

Plant-KBBE: Cornfed

Integration of advanced mapping and phenotyping methods to identify key alleles for building European maize ideotypes

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Introduction

Maize has proven to be a highly efficient crop for feed and energy production due to its C4 metabolism, its biomass yield and composition. The objectives of this trinational project are to i) develop biological resources for genetic analysis, ii) find key alleles defining maize biomass ideotypes, iii) develop markers linked to key loci enabling marker assisted selection, and iv) establish a European maize resource database.

Biological resources

Different biological resources are developed as a basis for linkage and linkage disequilibrium (LD) mapping:

- A panel of 750 highly diverse inbred lines will be assembled.
- A multi-parental advanced generation inter-cross design (MAGIC) will be set up and 800 DH lines will be extracted.
- Two nested association mapping (NAM) populations, a European flint connexion and an early dent connexion will be created (Fig. 1).
- Introgression lines of founders used in the NAM population and an early B73 line as recurrent parent will be established for *de novo* QTL mapping, validation of association genetics effects, QTL fine mapping and map based cloning.

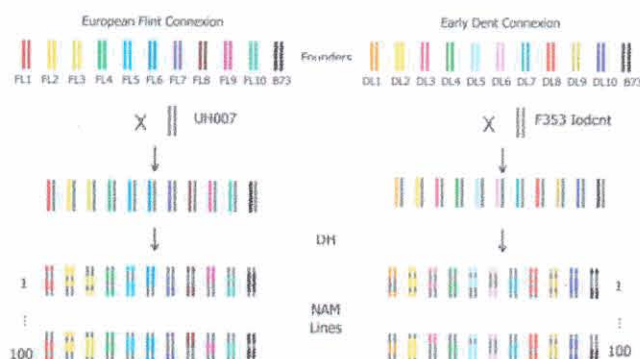


Fig. 1: Nested association mapping populations. This design illustrates the construction of the two NAM populations for the flint and dent connexion (mod. after Yu et al. 2008). For the flint connexion 10 founders will be crossed to a flint reference line. From each cross, 100 DH lines will be extracted and tested with a dent reference line. *Vice versa* for the dent connexion.

Acknowledgements

The project is funded in the framework of the Transnational (France, Germany, Spain) Cooperation within the PLANT-KBBE Initiative, with funding from the Agence Nationale de la Recherche (ANR), the Federal Ministry of Education and Research (BMBF), and the Ministry of Science and Innovation (MICINN).

References

Yu et al. 2008, *Genetics* 178(1): 539-551

Project outline

On the phenotypic level, low temperature response, leaf growth, water use efficiency, biomass accumulation and composition will be assessed. Phenotyping is conducted under field, semi-controlled and greenhouse conditions. After large scale polymorphism discovery using next generation sequencing techniques, high-density genotyping for linkage and LD mapping will be performed (Fig. 2 and 3).

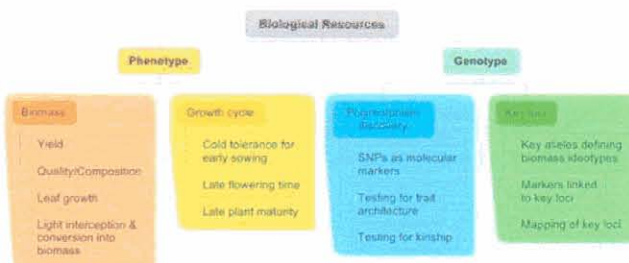


Fig. 2: Investigations on the phenotypic and genotypic levels.



Fig. 3: Controlled environment trial (Lernnatec platform) at IPK Gatersleben).

Outlook

Cornfed will provide directly applicable results in terms of alleles discovered at loci defining desired ideotypes. Markers for key alleles will allow predictive inference in genetic material important for breeding. The genetic architecture for traits of interest will be revealed. The magnitude and organisation of LD between and within genetic groups and its consequences for LD mapping will be elucidated by high-density genotyping. Sequencing, genotyping and phenotyping data will be accessible through a central database updated during the progress of the project.