Napiergrass (*Cenchrus purpureus* Schumach.) is a tropical forage grass and a promising lignocellulosic biofuel feedstock due to its high biomass yield, persistence, and nutritive value. However, its utilization for breeding has lagged behind other crops due to limited genetic and genomic resources. In this study, next-generation sequencing was first used to survey the genome of napiergrass. Napiergrass sequences displayed high synteny to the pearl millet genome and showed expansions in the pearl millet genome along with genomic rearrangements between the two genomes. Furthermore, to construct a high density genetic map of napiergrass, genotyping-by-sequencing (GBS) was employed in a bi-parental population of 185 F1 hybrids. A total of 512 million high quality reads were generated and 287,093 SNPs were called by using multiple de-novo and reference-based SNP callers. Single dose SNPs were used to construct the first high density linkage map that resulted in 1,913 SNPs mapped to 14 linkage groups, spanning a length of 1,410 cM and a density of 1 marker per 0.73 cM. This map can be used for many further genetic and genomic studies in napiergrass and related species.

**INTRODUCTION**

- Napiergrass (elephant grass) is a tropical perennial C4 grass.
- It is an allotetraploid \(2n = 4x = 28, A' A'' B'B''\)
- Cultivated primarily for forage and widely used by smallholder dairy farmers in Africa
- Important cellulosic energy crop due to its high dry biomass yield
- Dry matter yield is highest in napiergrass compared to other bioenergy crops like sorghum, switchgrass, or sugarcane.
- Breeding of napiergrass for desirable traits is lagging
  - Little genetic information available
  - Absence of genetic map
  - Absence of reference genome
  - Molecular tools haven’t been deployed in breeding programs
- Molecular tools haven’t been deployed in breeding programs

**OBJECTIVES**

- Compare software for SNP calling in napiergrass
- Construct high-density genetic map of napiergrass
- Investigate genomic and genetic architecture of napiergrass

**MATERIALS & METHODS**

- Contrasting napiergrass parents 
  - N190 and N122 were crossed
- N190
  - Late flowering
  - Reduced number of thick tillers
  - High biomass but not persistent
- N122
  - Early flowering
  - Prolix tillering with thin stalks
- Mapping population of 185 F1 hybrids was developed
- DNA was extracted from leaves using Dellaporta protocol
- DNA samples were submitted to Cornell University for Genotyping by Sequencing (GBS)
- Enzyme used for digestion in GBS: PstI
- Sequenced on 2 lanes of Illumina HiSeq 2000
- SNPs were called according to the software used
- Linkage map was constructed using JoinMap 4.1
  - Marker grouping: LOID 20
  - Regression-mapping algorithm
  - Kosambi function
- Four different software pipelines were compared
  - TASSEL de-novo UNEAK
  - TASSEL de-novo SNAP
  - SNPs called
  - Mapped SNPs
  - Mapped SNPs (%)

**RESULTS**

- 1,913 single dose SNPs were mapped to 14 linkage groups, spanning a length of 1,410 cM and a density of 1 marker per 0.73 cM (Fig. 3)
- Genetic map had 1,913 SNP markers grouped into 14 linkage groups, spanning a length of 1410 cM and a density of 1 marker per 0.73 cM.
- TASSEL de-novo UNEAK showed the highest percentage of SNPs mapped followed by stacks and Stacks (Fig. 4)
- TASSEL de-novo UNEAK showed the highest percentage of SNPs mapped followed by Stacks and SAMtools (Fig. 4)
- GBS was successfully used to construct a high density genetic map of napiergrass
- The genetic map had 1,913 SNP markers grouped into 14 linkage groups, spanning a length of 1410 cM and a density of 1 marker per 0.73 cM.
- TASSEL de-novo UNEAK pipeline retained highest number of SNPs on genetic map followed by STACKS.
- Tags of napiergrass showed high collinearity to pearl millet genome.
- For most of the pearl millet chromosome, there were two corresponding regions on the napiergrass genome.

**CONCLUSION**

- GBS was successfully used to construct a high density genetic map of napiergrass
- The genetic map had 1,913 SNP markers grouped into 14 linkage groups, spanning a length of 1410 cM and a density of 1 marker per 0.73 cM.
- TASSEL de-novo UNEAK pipeline retained highest number of SNPs on genetic map followed by STACKS.
- Tags of napiergrass showed high collinearity to pearl millet genome.
- For most of the pearl millet chromosome, there were two corresponding regions on the napiergrass genome.

**REFERENCES**


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