Short Commentary   **Open Access**

Association Mapping for Drought Tolerance in Barley

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Short Commentary

Barley is one of the world's most important crops with uses ranging from food and feed production representing the fourth most abundant cereal in both area and harvested tonnage. Barley is the best suitable crop for genetic studies, because of its diploid nature with a relatively small number of large chromosomes and has been widely used as a genetic model. With the advance of new genomics platforms, transcriptome, metabolome analyses and bioinformatics, the dissection of various quantitative traits and the determination of their chromosomal locations which in turn led to the identification of a number of marker–trait associations in various crop species including barley become feasible.

Drought tolerance is defined as the ability of a plant to survive, grow, and produce a harvestable yield with limited water supply or under periodic conditions of water deficit [1]. Increased frequency of droughts negatively affect plant development, growth, yield, and ultimately production of crop species. In the light of climate changes other factors that affect the sustainability of the world's resources and its consequences on food security, development of drought tolerant cultivars is therefore essential for maintaining yields under climate change conditions and for the extension of agriculture to sub-optimal cropping areas [2]. Given the complexity of the genetic control of drought tolerance (polygenic inheritance, low-heritability, and high G×E interactions), marker-assisted breeding has not contributed significantly to crop improvement for drought tolerance. However, progress has been made in the last two decades in understanding the genetic basis of drought tolerance in crop plants which is a prerequisite for the application of marker-assisted breeding in the development of cultivars with improved tolerance [3].

Conventional Quantitative Trait Loci (QTLs) analysis applying molecular markers on bi-parental populations is one of the most suitable methods for identifying genes that are involved in drought tolerance. However, it necessitates the development of a genetic linkage map and is identified based on linkage equilibrium in bi-parental population undergoes just a few cycles of recombination which limits the resolution of genetic maps and identified QTLs. Besides, in conventional QTL analysis several factors affect the detection of QTLs including the type, size and structure of the population, the number of environments sampled, calculation method, and number of molecular markers. Therefore association mapping, which has been successfully applied in human genetics to detect quantitative trait loci (QTL) of complex diseases and is dependent on the structure of linkage disequilibrium of alleles at different loci, is an alternative powerful approach for fine mapping of quantitative traits [4-6]. Linkage disequilibrium (LD) is affected by several biological factors such as recombination rate, selection, mutation, and population admixture. In plants, LD has been shown to extend from hundreds of base pairs to hundreds of kilobase pairs, depending on the species and type of analyzed population. The extent of LD determines whether a sufficient number of markers can be implemented to scan the entire genome or candidate genes association analyses is required [7-9].

The rapid development of genotyping platforms, e.g., Genotyping-by-sequencing (GBS) has facilitated the application of association mapping for a range of genetics studies and breeding applications [10]. Barley is a diploid and could serve as good model for cereal crops such as wheat, which has an even larger and more complex, hexaploid genome of 17 GB. Despite its complex and huge genome (5.1 GB), a sequence-enriched physical and genetic map of barley was recently accomplished and could serve as an excellent resource for future genetic studies and crop improvement [11,12].

The main challenge in association analysis is to separate associations between markers and traits resulting from physical linkage of genes from those that are generated as a result of population structure and kinship association. Therefore, to overcome this problem, the QK mixed model should be considered in association analysis to control population structure and kinship. The QK method was essentially developed to abolish false associations caused by population structure and kinship. Association mapping is a powerful approach that could be successfully implemented to identify significant marker–trait associations through linkage equilibrium in barley with high mapping resolution as well as less research effort [13,14].

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