

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

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CONCLUSIONS & PERSPECTIVES

- We present the first **high-density genetic linkage map** for Scots pine, with a consensus length of **1269.05 cM** and **18536 markers** across **12 linkage groups**.
- This genetic map will be useful for **improving the genome assembly** by assigning unlocalized scaffolds to chromosomes.
- Comparative recombination rates** studies will be carried out between pine (shorter maps) and spruce (longer maps) species using genetic distances.

Table 1: Genetic map metrics for each mother tree (AC1017 and Y3088, megagametophytes number in parenthesis) and the consensus map. **LG:** Linkage group. **Length** in cM.

LG	AC1017 (n = 433)		Y3088 (n = 1091)		Consensus	
	Markers	Length	Markers	Length	Markers	Length
I	796	107.96	665	113.95	1282	114.07
II	487	90.86	909	105	1400	105.59
III	737	98.26	1086	100.19	1755	101.86
IV	744	103.83	904	114.89	1415	115.53
V	959	104.62	992	79.64	1566	111.78
VI	717	93.53	988	111.78	1530	93.67
VII	812	105.65	1185	99.35	1857	123.58
VIII	855	108.64	912	91.07	1835	99.35
IX	869	93.67	1152	104.82	1634	110.24
X	1021	123.58	1063	108.74	1345	94.44
XI	852	103.8	850	94.07	1337	90.86
XII	940	97.63	990	105.54	1580	108.08
Total	9789	1232.03	11696	1229.04	18536	1269.05

Table 2: Comparative metrics of genetic maps in *Picea* and *Pinus* species. **Length** in cM. Modified from Ritland *et al.*, *Genetic mapping in conifers* (2011).

Species	Marker type	Marker number	Length
<i>Picea abies</i>	SNP	21056	3556
<i>Picea glauca</i>	AFLP, ESTP, SNP, SSR	821	2304
<i>Picea mariana</i>	AFLP, ESTP, SNP, RAPD, SSR	835	1850
<i>Pinus brutia</i>	AFLP, SAMPL, ESTP, SSR	1111	1770
<i>Pinus pinaster</i>	Isozymes, RAPD	463	1860
<i>Pinus radiata</i>	RFLP, SSR	173	1223
<i>Pinus taeda</i>	AFLP	508	1528

INTRODUCTION & METHODS SUMMARY

- Scots pine (*Pinus sylvestris*) is the most **widely distributed** Pinaceae species in the world.
- Important species for **wood production** in Sweden.
- Large** (>20Gbp) and **highly repetitive** genome.
 - Linkage maps are important for **genome-wide association** and **evolution** studies. Also, for improving fragmented genome assemblies.
- Haploid megagametophytes were manually separated from seeds and grounded in liquid nitrogen.
- DNA extraction and genotyping with Psyl50K SNP array.
 - Map creation with OneMap and LPmerge.

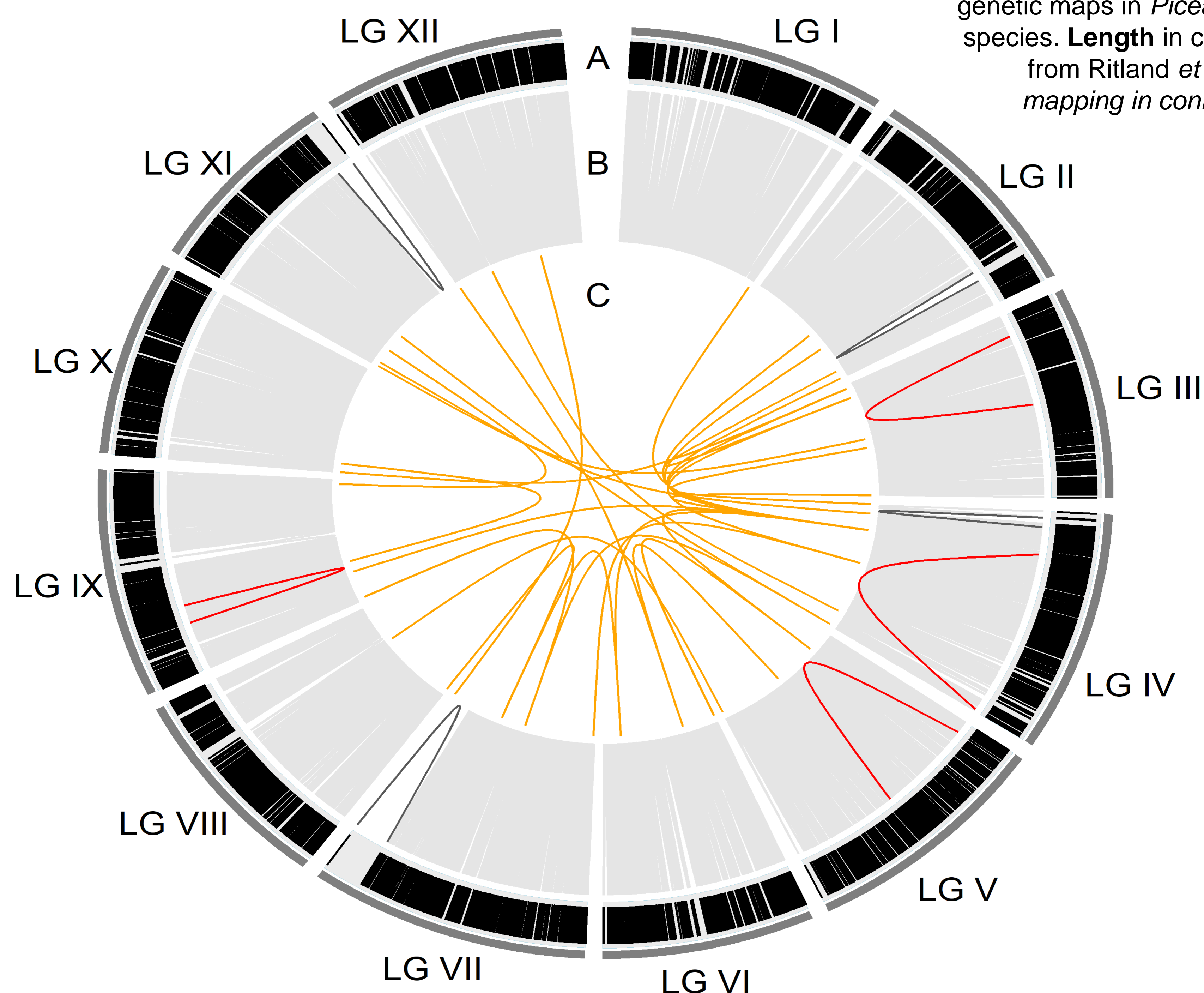


Figure 1: Circos plot of the consensus map. **A)** Marker distribution across linkage groups (LG). Black vertical lines represent markers (18536 in total) arranged according to their positions in cM. **B-C)** Dark gray lines link markers separated more than 5cM in the same LG. Red and orange lines represent mismatches between LG and annotated chromosome for markers in the same LG (red lines; panel B) or in different LGs (orange lines; panel C).



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SLU Breeding Network Meeting
"Breeding 360: Collaboration across disciplines"
May 6th – 7th, 2025
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