**High-density genetic linkage map for Scots pine (*Pinus sylvestris*) based on SNP array genotyping**

Maximiliano Estravis Barcala and Harry X. Wu

Linkage genetic maps serve as a complement to genome assemblies by helping to merge scaffolds and contigs, or to separate chimeric sequences. Linkage maps deal with recombination rates (genetic distance) rather than nucleotide distance, being an important tool for genome-wide association and adaptive evolution studies. Genetic map construction is facilitated in conifers due to the presence of a multicellular female gametophyte, each one representing a unique meiotic product, and thus avoiding the need of complicated crossing designs. In this study we present the first ultra-dense haploid genetic map for Scots pine (*Pinus sylvestris*), the second most important forestry species in Sweden. Haploid megagametophytes from two mother trees were manually separated from the maternal tissue and grounded, followed by DNA extraction and genotyping with the recently published Psyl50K SNP array. After quality filtering, a total of 12,851 SNPs and 1,091 individuals were kept for mother Y3088, and 11,646 SNPs and 433 individuals for AC1017. OneMap was used for map construction, which comprises linkage groups creation, ordering, and mapping. These steps were done for each mother separately, and then a consensus map was built. We present the genetic map consisting of twelve linkage groups, corresponding in most cases with the species’ twelve chromosomes in the latest genome assembly. We discuss markers which were assigned to the linkage groups but not to chromosomes in the current genome assembly, rather to unlocated scaffolds. For these cases, the genetic map will help to make the assembly more contiguous and trustworthy.