Genebank genomics and pangeneome analysis in barley to make barley diversity accessible at species’ scale

Only 15 years ago a whole genome assembly of barley was far out of sight. Ten years ago a draft sequence integrated into a physical map changed this picture and today multiple barley genomes are assembled to chromosome-scale and many thousands of genotypes were captured by different means of re-sequencing. The genomic revolution has democratized genome sequencing and assembly in the AgGenomics era and there is no reason this trend will change. Today sequencing and assembly of an entire unknown barley haplotype has become a task within a single PhD study and does no longer require multinational consortia. Extrapolating this development into the near future it seems realistic that we will have access to genome diversity of our important crops at species’ scale, including wild progenitors and representatives of the secondary and tertiary genepools. Are we ready to make efficient use of this kind and dimensionality of information? In Research? In Breeding? This topic, recent progress and the related questions will be discussed during the Kjeldgaard lecture.