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

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Abstract (approx. 200 words)**:**

Linkage genetic maps serve as a complement to genome assemblies by helping to merge scaffolds and contigs, or to separate chimeric sequences. Importantly, linkage maps deal with recombination rates (genetic distance) rather than nucleotide distance, being an important tool for genome-wide association and adaptive evolution studies. Breeding can be accelerated and more precise by knowing the genetic linkage between molecular markers (like SNPs) and QTLs associated to important economic traits. 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. 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 show how this genetic map can help better understand the genomic landscape of this important forestry species with applications in comparative recombination studies, genotype-phenotype association, and genomic selection.

Key words:
Linkage maps – *Pinus sylvestris* – SNP array – High-throughput genotyping