COMMENTARY

Genetic mapping

Simegn Alemu *

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ABSTRACT

On analysis of all individuals collected from sample populations biological assay is based. Extensively used in gene mapping through bulked segregant analysis with biparental populations, bulked sample analysis (BSA), has been, mapping by sequencing with major gene mutants and pooled genome wide association study using extreme variants, which works with selected and pooled individuals.

Key words: Gene mapping; Genomics; Phenotype; Genes

DESCRIPTION

BSA significantly reduces the scale and cost by simplifying the procedure, compared to conventional entire population analysis. The bulks can be built by selection of representative samples from any populations and all types of segregants and variants or extremes that represent wide ranges of phenotypic variation for the target trait. Methods and procedures for bulking, sampling and multiplexing are described. Microarrays and high-throughput sequencing at all levels of DNA, RNA and protein the samples can be analysed using individual markers. By, genetic architecture, selection of extreme individuals, population size, sequencing strategies, of the trait and marker density the power of BSA is affected. BSA will facilitate plant breeding through marker assisted selection and selective phenotyping development of diagnostic constitutive markers, agronomic genomics.

For two contrasting groups of individuals from any population as suggested the pooled DNA analysis can be used not just for those from biparental segregating populations. Such as major gene mutants and their corresponding wild types which are strategically different from MutMap using bulked segregants from the mutant derived population first, the same principle has been used in mapping by sequencing using two contrasting groups. Second, bulked for sequencing and genomewide association study the individuals with extreme phenotypes from natural populations.

Pooled samples from genetics and breeding populations and all analyses using selected in this article, the term bulked sample analysis is used. To achieve the best representativeness by selecting only a part of individuals from the entire sample set and pooling as bulks we define BSA as a sampling–bulking method. Samples that represent individuals collected from populations and markers that represent all types of biomarkers at DNA, RNA and protein levels, to generalize the concept, we define these two important components involved in BSA.

CONCLUSION

Selective assay, by which only individuals with extreme phenotypes are analysed, such as selective genotyping to maintain the statistical power by reducing cost and simplifying analytical process, has been proposed. Analyse as a pool and bulk all the individuals selected from each tail of the population, a further significant cost reduction. For example is to, pooled DNA analysis for marker identification was developed by two groups independently but named differently as bulked segregant analysis and DNA pooling. Increased tail sizes and high density markers so that there is no need to validate the putative markers, more recently, bulked segregant analysis has been modified to locate the target genes, by genotyping the entire populations using the positive markers by using large populations.

Department of Genetics, Beni Suef University, Beni Suef, Egypt
Correspondence: *Simegn Alemu, Department of Genetics, Beni Suef University, Beni Suef, Egypt, E-mail: alemusimegn22@gmail.com*

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