





P 14 - Topic: Harnessing Diversity for Triticeae Improvement

### **High-throughput genotyping of Swiss bread and spelt wheat identifies unused gene pools for breeding**

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**Key message:** High-throughput genotyping of bread and spelt wheat landraces and modern cultivars with a 15K wheat SNP array reveals differences in their gene pools.

Modern cultivars of cereals carry only a fraction of the genetic diversity present in their wild progenitors and old landraces. The reduction of genetic diversity was caused by the use of only a limited number of plants during domestication and breeding. Genebanks are an important resource to preserve the genetic diversity of old landraces and wild progenitors. In addition, the accessions from genebanks may harbor agriculturally important genes that were missed during domestication and modern breeding. The direct use of landraces in breeding is limited, because they often also show undesired traits. Therefore, a detailed genetic characterization is necessary to make genebank material more accessible for modern breeding and to facilitate the separation of desired from unwanted traits.

We genotyped 502 bread wheat and 294 spelt wheat accessions from the Swiss National database with a 15K wheat SNP array. The bread wheat and spelt wheat are both hexaploid (AABBDD) and close relatives that can be interbred with each other. The genotyped accessions included landraces, mainly from Switzerland, as well as modern cultivars. The data revealed that bread wheat accessions are genetically different from spelt wheat accessions. This clear separation was also visible in all three sub-genomes. In addition, a set of bread wheat landraces that were diverse from modern cultivars was identified. Those accessions are promising targets for identification of novel genes, since they were likely missed in the Swiss wheat breeding program. The genotypic data facilitates the transfer of novel genes from landraces into modern cultivars.