The research has developed high- density SNP genetic map in pearl millet. This map is also part of the results being used by the larger multi-institutional pearl millet genome project in publishing comprehensive pearl millet genetic map. The SNP genetic map has been used for identifying probable QTLs for several important traits useful for producing higher yielding pearl millet varieties for southeast USA.

Development of high density genetic map and its utility in QTL mapping for agronomic traits in pearl millet

Who cares and why?

Pearl Millet is known for drought tolerance and its ability to grow on low fertility soils. It is a multi-purpose crop which can be used for grazing as well as grain. The grain is gluten free and much in demand as whole grain as well as flour in health food stores and also has become a general shelf item in all grocery stores. Pearl millet flour is much in demand by immigrants from Indian subcontinent and from Sahel Africa.
Climate in the Southern United States is suitable for growing pearl millet. Georgia farmers are familiar with this because it is a widely accepted for cattle forage. The production and harvesting of pearl millet can be carried out using the existing farm machinery for grain production. Therefore, research to introduce pearl millet into Georgia agriculture makes sense as it will provide much needed high return enterprise to local farmers. Improvement of pearl millet for higher grain yields under Southeastern environmental conditions has been undertaken under the project to improve the adaptability and value of pearl millet for US growers.

Pearl millet is a highly cross-pollinated species and has a large genome size of ~2350 Mb. This crop lacks a reference genome and, therefore, development of genomic resources is essential to enhance genomic-based studies. The detailed information gained from genomic studies will further aid in development of germplasm suitable for domestic use. Pearl millet germplasm development requires improvement in several physiological and agronomical traits that can increase the feed quality and yields. Therefore, identifying the genetic basis of underlying traits will support breeding programs for pearl millet crop improvement. This project was undertaken to develop a dense genetic map in pearl millet which can be used in downstream analysis such as QTL mapping and genomic selection.

What has the project done so far?

We have completed several milestone achievements in this project. Recombinant inbred population obtained from two parents, Tift 99B and Tift 454, were used in this study. Both these parents are dwarf, early grain types that were developed and used by USDA ARS and UGA, Tifton in producing a commercial hybrid known as Tiftgrain 102. These parental lines were shown to be resistant to rust, pyricularia leaf spot and nematode damage. We have developed a high density genetic map using Genotyping-by-Sequencing. Sequencing of 184 RILs produced a large dataset for SNP calling. Several combinations of methods such as hierarchical clustering, bootstrapping and assembly were adopted and yielded a linkage map with thousands of markers. We have developed a linkage map with ~16,000 SNPs and ~ 275,000 anchored sequence tags. The linkage map consists of seven distinct linkage groups which span a total genetic length of ~470cM. To our knowledge, this is the first

high density linkage map in pearl millet. The data is also shared with Cornell University working on diverse mapping population and diversity population. The GBS markers were also used for genome assembly and ordering scaffolds in genome sequencing project led by ICRISAT. The project was also undertaken to phenotype several agronomic and physiological traits in the field. We were able to validate the utility of map using several phenotypic traits and identified QTLs influencing these traits. Identification of potential regions influencing digestibility are underway.

Through this project potential collaborations were developed with other universities and institutes such as Alabama A&M University, Cornell University, USDA-ARS, Tifton and ICRISAT, India. This project has also funded and supported several graduate students.

Impact Statement

GBS is an efficient tool for generating maps with high density markers in pearl millet which lacks reference genome and hence other researchers can use a similar approach for creating high resolution maps.
The results from this study facilitates pearl millet research community such as genome assembly and ordering chromosomes in pearl millet genome sequencing projects and other related projects. It will also help other researchers working on pearl millet mapping population in calling SNPs using tags in this population while constructing linkage maps.

This project will identify potential genomic regions of interest for agronomic traits. The identified markers will be used in making decisions for selection of lines to be used in making crosses. This will facilitate breeders in developing inbred lines through marker-assisted selection. Results generated by this project will be disseminated to farmers, researchers, extension personnel, breeders and other stakeholders.

What research is needed?

Further research is needed in validating the potential markers in their utility for marker-assisted selection and genomic selection and identification of suitable varieties through multi-location trials and testing. Extensive research is also needed to conduct expression studies involving high-throughput sequencing and phenotyping procedures.

Want to know more?
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