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Optical processing for the analysis of genetic data sequencing

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An optical image processing technique can be proposed for analyzing and exploring DNA sequences. The approach uses the powerful computing capability of optical correlation to provide real-time processing of the genomic data. Instead of representing the symbolic DNA sequences in numeric form, they are converted and treated as 2-D images for matching purposes. Both images of the reference and the target DNA sequences are combined and presented as a joint input image to an optical joint transform correlator (JTC) set-up for a real-time processing. This JTC-based approach is capable to search for similarity/dissimilarity between two tested DNA sequences. The optical approach can facilitate the exhaustive search algorithms for locally and/or globally DNA alignment. Simulations experimental results on actual DNA sequences will be presented to demonstrate the effectiveness of the proposed optical approach.

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Identification and verification of QTL associated with frost tolerance using linkage mapping and GWAS in winter faba bean

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Frost stress is one of abiotic stresses, which cause a significant reduction in winter faba bean yield in Europe. The main objective of this work is to genetically improve frost tolerance in winter faba bean by identifying and validating QTL associated with frost tolerance to be used in marker-assisted selection. Two different genetic backgrounds were used a biparental population (BPP) consisting of 101 inbred lines and 189 genotypes from single seed descent (SSD) from the Gottingen Winter Bean Population (GWBP). All experiments were conducted in a frost growth chamber under controlled conditions. Both populations were genotyped using the same set of 189 SNP markers. Visual scoring for frost stress symptoms was used to define frost tolerance in both populations. In addition, leaf fatty acid composition (FAC) and proline content were analyzed in BPP as physiological traits. QTL mapping (for PBB) and genome wide association studies (for GWBP) were performed to detect QTL associated with frost tolerance. High genetic variation between genotypes and heritability estimates were found for all traits. QTL mapping and GWAS identified new putative QTL associated with promising frost tolerance and related traits. A set of common 54 SNP markers in both two different genetic backgrounds showed a high genetic diversity with polymorphic information content ranged from 0.31 to 0.37 and gene diversity ranged from 0.39 to 0.50, indicating that these markers could be used for genotyping any faba bean population. Five SNP markers showed a significant marker-trait association with frost tolerance and related traits in both populations. Moreover, synteny analysis between *Medicago truncatula* (model legume) and faba bean genomes was performed to identify candidate genes of these markers. Collinearity was evaluated between the faba bean genetic map constructed in this study and the faba bean consensus map, resulting in identifying possible genomic regions in faba bean which may control frost tolerance genes. The two genetic backgrounds were useful in detecting new variation to improve frost tolerance in winter faba bean. Of the five validated SNP markers, one (VF_Mt3g086600) was found to be associated with frost tolerance and FAC in both populations. This marker was also associated with winter hardiness and high yield in earlier studies. This marker is located in a gene of unknown function.

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