Pangenomes of the Triticeae

Abstract

The genomic revolution, started by the introduction of high-throughput next generation sequencing technology in combination with improved compute power and algorithms, has made *de novo* sequencing and assembly, almost independent of genome complexity, a routine task. While sequencing of the multigigabase genomes of the Triticeae crop species barley, wheat, rye and wild relatives initially required the formation and collaboration of large research consortia, it is now feasible to sequence entire Triticeae genomes just as a part of a map-based cloning project. This opens the perspective towards systematically unlocking the crop genome diversity at species scale. Entire genebank collections of wheat and barley of the Federal ex situ Genebank of IPK Gatersleben are / were genotyped by sequencing, providing global population diversity resolution, which is used as a foundational information for pangenome sequencing. More than 75 barley genomes, including 25 wild *H. vulgare* ssp. *spontaneum*, were assembled into chromosome scale scaffolds using PACBIO Hifi and Hi-C data. Furthermore, a pangenome initiative is working towards a genus *Hordeum* pangenome. Further pangenome activities are underway in wheat, rye and oats.