Linkage Disequilibrium and Population Genetics in Spring Barley

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Analysing Linkage Disequilibrium (LD) and population structure is crucial for conducting genome wide association studies to lower the outcome of false positive marker-trait associations and to provide insight into the genomic constitution of the population analysed. Therefore, we genotyped 716 spring barley (*Hordeum vulgare*) lines containing high yielding accessions of actual breeding programs from two German breeding companies and a set of landraces from the fertile crescent, Africa and the Far East by iSelect SNP array technology enveloping 7800 markers. Results from LD analysis on the germplasm described above including an explanation of the methodology applied using a yet unpublished high density genetic map of the barley genome are presented. Furthermore detection of population structure has been performed by several approaches. A very common method is Bayesian clustering with the program *STRUCTURE*. There, the usage of linkage and allele frequency models shows enhanced estimation of population structure resulting in three clusters, whereas simple models can produce overestimated outputs up to 17 clusters. Besides multivariate analysis like principle component analysis and multidimensional scaling (MDS) reveals genetic diversity and is much faster, which is of special importance concerning the increasing amount of genetic information available. Two major findings from MDS are that on the one hand landraces clearly distinguish from breeders lines. On the other genetic diversity detected within the breeder's lines is much higher than within the landraces arising from the fact that the marker set was developed using breeders genotypes and therefore miss to detect diversity in wild relatives alleles.