

Genome-Wide association mapping of frost tolerance in Pisum sativum

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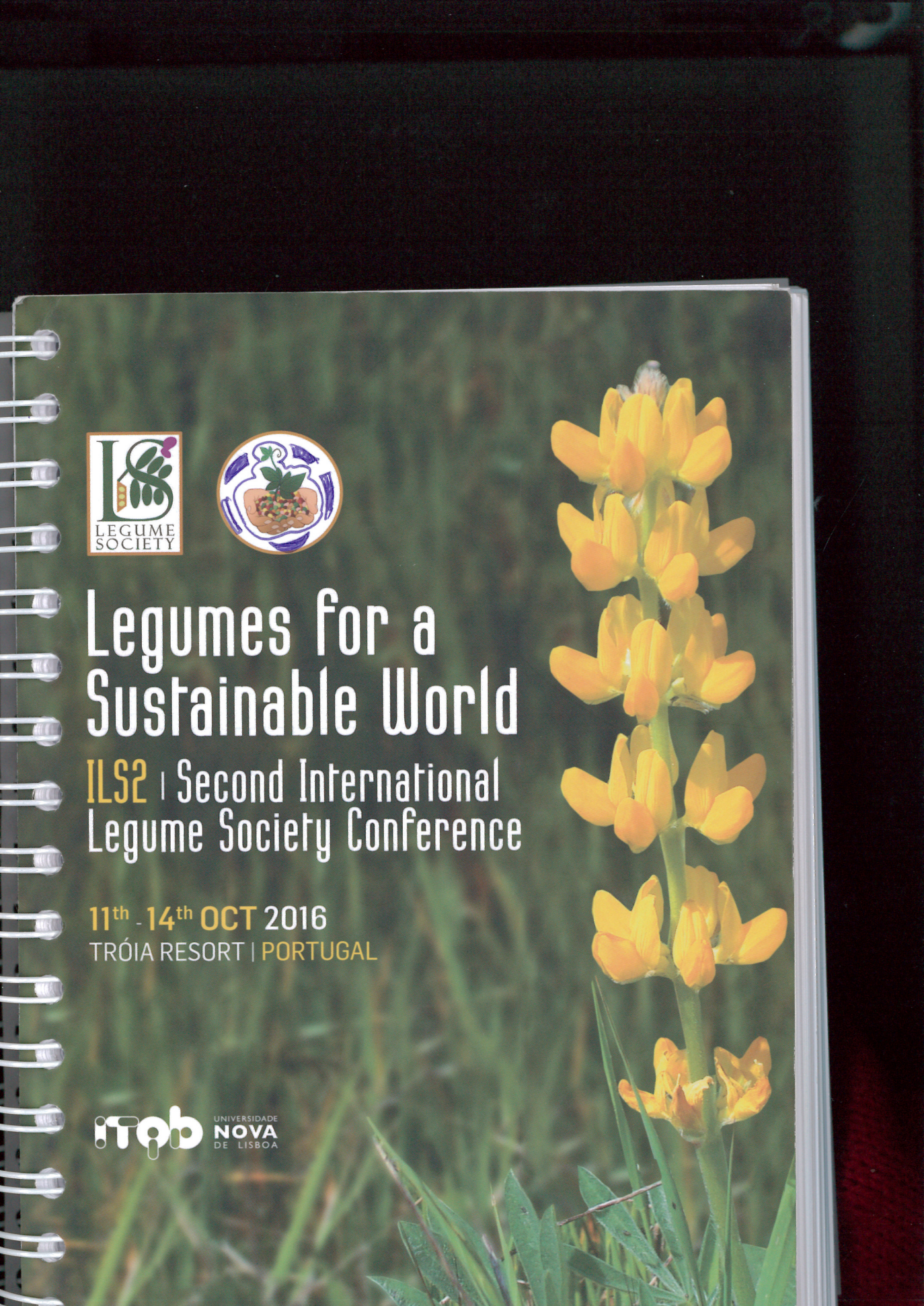
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Genome-Wide association mapping of frost tolerance in *Pisum sativum*

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Genome Wide Association Mapping was performed in pea. Accessions from the pea reference collection where phenotyped for frost in field and controlled conditions, and genotyped using Infinium®BeadChip 15K SNPs (Tayeh et al., 2015). After applying filters of quality control, we obtained 363 accessions and 10739 loci for GWA study. Association analyses were conducted with FaST-LMM software using a mixed model that included a relatedness kinship matrix (K) and a population structure matrix (Q) to control for false positives. The K matrix was generated using two approaches. In the first one, the kinship matrix was estimated with all the 10739 markers. In the second approach, we estimated the kinship, called "K-chr", with all the markers other than those located on the same chromosome as the marker being tested (Rincent et al., 2014). Simulations revealed that Rincent's approach was more powerful than the mixed model taking into account a general kinship (estimated for all chromosomes). The GWA study identified 8 loci distributed over different chromosomes comprising 61 SNPs significantly associated with frost tolerance. Results confirmed 3 QTLs that were previously mapped using bi-parental populations and identified 3 novel tolerance loci. Several potential-candidate genes were found corresponding to these SNPs. Additionally, the analyses allowed to identify haplotypes with increased frost tolerance and accessions with favourable alleles for this trait.