

Developing new breeding approaches and genetic analysis in bambara groundnut – linkage and association analysis in MAGIC populations (Code: Bam1-006)

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Background Information

Bambara groundnut (*Vigna subterranea* L. Verdc) has potential to contribute to global food and nutritional security. However, typical of most underutilised crop species, there are no improved varieties/cultivars of Bambara groundnut developed via controlled breeding programmes. Landraces which have been selected by farmers remain the only source of planting materials. The concept of ideotype crop varieties/cultivars that combine superior yield potential and desirable agronomic traits with maximum adaptability to specific ecologies is the aim of breeding programmes. Availability of improved varieties is also one of the main motivating factors leading to large scale cultivation of crops by farmers. Uniformity of agronomic traits allows synchronization of cultural practices (leading to efficiency and cost effectiveness in farm management) and it is one condition needed for successful mechanisation of agriculture. The development of varieties of Bambara groundnut with uniform and desirable agronomic traits is necessary, if the potential of this underutilised crop species is to be effectively harnessed for global food and nutritional security.

Moreover, not much is known about the genetic inheritance of important agronomic traits in Bambara groundnut. Linkage analysis using advanced approaches that generate high density maps (DART Seq, SSRs) can provide important information on the genetic inheritance of agronomically important traits. Association Genetics is now becoming feasible in underutilised crops, with saturation using high density markers now possible. In inbreeding species, dominant markers are fully informative, making the use of both dominant and co-dominant marker types derived from DARTSeq-based association mapping feasible in Bambara groundnut.

To effectively utilise resources and save valuable time, the need for permanent multi-utility germplasm resources to tackle various genetic questions while generating valuable novel recombinants of genotypes for introduction, evaluation and selection within different environments is of huge significance. The 'second/next generation' breeding germplasm resource or breeding populations appears to meet these strategic breeding needs and could present a paradigm shift for breeding and genetic studies in plants species. Of the various types of the second/next generation breeding populations, Multi-parental Advance Generation Inter-cross (MAGIC) appears very useful to plant breeders and is becoming increasingly popular. It has the advantage of integrating multiple sources of alleles into a single population and the early generations of population development allows conventional linkage mapping and QTL analysis, along with fine mapping at later generations. As such, MAGIC populations represent a potentially new way to integrate the best aspects of linkage analysis with association mapping, while generating germplasm for selection within different environments.

Objective(s)

This project therefore proposes to begin the development of high yielding varieties of Bambara groundnut with desirable uniform agronomic traits (e.g. shorter flowering and maturity period, cream coloured testa, etc.) through novel breeding approaches, coupled with molecular genetic analysis to understand the basis of agronomically important traits.

Proposed methodology

Eight founder parental lines will be involved in the development of the MAGIC population. Important breeding objectives such as testa colour, yield potential, geographical location adaptability, crop architecture and phenology, days to physiological maturity etc. will be taken into consideration in selecting founder parental lines. At the early stage of the population development, linkage and QTL analysis (DArT Seq, SSRs) of important agronomic traits will be carried out followed by fine mapping (DArT Seq) at the latter stages.

Expected outcomes

The following outcomes are envisaged from the successful completion of the project;

1. Develop (or at least start the development of) Bambara groundnut ideotypes (varieties) for the different agro-ecological zones where the crop is grown across Africa and South East Asia.
2. Linkage maps and QTL analysis of important agronomic traits in Bambara groundnut to aid future breeding programmes.
3. A permanent germplasm resource for association genetics and/or comparative genomic analysis of agronomic traits in Bambara groundnut.