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**Research Article**

# Indicators for the on-farm assessment of crop cultivar and livestock breed diversity: A survey-based participative approach

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## Abstract

Agrobiodiversity plays a fundamental role in guaranteeing food security. However, still little is known about the diversity within crop and livestock species: the genetic diversity. In this paper we present a set of indicators of crop accession and breed diversity for different farm types at farm-level, which may potentially supply a useful tool to assess and monitor faming system agrobiodiversity in a feasible and relatively affordable way.

A generic questionnaire was developed to capture the information on crop and livestock species in 12 European case study regions and in Uganda by 203 on-farm interviews. Through a participatory approach, which involved a number of stakeholders, eight potential indicators were selected and tested. Five of them are recommended as potentially useful indicators for agrobiodiversity monitoring per farm: (1) crop-species richness (up to 16 crop species), (2) crop-cultivar diversity (up to 15 crop cultivars, 1-2 on average), (3) type of crop cultivars (3 % of all crop cultivars in Europe, 31 % in Uganda), (4) livestock-species diversity (up to 5 livestock species), and (5) breed diversity (up to 5 cattle and 8 sheep breeds, on average 1-2).

We demonstrated that the selected indicators are able to detect differences between farms, regions and dominant farm types. Given the present rate of agrobiodiversity loss and the dramatic effects that this may have on food production and food security, extensive monitoring is urgent. A consistent survey of crop cultivars and livestock breeds on-farm will detect losses and help to improve strategies for the management and conservation of on-farm genetic resources.

**Key words:** Agrobiodiversity, indicators, participatory, cultivars, breeds, landraces

## 1 Introduction

Biodiversity comprises genetic, species and habitat diversity that represent the variety of living organisms and the multitude of ecosystems in which they live in. Since the publication of the book ‘Biodiversity’ by Wilson (1988) and the ‘Rio Earth Summit’ in 1992, the concept of biodiversity has been expanded to include the key factors for sustainable development, on which natural and anthropogenic systems and their inhabitants’ rely (CBD 2010). Biodiversity and agricultural land-use became the focus of political strategies for sustainable economic growth and of conservation strategies to protect biodiversity associated with farmland. This agrobiodiversity, a sub-set of biodiversity, comprises the diversity and management of crop and livestock species used in different agro-ecosystems as well as the genetic diversity within and among crop accessions (i.e. commercial cultivars and landraces), livestock breeds and crop wild relatives (CWR) associated with farmland (Love and Spaner 2007; Buiteveld et al. 2009; Turner et al. 2011). Moreover, it considers traditional ecological knowledge, technologies, and farming and food practices (Brookfield and Stocking 1999). Whilst agricultural production often reduces biodiversity due to the expansion of intensively managed farm land, a wide range of agricultural management practices do also protect diverse ecosystems which would vanish during natural evolution (Gomiero et al. 2011). For millennia, farmers and - more recently – breeders have contributed to crop accessions and livestock breed diversity by selecting and breeding. Genetic diversity, the diversity within and among crop accessions, livestock breeds and CWR, can improve important ecosystem services including pollinator attraction and pest control, which are crucial for agricultural productivity and stability at a large scale (Hajjar et al. 2008; Zhu et al. 2000). Genetic diversity *per se* plays a key role for local and global food security (Altieri 1999). Breeding methods such as targeted cross-fertilization and the introgression of genetic material from wild relatives increase crop and livestock yields and provide a continuous basis for the protection of crops from diseases (Vavilov 1926; Hall and Richards 2013; FAO 1993; Jarvis and Hodgkin 1999).

Major threats to agrobiodiversity and, therefore, to genetic diversity of domesticated and wild plant and animal species arise from the intensification, specialization and mechanization of agricultural production as well as from climatic and socio-economic changes worldwide (FAO 2007; Fowler and Hodgkin 2004; Brush 2004). The increase of productivity to fulfill changing market demands is among the most threatening factors leading to genetic erosion, i.e. the loss of genetic diversity in the form of alleles and genotypes as well as domestic crop accessions and livestock breeds (Veteläinen et al. 2009). Genetic erosion has been reported on both regional and global scales. Approximately 75 % of crop genetic resources that have been cultivated previously, were lost by the end of the 19th century (FAO 1993). In Europe and the Caucasus region, 34% of mammalian and 51% of avian breeds are at risk of extinction, while 17% and 5% have already been lost within the same period of time (FAO 2013a; BfN 2008). The replacement of crop and livestock landraces by single, uniform high-performance cultivars and breeds has been reported for various regions (Veteläinen et al. 2009). For instance, in Southern Italy, 70 % of landraces have been lost within three decades (Hammer et al. 1996). In Europe and North America, the replacement of landraces by modern cultivars and breeds reached almost 100 % in 1970 for specific species (van de Wouw et al. 2010). In approximately 130 countries, the dairy cattle breed 'Holstein-Friesian' replaced numerous local breeds and is dominating today (FAO 2007). These are only few examples which hardly represent the true extend of what has been lost. Nevertheless, there is still a lack of consistent procedures for data collection that would allow detailed insight into crop accessions and livestock breeds as well as crop wild relatives conserved at farm, regional or international scales (FAO 2013a; FAO 2013b). These data collections are crucial for the development, improvement and implementation of valuable indicators for the estimation, evaluation and conservation of crop and livestock genetic resources (FAO 2013b).

Genetic diversity indicators are required to detect genetic diversity and, moreover, to detect changes (e.g. genetic erosion of and within crop accessions and livestock breeds), and to monitor progress toward defined goals such as the reduction or the prevention of biodiversity loss by 2020 (CBD 2010) and to provide an early warning system (FAO 2002). General and feasible indicators for genetic diversity such as 'Total area of transgenic crops (ha)' have been proposed and are utilized by various organizations, e.g. the Organization for Economic Co-operation and Development (OECD 2008). These indicators are meant to summarize and represent complex information such as the diversity in an ecosystem. Nevertheless, there is currently no generally accepted standard procedure on how to measure inter-specific and intra-specific (inter-varietal) diversity at large scale within agricultural systems.

The most precise approach to measure genetic diversity, directly at the gene level, is the use of molecular genetic methods. Molecular markers are applied to plant and animal species in order to study fundamental patterns of genetic diversity, relatedness among individuals or populations or to identify valuable genetic resources in natural or semi-natural populations as well as of domesticated crop and livestock (Agarwal et al. 2008; Last et al. 2013). However, the lack of markers for certain species and the substantial requirement for sample collection and analyses make these methods less practicable for the assessment of on-farm genetic diversity on a large scale. Recently, Bonneuil et al. 2012 presented a study comparing the richness of crop accessions, the spatial distribution as well as the genetic distance among and within accessions in wheat based on molecular markers. While this represents a very thorough approach to estimating crop genetic diversity at a large scale, it was applied to only a single species and did not consider the farm level. We aimed at a technically less demanding approach considering many species and estimating on farm diversity

A survey-based determination of on-farm genetic diversity cannot detect genetic variation at the gene level, but provides a feasible approach to estimate crop accession and breed diversity as well as the abundance of landraces on a larger scale (Cebolla-Cornejo et al. 2007; Teklu and Hammer 2006). Crop accession and breed diversity represent a rough estimator of genetic diversity at farm-scale. Nonetheless, both can be essential to farming enterprise. Moreover, crop and livestock genetic diversity at various levels are the intentional genetic diversity on farms. Depending on the farm type, the diversity of crop accession and/or breed diversity may contribute to agrobiodiversity (Vandermeer et al. 1998). Knowledge of on-farm genetic diversity and processes of genetic erosion mostly rely on survey-based strategies using questionnaires or on-farm interviews (Jarvis et al. 2008; Hammer et al. 1996). Potential indicators that are derived from such questionnaires include the number of plant and animal species, crop accessions and livestock breeds, population size, and diversity indices such as the Simpson’s index (Simpson 1949), which takes into account relative abundance and evenness of accession diversity on a farm or within a region (Brown 2010).

This paper presents five indicators for the estimation of genetic diversity, i.e. crop accession or breed diversity, at farm level. As part of the EU FP7 BioBio project (BioBio 2012), which aimed at identifying and testing biodiversity indicators for organic/low-input and conventional farming systems in Europe and another non-European case study, scientific standards and stakeholders were considered in the indicator selection process (Herzog et al. 2012). We developed a questionnaire to survey data associated with crop and livestock genetic diversity on farms from different farm types. We tested whether the survey method applied and the obtained data were usable to compute proposed indicators and if they were applicable to different farm types and case study regions. Additionally, we evaluated the potential role of such indicator values for developing strategies to conserve or increase crop cultivar and livestock breed in agro-ecosystems.

## 2 Material and methods

The development of indicators for genetic diversity within the EU FP7 project 'BioBio' comprised i) a literature-based indicator review, ii) an indicator evaluation by scientific experts and stakeholders, iii) the questionnaire development for on-farm survey of crop accession and breed diversity, iv) the collection of data from 217 farms of 14 cases study regions in selected countries in Europe and Uganda (Table 1, Figure 1) through interviews using the questionnaire, and v) the indicator evaluation and selection based on the data.

In the BioBio project, twelve study regions (Table 1, Figure 1) were selected to reflect major farm types in Europe as well as a large gradient of climatic conditions and major High Nature Value (HNV) farmland regions (Andersen et al. 2003). The definition of farm types follows the classification of the EC Commission Decision 1985 85/377/EEC, establishing a Community typology for agricultural holdings and relates to the type of farm activity (arable farming, livestock farming, mixed farming and permanent crops). 'Production system' relates to the classifications such as organic farming, integrated farming, conventional farming, etc.. In the first phase, methodologies and indicators were applied in 12 European case study regions. After the first phase, the applicability of the questionnaire has been revised and adapted. Main criteria were the availability of the data and the comprehensibility of the questionnaire with regard to farm type. In the second phase, the applicability of the questionnaire was further tested in Ukraine and Uganda, in quite different agro-ecological zones and policy contexts (Herzog et al. 2012). To reduce farm selection bias within study regions, the regions were selected to be as homogeneous as possible with respect to environmental conditions (exposition, elevation, soil, temperature, precipitation). In each region, 8 to 10 organic and an equal number of non-organic farms were selected at random for this study (see Arndorfer et al. 2010 for a detailed description of study regions and farm selection). During on-farm interviews, the applicability of the questionnaire and the availability of the requested data were evaluated.

### 2.1 Indicator review and evaluation by scientific experts and stakeholders

Indicators for the estimation of genetic diversity of crop and livestock species were reviewed based on scientific literature and on reports elaborated by the Organization for Economic Co-operation and Development (OECD), the European Environment Agency (EEA) and the Convention on Biological Diversity (CBD) (OECD 2008; EEA 2007; CBD 2003). A preliminary set of indicators (Table 2, see Dennis et al. 2009 for complete set) was submitted to 20 members of the Stakeholder Advisory Board (SAB) and evaluated according to specific selection criteria (Pointereau and Langevin 2012). The SAB was composed of representatives with environmental and conservation interests, e.g. international, national, and regional authorities, research and education bodies as well as farmers' and consumers associations and nongovernmental organizations. The main selection criteria were attractiveness to specific stakeholder groups and feasibility for monitoring. The preferred genetic indicators combined the ability to assess the impact of farming on genetic diversity (i.e. crop cultivar and breed diversity), to support policy-making in the agro-environmental sector, to label agricultural products, to raise awareness on biodiversity and to maintain standardized protocols for the assessment of genetic diversity in agricultural production systems (Pointereau and Langevin 2012).

### 2.2 Questionnaire development and completion

Information for the assessment of crop and livestock genetic diversity was gathered using a questionnaire which was completed during on-farm interviews (Genetic Diversity Questionnaire; Suppl.1; (BioBio 2012)). The questionnaire was divided into four sections taking into account specific aspects of different farm types (Table 1). Three sections covered the survey of arable, vegetable and tree crop species and accessions occurring on the farm. First, the land surface covered by each accession as well as additional information on the type of the seed material (commercial cultivars or landraces) and the application of on-farm seed multiplication (yes/no) as part of the production was recorded. In the fourth section farmers described selected phenotypic characteristics of eight selected arable (wheat, barley and potato), vegetable (carrot, *Allium* spp.) and tree or permanent crops (apple, cherry, and grape). Since names and characteristics of commercial cultivars in Europe are listed based on standardized protocols and they are publicly available, phenotypic characteristic within study sites where only surveyed for accessions without listed names (unknown name) or landraces. To standardize the description of the eight selected crop species, we provided a list of descriptors, which were selected from descriptor lists of Bioversity International (2010). In addition to crop genetic diversity, information on livestock species which were a relevant part of the farming enterprise and the names of corresponding breeds occurring on the farm were recorded during interviews. Each unique cross was counted as a different crossbreed even if represented by only one individual.

### 2.3 Evaluation of indicators

Based on the farmer interviews, indicators were divided into three categories depending on whether they: a) were practicable, i.e. data could be easily and correctly surveyed, b) were not redundant, i.e. not strongly correlated with each other (data not shown), and c) revealed variability within the data, i.e. allowed the detection of differences between farms. Indicators which met these criteria were classified as ‘**selected indicators**’. Indicators for which the survey-based approach provided only inconsistent data or a subsequent analysis was not possible due to lacking data or analysis tools were classified as ‘**research indicators**’. Indicators for which the collected data was imprecise or incomplete (i.e. no data returned or interviews were completed on less than three quarter of selected farms within a case study) were classified as ‘**discarded indicators**’. Correlations between indicator values and farm parameters (i.e. farm size) within case study regions were excluded by correlation analysis. Differences in indicator values among organic and non-organic, and among case study regions were tested using the non-parametric pairwise Mann Withney U group means using test and the Holm-correction for multiple testing implemented in the statistical software R (R Development Core Team 2011).

## 3 Results and discussion

We completed 203 farm interviews in 12 European case study regions and in Uganda (Table 4). The time effort for a single interview depended on the size and the complexity of the farm. On average, the interview duration was 50 min (10 to 100 min). Due to incomplete data for the Dutch case study region (NL, horticulture), this case study was excluded from further analysis. There, the simplistic questionnaire was not able to capture the complexity of repeated cultivation of various vegetable species and accessions within one field site at a certain time point. A clear specification of the time point or time frame and a more detailed instruction to the use of the applied questionnaire (e.g. how to handle specific farm types and production system explained by case example) in advance is necessary. For such complex systems, the questionnaire would need to be adjusted as it was done for the Ugandan case study region. There, the questionnaire aimed at capturing crops and accessions grown within one season in order to capture multiple crops and accessions grown on a repeatedly cultivated plot. Alternatively, the use of farmers' books in order to record the whole data set of the previous season or a limited data set, e.g. reduced to defined production periods, could be evaluated. For the remaining case study regions, indicators were calculated based on the data received using the questionnaire and evaluated according to criteria described in section 2.3. Five indicators were retained for further analysis, one was recommended for further research applications and two indicators were discarded (Table 3).

### 3.1 Recommended indicators

The five indicators '**Crop-Species Richness**', '**Crop-Cultivar Diversity**', '**Type of Crop Accessions**', '**Livestock-Species Richness**' and '**Breed Diversity**' are recommended for further application. Data required for the calculation of these indicators, e.g. precise names of crop and livestock species, crop accessions and livestock breeds or their type, were easily accessible. Farmers provided detailed information during the interview for the calculation of the indicator values per farm. Indicator values differed between farms and the results were of interest to stakeholders.

'**Crop-Species Richness**' (CSR) was calculated based on the total numbers of arable, vegetable, tree and forage crops and was expressed as crop species richness, i.e. the total number of natural or cultivated populations of plant species for agricultural purpose per farm. Crop species were grown on 174 out of 203 farms. No crop species were recorded in the 16 farms of the Bulgarian case study region and on 13 single farms across all other case study regions, which focused on grassland based livestock production (Table 4). Crop as well as livestock indicators were only calculated for farms on which they were present. A total of 91 different crop species were recorded across all case study regions. CSR in organic and non-organic farms within case study regions did not differ significantly ($p > 0.05$). The median of CSR per case study region ranged from 1 in the Italian case study region to 11 in the German case study region, where CSR was significantly higher ($p < 0.05$) than in the other regions. In the mixed farm type of German case study region, sown grasslands were as abundant as field crops and contained multiple cultivated forage crops species such as red clover (*Trifolium pratensis*), perennial ryegrass (*Lolium perenne*) or meadow fescue (*Festuca pratensis*), leading to a high CSR per farm. In the Italian case study region, CSR was significantly lower than in all other case study regions ($p < 0.05$), due to the focus on wine production, where a single crop species (*Vitis vinifera*) dominated. Other crop species such as olives (*Olea europaea*) or Durum wheat (*Triticum durum*) were only detected on few single Italian farms and were not part of the main production system. In the Spanish case study region 'Olive plantation', olives groves were the main production system, but compared to the Italian vineyards, almost each farm cultivated further crop species such as cork oaks (*Quercus* spp.) or *Vitis vinifera.* The loss of crop species within farming systems will result in the disappearance of the corresponding accessions and, therefore, affect the on-farm biodiversity. It will also entail a reduction of the richness of farm habitats at farm level, e.g. arable as well as forage crop production sites, and the associated wild species, e.g. segetal flora. On the other hand, some farm type – such as the Spanish Dehesas (cork oaks) – may require large areas, whilst being relatively poor in number of crop species. Although this means low CSR at the farm level, such farm types may nevertheless contribute valuable ecosystems at a regional level. Therefore, changes to farm-level CSR should also be interpreted in a regional context.

'**Crop-Cultivar Diversity**' (CCD) was calculated as the total number of accessions (commercial cultivars, landraces and 'unknown') divided by CSR (crop-species richness) per farm. Since the indicator CCD harbors a certain ambiguity by not revealing the distribution of cultivars within species, CCD has always to be considered together with the crop species diversity on farm. The median of CCD ranged from one in the Spanish, Hungarian and Ukrainian case study regions, to 6.5, in the Italian case study region (Table 4). The lowest CCD per farm was one and was found on 45.4 % of the investigated farms. CCD in organic and non-organic farms within case study regions did not differ significantly ($p > 0.05$). Within the farm type 'arable crops', crop species such as cereals or vegetables were often grown as monocultures of single accessions. These populations, characterized by a substantial degree of uniformity, are cultivated in order to improve economic performance and simplify post-harvest procedures (Buiteveld et al. 2009). The highest CCD was 15, detected on a single Italian farm, where grapes (*Vitis vinifera*) were cultivated. The farm type (Table 1) had significant impact on the CCD per farm. For farm types such as ‘arable crops’ as well as in the German case study region, the median of CCD ranged between one and two (Table 4). These values were comparable with those found in a survey of on-farm accession diversity of major crop species worldwide (Jarvis et al. 2008). On the vineyard based farms in the Italian cases study region the CCD was significantly higher than in all other case study regions ($p < 0.05$). Farmers grow different accessions to produce different kinds of wines in order to have a larger product range to offer, which results in a high accession diversity per farm. Moreover, high accession diversity can spread economic risks caused by unfavorable weather conditions or pest and disease outbreaks (Zhu et al. 2000). In the Spanish case study region, where cork oaks were cultivated, three oak species (*Quercus ilex*, *Q. suber*, *Q. pyrenaica*), dominant within the Dehesa-ecosystem in central-western Spain, were recorded but accessions could not be distinguished (Plieninger et al. 2010). Consequently, CSR was three, if all three *Quercus* species were present on a farm and CCD per farm was one. Only in single cases multiple accessions of additional crops such as rye, barley or Italian ryegrass were cultivated under the oak trees, increasing CCD. While CCD can provide a valuable tool for the detection of varietal diversity and genetic erosion within a crop species on most farm types, its use in semi-natural populations, e.g. cork oaks or permanent grassland, is limited. For the investigation of crop accession diversity within these farm types, approaches based on morphological or molecular markers would be preferable and have previously been used to detect high genetic variability within cork oaks (Fufa et al. 2005; Wilson 1988; Martín et al. 2009). The value of the number of crop accessions as a measure of genetic diversity may to some extent depend on the species, its reproduction system and the geographical scale of the investigation. While Ford-Lloyd et al. (2008) observed good correlation between the number of rice landraces and average allelic richness, the number of cultivars was only poorly correlated to genetic diversity in a study investigating wheat (Bonneuil et al. 2012). In the present study, different species with different reproduction systems were considered on a relatively large geographical scale and therefore, some correlation between the number of accessions and genetic diversity may be expected.

We suggest the sub-indicator ‘Percentage of rare crop accessions per species’ as a supplement to CCD. For proof of concept, we calculated this indicator for the tree crop *Malus domestica* in the Swiss case study region (Table 3). Eleven endangered *M. domestica* accessions were identified using the database of ‘ProSpecieRara’ Switzerland (ProSpecieRara 2013). The percentage of endangered accessions per farm in the Swiss case study region ranged from 0 to 100 % (Figure 2). The majority (> 50 %) of apple tree accessions planted represented accessions classified as locally endangered. Farms with 100 % endangered accessions substantially contribute to the conservation of on-farm crop accession diversity. However, although this kind of information is in demand by stakeholders, general utilization is difficult for various reasons. A general list revealing the conservation status of accessions along the same lines as the ‘IUCN Red List of Threatened Species’ is not available. Commercial accessions, which were predominantly grown in the European case study regions, are not considered as endangered or under risk if conserved in a gene bank (FAO 2002). Thus, the definition of ‘endangered’ is inconsistent on a local and global level and might be of different significance within modern and traditional farming systems (FAO 2002). These differences may lead to an inconsistent conservation of crop and accession diversity.

The indicator ‘**Type of Crop Accessions**’ (TCA) considers the presence of landraces, which are mostly heterogeneous populations of crop species locally adapted and valuable as genetic resources. Landraces are highly threatened in European agricultural production systems (Veteläinen et al. 2009). In total, only 6 landraces were recorded on 187 farms from case study regions within 11 European countries. Two olive (*Olea europaea*) landraces were detected within the Spanish Dehesas, a single winter wheat (*Triticum aestivum*) landrace was recorded in the German case study region and three landraces were recorded for grape (*Vitis vinifera*) detected in the Spanish olive groves. In European countries, landraces of cereals such as oat have been drastically reduced by up to 100 % (Veteläinen et al. 2009; Ahokas and Manninen 2000; Teklu and Hammer 2006). Very rarely they are part of the actual production on farm, but they are maintained to meet private interest such as the conservation of ‘family heritage’. In contrast, landraces were of considerable importance in Uganda. On the 16 farms of the Ugandan case study region, 15 crop species were cultivated in total (Table 5). Thirty-one percent of the corresponding accessions were classified as landraces and 21 % were of unknown type (data not shown). Most landraces were recorded for banana (Table 5), which is the most abundant crop species in this case study region, mainly indigenous and an important food source in Uganda (Tushemerehe et al. 2001; FAO 2012). In Europe, landraces have become very rare and the appropriateness of the respective indicator may therefore be questionable. Yet, we still recommend recording this information in on-farm surveys because (i) it is easily obtained, (ii) it permits the localization of populations, (iii) it can yield insights into the importance of preserving local accessions of landraces by farmers, and (iv) it is an issue perceived as important by some farmers and other stakeholder groups. In countries such as Uganda, where subsistence farming prevails, the indicator TCA gives an indication of the genetic diversity of individual crop species and indirectly, on farmers’ dependence on commercial cultivars. Likewise, the indicator provides a point of departure for monitoring trends in landrace cultivation and the status of genetic resources maintained on-farm.

‘**Livestock-Species Richness**’ (LSR) addresses the total number of livestock species occurring per farm. Within selected case study regions and on corresponding farms, cattle and sheep were the dominating species representing a relevant part of the enterprise on most of the farms. The highest LSR (4) was detected within the Spanish Dehesas (Table 4). There, pigs, goats and horses were part of the enterprise, too. On average, farmers are keeping one to two species as part of their enterprise. Although further species have been detected on single farms (e.g. chicken), they were not surveyed due to their irrelevance for the farming enterprise. The same applies for single cows or chicken on Ugandan farms which contributed to farmers livelihood, but were not included to the survey due to their irrelevance for the enterprise on the selected farms. Nevertheless, in order to achieve completeness of data about on-farm breed diversity, future studies need to consider all livestock breeds per farm. In Europe, livestock breeds are also kept by farmers for other purposes that commercial use in enterprises. Governments, non-governmental organization or private farmers (e.g. hobby farmers) preserve noncommercial breeds and their diversity *in situ* for conservation purposes (Woelders et al. 2006). In developing countries, this is of major importance because subsistence farming is significantly contributing to farmers’ and families’ livelihood, while relying on the advantage of local breeds and their diversity. LSR in organic and non-organic farms within case study regions did not differ significantly ($p > 0.05$).

‘**Breed Diversity**’ (BD) addresses the total number of livestock breeds (breeds and crossbreeds) occurring per farm, divided by the livestock species richness per farm. The total number of cattle, sheep, pig, goat and horse breeds and crossbreeds, detected across all farms and case studies with livestock, was 40, 30, 1, 1 and 1, respectively. The median of BD per farm ranged between one and two (Table 4). The highest BD was recorded in the Welsh (4.5) and the Swiss case study region (5; Table 4). In both regions, cattle BD was significantly higher compared to all other case study regions where livestock was present on farm ($p < 0.05$). Nevertheless, in most case study regions production was primarily focused on a single breed or crossbreed. BD in organic and non-organic farms within case study regions did not differ significantly ($p > 0.05$). The indicator BD represents a valuable measurement of on-farm breed diversity with regard to selected livestock species.

We suggest testing the sub-indicator ‘Percentage of rare breeds per species’ occurring per farm (Table 3). For the Swiss case study region, information on endangered breeds originated from the database of ‘ProSpecieRara’ Switzerland (ProSpecieRara 2013). Only one cattle breed (i.e. according to the guidelines of ‘ProSpecieRara’) was identified, which represented 20 % of the cattle breeds present on a single farm in the Swiss case study region. None of the sheep breeds recorded within this case study region were classified as rare by ‘ProSpecieRara’. However, based on the classification of FAO (Food and Agriculture Organization of the United

Nations), none of the surveyed cattle or sheep breed in the Swiss case study region is ‘under risk’ (DAD-IS 2013, EFABIS 2014). Again, the utilization of rare or endangered animal breeds as indicators for inter-breed diversity on a farm is challenging. In national and international databases such as provided by the FAO ‘Domestic Animal Diversity Information System’ or the ‘European Farm Animal Biodiversity Information System’ (DAD-IS 2013; EFABIS 2014; FAO 2013a), neither data on crossbreeds (cattle and sheep), which are predominantly utilized on farms, nor the conservation status are directly available for a high proportion of breeds (Martyniuk et al. 2010). Although such databases such as provided through DAD-IS or EFABIS are constantly improving, they are still widely lacking on-farm information. Consequently, they do not allow for gathering information about the spatial distribution of breeds and crossbreeds at smaller scales such as regional or national levels. Moreover, breeds kept by other livestock owners such as hobby farmers might be captured insufficiently. Other classification systems such as locally adapted versus exotic as well as local versus transboundary breeds are highly recommended since they would allow a spatial distribution of breeds at global or national scale (FAO 2013b). However, corresponding data at regional or on-farm levels are still lacking.

Although ‘**Breed Diversity**’ and the corresponding sub-indicator do not estimate genetic diversity at the gene level within populations of a specific breed or the genetic distance among individuals present on a farm, they allow the evaluation of genetic resources that are utilized at inter-breed level and, therefore, conserved on-farm. The survey of breeds, i.e. names and abundance of breeds that are utilized, can contribute to complete national and international lists or databases. They still contain gaps with regard to spatial breed occurrence and, therefore, the classification of the endangerment status of various species in agricultural production is still not considering the full range of information on livestock breeds on farms. The survey of data on the geographical distribution of breeds remains the most fundamental step for breed diversity analysis. Large progress has been made with regard to the identification and molecular-genetic mapping of breeds (i.e. cattle, sheep, goats, etc.) on the global scale (Groeneveld et al. 2010; Martín-Burriel et al. 2011). The combination of both types of information will be crucial for subsequent conservation and protection processes.

In general, the values obtained for the five recommended indicators are dependent on the unique geographical conditions and the farming types present in the selected regions and values should therefore only be compared taking into account the influence of these external factors.

### 3.2 Indicators for further research

'**Pedigree-based genetic diversity**' can be estimated using the coefficient of parentage (COP), i.e. the probability that two accessions are identical by descent, estimated by using pedigree lineage (Malécot 1947). In addition to the various applications in crop breeding (Cowling 2007), COP can be used to estimate genetic diversity among accessions or to investigate regional crop diversity over time and space (van Esbroeck et al. 1998). Nevertheless, the measurement of the COP is only feasible for crop species for which the pedigree is known and publicly available, e.g. wheat, rice or barley. Accessions that are historically undocumented such as traditional accessions or landraces cannot be subjected to pedigree analysis (Veteläinen et al. 2009). Therefore, we focused on the case study regions Austria, Germany and France, where wheat was the most abundant crop species and present on all farms. The information on wheat accessions, i.e. the accession name, was easily obtained from the questionnaire survey. While the questionnaire will provide data on cultivars present on farm, it is not necessary to receive pedigree data. However detailed pedigree information for the calculation of the COP of the wheat accessions was not readily available because the information was either scattered in multiple databases, or kept confidential by private breeders or breeding companies. This indicator would be meaningful, if the pedigree information of accessions were publicly available.

### 3.3 Discarded indicators

The proposed indicator '**Crop-Cultivar Phenotypic Diversity**' was discarded after only few data were received from the European case study regions during the first survey phase. Although the morphological or phenotypic assessment is a common and informative tool to estimate genetic diversity on the intra-specific and inter-varietal level (Mohammadi and Prasanna 2003), the survey-based approach as applied in this study cannot be recommended for several reasons. First, the number of crop species and corresponding crop accession on a single farm can be quite large and a survey addressing multiple descriptors for all of them is time consuming. Second, a large database of the descriptors that would be required to address all these species is not applicable using a questionnaire. Here, a web-based questionnaire on a field computer linked to multiple online-databases could be a solution. Third, the focus on only a few major crops reduced the comparability among farms. Nevertheless, farmers provided very precise information on selected descriptors, but only less than ten accessions across all case studies were commercial cultivars of unknown name or landraces and, consequently, were surveyed by phenotypic descriptors. Especially when accessions were of 'unknown type' (without a given accession name), the corresponding morphological information made them differentiable and, therefore, countable for the indicator ‘**Crop-Cultivar Diversity**’. However, the assessment of ‘**Crop-Cultivar Phenotypic Diversity**’ in case studies such as Uganda might be very useful. There, this approach could help differentiating crop accession as well as landraces from each other, because accession names are less standardized. An optimized survey-based approach could still be implemented using an online questionnaire, based on a database containing a large variety of crop species and the corresponding descriptors. In general, this will improve the survey of phenotypic data of many crop species and corresponding accessions in the field. In Uganda, this could reveal a better estimate of accession diversity based on phenotypic information. Nevertheless, capturing phenotypic data of multiple crops species and accession on Ugandan farms would require are more complex and preferable web-based survey (e.g. electronic survey tools linked to data bases).

‘**On-Farm Seed-Multiplication**’ was not practiced in any of the case study regions in Europe with the exception of one farm. Therefore, it was discarded as an indicator. Nonetheless, information on on-farm seed-multiplication could provide valuable information about accession development on farm and the current status of genetic resources which farmers are working with. On the other hand, in Uganda landraces are of much greater importance (see 3.1, ‘**Type of Crop Accessions**’). There, seed-multiplication is an important farming practice to multiply own seed material for further seasons and to keep or sell their landraces. The extensive use of landraces is an important part of subsistence providing natural insurance, e.g. against pests and diseases, vagaries of the market or weather, without spending high prices for improved cultivars (Zhu et al. 2000). Furthermore, landraces or indigenous accessions are cultivated to meet needs and diverse purposes within the socio-economic context, e.g. banana accessions for cooking, animal feed, mulch production and brewing of beer (Jarvis et al. 2008; Tushemerehe et al. 2001).

## 4. Conclusion

Within the activity of this project, for the first time, an identification and testing exercise has been carried out in order to develop a set of indicators to estimate agricultural genetic diversity, i.e. crop accession and breed diversity, at the farm scale, through the active participation of scientific experts and national and international stakeholders and farmers. The tested survey-based approach using on-farm questionnaires and interviews revealed to be a promising and simple tool to obtain demographic information on crop species, crop cultivar, and livestock species and breed diversity within multiple farm types The improvement of the questionnaire, e.g. by giving more precise definitions or categories for data recording, by organizing test surveys in order to prove the understandability and applicability of the questionnaire, or using an online questionnaire connected to large databases could increase the quality of data provided. Within the EU, information on crops and livestock species could be added to the data, since this is already gathered by countries or the EU in order to calculate and control relevant farm subsidies. Moreover, the comparability of different farm types could be improved by statistical modelling techniques which consider the possible impact of farming system or the geographical region as well as factors related to the selection process (e.g. climate, farm size, policy frameworks or market behavior). The selected indicators could provide a baseline of the current state of crop accession and breed diversity in agricultural production systems. Additionally, a large scale survey of crop accessions and livestock breeds as well as their corresponding landraces would help to document the risk status of crop accessions and livestock breeds in a specific region and would provide estimates on genetic erosion within species in agricultural production. Therefore, we propose that the selected set of indicators to be included into indicator sets for agrobiodiversity assessments.

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## References

Agarwal M, Shrivastava N, Padh H (2008) Advances in molecular marker techniques and their applications in plant sciences. Plant Cell Reports 27 (4):617-631. doi:10.1007/s00299-008-0507-z

Ahokas H, Manninen M-L (2000) Retrospecting genetic variation of Finnish oat (*Avena sativa*) landraces and observations on revived lines grown prior to 1957. Genetic Resources and Crop Evolution 47 (3):345-352. doi:10.1023/a:1008731320865

Altieri MA (1999) The ecological role of biodiversity in agroecosystems. Agriculture Ecosystems and Environment 74 (1-3):19-31. doi:10.1016/s0167-8809(99)00028-6

Andersen A, Baldock D, Bennett H, Beaufoy G, Bignal E, Brouwer F, Elbersen B, Eiden G, Godeschalk F, McCracken D, Niuwenhuizen W, Van Eupen M, Hennekens S, Zervas G (2003) Developing a high nature value farming area indicator. Internal Report for the European Environment Agency. Institute for European Environmental Policy (IEEP), Copenhagen, Denmark, Copenhagen, Denmark

Arndorfer M., et al. (2010) Delimitation of BIOBIO Case Study Regions and the Selection of Case Study Farms. Deliverable 3.1 of the EU FP7 research project Indicators for Biodiversity in organic and low-input farming systems.

BfN (2008) Nature data 2008. Federal agency for Nature Conservation (BfN), Bonn, Germany, Bonn, Germany

BioBio Homepage - Biodiversity Indicators for European Farming Systems, www.biobio-indicator.org (2012) Agroscope Reckenholz-Tänikon Research Station ART.

Bonneuil C, Goffaux R, Bonnin I; Montalent P; Hamon C; Balfouriri F; Goldringer I (2012) A new integrative indicator to assess crop genetic diversity. Ecological Indicators 23: 280-289

Brookfield H, Stocking M (1999) Agrodiversity: Definition, description and design. Global Environmental Change 9 (2): 77-80. doi: 10.1016/S0959-3780(99)00004-7

Brown AHD (2010) Indicators of genetic diversity, genetic erosion and genetic vulnerability for plant genetic resources for food and agriculture. The second report on the state of the world's plant genetic resources for food and agriculture. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy

Brush SB ( 2004) Farmers' bounty: Locating crop diversity in the contemporary world. Yale University Press, New Haven, CT, USA

Buiteveld J, van Veller MGP, Hiemstra SJ, ten Brink B, Tekelenburg T (2009) An exploration of monitoring and modelling agrobiodiversity: From indicator development towards modelling biodiversity in agricultural systems on the sub-specific level. Report 2009/13. Wageningen, The Netherlands

CBD (2003) Proposed biodiversity indicators relevant to the 2010 target (Meeting document: UNEP/CBD/SBSTTA/9/INF/26). Ninth Meeting of the Subsidiary Body on Scientific, Technical and Technological Advice (SBSTTA 9), Montreal, Canada

CBD (2010) Implementation of Strategic Plan for Biodiversity 2011–2020, including the Aichi Biodiversity Targets, http://www.cbd.int/sp/targets/default.shtml. Convention on Biological Diversity, Montreal, Canada

Cebolla-Cornejo J, Soler S, Nuez F (2007) Genetic erosion of traditional varieties of vegetable crops in Europe: Tomato cultivation in Valencia (Spain) as a case study. International Journal of Plant Production 1 (2):113-128

Cowling WA (2007) Genetic diversity in Australian canola and implications for crop breeding for changing future environments. Field Crops Research 104 (1-3):103-111. doi:http://dx.doi.org/10.1016/j.fcr.2006.12.014

Crop descriptors (2010) http://www.bioversityinternational.org/publications/search/results.html?t=11&pageTitle=Yes, Bioversity International, Rome, Italy

DAD-IS (2013) Domestic Animal Diversity Information System, http://faostat3.fao.org/home/index.html#VISUALIZE. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy

EEA (2007) Halting the loss of biodiversity by 2010: Proposal for a first set of indicators to monitor progress in Europe. EEA Technical Report No 11/2007. Copenhagen, Denmark

EFABIS (2014) European Farm Animal Biodiversity Information System, http://www.eaap.org/content/efabis.htm. European Federation of Animal Science (EAAP), Milan, Italy

Harvesting nature's diversity (1993) http://www.fao.org/DOCREP/004/V1430E/V1430E00.HTM. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy

FAO (2002) Review and development of indicators for genetic diversity, genetic erosion and genetic vulnerability (GDEV): Summary report of a joint FAO/IPGRI workshop (Rome, 11-14 September, 2002). Food and Agricultural Organization of the United Nation (FAO), Rome, Italy

FAO (2007) The state of the world’s animal genetic resources for food and agriculture, http://www.fao.org/docrep/010/a1250e/a1250e00.htm. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy

FAO (2013a) Status and trends of animal genetic resources - 2012, http://www.fao.org/docrep/meeting/027/mg046e.pdf. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy

FAO (2013b) Fourteenth regular session of the Commission on Genetic Resources for Food and Agriculture (Rome, 15 – 19 April). Food and Agriculture Organization of the United Nations (FAO), Rome, Italy

FAOSTAT (2012) http://faostat3.fao.org/home/index.html#VISUALIZE. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy

Ford-Lloyd BV, Brar D, Khush GS, Jackson MT, Virk PS (2008) Genetic erosion over time of rice landrace agrobiodiversity. Plant Genetic Resources: Characterization and Utilization 7: 163-168. doi: 10.1017/S1479262108137935

Fowler C, Hodgkin T (2004) Plant genetic resources for food and agriculture: Assessing global availability. Annual Review of Environment and Resources 29:143-179

Fufa H, Baenziger PS, Beecher BS, Dweikat I, Graybosch RA, Eskridge KM (2005) Comparison of phenotypic and molecular marker-based classifications of hard red winter wheat cultivars. Euphytica 145:133-146

Gomiero T, Pimentel D, Paoletti MG (2011) Environmental impact of different agricultural management practices: Conventional vs. organic agriculture. Critical Reviews in Plant Sciences 30 (1-2):95-124

Groeneveld LF, Lenstra JA, Toro MA; Scherf B, Pilling D, Negrini R, Finlay EK, Jianlin H, Groeneveld E, Weigend S, The GLOBALDIV Consortium (2010) Genetic diversity in farm animals – A review. Animal Genetics 41: 6-31. doi:10.1111/j.1365-2052.2010.02038.x

Hajjar R, Jarvis DI, Gemmill-Herren B (2008) The utility of crop genetic diversity in maintaining ecosystem services. Agriculture Ecosystems and Environment 123 (4):261-270. doi:10.1016/j.agee.2007.08.003

Hall AJ, Richards RA (2013) Prognosis for genetic improvement of yield potential and water-limited yield of major grain crops. Field Crops Research 143 (0):18-33. doi:10.1016/j.fcr.2012.05.014

Hammer K, Knupffer H, Xhuveli L, Perrino P (1996) Estimating genetic erosion in landraces - Two case studies. Genetic Resources and Crop Evolution 43 (4):329-336

Herzog F, Balazs K, Dennis P, Friedel J, Jeanneret P, Geijzendorffer I, Kainz M, Pointereau P (2012) Biodiversity indicators for European farming systems, Vol. 17. ART-Schriftenreihe, Zurich, Switzerland

Jarvis DI, Brown AHD, Cuong PH, Collado-Panduro L, Latournerie-Moreno L, Gyawali S, Tanto T, Sawadogo M, Mar I, Sadiki M, Hue NT-N, Arias-Reyes L, Balma D, Bajracharya J, Castillo F, Rijal D, Belqadi L, Rana R, Saidi S, Ouedraogo J, Zangre R, Rhrib K, Chavez JL, Schoen DJ, Sthapit B, De Santis P, Agarwal M, Shrivastava N, Padh H (2008) Advances in molecular marker techniques and their applications in plant sciences. Plant Cell Rep 27:617-631 doi:10.1007/s00299-008-0507-z

Ahokas H, Manninen M-L (2000) Retrospecting genetic variation of Finnish oat (Avena sativa) landraces and observations on revived lines grown prior to 1957 Genetic Resour Crop Ev 47:345-352 doi:10.1023/a:1008731320865

Altieri MA (1999) The ecological role of biodiversity in agroecosystems. Agr Ecosyst Environ 74:19-31 doi:10.1016/s0167-8809(99)00028-6

Andersen A, Baldock D, Bennett H, Beaufoy G, Bignal E, Brouwer F, Elbersen B, Eiden G, Godeschalk F, McCracken D, Niuwenhuizen W, Van Eupen M, Hennekens S, Zervas G (2003) Developing a high nature value farming area indicator. Internal Report for the European Environment Agency (EEA), Institute for European Environmental Policy (IEEP), Copenhagen, Denmark

Arndorfer M, Angelova S, Balázs K, Bogers MIM, Centeri C, Choisis J-P, Choisis N, Dennis P, Eiter S, Falusi E, Fjellstad W, Friedel JK, Geijzendorffer I, Gomiero T, Griffioen AJ, Guteva Y, Jongman R, Juárez E, Kainz M, Kelemen E, Lüscher G, Mayr J, Moreno G, Paoletti MG, Podmaniczky L, Sarthou J-P, Skutai J, Stoyanova S, Schneider M, Siebrecht N, Wolfrum S, Wilkes J, Zanetti T (2010) Delimitation of BioBio case study regions and the selection of case study farms. Deliverable 3.1 of the EU FP7 research project: Indicators for biodiversity in organic and low-input farming systems. BOKU, Vienna, Austria. http://www.biobio-indicator.org/deliverables/D31.pdf. Accessed 30 June 2014

BioBio (2012) Biodiversity indicators for European farming systems. Agroscope Reckenholz-Tänikon Research Station ART, Zurich, Switzerland. www.biobio-indicator.org. Accessed 30 June 2014

Bioversity International (2010) Crop descriptors. Bioversity International, Maccarese, Italy. http://www.bioversityinternational.org/e-library/publications/categories/descriptors/. Accessed 30 June 2014

Bonneuil C, Goffaux R, Bonnin I, Montalent P, Hamon C, Balfouriri F, Goldringer I (2012) A new integrative indicator to assess crop genetic diversity. Ecol Indic 23:280-289 doi:10.1016/j.ecolind.2012.04.002

Brookfield H, Stocking M (1999) Agrodiversity: Definition, description and design. Global Environ Chang 9:77-80 doi:10.1016/S0959-3780(99)00004-7

Brown AHD (2010) Indicators of genetic diversity, genetic erosion and genetic vulnerability for plant genetic resources for food and agriculture. The second report on the state of the world's plant genetic resources for food and agriculture. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy

Brush SB (2004) Farmers' bounty: Locating crop diversity in the contemporary world. Yale University Press, New Haven, CT, USA

Buiteveld J, van Veller MGP, Hiemstra SJ, ten Brink B, Tekelenburg T (2009) An exploration of monitoring and modelling agrobiodiversity: From indicator development towards modelling biodiversity in agricultural systems on the sub-specific level. Report 2009/13. Centre for Genetic Resources (CGN), Wageningen, The Netherlands

CBD (2003) Proposed biodiversity indicators relevant to the 2010 target (Meeting document: UNEP/CBD/SBSTTA/9/INF/26). Ninth Meeting of the Subsidiary Body on Scientific, Technical and Technological Advice (SBSTTA 9). Convention on Biological Diversity (CBD), Montreal, Canada

CBD (2010) Implementation of Strategic Plan for Biodiversity 2011-2020, including the Aichi Biodiversity Targets. Convention on Biological Diversity (CBD), Montreal, Canada. http://www.cbd.int/sp/targets/default.shtml. Accessed 30 June 2014

Cebolla-Cornejo J, Soler S, Nuez F (2007) Genetic erosion of traditional varieties of vegetable crops in Europe: Tomato cultivation in Valencia (Spain) as a case study. Int J Plant Prod 1:113-128

Cowling WA (2007) Genetic diversity in Australian canola and implications for crop breeding for changing future environments. Field Crops Res 104:103-111 doi:10.1016/j.fcr.2006.12.014

DAD-IS (2012) Domestic Animal Diversity Information System. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy. http://faostat3.fao.org/home/index.html#VISUALIZE. Accessed 30 June 2014

Dennis P, Arndorfer M, Balázs K, Bailey D, Boller B, Bunce RGH, Centeri C, Corporaal A, Cuming D, Deconchat M, Dramstad W, Elyakime B, Falusi E, Fjellstad W, Fraser MD, Freyer B, Friedel JK, Geijzendorffer I, Jongman R, Kainz M, Marcos GM, Gomiero T, Grausgruber-Gröger S, Herzog F, Hofer G, Jeanneret P, Kelemen E, Kölliker R, Moakes SR, Nicholas P, Paoletti MG, Podmaniczky L, Pointereau P, Sarthou J-P, Siebrecht N, Sommaggio D, Stoyanova S, Teufelbauer N, Viaggi D, Vialatte A, Walter T, Widmer F, Wolfrum S (2009) Conceptual foundations for biodiversity indicator selection for organic and low-input farming systems. Deliverable 2.1 of the EU FP7 Project BioBio. http://www.biobio-indicator.org/deliverables/D21.pdf. Accessed 30 June 2014

EEA (2007) Halting the loss of biodiversity by 2010: Proposal for a first set of indicators to monitor progress in Europe. EEA Technical Report No 11/2007. European Environmental Agency (EEA), Copenhagen, Denmark

EFABIS (2014) European Farm Animal Biodiversity Information System. European Federation of Animal Science (EAAP), Milan, Italy. http://www.eaap.org/content/efabis.htm. Accessed 30 June 2014

FAO (1993) Harvesting nature's diversity. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy. http://www.fao.org/DOCREP/004/V1430E/V1430E00.HTM. Accessed 30 June 2014

FAO (2002) Review and development of indicators for genetic diversity, genetic erosion and genetic vulnerability (GDEV): Summary report of a joint FAO/IPGRI workshop (Rome, 11-14 September, 2002). Food and Agricultural Organization of the United Nation (FAO), Rome, Italy

FAO (2007) The state of the world’s animal genetic resources for food and agriculture. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy. http://www.fao.org/docrep/010/a1250e/a1250e00.htm. Accessed 30 June 2014

FAO (2013) Status and trends of animal genetic resources - 2012. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy. http://www.fao.org/docrep/meeting/027/mg046e.pdf. Accessed 30 June 2014

FAO (2013) Status and trends of animal genetic resources - 2012. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy. http://www.fao.org/docrep/meeting/027/mg046e.pdf. Accessed 30 June 2014

FAO (2013b) Fourteenth regular session of the Commission on Genetic Resources for Food and Agriculture (Rome, 15 – 19 April). Food and Agricultural Organization of the United Nation (FAO), Rome, Italy

FAOSTAT (2012) The Statistics Division of the FAO. Food and Agricultural Organization of the United Nation (FAO), Rome, Italy. http://faostat3.fao.org/home/index.html#VISUALIZE. Accessed 30 June 2014

Ford-Lloyd BV, Brar D, Khush GS, Jackson MT, Virk PS (2008) Genetic erosion over time of rice landrace agrobiodiversity. Plant Gene Resour 7:163-168 doi:10.1017/S1479262108137935

Fowler C, Hodgkin T (2004) Plant genetic resources for food and agriculture: Assessing global availability. Ann Rev Environ Resour 29:143-179 doi: 10.1146/annurev.energy.29.062403.102203

Fufa H, Baenziger PS, Beecher BS, Dweikat I, Graybosch RA, Eskridge KM (2005) Comparison of phenotypic and molecular marker-based classifications of hard red winter wheat cultivars. Euphytica 145:133-146 doi: 10.1007/s10681-005-0626-3

Gomiero T, Pimentel D, Paoletti MG (2011) Environmental impact of different agricultural management practices: Conventional vs. organic agriculture. Crit Rev Plant Sci 30:95-124 doi:10.1080/07352689.2011.554355

Groeneveld LF, Lenstra JA, Toro MA, Scherf B, Pilling D, Negrini R, Finlay EK, Jianlin H, Groeneveld E, Weigend S, The GLOBALDIV Consortium (2010) Genetic diversity in farm animals - A review. Anim Genet 41:6-31 doi:10.1111/j.1365-2052.2010.02038.x

Hajjar R, Jarvis DI, Gemmill-Herren B (2008) The utility of crop genetic diversity in maintaining ecosystem services. Agric Ecosyst Environ 123:261-270 doi:10.1016/j.agee.2007.08.003

Hall AJ, Richards RA (2013) Prognosis for genetic improvement of yield potential and water-limited yield of major grain crops. Field Crops Res 143:18-33 doi:10.1016/j.fcr.2012.05.014

Hammer K, Knupffer H, Xhuveli L, Perrino P (1996) Estimating genetic erosion in landraces - Two case studies Genet Resour Crop Ev 43:329-336 doi: 10.1007/BF00132952

Herzog F, Balázs K, Dennis P, Friedel JK, Jeanneret P, Geijzendorffer I, Kainz M, Pointereau P (2012) Biodiversity indicators for European farming systems. Vol. 17. ART-Schriftenreihe, Zurich, Switzerland

Jarvis DI, Brown AHD, Cuong PH, Collado-Panduro L, Latournerie-Moreno L, Gyawali S, Tanto T, Sawadogo M, Mar I, Sadiki M, Hue NT-N, Arias-Reyes L, Balma D, Bajracharya J, Castillo F, Rijal D, Belqadi L, Rana R, Saidi S, Ouedraogo J, Zangre R, Rhrib K, Chavez JL, Schoen DJ, Sthapit B, De Santis P, Fadda C, Hodgkin T (2008) A global perspective of the richness and evenness of traditional crop-variety diversity maintained by farming communities. Proc Natl Acad Sci 105:5326-5331 doi:10.1073/pnas.0800607105

Jarvis DI, Hodgkin T (1999) Wild relatives and crop cultivars: Detecting natural introgression and farmer selection of new genetic combinations in agroecosystems. Mol Ecol 8:S159-S173 doi:10.1046/j.1365-294X.1999.00799.x

Last L, Widmer F, Fjellstad W, Stoyanova S, Kölliker R (2013) Genetic diversity of natural orchardgrass *Dactylis glomerata* L. populations in three regions in Europe. BMC Genet 14:102 doi:10.1186/1471-2156-14-102

Love B, Spaner D (2007) Agrobiodiversity: Its value, measurement, and conservation in the context of sustainable agriculture. J Sustainable Agric 31:53-82 doi:10.1300/J064v31n02_05

Malécot G (1947) Les mathématiques de l'hérédité. Masson et Cie, Paris, France

Martín MA, Navarro-Cerrillo R, Ortega P, Alvarez JB (2009) The use of cotyledon proteins to assess the genetic diversity in sweet holm oak. J of Fore Sci 55:526-531

Martín-Burriel I, Rodellar C, Cañón J, Cortés O, Dunner S, Landi V, Martínez- Martínez A, Gama LT, Ginja C, Penedo MCT, Sanz A, Zaragoza P, Delgado JV (2011) Genetic diversity, structure, and breed relationships in Iberian cattle. J Anim Sci 89:893-906 doi:10.2527/jas.2010-3338

Martyniuk E, Pilling D, Scherf B (2010) Indicators: Do we have effective tools to measure trends in genetic diversity of domesticated animals? Animal Gene Resour 47:31-43 doi:10.1017/S2078633610001013

Mohammadi SA, Prasanna BM (2003) Analysis of genetic diversity in crop plants - Salient statistical tools and considerations. Crop Sci 43:1235-1248 doi:10.2135/cropsci2003.1235

OECD (2012) Environmental Performance of Agriculture in OECD countries since 1990: 8. Biodiversity (genetic, wild species and ecosystem diversity). Organisation for Economic Co-operation and Developement (OECD), Paris, France. http://stats.oecd.org/viewhtml.aspx?QueryName=522&QueryType=View. Accessed 30 June 2014

Plieninger T, Rolo V, Moreno G (2010) Large-scale patterns of Quercus ilex, Quercus suber, and Quercus pyrenaica regeneration in Central-Western Spain. Ecosystems 13:644-660 doi:10.1007/s10021-010-9345-2

Pointereau P, Langevin B (2012) Report on the contribution of the stakeholders to the selection of the biodiversity indicators for organic and low input farming systems (Deliverable D7.1). BioBio Indicators for biodiversity in organic and low-input farming systems (Project No. 227161). Solagro, Toulouse, France. http://www.biobio-indicator.org/deliverables/D713.pdf. Accessed 30 June 2014

ProSpecieRara (2013) Tiere. Schweizerische Stiftung für die kulturhistorische und genetische Vielfalt von Pflanzen und Tieren, Basel, Switzerland. http://www.prospecierara.ch/de/tiere. Accessed 30 June 2014

R Development Core Team (2011) R: A language and environment for statistical computing. R foundation for statistical computing, Vienna, Austria. http://www.r-project.org/. Accessed 30 June 2014

Simpson EH (1949) Measurement of diversity. Nature 163:688-688 doi:10.1038/163688a0

Teklu Y, Hammer K (2006) Farmers' perception and genetic erosion of tetraploid wheats landraces in Ethiopia. Genet Resour Crop Ev 53:1099-1113 doi:10.1007/s10722-005-1145-8

Turner N, Luczaj L, Migliorini P, Pieroni AL, Dreon AL, Sacchetti LE, Paoletti MG (2011) Edible and tended wild plants, traditional ecological knowledge and agroecology. Crit Rev Plant Sci 30:198-225 doi:10.1080/07352689.2011.554492

Tushemerehe WK, Kashaija IN, Tinzaara W, Nankinga C, New S (2001) Banana production manual: A guide to successful banana production in Uganda. National Agricultural Research Organisation (NARO), Entebbe, Uganda

van de Wouw M, Kik C, van Hintum T, van Treuren R, Visser B (2010) Genetic erosion in crops: Concept, research results and challenges. Plant Gene Resour 8:1-15 doi:10.1017/S1479262109990062

van Esbroeck A, Bowman DT, Calhoun DS, May OL (1998) Changes in the genetic diversity of cotton in the USA from 1970 to 1995. Crop Sci 38:33-37 doi:10.2135/cropsci1998.0011183X003800010006x

Vandermeer J, van Noordwijk M, Anderson J, Ong C, Perfecto I (1998) Global change and multi-species agroecosystems: Concepts and issues. Agric Ecosyst Environ 67:1-22 doi:10.1016/S0167-8809(97)00150-3

Vavilov N (1926) Studies on the origin of cultivated plants. Bulletin of Applied Botany and Plant-Breeding 26:139-248

Veteläinen M, Negri V, Maxted N (2009) European landraces: On-farm conservation managment and use. Bioversity Technical Bulletin No. 15. Bioversity International, Italy, Rome

Wilson EO (1988) Biodiversity. The National Academies Press, Washington, DC, USA

Woelders H, Zuidberg CA, Hiemstra SA (2006) Animal genetic resources Conservation in the Netherlands and Europe: Poultry perspective. Poult Sci 85:216-222 doi:10.1093/ps/85.2.216

Zhu YY, Chen HR, Fan JH, Wang YY, Li Y, Chen JB, Fan JX, Yang SS, Hu LP, Leung H, Mew TW, Teng PS, Wang ZH, Mundt CC (2000) Genetic diversity and disease control in rice. Nature 406:718-722 doi:10.1038/35021046

# TABLES AND FIGURES

**Table 1** — Description of regions and farm types for 14 case study regions in Europe, Ukraine and Uganda.

| Country (Region) | Code | Farm Type (main crop/livestock) | Climatic Region | High-Nature Value System |
|---|---|---|---|---|
| Austria (Marchfeld) | AT | Arable crops | Continental | No |
| France (Gascony) | FR | Arable crops | Mediterranean | No |
| Switzerland (Swiss Alps) | CH | Permanent crops - Grassland with livestock (cattle) | Alpine | No |
| Bulgaria (Rhodope Mountains) | BG | Permanent crops - Grassland with livestock (sheep) | Mediterranean | Yes |
| Hungary (Homokhátság) | HU | Permanent crops - Grassland with livestock (sheep) | Pannonian | Yes |
| Norway (Hedmark) | NO | Permanent crops - Grassland with livestock (sheep) | Boreal | No |
| United Kingdom (Wales) | UK | Permanent crops - Grassland with livestock (cattle, sheep) | Atlantic | No |
| Germany (Southern Bavaria) | DE | Mixed crops - Arable and permanent crops (grassland) with livestock (cattle) | Continental | No |
| Italy (Veneto) | IT | Permanent crops (Vineyards) | Mediterranean | No |
| Spain (Extremadura) | ES_D | Permanent crops - Cork oaks/grassland with livestock (cattle) | Mediterranean | Yes |
| Spain (Extremadura) | ES_O | Permanent crops (Olive plantations) | Mediterranean | No |
| Netherlands (Gelderland) | NL | Horticulture | Atlantic | No |
| Ukraine (Kiev Province) | UA | Arable crops | Continental | No |
| Uganda (Kayunga Region) | UG | Mixed crops (permanent and arable crops | Tropical (humid) | n.a. |

**Table 2** — The preliminary set of data-survey approaches for the establishment of genetic diversity indicators. Five approaches to genetic-diversity estimation were summarized according to indicators they could provide and evaluated with regard to selection criteria by stakeholders and scientists. (* = low, ** = moderate and *** = high.)

| | | Stakeholders' and Scientists' Pre-evaluation according to | | | | | |
|---|---|---|---|---|---|---|---|
| Indicator Base | Indicator | Variation detected | Sample throughput | Reliability | Labor effort | Technical skills required | Tested in the project |
| Survey | Number of cultivars, breeds and landraces | * | *** | * | * | * | x |
| Survey | Type (cultivars, landraces) | * | *** | ** | * | * | x |
| Survey | Cultivation area per crop | * | *** | ** | * | * | x |
| Pedigree | Coefficient of parentage | ** | ** | *** | ** | * | x |
| Phenotypic characteristics | Genetic variance, mean | * | *** | ** | *** | * | x |
| Protein marker (e.g. Isozyme) | Diversity, genetic distance | ** | ** | ** | ** | ** | |
| Molecular genetic marker [a] | Diversity, genetic distance | ** - *** | * - *** | * - *** | ** - *** | ** - *** | |

[a] Depending on marker type

**Table 3** — Proposed indicators for the survey-based estimation of on-farm genetic diversity of crop and livestock species classified according to selection status.

| Indicator Name | Selection Status | Unit | Sub-Indicator |
|---|---|---|---|
| ‘Crop-Species Richness’ (CSR) | Selected | Number of crop species per farm | |
| ‘Crop-Cultivar Diversity’ (CCD) | Selected | Total number of accessions per farm (across all crop species) divided by CSR | Percentage of rare cultivars per species and farm |
| ‘Type of Crop Accessions’ (TCA) | Selected | Percentage of landraces per farm | |
| ‘Livestock-Species Richness’ (LPR) | Selected | Number of livestock species per farm | |
| ‘Breed Diversity‘ (BD) | Selected | Average number of breeds (cattle and sheep) per farm | Percentage of rare cattle breeds<br>Percentage of rare sheep breeds |
| ‘Pedigree-Based Genetic Diversity’ | Research | Name of crop species and pedigree information (if available) | - |
| ‘Crop-Cultivar Phenotypic Diversity’ | Discarded | Phenotypic diversity of selected crop species | - |
| ‘On-Farm Seed-Multiplication’ | Discarded | Seed management performance | - |

**Table 4** — The number of crop, species, livestock species, crop accessions, and livestock breeds utilized per case study region. For each case study region, the number of farms (n), the number of farms where crops (a) and/or livestock (b) was present, the median (med), and the minimum (min) and maximum (max) values are presented.

| Case Study | | Crop-Species Richness | | | | Crop-Cultivar Diversity | | | | Livestock-Species Richness | | | | (Livestock) Breed Diversity | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | n | a | med | min | max | a | med | min | max | b | med | min | max | b | med | min | max |
| AT | 16 | 16 | 6.0 | 4.0 | 14.0 | 16 | 1.3 | 1.0 | 1.7 | 0 | - | - | - | 0 | - | - | - |
| FR | 16 | 15 | 4.0 | 1.0 | 14.0 | 15 | 1.3 | 1.0 | 1.8 | 0 | - | - | - | 0 | - | - | - |
| UA | 6 | 6 | 5.0 | 5.0 | 5.0 | 6 | 1.0 | 1.0 | 2.6 | 0 | - | - | - | 0 | - | - | - |
| CH | 19 | 19 | 4.0 | 2.0 | 7.0 | 16 | 2.2 | 1.0 | 5.5 | 19 | 1 | 1 | 1 | 19 | 2.0 | 1.0 | 5.0 |
| BG | 16 | 0 | - | - | - | 0 | - | - | - | 16 | 1 | 1 | 2 | 16 | 1.0 | 1.0 | 3.0 |
| HU | 18 | 17 | 3.0 | 1.0 | 9.0 | 17 | 1.0 | 1.0 | 1.1 | 18 | 1 | 1 | 2 | 18 | 1.0 | 1.0 | 2.0 |
| NO | 12 | 11 | 5.0 | 2.0 | 6.0 | 11 | 1.2 | 1.0 | 1.5 | 12 | 1 | 1 | 1 | 12 | 1.0 | 1.0 | 2.0 |
| UK | 20 | 10 | 3.5 | 2.0 | 6.0 | 10 | 2.1 | 1.0 | 3.3 | 9 | 2 | 1 | 2 | 9 | 2.0 | 1.0 | 4.5 |
| DE | 16 | 16 | 11.0 | 3.0 | 16.0 | 16 | 1.5 | 1.0 | 2.4 | 16 | 1 | 1 | 1 | 16 | 1.0 | 1.0 | 1.0 |
| IT | 18 | 18 | 1.0 | 1.0 | 2.0 | 18 | 6.5 | 1.0 | 15 | 0 | - | - | - | 0 | - | - | - |
| ESD | 10 | 10 | 3.5 | 1.0 | 5.0 | 4 | 1.0 | 1.0 | 1.0 | 10 | 2 | 1 | 4 | 10 | 2.0 | 2.0 | 3.0 |
| ESO | 20 | 20 | 2.5 | 1.0 | 9.0 | 20 | 1.0 | 1.0 | 1.0 | 9 | 1 | 1 | 1 | 9 | 1.0 | 1.0 | 1.0 |
| UG | 16 | 16 | 5.5 | 2.0 | 9.0 | 16 | 1.7 | 1.4 | 2.2 | 0 | - | - | - | 0 | - | - | - |

**Table 5** — Crop species and corresponding share of cultivars and landraces recorded on 16 selected farms in the Ugandan case study region.

| Crop Species | Number of Plots within CS | Cultivars (%) | Landraces (%) | Unknown (%) |
|---|---|---|---|---|
| Banana (*Musa* spp.) | 42 | 26.2 | 66.7 | 7.1 |
| Potato (*Solanum tuberosume*) | 27 | 7.4 | 55.6 | 37.0 |
| Common Bean (*Phaseolus vulgaris*) | 26 | 42.3 | 57.7 | 0.0 |
| Pineapple (*Ananas comosus*) | 18 | 50.0 | 50.0 | 0.0 |
| Maize (*Zea mays*) | 17 | 76.5 | 11.8 | 11.8 |
| Coffee (*Coffea*) | 15 | 33.3 | 66.7 | 0.0 |
| Pawpaw (*Asimina triloba*) | 14 | 42.9 | 50.0 | 7.1 |
| Cowpea (*Vigna unguiculata*) | 1 | 0.0 | 100.0 | 0.0 |
| Cabbage (*Brassica oleracea*) | 2 | 50.0 | 50.0 | 0.0 |
| Peanut (*Arachis hypogaea*) | 2 | 100.0 | 0.0 | 0.0 |
| Cassava (*Manihot esculenta*) | 2 | 0.0 | 100.0 | 0.0 |
| African Eggplant (*Solanum aethiopicum*) | 1 | 0.0 | 100.0 | 0.0 |
| Tomato (*Solanum lycopersicum*) | 1 | 100.0 | 0.0 | 0.0 |
| Sugarcane (*Saccharum officinarum*) | 1 | 100.0 | 0.0 | 0.0 |
| Soybean (*Glycine max*) | 1 | 100.0 | 0.0 | 0.0 |

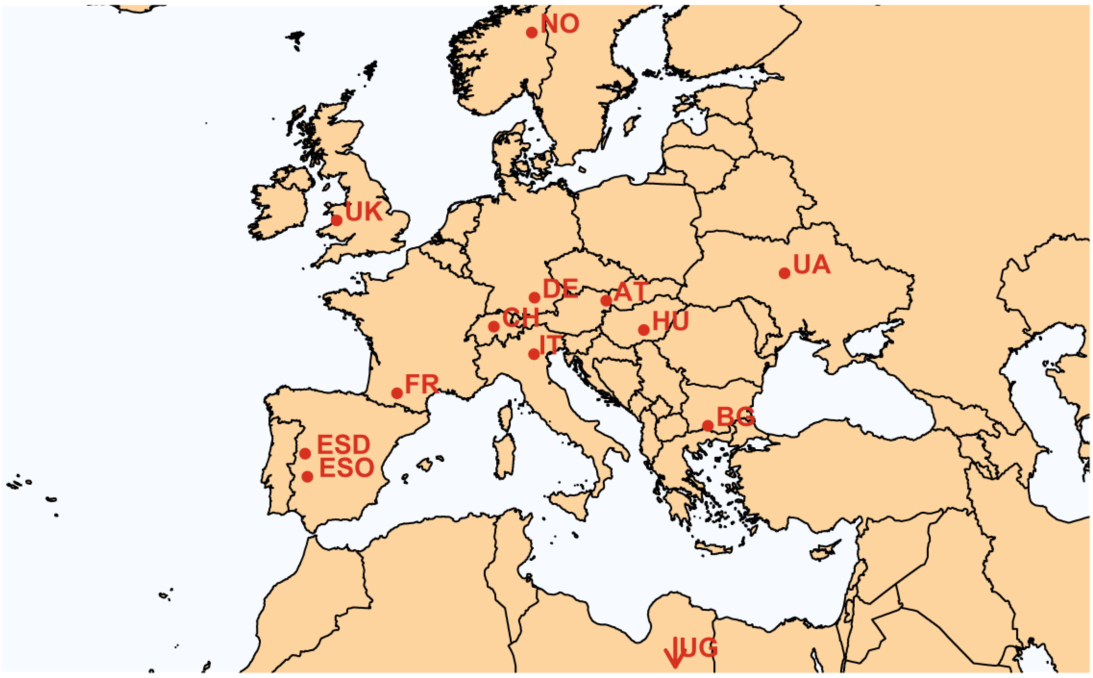

Fig. 1 — The spatial distribution of 12 case study regions within the European territory and one in Uganda.

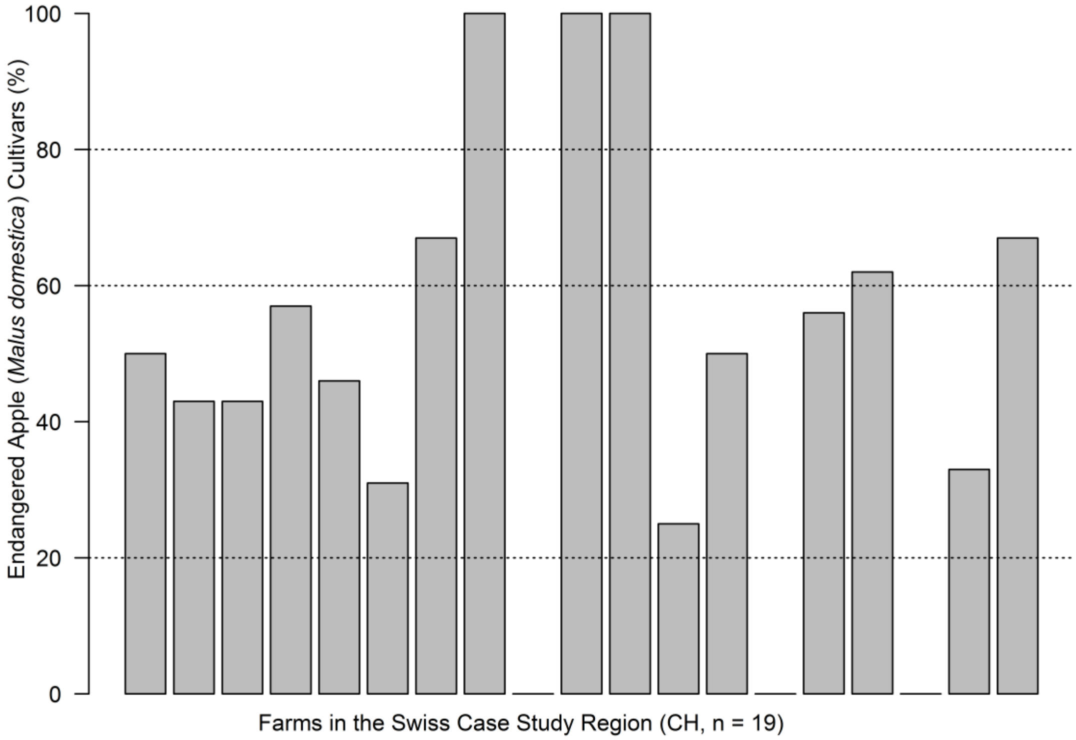

**Fig. 2** — Percentage of endangered apple (*Malus domestica*) accessions (bars) per farm in the Swiss case study region. Numbers within the grey bars represent the total amount of apple accessions recorded per farm.

## Supplementary material

**Suppl.1** Genetic Diversity Questionnaire