Core collections were devised as a tool for researchers and plant breeders to explore and utilise the genetic diversity of germplasm collections. In Spain, four investigation groups are collaborating to create the core collection of the durum wheat collection maintained at the National Genetic Resources Centre (CRF-INIA). The objective of this work was to select 200 entries which could glean most of the genetic diversity contained in the whole collection. This subsample will be genetically characterised with molecular markers and evaluated for different traits to select about 60 accessions for the core collection.

The procedure to select the 200 entries followed these steps:

1) Determination of domain
The domain was established as 555 accessions of landraces and old cultivars

2) Division into genetically distinct types: taxonomic and agro-ecological regions
Accessions classified in five taxonomic groups: T. turgidum conv. durum, T. turgidum conv. turgidum, T. turidum conv. polonicum, T. turgidum ssp. dicoccum y T. monococcum L. Between four and 31 entries were allocated per agro-ecological region.

3) Determination of the basic unit (province)
Between 1 and 20 entries were allocated per province.

4) Choice of the entries.
Choice of entries for each province was done maximizing the diversity in agro-morphological and biochemical traits (gliadins and glutenins), and in altitude and type of soil of the collection site, if available. The einkorn accessions were selected maximizing their diversity using microsatellites. The proportions used were logarithmic for the agro-ecological regions and taxonomic groups, and linear for provinces.

Nine agro-ecological regions were established based on a cluster analysis of historical wheat yield records for the Spanish provinces. The allocation of number of accessions per group was proportional to the local varieties described in each province in the 50’s.

The 200 selected entries were validated showing that the range of variation for geographic parameters (longitude, latitude and altitude) and agro-morphological characters of each agro-ecological region were included.

The 200 entries are now being characterized for four gliadin loci (Gli-A1, Gli-B1, Gli-A2, and Gli-B2) and 39 microsatellites selected with a high degree of polymorphism and distributed in all chromosomes.

The analysis of all information together with evaluation data (quality, disease resistances...) will allow choosing about 60 accessions for the core collection.

Reference

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