A Strategy of Soybean Molecular Breeding

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Abstract

Soybean molecular breeding represents development of soybean breeding, which includes marker-assisted selection (MAS) breeding, transgenic breeding and molecular design. In this paper, we introduced a strategy of molecular breeding based on the mini-core collection. By series of concentration of genetic diversity within a huge amount of germplasm, the mini core collection was extracted from core collection derived from the primary core collection. A few accessions with favorite trait such as 28k null and low content of β subunit were identified among a large range of variation, indicating representative of mini core collection. By using the mini core collection as donor parents, some elite cultivars as recipient parent had showed the potential of improvement of both yield and quality. The results indicate that this strategy can be benefit for both gene discovery and marker assisted selecting breeding.

Key words

Soybean, molecular marker, gene, selection, core collection, germplasm

Media summary

A strategy of molecular breeding based on the mini-core collection was established, which can be benefit for both gene discovery and marker assisted selection breeding.

Introduction

Soybean is originated in China and has been planted for over 3000 years. It is an important plant source of protein and edible oil. Since 1923, by using conventional breeding methods, a number of cultivars have been developed for soybean production, which plays an important role in the promotion of soybean production and ensuring consumption demand. However, since 1995, China started importing soybean, which was mainly transgenic soybean. The imports amount has been steadily rising up to 0.82 million tons in 2007, accounting for two-thirds of the domestic soybean market. China's soybean production was unable to meet the growing domestic consumption demand, because China's soybean yield level is not only lower than the world average level, but also far below the level of the world's top three main soybean-producing countries, United States, Brazil and Argentina. Since China's areas of arable land are limited and steady declined, it is only choice to increase the total production of soybean by improving the yield level. In national soybean GeneBank, that houses the most of the world soybean germplasm collection of over 23000 accessions, less than 1% of the accessions was used in developing 1500 cultivars from 1923 to 2005. Thus most cultivars have a narrow genetic base. This exiguous use of germplasm is due to lack of reliable information on traits of economic importance. Therefore core collection has been established and utilized for improving the soybean yield.

Development of soybean core collection

Based on the passport data and agronomic traits of these germplasm, a total of 20 sampling methods were compared. The primary core collection was then selected by the best method

(Qiu et al., 2003) and artificially adding accessions with traits that not included (Wang et al., 2006).　Then this collection was analyzed by a core set of SSR loci, which identified with 80 autumn soybean accessions (Xie et al., 2003) and confirmed with 190 random soybean accessions from the whole country (Wang et al., 2003).　The core collection established with both SSR data and agronomic traits were more representative than those chosen on the basis of either (Wang et al., 2006).　The mini core collection (1% entire accessions) concentrated the most genetic diversity from core collection.

Evaluation of phenotypes and genotypes

The mini core collection was subjected to (1) replicated multilocational evaluations to identify traits of economic importance for genotype x environment interactions, (2) analyzing some quality traits such as lacking allergic protein 28K and lipoxygenase null, protein content and quality (11S/7S) as well as oil content, (3) identification of resistance such as soybean cyst nematode, soybean mosaic virus and salinity etc. Meanwhile, it was sequenced for candidate genes of some important traits and genotyped by using markers of SSRs (Wang et al., 2003), SNPs, SCARs etc. The results showed that the core collections had vast diversity with lower ratio for the targeted traits (Zhang et al., 2006), indicating that the core collection would provide an effective platform in proper exploitation of soybean germplasm resources for the study of complex traits and discovering novel favorite traits for crop genetic development.

Mini-core collection based backcross

The local modern elite cultivars adapted to various cultivated regions were used as recipient parents to cross and backcross with each of the accession within the mini-core collection as donor parents. It is obviously needed to backcross at least twice so that the introgression lines appeared to be adapted the local environment. It is proved by analyzing pedigrees of 195 Chinese modern soybean cultivars, because the Tokachi-Nagaha introduced from Japan had contribution rate of 0.78-50.00%, in which 12.50%, 6.25% and 25％ derived about 77.3% of the total cultivars (Guo et al., 2007). A series of introgression lines with few fragments from donor parents were selected for different favorite trait. The introgression lines carried similar fragment among various cultivar backgrounds or carried various fragment among same cultivar will be compared for mapping the important traits. So far, the potential improvement of yield and quality has been observed by using recipient parent as checks.　The pyramiding important traits have been undertaking among the introgression lines.

Molecular markers assisted selection

Soybean target gene selection is also known as foreground selection. Reliability of foreground selection depends primarily on the close linkage degree between genetic markers and the target gene. Some screened and developed molecular markers is been using for selection of important traits such as SCN, SMV and salinity resistances among the introgression lines. Selection of other parts of genome except the part of target gene referred as background selection. The MAS for the background increased recovery rate of the recurrent parent had been studied (Duan et al., 2002). However, two issues needs to be considered. One is how to identify the advanced backcrosses in order to increase the background recovery rate of recurrent parent since there are making many crosses for each year. The other thing is related to the backcrossing times. When 102 near isogenic lines (Backcross six times) were identified with scattered markers over the whole genome, most of the NIL consisted of over 3 fragments from the donor parents. The results indicated that the actual recovery rates of recipient parent genome were usually lower than the theoretical ones, which means more backcrosses will be needed if introgression line has to keep only few fragments from genome of donor parent.

Prospect of soybean molecular breeding

The key of soybean molecular breeding for this strategy is to discovery and use genes. By developing the genome wide introgression lines based on mini-core collection, the genes will be discovered and identified in a large-scale by using association analyses. In order to achieve the directional and highly efficient precision breeding by cooperating molecular breeding with the traditional breeding, the increase knowledge of soybean genomics, bioinformatics etc will be very helpful. It is also possible to realize soybean cultivar molecular design breeding, if design theory and methods will be developed accompany with the construction of digital industrial system for soybean breeding.

Conclusion

A representative mini core collection was established by using passport data, agronomic traits and SSR markers. It has been further evaluated for important traits and found favorite traits for mining novel genes. Meanwhile, this mini core collection was transferred to different elite cultivars background for large scale gene discovery and molecular breeding.

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