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European Avena genetic resources characterization for quality and agronomic traits.

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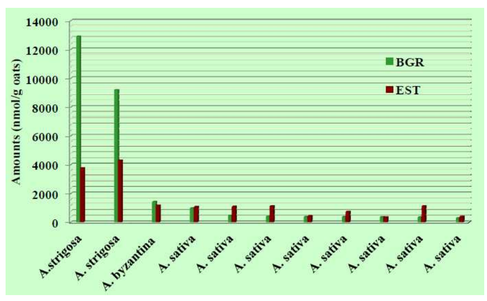
The AVEQ project: from phenotyping to genotyping

In the AveQ European cooperative project genebank material and oat varieties have been evaluated for traits considered important for future oat breeding in a European premium market. Six hundred fifty five oat accessions were selected- including current commercial cultivars as well as cultivated, marginally cultivated and wild genebank material- representing twelve *Avena* species, more than 100 years of breeding history and more than 30 countries of origin. All the accessions were evaluated in two-year field trials in seven European locations (Estonia, Sweden, Poland, France, Italy, Romania and Bulgaria) for some morphological and agronomic traits – including yield and disease resistance. In each experiment eleven standard cultivars have been included. In addition, a subset of about 150 accessions was genotyped using the Illumina 6K Oat Array, with the ultimate aim to perform association mapping for cold tolerance and quality traits.

Quality traits

All samples were analysed for protein, fat and total ß-glucan, and a subset of about 80 accessions were additionally analysed for soluble ß-glucan, starch, dietary fibre components (uronic acids, Klason lignin, and non- starch polysaccharides) and antioxidants (tocols and avenanthramides). For example, avenanthramides content in different *Avena* species is shown in Fig. 1.



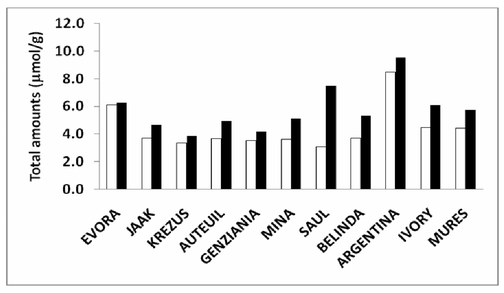


Fig 1. (left) Avenanthramides 2c, 2p and 2f content in different *Avena* species.

Fig 2. (right) Avenanthramides 2c, 2p and 2f content in standard cultivars.

Cold Tolerance

Cold tolerance was evaluated in open field trials in three environments (Italy, Romania and Bulgaria). In addition, chlorophyll fluorescence analysis (Fv/Fm) in controlled environments was used to confirm cold tolerance in a subset of about 200 accessions (Set 1 + Set 2). Five experiments with different stress temperatures (-6, -7, -10, -12 °C) for each set were carried out and relative rank based on a total of 30 measurements was calculated.

Set 1

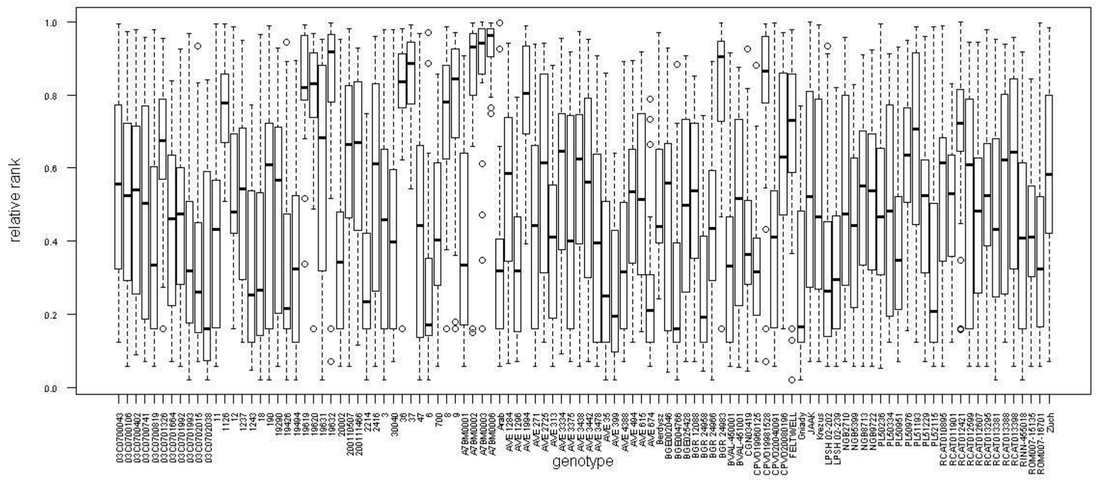


Fig 3. Cold tolerance variability based on chlorophyll Fv/Fm measurements in Set 1.

Set 2

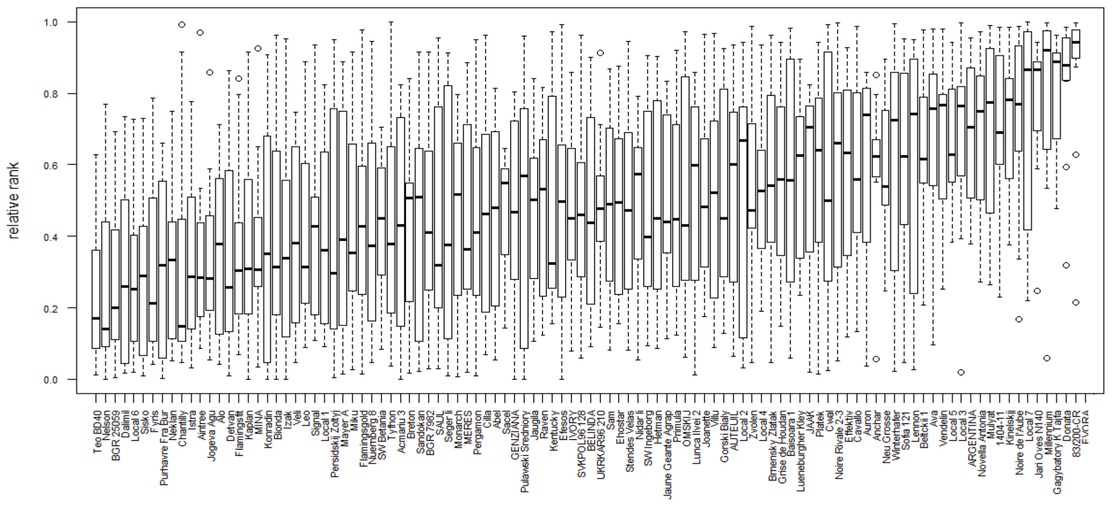


Fig 4. Cold tolerance variability based on chlorophyll Fv/Fm measurements in Set 2.

Genotyping

A subset of about 150 accessions (*A. sativa* + 5 *A. strigosa* accessions), including standard cultivars, was genotyped using the Illumina 6K Oat Array, which contains nearly 5000 SNP markers. Data were filtered to eliminate failed (Fig. 5) and monomorphic markers, reducing the final number of informative SNPs to about 2000. Population structure was investigated by means of Principal Component Analysis (Figures 7 and 8).

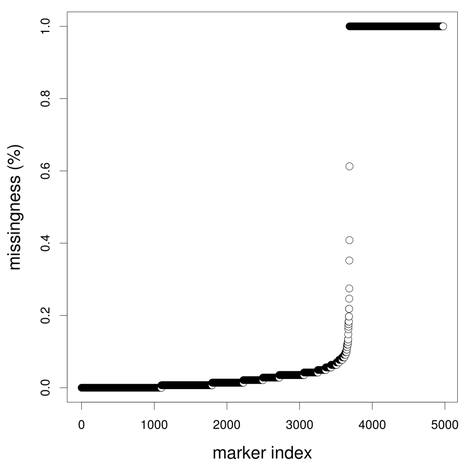


Fig 5. Percentage of missingness per marker (before filtering).

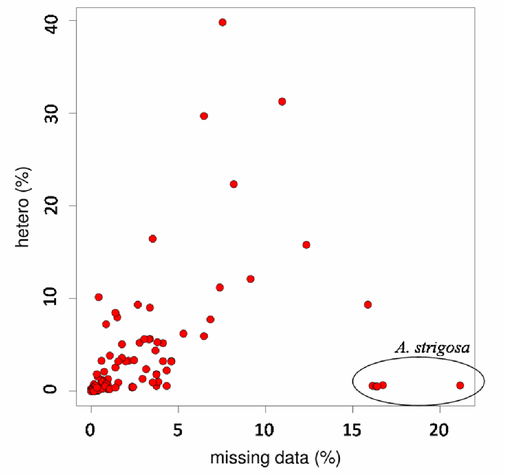


Fig 6. Heterozygous markers percentage vs. missingness per individual (after filtering).

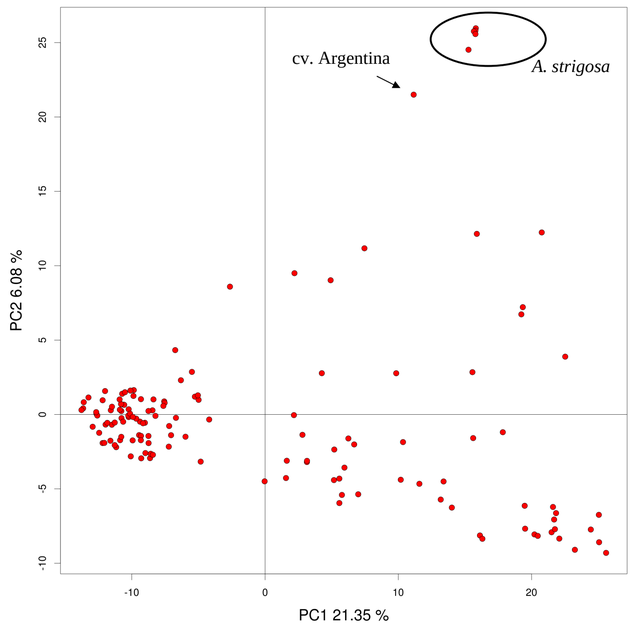


Fig 7. Principal Component Analysis. PC1 vs. PC2 .

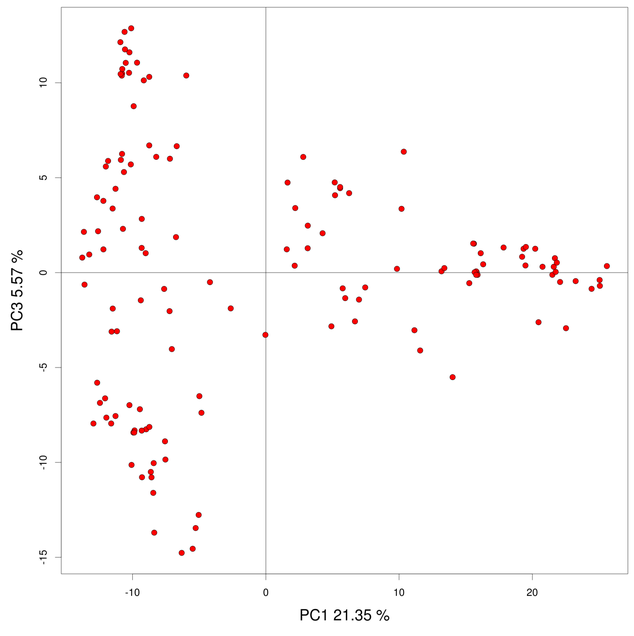


Fig 8. Principal Component Analysis. PC1 vs. PC3 .

Acknowledgements

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