Identification of molecular markers linked to multiple rust resistance traits in Kazakh bread wheat

Abstract:

Bread wheat (*Triticum aestivum*), is considered as the second most important staple crop in the world after rice, providing the food for approximately one third of the world's population. It represents approximately 20% of the global major cereal crop production with 759.5 million tonnes (FAO, 2018), and thus plays a key role in global food security. Due to the increasing food demand of an increasing human population, bread wheat production is only likely to increase in its importance in the future (Tadesse et al. 2016). Of the approximately 46 fungal diseases of wheat that have been documented, rust diseases are the most economically important. Controlling these destructive fungal diseases through rust resistance breeding is the most effective and environmentally friendly approach to minimize the yield losses and bring more financial benefits to plant breeders, farmers and consumers (Singh, 1998; Vida, 2009; Herrera, 2011). To ensure a diverse pool of genetic-based resistance is available for breeding, identification of new and effective major rust resistance genes from different germplasms of global wheat cultivars is essential.

Recent advances in molecular marker technology have created effective tools for selective breeding which has several advantages over traditional phenotype-based trait selection. Marker-assisted selection (MAS) has also been widely used to target wheat rust resistance genes. Molecular markers offer powerful tools to tag rust resistance genes and as a part of MAS can be used in the improvement of plant breeding efficiency. This research project aims to identify PCR-based markers associated with important leaf and stem rust resistance genes, and then develop these markers into highly accurate and easy-applicable PCR-based markers for using in breeding programs. In this study, PCR-based molecular markers used for MAS included; length SSR (Simple sequence repeat) polymorphic markers, Cleaved amplified polymorphic sequences (CAPS), and SNP (Single nucleotide polymorphism). The aims of this research are;

1) To identify the PCR-based markers (length polymorphic marker, SNP and CAPS markers) linked to rust resistance genes in Kazakh wheat varieties the identified disease resistance genes.
2) To develop a MAS strategy using the identified molecular markers to detect the candidate resistance genes in selected Kazakh bread wheat varieties.

The results of recent work provided further information about polymorphic fragments of *Lr22a* and *Sr2* amplified from different homoeologous genomes. The complete sequences of cloned fragments will be useful for genome-specific primer design to avoid the cross-amplification in the PCR of target in paralogs from the same genome and from homologs and paralogs in the homoeologuos genomes. In addition, one SNP identified at recognition site of *Bco*DI restriction enzyme can be used for developing CAPS marker, allowing the differentiation PCR products from target genome than other genomes. Furthermore, the successful development of CAPS marker for *Lr51* revealed an additional easy, cheap and reliably score-able marker which can be routinely used to track *Lr51* in not only Kazakh wheat varieties but also worldwide wheat germplasms. More importantly, the designed Amplifluor-like SNP system showed the level of effectiveness and accuracy in allelic discrimination of *Lr*51, indicating the potential use of this cost-effective genotyping technique in future genotyping studies involving this leaf rust resistance trait.