

Two Methods for Duplication Assessments within Nordic Oat Accessions at the Canadian National Genebank

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Introduction

Putative duplicates are accessions that have the same accession name and are represented by two or more entries (accessions) in the genebank collection. Duplication of accessions within a genebank is not unusual, particularly in older cultivars. It is confusing to genebank clients and a burden for curators and genebank budgets. This study applies two methods to assess intra-collection duplication within 339 Nordic oat (*Avena sativa* L.) accessions preserved by Plant Gene Resources of Canada (PGRC).

Material and Methods

The Nordic oats had 52 duplication groups, which included 230 of the 339 accessions. A field assessment, which was based on visual inspection of field plots during two growing seasons, was conducted to detect distinct phenotypes within each duplication group. Simultaneously, a descriptor assessment using seven characters with altogether sixteen character states was used in both years for the same purpose (Figure 1).

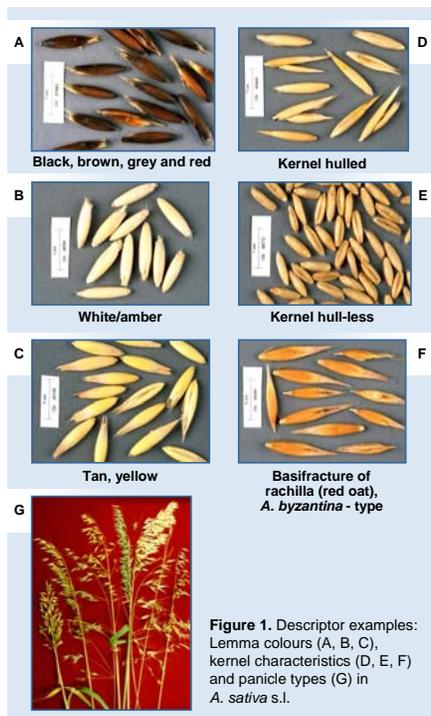


Figure 1. Descriptor examples: Lemma colours (A, B, C), kernel characteristics (D, E, F) and panicle types (G) in *A. sativa* s.l.

Results

- The combined results of both assessments and both years indicated that among the 230 accessions in the 52 duplication groups only 118 accessions could be identified as distinct. This would allow for a reduction of 33% of the 339 Nordic oat accessions at PGRC.
- The field assessment method detected less (75%) distinct accessions than the descriptor assessment (84%), but repeatability was higher in the field assessment (70%) than in the descriptor assessment (64%) (Figure 2).
- As a tendency, duplication groups that contained many accessions, also contained more distinct phenotypes, but there were exceptions (Figure 3).
- Duplication groups of older cultivars did not necessarily contain more distinct accessions (Figure 4).
- Despite similar accession names (passport data), there often were considerable differences between putative duplicates.

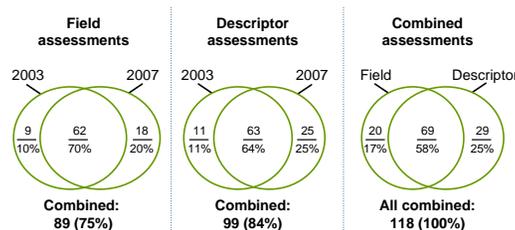


Figure 2. Set diagrams showing absolute numbers (upper row) and relative numbers (lower row) of distinct accessions within 54 duplication groups comprising 230 accessions in total. The years of assessment and the assessment methods are indicated. The overlapping area (intersection) of the two sets contains the number of accessions that was detected as distinct in both years or by both assessment methods. The union of two sets represents the combined assessments.

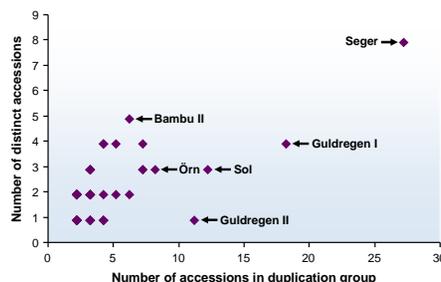


Figure 3. Number of distinct accessions and number of accessions within 52 duplication groups of Nordic oat. Many dots represent several value pairs. Some names of duplication groups are shown.

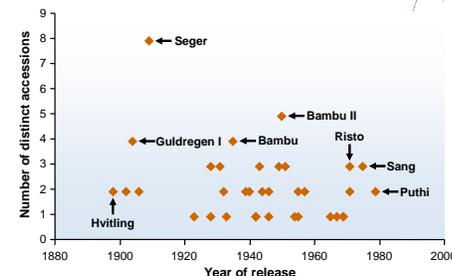


Figure 4. Number of distinct accessions and year of release of the cultivar name of the duplication group within 35 duplication groups of Nordic oat that had a year of release of the respective cultivar recorded. Some names of duplication groups are shown.

Discussion

The field assessment requires an experienced germplasm evaluator, but has the potential to handle a large numbers of germplasm accessions and detects functional, fitness related, and user-relevant diversity. Combination of field assessment with descriptor assessment and more sophisticated methods on selected subgroups may be the most efficient method for determination of internal duplication in genebank collections. Combining phenotypically similar accessions of duplication groups may be the best way to consolidate the collection without loss of genetic diversity.

Conclusions

- Passport data are not sufficient to describe intra-collection duplication.
- Phenotypic assessments are a useful first approach to assess duplication.
- More sophisticated methods using molecular markers could be applied to refine the diversity analysis within duplication groups.

Acknowledgement

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