	0.22	-4.E-08	0.47	0.25	8.E-04
MMS1	Base + SNV	0.61	0.21	-5.E-07	0.46	0.25	-4.E-03
MMS1	Base + Norris d2g9	0.58	0.22	-4.E-08	0.44	0.26	-8.E-05
MMS1	Base + SaGo d1s33	0.52	0.24	-8.E-08	0.39	0.27	5.E-04

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

XIII (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	Base	0.54	0.23	2.E-07	0.39	0.27	-3.E-03
PGS_{red}	SNV	0.61	0.21	2.E-07	0.44	0.26	-3.E-03
PGS_{red}	Norris d1g3	0.53	0.23	-5.E-08	0.39	0.27	3.E-04
PGS_{red}	Norris d1g5	0.52	0.24	-5.E-08	0.41	0.26	2.E-03
PGS_{red}	Norris d1g9	0.54	0.23	-4.E-08	0.40	0.27	2.E-03
PGS_{red}	Norris d1g13	0.50	0.24	-7.E-08	0.41	0.27	-1.E-03
PGS_{red}	Norris d1g17	0.57	0.22	-5.E-08	0.45	0.26	4.E-03
PGS_{red}	Norris d1g25	0.60	0.22	-8.E-08	0.43	0.26	4.E-03
PGS_{red}	Norris d1g33	0.59	0.22	-1.E-07	0.41	0.26	4.E-03
PGS_{red}	Norris d1g41	0.60	0.22	-9.E-08	0.43	0.26	2.E-03
PGS_{red}	Norris d2g3	0.49	0.24	-4.E-08	0.37	0.27	-8.E-04
PGS_{red}	Norris d2g5	0.50	0.24	-4.E-08	0.42	0.26	-2.E-03
PGS_{red}	Norris d2g9	0.55	0.23	-4.E-08	0.40	0.27	2.E-03
PGS_{red}	Norris d2g13	0.49	0.24	-4.E-08	0.39	0.27	-1.E-03
PGS_{red}	Norris d2g17	0.54	0.23	-4.E-08	0.40	0.27	-2.E-03
PGS_{red}	Norris d2g25	0.53	0.23	-3.E-08	0.41	0.27	2.E-03
PGS_{red}	Norris d2g33	0.52	0.24	-8.E-08	0.38	0.27	2.E-03
PGS_{red}	Norris d2g41	0.59	0.22	-1.E-07	0.45	0.26	9.E-04
PGS_{red}	SaGo d1s3	0.54	0.23	-3.E-08	0.42	0.26	-1.E-03
PGS_{red}	SaGo d1s5	0.53	0.23	-5.E-08	0.41	0.26	-3.E-03
PGS_{red}	SaGo d1s9	0.51	0.24	-4.E-08	0.43	0.26	1.E-03
PGS_{red}	SaGo d1s13	0.51	0.24	-3.E-08	0.38	0.27	-3.E-03
PGS_{red}	SaGo d1s17	0.48	0.25	-2.E-08	0.36	0.28	3.E-03
PGS_{red}	SaGo d1s25	0.59	0.22	-3.E-09	0.43	0.26	2.E-03
PGS_{red}	SaGo d1s33	0.63	0.21	-6.E-08	0.42	0.26	3.E-03
PGS_{red}	SaGo d1s41	0.57	0.23	-7.E-08	0.40	0.27	4.E-03
PGS_{red}	SaGo d2s3	0.47	0.25	2.E-08	0.38	0.27	-4.E-04
PGS_{red}	SaGo d2s5	0.48	0.25	-2.E-08	0.36	0.28	3.E-03
PGS_{red}	SaGo d2s9	0.49	0.24	-5.E-08	0.37	0.27	-1.E-03
PGS_{red}	SaGo d2s13	0.49	0.24	-5.E-08	0.39	0.27	-8.E-04
PGS_{red}	SaGo d2s17	0.56	0.23	-4.E-08	0.42	0.26	2.E-03
PGS_{red}	SaGo d2s25	0.55	0.23	-5.E-08	0.41	0.26	-3.E-03
PGS_{red}	SaGo d2s33	0.57	0.23	-3.E-08	0.42	0.26	1.E-03
PGS_{red}	SaGo d2s45	0.57	0.22	-1.E-08	0.42	0.26	-3.E-03
PGS_{red}	Base + SNV	0.56	0.23	4.E-08	0.40	0.27	-1.E-03
PGS_{red}	Base + Norris d1g25	0.60	0.22	-6.E-08	0.40	0.27	1.E-03
PGS_{red}	Base + SaGo d2s41	0.61	0.21	-5.E-08	0.44	0.26	-1.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XIV: Calibrations and cross validations for Nup_{MAT} within N0 with spectral data during fruit development

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.80	0.13	-3.E-08	0.77	0.14	1.E-03
MMS1	SNV	0.80	0.13	1.E-07	0.77	0.14	-7.E-04
MMS1	Norris d1g3	0.80	0.13	-1.E-08	0.79	0.13	6.E-04
MMS1	Norris d1g5	0.80	0.13	-1.E-08	0.77	0.14	2.E-03
MMS1	Norris d1g9	0.81	0.12	-5.E-08	0.78	0.14	5.E-03
MMS1	Norris d1g17	0.82	0.12	-3.E-08	0.79	0.13	2.E-03
MMS1	Norris d1g25	0.82	0.12	-2.E-08	0.79	0.13	2.E-03
MMS1	Norris d1g33	0.81	0.12	-3.E-08	0.77	0.14	-2.E-04
MMS1	Norris d1g41	0.82	0.12	-3.E-08	0.78	0.13	3.E-03
MMS1	Norris d2g3	0.79	0.13	-1.E-08	0.76	0.14	5.E-04
MMS1	Norris d2g5	0.79	0.13	-2.E-08	0.77	0.14	-6.E-04
MMS1	Norris d2g9	0.80	0.13	-1.E-08	0.77	0.14	-2.E-05
MMS1	Norris d2g13	0.80	0.13	-2.E-08	0.78	0.13	2.E-04
MMS1	Norris d2g17	0.82	0.12	-1.E-08	0.79	0.13	4.E-03
MMS1	SaGo d1s3	0.82	0.12	-1.E-08	0.78	0.14	-3.E-04
MMS1	SaGo d1s5	0.81	0.13	-3.E-08	0.78	0.14	1.E-03
MMS1	SaGo d1s9	0.80	0.13	-2.E-08	0.78	0.14	4.E-04
MMS1	SaGo d1s13	0.81	0.12	-3.E-08	0.78	0.13	-5.E-04
MMS1	SaGo d1s17	0.82	0.12	-8.E-09	0.78	0.13	1.E-03
MMS1	SaGo d1s25	0.82	0.12	-3.E-08	0.79	0.13	1.E-03
MMS1	SaGo d1s33	0.79	0.13	-4.E-08	0.77	0.14	7.E-04
MMS1	SaGo d1s41	0.79	0.13	-9.E-10	0.76	0.14	8.E-04
MMS1	SaGo d2s3	0.74	0.15	-2.E-08	0.70	0.16	-1.E-03
MMS1	SaGo d2s5	0.78	0.13	-2.E-08	0.75	0.14	1.E-03
MMS1	SaGo d2s9	0.79	0.13	-1.E-08	0.76	0.14	8.E-04
MMS1	SaGo d2s13	0.79	0.13	2.E-08	0.77	0.14	-1.E-03
MMS1	SaGo d2s17	0.81	0.13	-2.E-08	0.79	0.13	-8.E-04
MMS1	Base + Norris d1g13	0.81	0.12	-3.E-08	0.79	0.13	2.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XIV (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	Base	0.74	0.14	-3.E-08	0.69	0.16	-1.E-03
PGS_{red}	SNV	0.75	0.14	-3.E-08	0.70	0.16	-1.E-03
PGS_{red}	Norris d1g3	0.72	0.15	-2.E-08	0.66	0.17	-5.E-03
PGS_{red}	Norris d1g5	0.71	0.15	-2.E-08	0.67	0.17	-3.E-03
PGS_{red}	Norris d1g9	0.73	0.15	-2.E-08	0.70	0.16	-4.E-03
PGS_{red}	Norris d1g13	0.72	0.15	-3.E-08	0.70	0.16	-1.E-03
PGS_{red}	Norris d1g17	0.72	0.15	-1.E-08	0.69	0.16	-2.E-03
PGS_{red}	Norris d1g19	0.73	0.15	-2.E-08	0.70	0.16	-8.E-04
PGS_{red}	Norris d1g21	0.73	0.15	-2.E-08	0.69	0.16	-6.E-04
PGS_{red}	Norris d1g23	0.72	0.15	-2.E-08	0.67	0.16	-1.E-03
PGS_{red}	Norris d1g25	0.72	0.15	-2.E-08	0.68	0.16	-1.E-03
PGS_{red}	Norris d1g33	0.71	0.15	-3.E-08	0.69	0.16	-1.E-03
PGS_{red}	Norris d1g41	0.73	0.15	-1.E-08	0.69	0.16	1.E-03
PGS_{red}	Norris d2g3	0.68	0.16	-2.E-08	0.57	0.19	1.E-03
PGS_{red}	SaGo d1s3	0.73	0.15	-4.E-08	0.66	0.17	-1.E-03
PGS_{red}	SaGo d1s5	0.69	0.16	3.E-08	0.65	0.17	-2.E-03
PGS_{red}	SaGo d1s9	0.72	0.15	-2.E-08	0.69	0.16	-2.E-03
PGS_{red}	SaGo d1s13	0.73	0.15	-2.E-08	0.70	0.16	-2.E-03
PGS_{red}	SaGo d1s17	0.73	0.15	-3.E-08	0.71	0.16	-2.E-03
PGS_{red}	SaGo d1s25	0.74	0.15	-1.E-08	0.71	0.15	-2.E-03
PGS_{red}	SaGo d1s41	0.77	0.14	-3.E-08	0.71	0.16	-3.E-03
PGS_{red}	SaGo d1s43	0.76	0.14	-1.E-08	0.70	0.16	-4.E-03
PGS_{red}	SaGo d1s45	0.75	0.14	-2.E-08	0.70	0.16	-1.E-03
PGS_{red}	SaGo d1s51	0.74	0.15	-2.E-08	0.69	0.16	-3.E-03
PGS_{red}	SaGo d2s3	0.74	0.14	-2.E-08	0.62	0.18	-2.E-03
PGS_{red}	Base + SaGo d1s33	0.77	0.14	-6.E-09	0.71	0.15	-2.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XV: Calibrations and cross validations for Nup_{MAT} within N0 with spectral data during fruit development

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.77	0.14	-5.E-08	0.74	0.15	-8.E-04
MMS1	SNV	0.76	0.14	7.E-08	0.73	0.15	7.E-04
MMS1	Norris d1g3	0.81	0.13	2.E-07	0.76	0.14	3.E-03
MMS1	Norris d1g5	0.80	0.13	2.E-07	0.76	0.14	1.E-03
MMS1	Norris d1g13	0.79	0.13	9.E-09	0.74	0.15	6.E-05
MMS1	Norris d1g15	0.81	0.13	-9.E-09	0.76	0.14	-4.E-04
MMS1	Norris d1g19	0.78	0.14	-6.E-09	0.74	0.15	2.E-03
MMS1	Norris d1g29	0.79	0.13	-1.E-08	0.74	0.15	-7.E-05
MMS1	Norris d1g39	0.76	0.14	2.E-07	0.73	0.15	4.E-04
MMS1	Norris d2g3	0.77	0.14	1.E-07	0.74	0.15	3.E-03
MMS1	SaGo d1s3	0.78	0.14	2.E-08	0.74	0.15	3.E-04
MMS1	SaGo d1s5	0.78	0.14	2.E-07	0.73	0.15	1.E-03
MMS1	SaGo d1s7	0.81	0.13	1.E-07	0.76	0.14	-4.E-03
MMS1	SaGo d1s9	0.81	0.13	8.E-09	0.76	0.14	2.E-03
MMS1	SaGo d1s13	0.81	0.13	1.E-07	0.75	0.15	1.E-03
MMS1	SaGo d1s19	0.78	0.13	2.E-07	0.75	0.14	-9.E-04
MMS1	SaGo d1s29	0.77	0.14	2.E-07	0.75	0.15	8.E-04
MMS1	SaGo d1s39	0.76	0.14	1.E-07	0.73	0.15	4.E-04
MMS1	SaGo d2s3	0.76	0.14	2.E-07	0.69	0.16	2.E-03
MMS1	Base + Norris d1g3	0.77	0.14	1.E-07	0.73	0.15	3.E-03
MMS1	Base + SaGo d1s9	0.81	0.13	-1.E-07	0.75	0.15	2.E-03
PGS_{red}	Base	0.75	0.15	5.E-08	0.71	0.16	-3.E-03
PGS_{red}	SNV	0.71	0.16	8.E-09	0.68	0.16	1.E-03
PGS_{red}	Norris d1g3	0.79	0.13	7.E-09	0.64	0.17	3.E-04
PGS_{red}	Norris d1g5	0.79	0.13	2.E-07	0.66	0.17	4.E-03
PGS_{red}	Norris d1g7	0.72	0.15	2.E-07	0.68	0.16	5.E-03
PGS_{red}	Norris d1g9	0.71	0.16	2.E-07	0.67	0.17	3.E-03
PGS_{red}	Norris d1g13	0.74	0.15	2.E-07	0.68	0.16	5.E-03
PGS_{red}	Norris d1g15	0.71	0.15	6.E-09	0.68	0.17	1.E-03
PGS_{red}	Norris d1g19	0.71	0.16	2.E-07	0.67	0.17	9.E-04
PGS_{red}	Norris d1g29	0.79	0.13	2.E-08	0.65	0.17	1.E-03
PGS_{red}	Norris d1g39	0.77	0.14	2.E-08	0.71	0.16	-1.E-03
PGS_{red}	Norris d1g33	0.72	0.15	2.E-07	0.67	0.17	2.E-03
PGS_{red}	Norris d1g35	0.72	0.15	9.E-09	0.69	0.16	2.E-03
PGS_{red}	Norris d1g41	0.80	0.13	-7.E-10	0.72	0.15	-2.E-03
PGS_{red}	Norris d1g45	0.74	0.15	8.E-09	0.69	0.16	2.E-03
PGS_{red}	Norris d2g3	0.43	0.22	1.E-07	0.39	0.23	6.E-04

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XV (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	SaGo d1s3	0.79	0.13	2.E-08	0.62	0.18	2.E-03
PGS_{red}	SaGo d1s5	0.78	0.14	3.E-07	0.61	0.18	5.E-03
PGS_{red}	SaGo d1s7	0.79	0.13	9.E-09	0.68	0.17	2.E-03
PGS_{red}	SaGo d1s9	0.75	0.15	1.E-07	0.66	0.17	6.E-03
PGS_{red}	SaGo d1s13	0.75	0.14	2.E-07	0.69	0.16	4.E-03
PGS_{red}	SaGo d1s19	0.75	0.15	3.E-07	0.68	0.17	2.E-03
PGS_{red}	SaGo d1s29	0.78	0.13	6.E-09	0.71	0.16	-7.E-04
PGS_{red}	SaGo d1s39	0.78	0.13	2.E-07	0.72	0.15	3.E-03
PGS_{red}	SaGo d1s41	0.78	0.13	6.E-09	0.71	0.15	-9.E-04
PGS_{red}	SaGo d1s51	0.76	0.14	8.E-09	0.70	0.16	-1.E-03
PGS_{red}	SaGo d2s3	0.37	0.23	3.E-07	0.36	0.23	3.E-03
PGS_{red}	Base + SaGo d1s39	0.78	0.13	2.E-07	0.71	0.16	1.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XVI: Calibrations and cross validations for Seed DM across N levels with spectral data before flowering

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.55	6.10	2.E-07	0.52	6.31	5.E-02
MMS1	SNV	0.53	6.23	-1.E-06	0.50	6.47	6.E-02
MMS1	Norris d1g3	0.56	6.04	8.E-07	0.54	6.23	2.E-02
MMS1	Norris d1g5	0.55	6.12	3.E-07	0.52	6.35	4.E-02
MMS1	Norris d1g7	0.57	6.01	-2.E-07	0.53	6.28	4.E-02
MMS1	Norris d1g9	0.57	5.96	6.E-07	0.54	6.22	2.E-02
MMS1	Norris d1g11	0.57	6.02	8.E-07	0.53	6.28	3.E-02
MMS1	Norris d1g13	0.58	5.89	-8.E-07	0.53	6.25	2.E-02
MMS1	Norris d1g15	0.57	6.01	8.E-07	0.54	6.22	-1.E-03
MMS1	Norris d1g17	0.51	6.38	4.E-07	0.49	6.56	-3.E-02
MMS1	Norris d1g25	0.56	6.08	3.E-07	0.52	6.32	-6.E-03
MMS1	Norris d1g41	0.55	6.12	-9.E-08	0.52	6.32	-7.E-03
MMS1	Norris d2g3	0.53	6.27	4.E-07	0.50	6.46	4.E-02
MMS1	Norris d2g9	0.58	5.95	6.E-07	0.53	6.26	2.E-02
MMS1	Norris d2g17	0.56	6.04	6.E-07	0.53	6.30	-2.E-02
MMS1	Norris d2g25	0.57	6.01	2.E-06	0.54	6.20	-1.E-02
MMS1	Norris d2g37	0.57	6.01	2.E-06	0.53	6.29	2.E-02
MMS1	Norris d2g39	0.60	5.77	2.E-06	0.56	6.09	-2.E-02
MMS1	Norris d2g41	0.60	5.77	-9.E-07	0.56	6.09	-2.E-02
MMS1	Norris d2g43	0.57	6.02	8.E-07	0.53	6.26	7.E-03
MMS1	SaGo d1s3	0.53	6.24	4.E-07	0.50	6.50	4.E-03
MMS1	SaGo d1s9	0.57	5.99	1.E-06	0.52	6.33	4.E-02
MMS1	SaGo d1s17	0.56	6.03	5.E-07	0.53	6.26	2.E-02
MMS1	SaGo d1s23	0.56	6.05	1.E-06	0.53	6.25	-1.E-02
MMS1	SaGo d1s29	0.64	5.52	-1.E-07	0.58	5.97	6.E-02
MMS1	SaGo d1s41	0.58	5.94	2.E-07	0.55	6.13	1.E-02
MMS1	SaGo d2s3	0.54	6.23	6.E-07	0.48	6.61	7.E-02
MMS1	SaGo d2s9	0.53	6.25	6.E-07	0.50	6.49	4.E-02
MMS1	SaGo d2s17	0.54	6.17	5.E-07	0.51	6.38	3.E-02
MMS1	SaGo d2s19	0.57	6.01	1.E-06	0.54	6.20	2.E-02
MMS1	SaGo d2s21	0.57	6.01	5.E-07	0.54	6.24	-1.E-02
MMS1	SaGo d2s23	0.57	6.01	4.E-07	0.53	6.25	-8.E-04
MMS1	SaGo d2s25	0.57	6.01	6.E-07	0.54	6.23	-2.E-03
MMS1	SaGo d2s27	0.61	5.71	7.E-07	0.56	6.06	-4.E-02
MMS1	SaGo d2s29	0.60	5.76	3.E-08	0.56	6.06	-4.E-02
MMS1	SaGo d2s31	0.60	5.79	7.E-07	0.56	6.05	-5.E-02
MMS1	SaGo d2s33	0.59	5.82	-1.E-07	0.56	6.09	-2.E-02
MMS1	SaGo d2s41	0.56	6.08	-3.E-07	0.53	6.24	2.E-02

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XVI (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base + SNV	0.55	6.14	-7.E-07	0.51	6.43	-2.E-02
MMS1	Base + Norris d1g9	0.57	5.96	5.E-07	0.53	6.27	5.E-04
MMS1	Base + Norris d1g13	0.56	6.03	-6.E-07	0.53	6.29	-4.E-03
MMS1	Base + Norris d1g15	0.57	6.01	1.E-06	0.53	6.28	2.E-02
MMS1	Base + Norris d2g39	0.60	5.77	1.E-06	0.55	6.13	-4.E-03
MMS1	Base + Norris d2g41	0.60	5.77	-2.E-08	0.56	6.11	2.E-02
MMS1	Base + SaGo d1s25	0.56	6.08	1.E-07	0.54	6.20	-1.E-02
MMS1	Base + SaGo d1s27	0.64	5.48	-2.E-06	0.57	5.98	4.E-02
MMS1	Base + SaGo d2s27	0.61	5.71	-2.E-07	0.56	6.08	8.E-03
MMS1	Base + SaGo d2s29	0.60	5.76	2.E-07	0.56	6.09	2.E-02
PGS_{red}	Base	0.51	6.41	4.E-07	0.46	6.72	2.E-02
PGS_{red}	SNV	0.48	6.61	5.E-07	0.44	6.87	-1.E-02
PGS_{red}	Norris d1g3	0.43	6.88	5.E-07	0.37	7.28	5.E-03
PGS_{red}	Norris d1g9	0.49	6.53	6.E-07	0.42	7.00	2.E-02
PGS_{red}	Norris d1g17	0.49	6.54	4.E-07	0.45	6.79	1.E-02
PGS_{red}	Norris d1g25	0.48	6.56	3.E-07	0.44	6.86	9.E-03
PGS_{red}	Norris d1g37	0.51	6.36	4.E-07	0.45	6.83	7.E-03
PGS_{red}	Norris d1g39	0.52	6.35	4.E-07	0.45	6.81	-1.E-02
PGS_{red}	Norris d1g41	0.52	6.34	7.E-07	0.45	6.79	2.E-02
PGS_{red}	Norris d1g43	0.52	6.35	6.E-07	0.45	6.78	-1.E-02
PGS_{red}	Norris d1g45	0.49	6.50	6.E-07	0.44	6.83	2.E-02
PGS_{red}	Norris d2g3	0.42	6.97	6.E-07	0.34	7.48	-2.E-02
PGS_{red}	Norris d2g9	0.41	7.02	2.E-07	0.35	7.39	-6.E-02
PGS_{red}	Norris d2g17	0.47	6.64	3.E-07	0.42	7.00	7.E-04
PGS_{red}	Norris d2g21	0.49	6.52	4.E-07	0.44	6.87	-6.E-03
PGS_{red}	Norris d2g23	0.51	6.42	8.E-07	0.44	6.83	6.E-03
PGS_{red}	Norris d2g25	0.49	6.55	6.E-07	0.41	7.06	-5.E-02
PGS_{red}	Norris d2g27	0.49	6.50	3.E-07	0.43	6.93	4.E-02
PGS_{red}	Norris d2g41	0.47	6.67	5.E-07	0.42	7.00	8.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XVI (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	SaGo d1s3	0.46	6.74	2.E-07	0.38	7.22	-6.E-02
PGS_{red}	SaGo d1s9	0.45	6.77	6.E-07	0.39	7.14	-3.E-02
PGS_{red}	SaGo d1s17	0.46	6.70	2.E-07	0.41	7.04	-3.E-02
PGS_{red}	SaGo d1s25	0.47	6.65	4.E-07	0.44	6.87	-8.E-03
PGS_{red}	SaGo d1s37	0.48	6.58	2.E-08	0.44	6.88	-5.E-02
PGS_{red}	SaGo d1s39	0.48	6.60	5.E-07	0.44	6.84	1.E-02
PGS_{red}	SaGo d1s41	0.48	6.62	7.E-07	0.43	6.88	-1.E-02
PGS_{red}	SaGo d1s43	0.50	6.48	4.E-07	0.45	6.81	8.E-03
PGS_{red}	SaGo d1s45	0.50	6.48	9.E-07	0.44	6.82	1.E-02
PGS_{red}	SaGo d1s47	0.50	6.48	3.E-07	0.44	6.84	5.E-02
PGS_{red}	SaGo d1s49	0.50	6.48	5.E-07	0.45	6.81	1.E-02
PGS_{red}	SaGo d1s51	0.49	6.49	4.E-07	0.45	6.82	-2.E-02
PGS_{red}	SaGo d2s3	0.42	6.94	1.E-06	0.35	7.41	-2.E-02
PGS_{red}	SaGo d2s9	0.42	6.97	8.E-07	0.34	7.47	-4.E-03
PGS_{red}	SaGo d2s17	0.41	7.04	5.E-07	0.35	7.36	-2.E-03
PGS_{red}	SaGo d2s25	0.40	7.07	3.E-07	0.35	7.36	6.E-02
PGS_{red}	SaGo d2s37	0.47	6.63	5.E-07	0.41	7.05	-3.E-02
PGS_{red}	SaGo d2s39	0.49	6.52	5.E-07	0.42	7.01	8.E-03
PGS_{red}	SaGo d2s41	0.48	6.56	6.E-07	0.42	6.96	5.E-02
PGS_{red}	SaGo d2s43	0.45	6.77	6.E-07	0.41	7.02	3.E-02
PGS_{red}	Base + SNV	0.48	6.61	2.E-07	0.43	6.91	8.E-04
PGS_{red}	Base + Norris d1g41	0.52	6.34	6.E-07	0.45	6.82	1.E-03
PGS_{red}	Base + Norris d1g43	0.49	6.53	6.E-07	0.44	6.85	-1.E-02
PGS_{red}	Base + Norris d2g23	0.53	6.29	7.E-07	0.44	6.89	-2.E-02
PGS_{red}	Base + SaGo d1s43	0.50	6.48	8.E-07	0.44	6.83	4.E-02
PGS_{red}	Base + SaGo d1s49	0.50	6.48	2.E-07	0.44	6.83	1.E-02
PGS_{red}	Base + SaGo d2s39	0.49	6.52	4.E-07	0.42	6.97	-3.E-02
PGS_{red}	Base + SaGo d2s41	0.48	6.56	5.E-07	0.42	6.98	-3.E-02

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XVII: Calibrations and cross validations for Seed DM across N levels with spectral data during fruit development

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.53	6.27	-5.E-07	0.51	6.39	-1.E-02
MMS1	SNV	0.53	6.24	-5.E-07	0.50	6.48	3.E-02
MMS1	Norris d1g3	0.59	5.85	3.E-07	0.53	6.25	2.E-02
MMS1	Norris d1g5	0.60	5.79	8.E-07	0.54	6.18	5.E-02
MMS1	Norris d1g7	0.59	5.83	1.E-06	0.55	6.17	3.E-02
MMS1	Norris d1g9	0.62	5.60	3.E-07	0.57	6.00	3.E-02
MMS1	Norris d1g17	0.60	5.81	1.E-06	0.56	6.11	3.E-04
MMS1	Norris d1g25	0.58	5.90	4.E-07	0.54	6.19	-2.E-02
MMS1	Norris d1g41	0.60	5.79	-5.E-07	0.55	6.16	2.E-03
MMS1	Norris d1g57	0.60	5.80	2.E-06	0.55	6.14	2.E-02
MMS1	Norris d2g3	0.55	6.12	5.E-07	0.49	6.57	-4.E-02
MMS1	Norris d2g9	0.59	5.84	8.E-07	0.53	6.30	6.E-02
MMS1	Norris d2g11	0.59	5.82	4.E-07	0.54	6.23	3.E-02
MMS1	Norris d2g13	0.60	5.75	9.E-07	0.54	6.22	-4.E-02
MMS1	Norris d2g15	0.60	5.80	9.E-07	0.54	6.22	-3.E-02
MMS1	Norris d2g25	0.61	5.69	-7.E-07	0.53	6.25	-2.E-02
MMS1	Norris d2g57	0.61	5.69	-5.E-06	0.55	6.17	6.E-02
MMS1	SaGo d1s3	0.58	5.88	6.E-07	0.53	6.26	1.E-02
MMS1	SaGo d1s5	0.63	5.57	9.E-07	0.57	5.96	-1.E-02
MMS1	SaGo d1s9	0.63	5.59	-1.E-07	0.57	6.02	5.E-03
MMS1	SaGo d1s17	0.61	5.73	-2.E-07	0.57	6.03	-7.E-03
MMS1	SaGo d1s25	0.60	5.81	4.E-07	0.56	6.06	-3.E-02
MMS1	SaGo d1s41	0.58	5.89	7.E-07	0.55	6.15	-4.E-03
MMS1	SaGo d2s3	0.52	6.31	3.E-07	0.46	6.72	-1.E-02
MMS1	SaGo d2s9	0.54	6.17	3.E-07	0.50	6.49	3.E-02
MMS1	SaGo d2s11	0.61	5.73	5.E-07	0.53	6.28	5.E-02
MMS1	SaGo d2s13	0.59	5.85	5.E-07	0.51	6.41	-4.E-02
MMS1	SaGo d2s15	0.58	5.92	3.E-07	0.52	6.37	-1.E-02
MMS1	SaGo d2s17	0.61	5.71	-1.E-07	0.55	6.14	7.E-02
MMS1	SaGo d2s25	0.60	5.75	4.E-07	0.53	6.25	4.E-02
MMS1	SaGo d2s41	0.62	5.60	8.E-07	0.55	6.14	2.E-02
MMS1	SaGo d2s57	0.62	5.65	1.E-06	0.54	6.20	3.E-02

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. VXII (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base + SNV	0.53	6.24	-2.E-06	0.51	6.40	1.E-01
MMS1	Base + Norris d1g9	0.62	5.60	6.E-07	0.58	5.97	-4.E-02
MMS1	Base + Norris d2g17	0.62	5.66	1.E-06	0.54	6.24	-6.E-02
MMS1	Base + Norris d2g41	0.62	5.64	3.E-06	0.54	6.19	2.E-02
MMS1	Base + SaGo d1s7	0.58	5.92	-1.E-09	0.53	6.26	5.E-03
MMS1	Base + SaGo d2s17	0.63	5.55	6.E-07	0.55	6.13	-3.E-02
MMS1	Base + SaGo d2s41	0.58	5.89	9.E-08	0.53	6.30	-9.E-03
PGS_{red}	SNV	0.51	6.38	-4.E-07	0.49	6.53	-7.E-03
PGS_{red}	Norris d1g3	0.43	6.88	4.E-07	0.36	7.30	2.E-01
PGS_{red}	Norris d1g9	0.55	6.14	9.E-07	0.51	6.41	2.E-02
PGS_{red}	Norris d1g17	0.52	6.34	3.E-07	0.50	6.45	2.E-02
PGS_{red}	Norris d1g25	0.53	6.29	3.E-09	0.51	6.44	7.E-02
PGS_{red}	Norris d1g41	0.54	6.19	5.E-07	0.52	6.37	-2.E-02
PGS_{red}	Norris d2g3	0.61	5.70	5.E-07	0.43	6.93	9.E-02
PGS_{red}	Norris d2g5	0.64	5.45	6.E-07	0.51	6.39	3.E-02
PGS_{red}	Norris d2g7	0.64	5.45	6.E-07	0.47	6.64	2.E-02
PGS_{red}	Norris d2g9	0.58	5.95	6.E-07	0.51	6.41	8.E-02
PGS_{red}	Norris d2g17	0.56	6.05	-9.E-07	0.52	6.32	6.E-02
PGS_{red}	Norris d2g25	0.52	6.33	8.E-07	0.50	6.50	4.E-02
PGS_{red}	Norris d2g41	0.54	6.21	6.E-07	0.50	6.47	4.E-02
PGS_{red}	SaGo d1s5	0.59	5.87	5.E-07	0.48	6.58	8.E-02
PGS_{red}	SaGo d1s7	0.59	5.86	5.E-07	0.49	6.51	9.E-02
PGS_{red}	SaGo d1s9	0.54	6.21	4.E-07	0.49	6.54	1.E-01
PGS_{red}	SaGo d1s17	0.54	6.21	6.E-08	0.51	6.42	3.E-02
PGS_{red}	SaGo d1s41	0.51	6.38	4.E-07	0.49	6.53	2.E-02
PGS_{red}	SaGo d2s3	0.58	5.94	3.E-06	0.36	7.33	2.E-01
PGS_{red}	SaGo d2s9	0.61	5.70	2.E-07	0.46	6.71	2.E-01
PGS_{red}	SaGo d2s11	0.62	5.63	2.E-07	0.43	6.89	1.E-01
PGS_{red}	SaGo d2s13	0.64	5.51	2.E-07	0.50	6.45	1.E-01
PGS_{red}	SaGo d2s15	0.64	5.45	8.E-07	0.39	7.15	3.E-01
PGS_{red}	SaGo d2s17	0.64	5.47	8.E-07	0.46	6.72	1.E-01
PGS_{red}	SaGo d2s25	0.58	5.89	5.E-07	0.53	6.26	-8.E-04
PGS_{red}	SaGo d2s41	0.52	6.35	2.E-07	0.49	6.53	4.E-02

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XVIII: Calibrations and cross validations for Seed DM within N1 with spectral data before flowering

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	Base + SNV	0.53	6.25	7.E-07	0.49	6.52	5.E-03
PGS_{red}	Base + Norris d2g5	0.65	5.43	5.E-07	0.50	6.45	8.E-02
PGS_{red}	Base + Norris d2g17	0.56	6.05	7.E-07	0.52	6.38	-3.E-02
PGS_{red}	Base + SaGo d1s3	0.62	5.61	7.E-07	0.51	6.41	2.E-02
PGS_{red}	Base + SaGo d1s25	0.50	6.45	4.E-07	0.48	6.59	-3.E-02
PGS_{red}	Base + SaGo d2s25	0.58	5.89	7.E-07	0.53	6.28	7.E-03
MMS1	Base	0.37	6.83	-1.E-06	0.33	7.12	4.E-03
MMS1	SNV	0.36	6.92	-4.E-07	0.31	7.23	-8.E-03
MMS1	Norris d1g3	0.46	6.36	-1.E-06	0.32	7.14	8.E-02
MMS1	Norris d1g9	0.42	6.57	7.E-07	0.34	7.06	8.E-02
MMS1	Norris d1g15	0.41	6.65	-1.E-06	0.34	7.02	2.E-02
MMS1	Norris d1g17	0.67	4.98	-4.E-06	0.46	6.38	3.E-01
MMS1	Norris d1g19	0.65	5.12	-6.E-07	0.46	6.38	-4.E-02
MMS1	Norris d1g21	0.66	5.04	2.E-06	0.49	6.17	2.E-02
MMS1	Norris d1g25	0.62	5.30	2.E-06	0.45	6.42	1.E-01
MMS1	Norris d1g27	0.69	4.81	2.E-06	0.49	6.16	8.E-02
MMS1	Norris d1g29	0.65	5.11	-2.E-06	0.47	6.37	-7.E-02
MMS1	Norris d1g41	0.51	6.05	-5.E-07	0.41	6.74	9.E-02
MMS1	Norris d2g3	0.45	6.43	-2.E-07	0.30	7.27	1.E-02
MMS1	Norris d2g9	0.61	5.42	-3.E-07	0.42	6.62	-1.E-02
MMS1	Norris d2g15	0.59	5.52	-1.E-06	0.43	6.57	2.E-01
MMS1	Norris d2g17	0.64	5.20	-5.E-07	0.44	6.51	-5.E-02
MMS1	Norris d2g19	0.63	5.27	-3.E-06	0.49	6.18	8.E-04
MMS1	Norris d2g21	0.63	5.23	6.E-07	0.49	6.14	-5.E-03
MMS1	Norris d2g23	0.61	5.39	-2.E-06	0.48	6.26	2.E-01
MMS1	Norris d2g25	0.61	5.42	-8.E-07	0.46	6.36	3.E-02
MMS1	Norris d2g41	0.47	6.29	-9.E-07	0.38	6.84	1.E-02
MMS1	SaGo d1s3	0.43	6.52	-6.E-07	0.35	7.01	8.E-02
MMS1	SaGo d1s9	0.44	6.48	-4.E-07	0.35	6.96	1.E-02
MMS1	SaGo d1s11	0.41	6.66	-4.E-07	0.34	7.05	3.E-03
MMS1	SaGo d1s13	0.64	5.16	7.E-08	0.45	6.47	1.E-01
MMS1	SaGo d1s15	0.64	5.16	-2.E-06	0.47	6.30	1.E-02
MMS1	SaGo d1s17	0.66	5.00	-3.E-07	0.49	6.31	-2.E-02
MMS1	SaGo d1s19	0.64	5.15	-2.E-05	0.49	6.22	2.E-02
MMS1	SaGo d1s21	0.64	5.21	-3.E-06	0.47	6.31	2.E-02
MMS1	SaGo d1s23	0.64	5.22	-4.E-06	0.44	6.50	1.E-01
MMS1	SaGo d1s25	0.64	5.21	-1.E-06	0.48	6.23	4.E-02
MMS1	SaGo d1s41	0.63	5.26	4.E-06	0.51	6.10	3.E-02

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. VXIII (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	SaGo d2s3	0.49	6.16	-2.E-07	0.28	7.37	3.E-02
MMS1	SaGo d2s9	0.48	6.25	-9.E-07	0.32	7.14	1.E-01
MMS1	SaGo d2s17	0.45	6.41	-5.E-07	0.33	7.07	1.E-01
MMS1	SaGo d2s25	0.58	5.61	-8.E-07	0.43	6.59	-1.E-02
MMS1	SaGo d2s35	0.62	5.36	-3.E-06	0.48	6.25	7.E-02
MMS1	SaGo d2s37	0.64	5.20	-3.E-06	0.48	6.25	-5.E-03
MMS1	SaGo d2s39	0.63	5.23	-1.E-06	0.47	6.34	2.E-01
MMS1	SaGo d2s41	0.63	5.23	9.E-07	0.48	6.26	3.E-01
MMS1	SaGo d2s43	0.64	5.21	-2.E-06	0.49	6.20	1.E-01
MMS1	SaGo d2s45	0.64	5.21	-3.E-06	0.50	6.10	-1.E-02
MMS1	SaGo d2s47	0.64	5.22	3.E-06	0.51	6.07	-9.E-03
MMS1	SaGo d2s49	0.63	5.27	4.E-07	0.52	6.01	1.E-01
MMS1	SaGo d2s51	0.63	5.27	-5.E-07	0.49	6.22	8.E-02
MMS1	Base + SNV	0.36	6.92	5.E-07	0.31	7.21	6.E-03
MMS1	Base + Norris d1g23	0.66	5.01	3.E-07	0.48	6.24	2.E-01
MMS1	Base + Norris d1g27	0.50	6.11	2.E-07	0.38	6.82	1.E-01
MMS1	Base + Norris d2g17	0.59	5.53	1.E-06	0.41	6.69	-6.E-03
MMS1	Base + Norris d2g21	0.63	5.23	-1.E-06	0.49	6.19	6.E-02
MMS1	Base + SaGo d1s17	0.65	5.10	2.E-06	0.46	6.41	7.E-02
MMS1	Base + SaGo d1s19	0.60	5.43	6.E-07	0.44	6.54	8.E-02
MMS1	Base + SaGo d1s41	0.63	5.26	2.E-06	0.48	6.25	-7.E-02
MMS1	Base + SaGo d2s37	0.64	5.19	2.E-06	0.50	6.16	9.E-02
MMS1	Base + SaGo d2s45	0.64	5.21	-1.E-06	0.47	6.28	1.E-01
MMS1	Base + SaGo d2s49	0.63	5.28	-7.E-07	0.51	6.08	-7.E-02
PGS_{red}	Base	0.38	6.79	-2.E-07	0.27	7.38	-4.E-02
PGS_{red}	SNV	0.37	6.88	5.E-08	0.22	7.64	-9.E-02
PGS_{red}	Norris d1g3	0.30	7.22	-2.E-07	0.21	7.68	-1.E-02
PGS_{red}	Norris d1g9	0.39	6.72	-1.E-07	0.24	7.58	-5.E-02
PGS_{red}	Norris d1g15	0.37	6.86	-5.E-07	0.24	7.57	3.E-02
PGS_{red}	Norris d1g17	0.45	6.41	1.E-08	0.26	7.49	-2.E-02
PGS_{red}	Norris d1g19	0.31	7.16	-5.E-07	0.22	7.66	1.E-02
PGS_{red}	Norris d1g25	0.38	6.80	-7.E-07	0.27	7.42	-4.E-02
PGS_{red}	Norris d1g41	0.30	7.23	-3.E-07	0.22	7.64	-9.E-05

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. VXIII (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	Norris d2g3	0.21	7.68	-2.E-07	0.16	7.93	-4.E-02
PGS_{red}	Norris d2g9	0.27	7.38	-4.E-07	0.19	7.80	-6.E-02
PGS_{red}	Norris d2g17	0.25	7.48	-2.E-07	0.23	7.63	1.E-02
PGS_{red}	Norris d2g23	0.40	6.68	-3.E-07	0.23	7.57	2.E-01
PGS_{red}	Norris d2g25	0.44	6.44	-2.E-07	0.24	7.55	-2.E-02
PGS_{red}	Norris d2g27	0.38	6.81	7.E-08	0.23	7.66	2.E-01
PGS_{red}	Norris d2g41	0.30	7.23	-2.E-07	0.22	7.69	-1.E-01
PGS_{red}	SaGo d1s3	0.36	6.90	-2.E-07	0.20	7.74	-4.E-02
PGS_{red}	SaGo d1s7	0.25	7.49	-5.E-07	0.19	7.82	-3.E-02
PGS_{red}	SaGo d1s9	0.45	6.41	-5.E-08	0.22	7.65	1.E-01
PGS_{red}	SaGo d1s11	0.24	7.53	-4.E-07	0.19	7.79	-4.E-03
PGS_{red}	SaGo d1s13	0.42	6.60	-2.E-07	0.25	7.55	-7.E-02
PGS_{red}	SaGo d1s15	0.37	6.84	-3.E-07	0.23	7.60	-3.E-02
PGS_{red}	SaGo d1s17	0.44	6.45	-1.E-07	0.23	7.60	-3.E-02
PGS_{red}	SaGo d1s19	0.40	6.68	-3.E-07	0.24	7.57	-9.E-02
PGS_{red}	SaGo d1s25	0.30	7.25	-2.E-07	0.21	7.68	-2.E-02
PGS_{red}	SaGo d1s41	0.28	7.32	-6.E-07	0.24	7.57	7.E-04
PGS_{red}	SaGo d2s3	0.24	7.55	7.E-07	0.16	7.97	-7.E-03
PGS_{red}	SaGo d2s9	0.21	7.69	-4.E-07	0.17	7.87	-8.E-02
PGS_{red}	SaGo d2s15	0.24	7.53	-3.E-07	0.16	7.96	-5.E-02
PGS_{red}	SaGo d2s17	0.29	7.30	-1.E-07	0.19	7.90	-2.E-01
PGS_{red}	SaGo d2s19	0.22	7.61	-4.E-07	0.17	7.91	3.E-03
PGS_{red}	SaGo d2s25	0.22	7.64	-3.E-07	0.18	7.90	-7.E-03
PGS_{red}	SaGo d2s41	0.22	7.61	-4.E-07	0.20	7.77	1.E-02
PGS_{red}	Base + SNV	0.37	6.88	-9.E-07	0.24	7.56	-1.E-02
PGS_{red}	Base + Norris d1g9	0.23	7.56	-1.E-07	0.19	7.80	3.E-04
PGS_{red}	Base + Norris d1g17	0.45	6.41	-2.E-07	0.30	7.31	7.E-02
PGS_{red}	Base + Norris d1g25	0.38	6.80	-7.E-07	0.22	7.63	3.E-02
PGS_{red}	Base + Norris d2g25	0.43	6.53	-3.E-07	0.27	7.45	-3.E-03
PGS_{red}	Base + SaGo d1s9	0.25	7.50	-1.E-07	0.18	7.86	-9.E-03
PGS_{red}	Base + SaGo d1s13	0.39	6.72	-2.E-07	0.25	7.57	-4.E-05
PGS_{red}	Base + SaGo d1s17	0.40	6.70	-6.E-08	0.24	7.58	-2.E-02
PGS_{red}	Base + SaGo d2s17	0.23	7.56	-2.E-07	0.17	7.91	1.E-02

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XIX: Calibrations and cross validations for Seed DM within N1 with spectral data during fruit development

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.41	6.62	-3.E-07	0.37	6.90	2.E-02
MMS1	SNV	0.42	6.57	1.E-07	0.39	6.78	7.E-03
MMS1	Norris d1g3	0.51	6.04	-4.E-07	0.41	6.67	9.E-02
MMS1	Norris d1g9	0.57	5.64	-1.E-06	0.45	6.43	8.E-02
MMS1	Norris d1g11	0.56	5.76	-2.E-06	0.42	6.61	2.E-02
MMS1	Norris d1g13	0.60	5.45	2.E-06	0.45	6.43	9.E-02
MMS1	Norris d1g15	0.60	5.47	2.E-07	0.41	6.65	-9.E-02
MMS1	Norris d1g19	0.54	5.87	-9.E-07	0.40	6.75	3.E-02
MMS1	Norris d1g21	0.58	5.59	-1.E-06	0.42	6.63	8.E-02
MMS1	Norris d1g23	0.60	5.43	2.E-07	0.45	6.42	-1.E-01
MMS1	Norris d1g25	0.58	5.59	-3.E-06	0.45	6.46	2.E-04
MMS1	Norris d1g41	0.55	5.81	2.E-07	0.43	6.54	2.E-02
MMS1	Norris d2g3	0.61	5.41	-1.E-06	0.36	6.91	-5.E-02
MMS1	Norris d2g9	0.50	6.09	-4.E-07	0.35	6.99	6.E-02
MMS1	Norris d2g13	0.51	6.03	6.E-07	0.36	6.91	3.E-02
MMS1	Norris d2g15	0.64	5.18	-3.E-06	0.42	6.64	-3.E-02
MMS1	Norris d2g17	0.62	5.32	1.E-07	0.42	6.61	-5.E-02
MMS1	Norris d2g19	0.49	6.17	-9.E-07	0.36	6.91	5.E-02
MMS1	Norris d2g25	0.58	5.57	-2.E-06	0.37	6.90	5.E-02
MMS1	Norris d2g41	0.61	5.39	2.E-07	0.44	6.49	1.E-01
MMS1	SaGo d1s 3	0.51	6.06	-5.E-07	0.41	6.69	6.E-02
MMS1	SaGo d1s 9	0.53	5.90	6.E-07	0.42	6.62	1.E-02
MMS1	SaGo d1s 15	0.55	5.77	-1.E-06	0.44	6.50	-2.E-02
MMS1	SaGo d1s 17	0.57	5.67	-5.E-07	0.45	6.42	-6.E-02
MMS1	SaGo d1s 19	0.51	6.04	3.E-06	0.43	6.54	-4.E-03
MMS1	SaGo d1s 25	0.55	5.82	6.E-07	0.44	6.48	-7.E-02
MMS1	SaGo d1s 37	0.57	5.68	3.E-06	0.44	6.51	2.E-02
MMS1	SaGo d1s 39	0.59	5.67	-4.E-06	0.46	6.36	-8.E-03
MMS1	SaGo d1s 41	0.57	5.67	-1.E-06	0.45	6.44	2.E-03
MMS1	SaGo d2s 3	0.64	5.19	-1.E-07	0.33	7.16	-9.E-02
MMS1	SaGo d2s 5	0.64	5.21	-9.E-07	0.38	6.85	4.E-02
MMS1	SaGo d2s 7	0.58	5.59	-8.E-08	0.37	6.88	2.E-01
MMS1	SaGo d2s 9	0.61	5.42	4.E-07	0.40	6.73	1.E-02
MMS1	SaGo d2s 17	0.56	5.72	-6.E-07	0.42	6.60	2.E-01
MMS1	SaGo d2s 25	0.50	6.08	-5.E-07	0.37	6.86	6.E-02
MMS1	SaGo d2s 41	0.61	5.38	1.E-06	0.42	6.59	1.E-01

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XIX (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base + SNV	0.42	6.57	5.E-07	0.38	6.83	-1.E-02
MMS1	Base + Norris d1g17	0.47	6.31	4.E-08	0.37	6.87	3.E-02
MMS1	Base + SaGo d1s 39	0.57	5.67	-5.E-06	0.47	6.34	-7.E-02
MMS1	Base + SaGo d2s 3	0.60	5.43	-5.E-07	0.33	7.09	8.E-02
MMS1	Base + SaGo d2s 17	0.58	5.60	-2.E-07	0.43	6.58	9.E-02
MMS1	Base + SaGo d2s 41	0.59	5.54	-3.E-08	0.43	6.56	1.E-01
PGS_{red}	Base	0.47	6.30	4.E-06	0.37	6.89	5.E-02
PGS_{red}	SNV	0.51	6.05	2.E-06	0.42	6.67	8.E-02
PGS_{red}	Norris d1g3	0.51	6.02	-5.E-07	0.38	6.82	2.E-02
PGS_{red}	Norris d1g9	0.48	6.22	-3.E-07	0.39	6.77	1.E-01
PGS_{red}	Norris d1g17	0.48	6.20	-5.E-07	0.40	6.69	1.E-01
PGS_{red}	Norris d1g21	0.45	6.41	-6.E-08	0.35	7.01	7.E-02
PGS_{red}	Norris d1g23	0.52	6.00	-1.E-06	0.37	6.87	-9.E-03
PGS_{red}	Norris d1g25	0.52	5.99	-6.E-07	0.38	6.82	2.E-01
PGS_{red}	Norris d1g27	0.49	6.14	-1.E-06	0.38	6.81	4.E-02
PGS_{red}	Norris d1g41	0.42	6.58	-2.E-07	0.30	7.25	4.E-02
PGS_{red}	Norris d2g3	0.40	6.68	-9.E-08	0.25	7.53	-9.E-02
PGS_{red}	Norris d2g5	0.37	6.84	-2.E-07	0.24	7.56	-1.E-01
PGS_{red}	Norris d2g7	0.52	5.96	-4.E-07	0.33	7.13	-2.E-01
PGS_{red}	Norris d2g9	0.52	5.96	-3.E-07	0.37	6.87	6.E-02
PGS_{red}	Norris d2g11	0.49	6.17	2.E-08	0.38	6.82	1.E-01
PGS_{red}	Norris d2g17	0.46	6.36	-6.E-07	0.36	6.94	2.E-02
PGS_{red}	Norris d2g25	0.45	6.38	-1.E-07	0.36	6.98	-4.E-04
PGS_{red}	Norris d2g41	0.44	6.49	-4.E-07	0.33	7.10	-5.E-02
PGS_{red}	SaGo d1s 3	0.49	6.16	2.E-07	0.38	6.85	-2.E-02
PGS_{red}	SaGo d1s 9	0.48	6.20	-4.E-07	0.39	6.81	5.E-02
PGS_{red}	SaGo d1s 17	0.49	6.14	3.E-07	0.39	6.75	9.E-02
PGS_{red}	SaGo d1s 25	0.44	6.47	-5.E-07	0.34	7.05	2.E-03
PGS_{red}	SaGo d1s 39	0.45	6.40	8.E-08	0.37	6.90	5.E-02
PGS_{red}	SaGo d1s 41	0.55	5.80	3.E-07	0.38	6.85	2.E-01
PGS_{red}	SaGo d1s 43	0.45	6.41	-9.E-07	0.35	7.03	1.E-02
PGS_{red}	SaGo d2s 3	0.31	7.15	1.E-06	0.20	7.77	-4.E-02
PGS_{red}	SaGo d2s 9	0.33	7.04	-1.E-06	0.24	7.54	-4.E-02
PGS_{red}	SaGo d2s 15	0.49	6.15	4.E-08	0.34	7.08	-5.E-02
PGS_{red}	SaGo d2s 17	0.54	5.83	-4.E-07	0.34	7.06	-8.E-02
PGS_{red}	SaGo d2s 19	0.55	5.80	-6.E-07	0.33	7.10	-7.E-02
PGS_{red}	SaGo d2s 21	0.53	5.92	2.E-07	0.39	6.75	3.E-02
PGS_{red}	SaGo d2s 25	0.53	5.92	-1.E-07	0.40	6.73	4.E-02
PGS_{red}	SaGo d2s 41	0.42	6.57	-2.E-07	0.37	6.91	-6.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XIX (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	Base + Norris d1g17	0.46	6.33	-5.E-07	0.38	6.83	-4.E-02
PGS_{red}	Base + Norris d1g25	0.52	5.99	-6.E-07	0.38	6.81	1.E-01
PGS_{red}	Base + Norris d2g9	0.52	5.96	-6.E-07	0.37	6.90	8.E-03
PGS_{red}	Base + Norris d2g11	0.53	5.91	-6.E-08	0.40	6.72	7.E-02
PGS_{red}	Base + SaGo d1s 17	0.47	6.26	2.E-07	0.40	6.71	3.E-02
PGS_{red}	Base + SaGo d1s 41	0.45	6.40	-7.E-07	0.34	7.05	6.E-02
PGS_{red}	Base + SaGo d2s 19	0.55	5.80	-6.E-08	0.35	6.98	-2.E-02
PGS_{red}	Base + SaGo d2s 25	0.50	6.09	-3.E-07	0.40	6.70	7.E-02

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XX: Calibrations and cross validations for Seed DM within N0 with spectral data before flowering

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base	0.59	4.95	-4.E-06	0.55	5.18	-3.E-02
MMS1	SNV	0.62	4.79	2.E-06	0.56	5.16	5.E-02
MMS1	Norris d1g3	0.63	4.70	-3.E-07	0.56	5.17	6.E-02
MMS1	Norris d1g9	0.64	4.63	-8.E-07	0.58	5.02	4.E-02
MMS1	Norris d1g17	0.62	4.77	3.E-07	0.57	5.11	6.E-02
MMS1	Norris d1g23	0.62	4.77	-9.E-07	0.56	5.10	6.E-02
MMS1	Norris d1g27	0.64	4.64	-9.E-07	0.59	5.00	-2.E-02
MMS1	Norris d1g41	0.72	4.11	3.E-07	0.62	4.78	-9.E-03
MMS1	Norris d2g3	0.59	4.92	-5.E-07	0.55	5.23	5.E-02
MMS1	Norris d2g9	0.63	4.72	-6.E-07	0.57	5.08	-4.E-02
MMS1	Norris d2g17	0.63	4.71	-6.E-07	0.59	4.97	-2.E-03
MMS1	Norris d2g21	0.59	4.93	-6.E-07	0.57	5.12	4.E-03
MMS1	Norris d2g23	0.66	4.54	-6.E-07	0.60	4.93	6.E-02
MMS1	Norris d2g25	0.64	4.66	-2.E-07	0.59	4.96	6.E-02
MMS1	Norris d2g27	0.63	4.69	-4.E-07	0.58	5.02	-6.E-03
MMS1	Norris d2g41	0.61	4.85	-8.E-07	0.58	5.06	6.E-03
MMS1	SaGo d1s3	0.65	4.58	-6.E-07	0.55	5.19	-5.E-02
MMS1	SaGo d1s9	0.64	4.64	8.E-08	0.58	5.03	-3.E-02
MMS1	SaGo d1s17	0.64	4.61	2.E-07	0.59	5.00	-2.E-02
MMS1	SaGo d1s25	0.64	4.65	-3.E-07	0.59	4.99	9.E-03
MMS1	SaGo d1s27	0.74	3.94	-6.E-07	0.64	4.65	2.E-02
MMS1	SaGo d1s31	0.72	4.06	9.E-08	0.65	4.60	2.E-02
MMS1	SaGo d1s33	0.72	4.07	-1.E-06	0.63	4.75	3.E-02
MMS1	SaGo d1s35	0.72	4.09	-2.E-07	0.64	4.63	8.E-03
MMS1	SaGo d1s37	0.72	4.09	-1.E-06	0.65	4.58	2.E-01
MMS1	SaGo d1s39	0.72	4.09	-1.E-06	0.64	4.68	-2.E-03
MMS1	SaGo d1s41	0.72	4.10	1.E-06	0.64	4.64	1.E-01
MMS1	SaGo d1s43	0.72	4.11	-9.E-07	0.63	4.74	3.E-02
MMS1	SaGo d1s45	0.71	4.13	-4.E-07	0.65	4.58	9.E-02
MMS1	SaGo d2s3	0.56	5.12	-6.E-07	0.49	5.52	-2.E-03
MMS1	SaGo d2s9	0.61	4.81	-6.E-07	0.55	5.19	-8.E-02
MMS1	SaGo d2s17	0.63	4.67	-7.E-07	0.59	4.99	-2.E-03
MMS1	SaGo d2s19	0.65	4.55	-6.E-07	0.61	4.85	-3.E-02
MMS1	SaGo d2s21	0.63	4.68	-5.E-07	0.57	5.09	-2.E-02
MMS1	SaGo d2s23	0.67	4.42	-5.E-07	0.61	4.90	-3.E-02
MMS1	SaGo d2s25	0.63	4.71	-6.E-07	0.58	5.02	4.E-02
MMS1	SaGo d2s41	0.62	4.75	-5.E-07	0.58	5.01	4.E-04

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XX (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base + SNV	0.60	4.91	4.E-08	0.56	5.12	4.E-02
MMS1	Base + Norris d1g25	0.64	4.63	1.E-07	0.59	5.01	-3.E-02
MMS1	Base + Norris d2g23	0.66	4.54	-1.E-06	0.60	4.93	-2.E-02
MMS1	Base + Norris d2g25	0.66	4.53	-2.E-07	0.59	4.94	3.E-02
MMS1	Base + SaGo d1s29	0.63	4.71	-2.E-07	0.58	5.02	6.E-02
MMS1	Base + SaGo d2s19	0.63	4.68	-7.E-07	0.58	5.02	4.E-02
MMS1	Base + SaGo d2s23	0.67	4.42	-7.E-07	0.60	4.89	-3.E-02
PGS_{red}	Base	0.53	5.28	-7.E-07	0.48	5.59	-3.E-02
PGS_{red}	SNV	0.65	4.59	-1.1E-06	0.58	5.03	-7.0E-02
PGS_{red}	Norris d1g3	0.51	5.41	-5.E-07	0.43	5.84	-1.E-01
PGS_{red}	Norris d1g5	0.52	5.34	-3.E-07	0.47	5.68	-1.E-01
PGS_{red}	Norris d1g7	0.53	5.27	-8.E-07	0.47	5.67	-4.E-02
PGS_{red}	Norris d1g9	0.53	5.28	-3.E-07	0.47	5.62	-1.E-01
PGS_{red}	Norris d1g11	0.53	5.31	-3.E-07	0.49	5.58	-2.E-02
PGS_{red}	Norris d1g13	0.52	5.35	-5.E-07	0.48	5.58	-8.E-02
PGS_{red}	Norris d1g15	0.52	5.35	-5.E-07	0.47	5.65	-9.E-02
PGS_{red}	Norris d1g17	0.52	5.33	-7.E-07	0.48	5.57	-4.E-02
PGS_{red}	Norris d1g25	0.51	5.43	-3.E-07	0.48	5.62	-4.E-02
PGS_{red}	Norris d1g41	0.51	5.43	-6.E-07	0.47	5.68	-1.E-02
PGS_{red}	Norris d2g3	0.52	5.37	-4.E-07	0.36	6.24	7.E-02
PGS_{red}	Norris d2g7	0.52	5.38	-4.E-07	0.47	5.65	-8.E-02
PGS_{red}	Norris d2g11	0.52	5.33	-5.E-07	0.49	5.50	-4.E-02
PGS_{red}	Norris d2g17	0.52	5.33	-6.E-07	0.49	5.55	-5.E-02
PGS_{red}	Norris d2g25	0.50	5.46	-5.E-07	0.46	5.72	-4.E-02
PGS_{red}	Norris d2g41	0.50	5.48	-5.E-07	0.47	5.65	-1.E-02
PGS_{red}	SaGo d1s3	0.51	5.42	-7.E-07	0.43	5.91	-2.E-02
PGS_{red}	SaGo d1s7	0.52	5.37	-2.E-07	0.43	5.84	-5.E-02
PGS_{red}	SaGo d1s9	0.53	5.31	-4.E-07	0.45	5.73	-5.E-02
PGS_{red}	SaGo d1s11	0.51	5.41	-6.E-07	0.47	5.69	-9.E-02
PGS_{red}	SaGo d1s13	0.53	5.27	-5.E-07	0.49	5.55	-3.E-02
PGS_{red}	SaGo d1s15	0.53	5.28	-4.E-07	0.50	5.51	-5.E-02
PGS_{red}	SaGo d1s17	0.53	5.31	-7.E-07	0.49	5.54	-4.E-02
PGS_{red}	SaGo d1s19	0.53	5.33	-6.E-07	0.48	5.58	-2.E-02
PGS_{red}	SaGo d1s21	0.53	5.33	-7.E-07	0.50	5.52	-1.E-02
PGS_{red}	SaGo d1s23	0.53	5.32	-5.E-07	0.49	5.58	-3.E-02
PGS_{red}	SaGo d1s25	0.53	5.32	-5.E-07	0.49	5.52	-3.E-02
PGS_{red}	SaGo d1s27	0.52	5.34	-6.E-07	0.49	5.55	-2.E-02
PGS_{red}	SaGo d1s41	0.51	5.43	-6.E-07	0.48	5.61	-2.E-02

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XX (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	SaGo d2s3	0.53	5.30	6.E-07	0.36	6.26	-1.E-01
PGS_{red}	SaGo d2s9	0.45	5.75	-2.E-07	0.35	6.25	-2.E-01
PGS_{red}	SaGo d2s15	0.52	5.34	-4.E-07	0.44	5.79	-6.E-02
PGS_{red}	SaGo d2s17	0.53	5.30	-6.E-07	0.45	5.74	-1.E-01
PGS_{red}	SaGo d2s19	0.53	5.32	-5.E-07	0.46	5.69	-2.E-02
PGS_{red}	SaGo d2s21	0.54	5.27	-5.E-07	0.49	5.59	3.E-02
PGS_{red}	SaGo d2s23	0.53	5.28	-4.E-07	0.49	5.55	7.E-02
PGS_{red}	SaGo d2s25	0.52	5.33	-4.E-07	0.49	5.59	-4.E-02
PGS_{red}	SaGo d2s41	0.52	5.34	-4.E-07	0.49	5.55	-9.E-03
PGS_{red}	Base + SNV	0.56	5.11	-5.E-07	0.46	5.71	-6.E-02
PGS_{red}	Base + Norris d1g7	0.53	5.27	-8.E-07	0.48	5.59	-1.E-02
PGS_{red}	Base + Norris d1g9	0.53	5.28	-3.E-07	0.50	5.54	-2.E-02
PGS_{red}	Base + Norris d1g11	0.53	5.31	-3.E-07	0.49	5.52	-5.E-02
PGS_{red}	Base + Norris d2g9	0.54	5.24	-6.E-07	0.49	5.52	1.E-02
PGS_{red}	Base + SaGo d1s15	0.53	5.28	-7.E-07	0.50	5.53	-4.E-02
PGS_{red}	Base + SaGo d2s21	0.54	5.27	-4.E-07	0.47	5.66	8.E-02
PGS_{red}	Base + SaGo d2s23	0.53	5.28	-5.E-07	0.49	5.57	-1.E-02

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XXI: Calibrations and cross validation for Seed DM within N0 with spectral data during fruit development

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	SNV	0.61	4.82	1.E-06	0.58	5.08	5.E-02
MMS1	Norris d1g3	0.65	4.53	-5.E-07	0.58	5.08	1.E-01
MMS1	Norris d1g5	0.71	4.15	-1.E-06	0.60	4.93	4.E-02
MMS1	Norris d1g7	0.72	4.07	-5.E-07	0.63	4.72	-4.E-03
MMS1	Norris d1g9	0.72	4.11	-5.E-07	0.62	4.80	7.E-02
MMS1	Norris d1g17	0.68	4.38	-5.E-07	0.61	4.84	-5.E-02
MMS1	Norris d1g25	0.69	4.33	-1.E-07	0.61	4.83	-7.E-03
MMS1	Norris d1g39	0.69	4.27	-9.E-07	0.63	4.74	4.E-02
MMS1	Norris d1g43	0.68	4.37	-1.E-06	0.60	4.91	2.E-02
MMS1	Norris d2g3	0.61	4.81	-5.E-07	0.55	5.23	3.E-02
MMS1	Norris d2g5	0.62	4.76	-4.E-07	0.55	5.21	6.E-03
MMS1	Norris d2g7	0.69	4.29	1.E-07	0.58	5.06	-5.E-02
MMS1	Norris d2g9	0.69	4.29	-4.E-07	0.61	4.87	-8.E-04
MMS1	Norris d2g11	0.64	4.61	-4.E-07	0.58	5.03	-1.E-03
MMS1	Norris d2g17	0.65	4.57	-8.E-07	0.57	5.06	-2.E-02
MMS1	Norris d2g25	0.64	4.61	-2.E-07	0.56	5.14	3.E-02
MMS1	Norris d2g39	0.62	4.79	-3.E-07	0.57	5.09	-4.E-02
MMS1	Norris d2g43	0.59	4.93	-2.E-07	0.55	5.19	-6.E-02
MMS1	SaGo d1s3	0.61	4.81	-8.E-07	0.54	5.28	-3.E-02
MMS1	SaGo d1s5	0.66	4.54	-5.E-07	0.58	5.02	9.E-02
MMS1	SaGo d1s7	0.73	4.00	-1.E-06	0.61	4.83	2.E-02
MMS1	SaGo d1s9	0.71	4.19	-4.E-07	0.61	4.84	3.E-02
MMS1	SaGo d1s11	0.71	4.18	7.E-07	0.62	4.75	6.E-02
MMS1	SaGo d1s13	0.71	4.18	-4.E-07	0.61	4.83	1.E-01
MMS1	SaGo d1s15	0.69	4.28	-2.E-06	0.62	4.80	1.E-01
MMS1	SaGo d1s17	0.71	4.18	-2.E-06	0.61	4.85	5.E-02
MMS1	SaGo d1s19	0.69	4.30	-7.E-07	0.62	4.81	8.E-02
MMS1	SaGo d1s25	0.68	4.36	-1.E-06	0.61	4.86	-1.E-02
MMS1	SaGo d1s41	0.66	4.48	-8.E-07	0.61	4.85	5.E-03
MMS1	SaGo d2s3	0.60	4.90	-5.E-07	0.49	5.53	-1.E-02
MMS1	SaGo d2s9	0.59	4.96	-3.E-07	0.53	5.31	6.E-03
MMS1	SaGo d2s17	0.66	4.48	-5.E-07	0.58	5.01	5.E-03
MMS1	SaGo d2s21	0.60	4.87	-4.E-07	0.55	5.21	-4.E-02
MMS1	SaGo d2s23	0.72	4.10	-2.E-07	0.61	4.88	7.E-02
MMS1	SaGo d2s25	0.70	4.22	-4.E-07	0.60	4.92	2.E-02
MMS1	SaGo d2s27	0.62	4.79	-3.E-07	0.55	5.19	-5.E-02
MMS1	SaGo d2s41	0.63	4.68	-4.E-07	0.57	5.07	4.E-02

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XXI (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
MMS1	Base + SNV	0.61	4.82	-5.E-07	0.58	5.01	3.E-02
MMS1	Base + Norris d1g7	0.71	4.18	-9.E-07	0.62	4.77	2.E-02
MMS1	Base + Norris d1g41	0.72	4.12	-9.E-07	0.64	4.68	2.E-02
MMS1	Base + Norris d2g41	0.72	4.10	5.E-07	0.60	4.91	-8.E-02
MMS1	Base + SaGo d1s11	0.71	4.18	2.E-07	0.60	4.87	5.E-02
MMS1	Base + SaGo d2s23	0.72	4.10	-7.E-07	0.60	4.92	-2.E-02
PGS_{red}	Base	0.62	4.79	4.E-07	0.59	5.00	4.E-02
PGS_{red}	SNV	0.65	4.59	-1.E-06	0.58	5.03	-7.E-02
PGS_{red}	Norris d1g3	0.69	4.31	-9.E-07	0.51	5.46	1.E-01
PGS_{red}	Norris d1g5	0.69	4.27	-4.E-07	0.55	5.23	-5.E-02
PGS_{red}	Norris d1g7	0.64	4.63	-5.E-07	0.58	5.04	8.E-02
PGS_{red}	Norris d1g9	0.62	4.74	-3.E-07	0.57	5.09	9.E-02
PGS_{red}	Norris d1g17	0.65	4.59	-1.E-07	0.59	4.96	-4.E-02
PGS_{red}	Norris d1g25	0.54	5.25	-4.E-07	0.53	5.34	5.E-02
PGS_{red}	Norris d1g39	0.66	4.53	-5.E-07	0.60	4.90	-1.E-01
PGS_{red}	Norris d1g45	0.66	4.48	-4.E-07	0.60	4.87	-2.E-02
PGS_{red}	Norris d2g3	0.31	6.43	-5.E-07	0.30	6.54	2.E-01
PGS_{red}	Norris d2g7	0.68	4.38	-8.E-07	0.52	5.38	-6.E-02
PGS_{red}	Norris d2g9	0.71	4.20	-3.E-07	0.54	5.24	1.E-01
PGS_{red}	Norris d2g11	0.58	5.04	-8.E-07	0.48	5.60	6.E-02
PGS_{red}	Norris d2g17	0.69	4.27	-1.E-06	0.60	4.94	-6.E-02
PGS_{red}	Norris d2g25	0.62	4.75	-4.E-07	0.55	5.21	2.E-01
PGS_{red}	Norris d2g41	0.59	4.96	-6.E-07	0.54	5.30	-6.E-03
PGS_{red}	SaGo d1s3	0.69	4.32	-4.E-07	0.55	5.22	4.E-02
PGS_{red}	SaGo d1s5	0.68	4.39	-4.E-08	0.55	5.26	6.E-02
PGS_{red}	SaGo d1s9	0.63	4.69	-3.E-07	0.55	5.24	2.E-02
PGS_{red}	SaGo d1s17	0.63	4.70	-5.E-07	0.56	5.14	-2.E-04
PGS_{red}	SaGo d1s25	0.61	4.83	-1.E-06	0.57	5.10	-5.E-03
PGS_{red}	SaGo d1s41	0.64	4.63	-9.E-07	0.59	5.00	8.E-03
PGS_{red}	SaGo d2s3	0.31	6.44	-2.E-07	0.30	6.56	3.E-02
PGS_{red}	SaGo d2s9	0.35	6.25	-5.E-07	0.31	6.46	-4.E-02
PGS_{red}	SaGo d2s13	0.60	4.89	-5.E-07	0.42	5.96	-9.E-02
PGS_{red}	SaGo d2s15	0.70	4.23	-5.E-07	0.54	5.26	-2.E-03
PGS_{red}	SaGo d2s17	0.70	4.21	-5.E-07	0.53	5.32	4.E-02
PGS_{red}	SaGo d2s19	0.70	4.22	-4.E-07	0.58	5.04	-1.E-01
PGS_{red}	SaGo d2s21	0.70	4.26	-3.E-07	0.51	5.43	1.E-02
PGS_{red}	SaGo d2s23	0.62	4.75	-7.E-07	0.49	5.54	2.E-01
PGS_{red}	SaGo d2s25	0.68	4.38	-3.E-07	0.54	5.28	2.E-01
PGS_{red}	SaGo d2s41	0.67	4.41	-4.E-07	0.56	5.16	9.E-03

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

Tab. XXI (continued)

Wavelengths range	Pre-treatment	Calibration			Validation		
		R^2	RMSE	Bias	R^2	RMSE	Bias
PGS_{red}	Base + SNV	0.67	4.45	5.E-07	0.60	4.93	-8.E-02
PGS_{red}	Base + Norris d1g41	0.67	4.42	-8.E-07	0.59	4.96	-2.E-02
PGS_{red}	Base + Norris d2g9	0.64	4.66	-3.E-07	0.52	5.37	4.E-02
PGS_{red}	Base + Norris d2g17	0.69	4.27	-6.E-07	0.59	4.95	-2.E-01
PGS_{red}	Base + SaGo d1s3	0.69	4.32	-4.E-07	0.55	5.18	-1.E-01
PGS_{red}	Base + SaGo d1s41	0.64	4.63	-9.E-07	0.59	4.95	6.E-02
PGS_{red}	Base + SaGo d2s17	0.68	4.38	-6.E-07	0.50	5.45	-2.E-01
PGS_{red}	Base + SaGo d2s19	0.70	4.22	-4.E-07	0.51	5.44	8.E-02

Calibrations and cross validations that were not shown in chapter B, R^2 coefficient of determination, RMSE root mean square error in dt ha^{-1}, MMS1 305 – 950 nm, PGS_{red} 951 – 1350 + 1551 – 1760 nm, Norris Norris gap derivative transformation, SaGo Savitzky-Golay derivative transformation, d derivation, g gap size, s number of smoothing points, Base baseline offset correction, SNV standard normal variate transformation

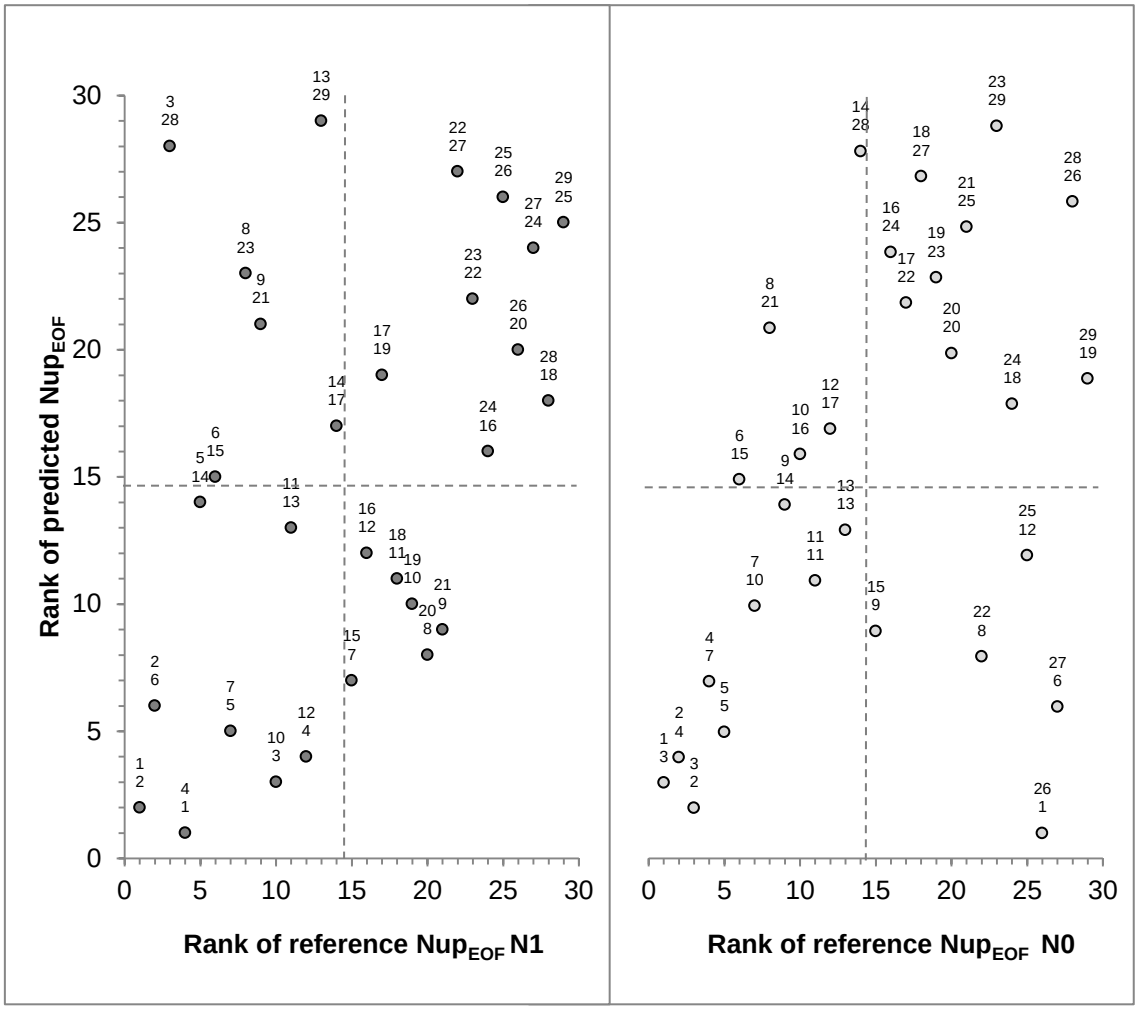

Fig. I: Nup$_{EOF}$ Ranks of genotypes for Nup$_{EOF}$ – Ranks of N1 means (left) and N0 means (right), spectral data before flowering across N1+N0

Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted mean derive from prediction across both N levels with MMS1 spectrum pre-treated with Norris gap 1st derivative gap size 9, Ranks are plotted within N levels

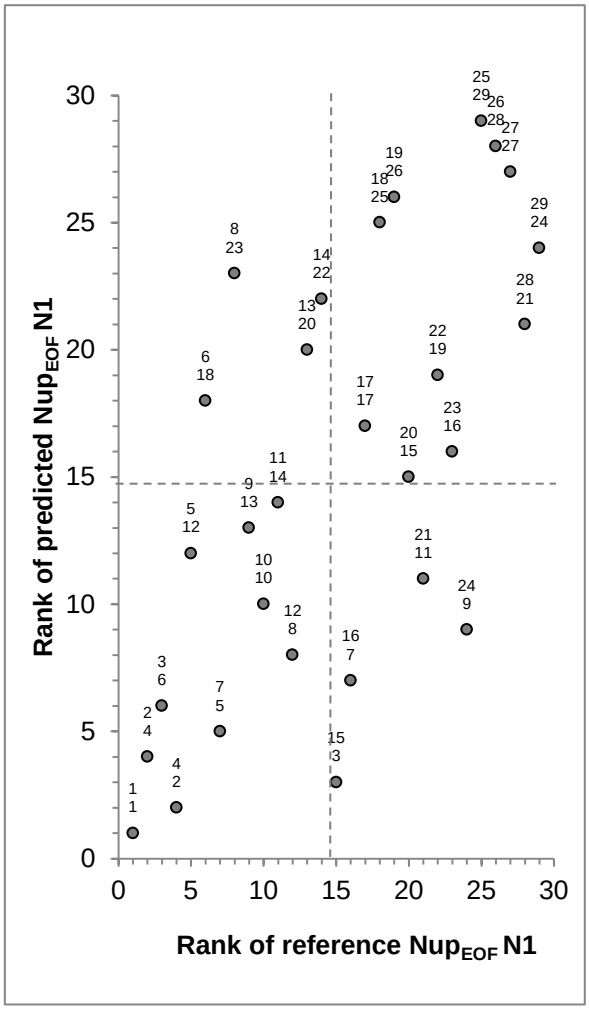

Fig. II: Nup$_{EOF}$ Ranks of genotypes for Nup$_{EOF}$ at N1, spectral data before flowering at N1

Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction within N1 with MMS1 pre-treated with Norris gap 1st derivative gap size 43

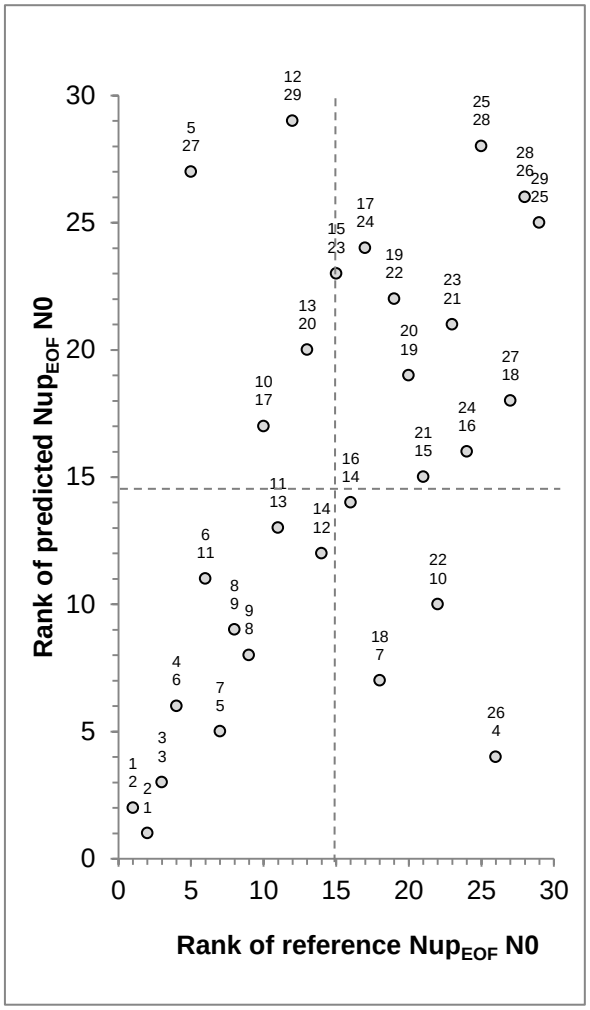

Fig. III: Nup$_{EOF}$ Ranks of genotypes for Nup$_{EOF}$ at N0, spectral data before flowering at N0

Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from predition within N0 with MMS1+PGS$_{red}$ pre-treated with Norris 2nd derivative gap size 9 (MMS1) and Savitzky Golay 1st derivative 13 smoothing points (PGS$_{red}$)

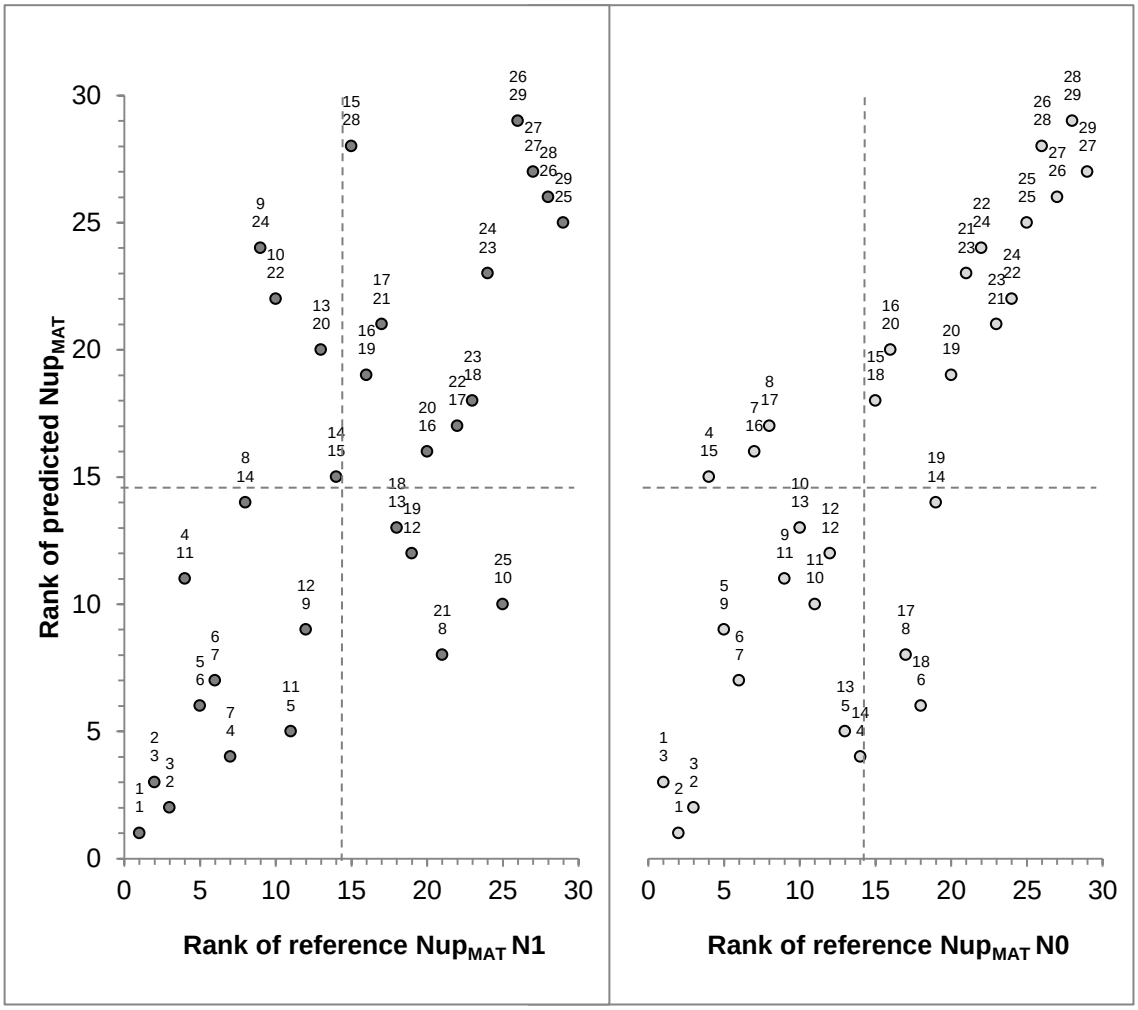

Fig. IV: Nup$_{MAT}$ Ranks of genotypes for Nup$_{MAT}$ – Ranks for N1 means (left) and for N0 means (left), spectral data before flowering across N1+N0

Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction across both N levels with MMS1 pre-treated with baseline offset correction followed by Savitzky Golay 1st derivative 17 smoothing points, Ranks are plotted within N levels

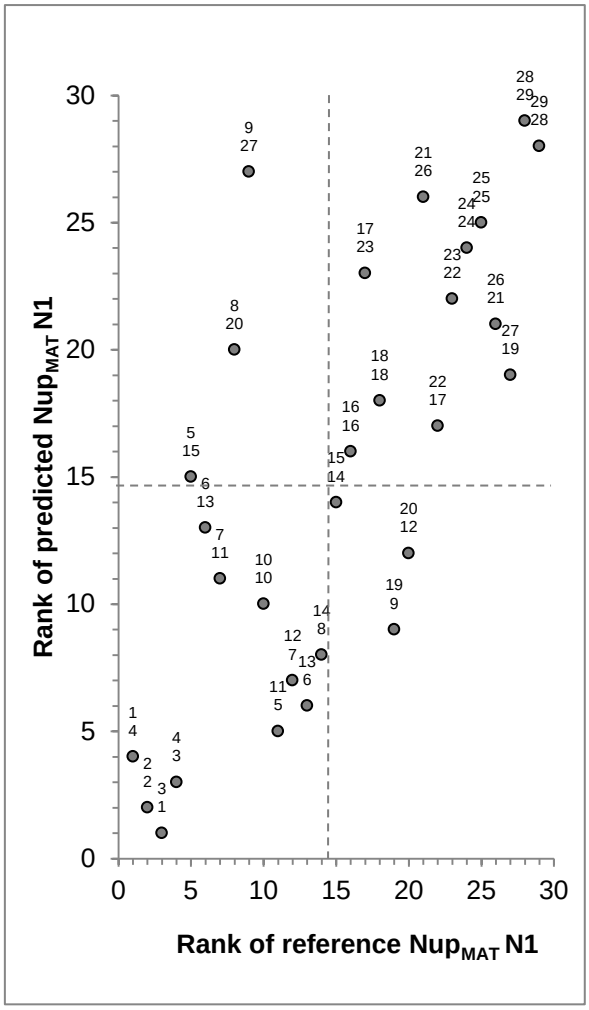

Fig. V: Nup$_{MAT}$ Rank of genotypes for Nup$_{MAT}$ at N1, spectral data before flowering at N1
Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction within N1 with MMS1 pre-treated with Norris gap 1st derivative gap size 41

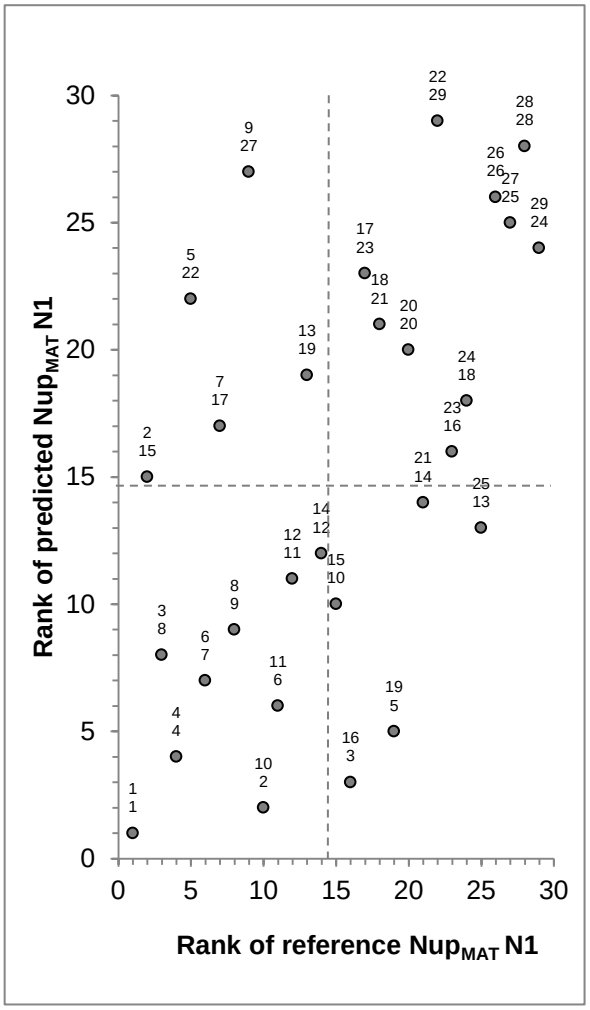

Fig. VI: Nup$_{MAT}$ Rank of genotypes for Nup$_{MAT}$ at N1, spectral data during fruit development at N1
Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction within N1 with MMS1 pre-treated with Norris gap 2nd derivative gap size 9

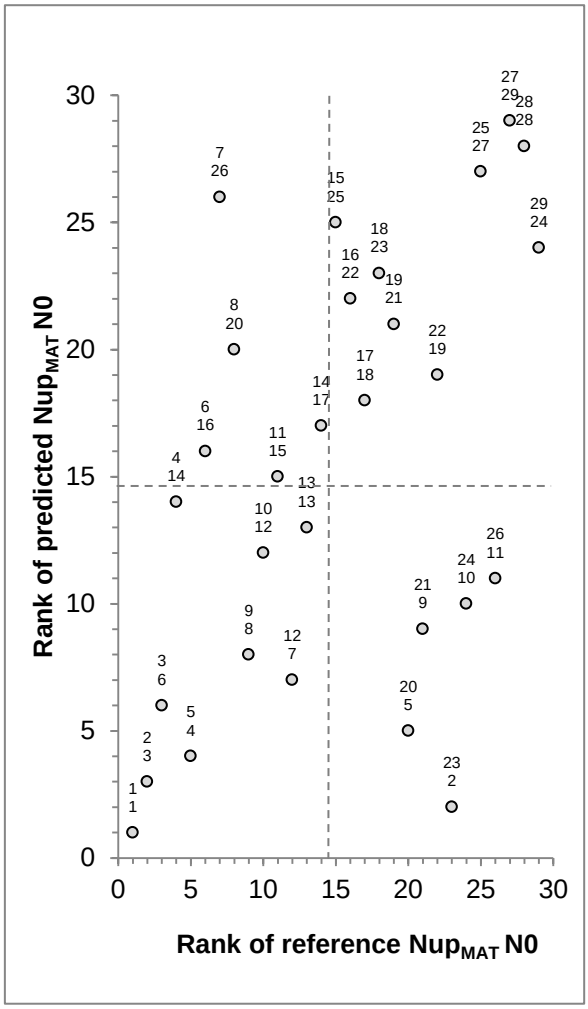

Fig. VII: Nup$_{MAT}$ Rank of genotypes for Nup$_{MAT}$ at N0, spectral data before flowering at N0

Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction within N1 with MMS1 pre-treated with Norris gap 1st derivative gap size 13

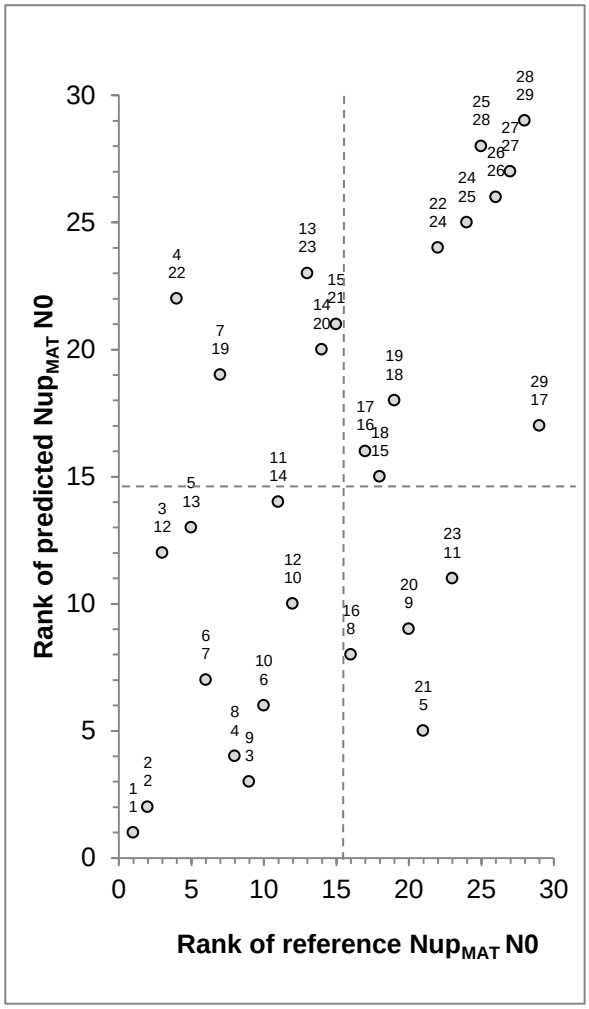

Fig. VIII: Nup$_{MAT}$ Rank of genotypes for Nup$_{MAT}$ at N0, spectral data during fruit development at N0

Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction within N1 with MMS1 pre-treated with Norris gap 1st derivative gap size 7

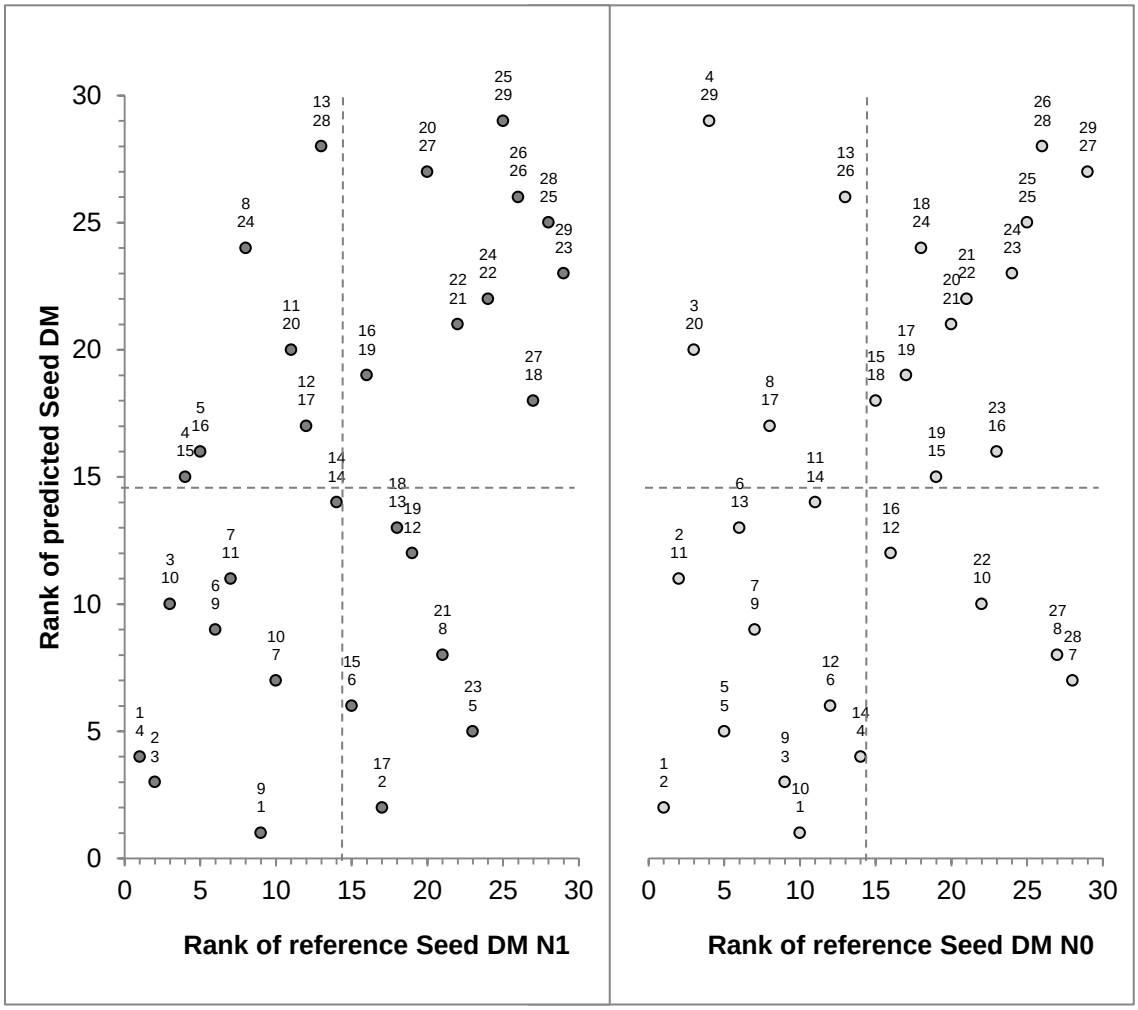

Fig. IX: Seed DM Rank of genotypes for Seed DM – Ranks for N1 means (left) and N0 means (right), spectral data before flowering across N1+N0

Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction across both N levels with MMS1 pre-treated with Savitzky Golay 1st derivative 25 smoothing points, Ranks are plotted within N levels

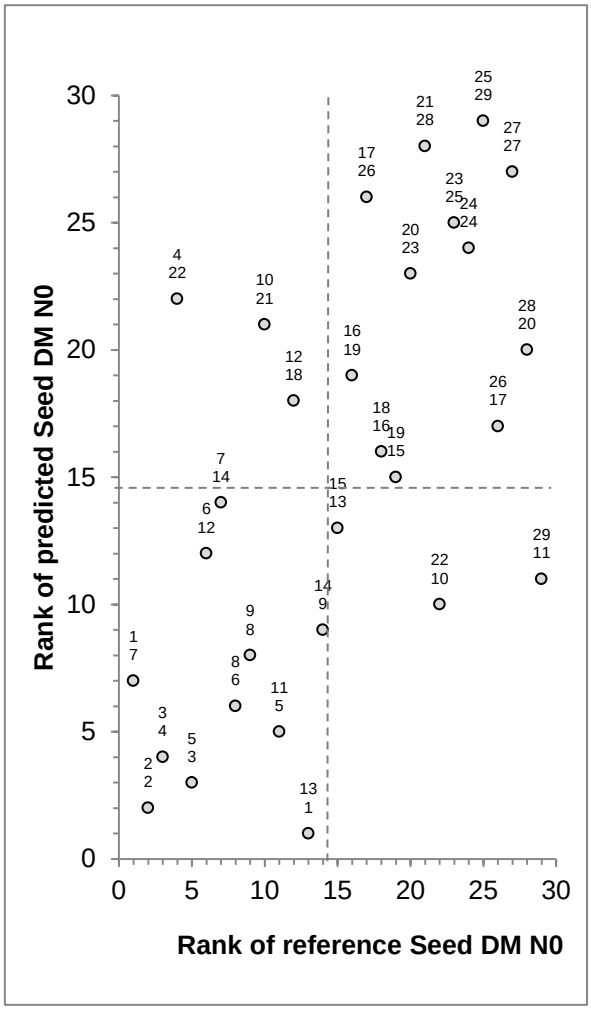

Fig. X: Seed DM Rank of genotypes for Seed DM at N0, spectral data before flowering at N0
Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction within N1 with MMS1 pre-treated with Savitzky Golay 1st derivative 29 smoothing points

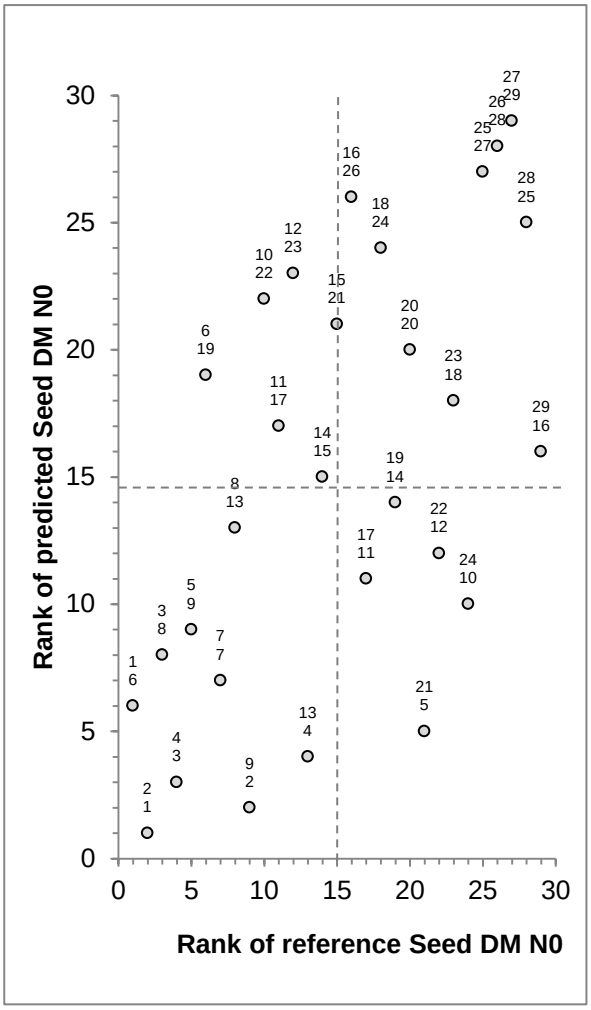

Fig. XI: Seed DM Rank of genotypes for Seed DM at N0, spectral data during fruit development at N0
Numbers above each point present rank of a genotype according to reference means (top) and predicted means (bottom), Plot is divided into four quadrants – genotypes in the bottom left showed good performance in field trials and were predicted to perform well, genotypes in the upper right performed bad in the field and were predicted to perform bad, predictions of genotypes in the bottom right and upper left were predicted contrary to their performance in field trials, Means of reference values derive from observation in the field, Predicted means derive from prediction within N1 with MMS1 pre-treated baseline offset correction

Tab. XXII: ANOVA for root traits and stem diameter s of EC10 field trial

Trait	Source	DF	MS	Var.cp	F		h²
RM_{0-20} [mg]	D	1	41.34	-1.41	0.59	*ns*	0 - **0** - 0
	R:D	2	69.57	-57.82	0.11	*ns*	
	G	9	950.72	-5.12	0.98	*ns*	
	DG	9	971.18	161.70	1.50	*ns*	
	RG:D	16	647.78	647.78			
	Total	37					
RM_{20-40} [mg]	D	1	1999.11	95.26	21.27	*	0 - **0** - 0
	R:D	2	93.98	3.38	1.56	*ns*	
	G	9	88.08	-3.33	0.87	*ns*	
	DG	9	101.38	20.61	1.69	*ns*	
	RG:D	18	60.16	60.16			
	Total	39					
RM_{40-60} [mg]	D	1	211.14	9.97	17.87	*ns*	0 - **0** - 0
	R:D	2	11.81	-2.00	0.37	*ns*	
	G	9	19.20	-7.46	0.39	*ns*	
	DG	9	49.03	8.63	1.54	*ns*	
	RG:D	18	31.76	31.76			
	Total	39					
StemDia [mm]	D	1	675.60	33.77	4411.87	**	-2.44 - **0.14** - 0.79
	R:D	2	0.15	-0.22	0.07	*ns*	
	G	9	2.99	0.11	1.17	*ns*	
	DG	9	2.56	0.13	1.11	*ns*	
	RG:D	18	2.30	2.30			
	Total	39					

D combination of measuring date and location, R:D replication within D, G genotype, DG interaction between D and G, RG:D interaction between R and G within D, DF degrees of freedom, MS mean squares, Var.cp variance component, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. C 3

Tab. XXIII: Means of genotypes for root traits and stem diameter of EC10 field trial

Genotype	RM_{0-20} [mg]	RM_{20-40} [mg]	RM_{40-60} [mg]	StemDia [mm]
PBY001	56.57	23.28	10.94	14.40
PBY007	105.43	21.21	7.98	15.99
PBY008	69.45	16.87	13.49	14.10
PBY015	77.36	22.59	8.30	14.74
PBY021	63.21	12.90	8.11	15.41
PBY022	74.92	16.48	7.32	14.82
PBY026	75.52	29.24	10.56	14.55
PBY027	48.32	19.47	6.15	13.87
PBY029	63.24	16.74	10.97	16.68
PBY061	76.58	23.28	10.13	14.83

An overview about trait abbreviations is given in Tab. C 3

Tab. XXIV: ANOVA for root traits and stem diameter of EC10 under controlled conditions

Trait	Source	DF	MS	Var.cp	F	h²
RS_{FM} [g]	G	9	50.638	7.3414	3.63 **	0.03 - **0.72** - 0.89
	R	4	82.264	6.8332	5.90 **	
	RG	36	13.931	13.9314		
	Total	49				
Tap_{FM} [g]	G	9	5.326	0.6499	2.56 *	-0.37 - **0.61** - 0.84
	R	4	1.951	-0.0125	0.94 *ns*	
	RG	36	2.077	2.0765		
	Total	49				
Lat_{FM} [g]	G	9	29.795	4.3008	3.59 **	0.02 - **0.72** - 0.89
	R	4	82.246	7.3956	9.92 **	
	RG	36	8.291	8.2906		
	Total	49				
RootDia [mm]	G	9	7.959	0.6967	1.78 *ns*	-0.98 - **0.44** - 0.78
	R	4	9.055	0.4580	2.02 *ns*	
	RG	34	4.475	4.4753		
	Total	47				
RootArea	G	9	16341.934	2208.8209	3.08 **	-0.14 - **0.68** - 0.87
	R	4	25906.974	2060.9144	4.89 **	
	RG	34	5297.830	5297.8296		
	Total	47				
$Dens_{Av}$ [mm]	G	9	14.408	0.6392	1.29 *ns*	-1.74 - **0.22** - 0.69
	R	4	34.494	2.3283	3.08 *	
	RG	34	11.212	11.2116		
	Total	47				
W_{Med} [mm]	G	9	267.815	12.3746	1.30 *ns*	-1.71 - **0.23** - 0.69
	R	4	240.187	3.4246	1.17 *ns*	
	RG	34	205.942	205.9415		
	Total	47				
W_{Max} [mm]	G	9	594.029	30.4941	1.35 *ns*	-0.78 - **0.50** - 0.80
	R	4	909.217	46.7659	2.06 *ns*	
	RG	34	441.559	441.5588		
	Total	47				
RTP	G	9	5861.944	-1037.2447	0.53 *ns*	0 - **0** - 0
	R	4	4161.073	-688.7094	0.38 *ns*	
	RG	34	11048.167	11048.1670		
	Total	47				
TD_{Med} [mm]	G	9	0.006	0.0003	1.39 *ns*	-1.48 - **0.30** - 0.72
	R	4	0.033	0.0029	7.86 **	
	RG	34	0.004	0.0043		
	Total	47				

G genotype, R replication, RG interaction between R and G, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. C 3

XXIV (continued)

Trait	Source	DF	MS	Var.cp	F		h²
TD_{Mean} [mm]	G	9	0.006	-0.0001	0.95	*ns*	0 - **0** - 0
	B	4	0.037	0.0031	5.81	**	
	BG	34	0.006	0.0064			
	Total	47					
$DD90_{Max}$ [mm]	G	9	0.064	-0.0044	0.75	*ns*	0 - **0** - 0
	B	4	0.272	0.0185	3.15	*	
	BG	34	0.086	0.0861			
	Total	47					
StemDia [mm]	G	9	14.324	1.3228	13.07	**	0.74 - **0.92** - 0.97
	B	9	0.759	-0.0338	0.69	*ns*	
	BG	81	1.096	1.0962			
	Total	99					

G genotype, R replication, RG interaction between R and G, h² heritability (bold) of genotype within variety type with 0.95 confidence interval, ** significant for α = 0.01, * significant for α = 0.05, *ns* not significant for α = 0.05, An overview about trait abbreviations is given in Tab. C 3

Tab. XXV: Means of genotypes for root traits and stem diameter of EC10 under controlled conditions

Genotype	RS_{FM} [g]	Tap_{FM} [g]	Lat_{FM} [g]	RootDia [mm]	RootArea	$Dens_{Av}$	W_{Med} [mm]	W_{Max} [mm]	RTP	$DD90_{Max}$ [mm]	TD_{Med} [mm]	TD_{Mean} [mm]	StemDia [mm]
PBY001	19.80	7.44	12.36	19.79	378.51	12.74	63.08	108.57	286.80	1.21	0.46	0.49	9.33
PBY007	19.82	5.89	13.93	18.66	385.57	12.33	59.14	114.43	257.40	1.33	0.50	0.52	10.68
PBY008	23.86	8.37	15.49	18.83	387.25	13.15	51.70	104.79	189.00	1.22	0.51	0.54	11.61
PBY015	13.79	5.75	8.04	16.67	265.49	9.34	46.91	96.13	222.05	1.06	0.44	0.48	9.09
PBY021	14.79	5.23	9.56	18.83	295.04	9.36	52.05	109.15	238.20	1.21	0.46	0.49	10.84
PBY022	16.31	6.29	10.02	18.68	263.81	8.65	57.20	107.63	252.80	1.25	0.45	0.48	9.38
PBY026	15.80	6.71	9.08	16.03	242.25	9.65	38.30	96.85	177.50	1.21	0.45	0.51	8.50
PBY027	15.84	6.86	8.98	16.32	277.86	11.20	44.26	80.12	240.00	1.18	0.44	0.47	9.37
PBY029	14.03	4.95	9.08	18.57	253.85	9.75	48.42	96.46	246.20	1.04	0.42	0.45	7.95
PBY061	15.99	5.99	10.01	17.75	316.58	8.85	51.61	86.21	196.40	1.43	0.52	0.56	11.06

DECLARATIONS

1. I, hereby, declare that this Ph.D. dissertation has not been presented to any other examining body either in its present or a similar form.

   Furthermore, I also affirm that I have not applied for a Ph.D. at any other higher school of education.

   Göttingen,

   Julia Rudloff

2. I, hereby, solemnly declare that this dissertation was undertaken independently and without any unauthorised aid.

   Göttingen,

   Julia Rudloff