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A novel strategy of genomic selection in breeding for soybeans Junyi Gai*, Nanjing Agricultural University, Jiangsu, China Xuegin Liu, Nanjing Agricultural University, Jiangsu, China Optimal cross design and precise progeny selection are major steps in conventional soybean breeding. Genomic selection (GS) is a marker-assisted selection procedure based on genome-wide SNP/marker information, which composes two links, establishing an index between required targets and SNPs/markers from a training population, and then using the index in progeny selection based on its genome-wide SNP/marker information. The GS was originally designed for animal breeding, especially for progeny selection, but not for optimal cross design in plants. Therefore, a novel GS strategy for both optimal cross design and precise progeny selection is expected. In soybean, the collected germplasm is a genetic reservoir from which all the varieties were developed. If the genetic constitution in terms of gene/QTL-allele composition of all breeding target traits in the reservoir has been explored, the genetic constitution of its derived parental materials can be inferred from their genome-wide markers. Since this kind of QTL/allele-marker relationship was obtained from the permanent reservoir rather than a temporary sample, the genetic information can be used everywhere in an ecoregion successively. In soybean breeding, the optimal cross design determines its progeny selection potential, therefore, is a key GS stage. Then the progeny GS should be based on the genetic constitution of the progenies. At this stage, the needed marker information will be limited only on the involved QTL-alleles (dozens for a single trait and hundreds for multiple traits), not necessary a whole set of genome markers, so the genotyping work for progenies can be reduced. Accordingly, the suggested novel GS strategy in soybeans is based on QTL-allele dissection of the reservoir and composes GS for optimal crosses and GS for progeny selection. Its prerequisite is a precise QTLallele dissection in the reservoir. We have developed a novel RTM-GWAS procedure which can meet the requirement and is ready for demonstration.