

Unlocking the genetic potential of an indigenous forage, lablab (*Lablab purpureus* L.) collection by the whole genome sequencing approach

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Context

Globally, livestock production is a prominent source of protein and income particularly for smallholder farmers of Africa; its production and productivity is dependent on access to health interventions, quality feed and livestock genetics. In the current scenario, feed availability in Sub-Saharan Africa (SSA) is challenged due to biotic and abiotic factors which are exacerbated by climate change and dwindling arable lands. Lablab (*Lablab purpureus* L.) is mainly known as a pulse or vegetable crop but is also an important source of animal feed in SSA, particularly known for its drought tolerance and high quality. This research aims to develop phenotypic metadata and a genomics database for lablab, thereby enabling advanced plant breeding procedures, such as genomic selection and marker assisted breeding at National Agricultural Research Systems (NARS). The data generated in this action will be made publicly available in order to facilitate application of genomics-based breeding at NARS.



Fig 1. Lablab accessions with different seed coat colour at ILRI gene bank (A) and field evaluation of 143 lablab accessions (B)

Findings

Field evaluations showed significant variations in agro-morphological and feed quality traits. For example, accessions showed significant variation in terms of plant height, fresh weight and dry weight. The genotyping generated more than a million high quality genome-wide SNPs, after mapping reads to a reference genome (Njaci et al 2022) which were used to assess genetic diversity (Fig 2A). Genome wide association study (GWAS) identified candidate loci associated with traits of interest such as fresh weight and other phenotypic traits measured in this study (Fig 2B).

Methods

More than 300 lablab accessions are conserved at the ILRI forage gene bank (Fig 1A). One hundred and forty-three accessions which represented as broad a diversity of the whole collection as possible were phenotyped at three locations (Bishoftu, Melkassa, Mieso), with different agro-ecologies, in Ethiopia (Fig 1B). The same accessions were also sequenced on an Illumina platform using paired-end 2 × 150 bp short-reads at 10x depth.

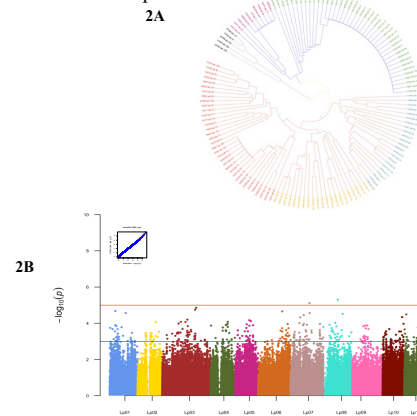


Fig 2. Clustering of lablab accessions based on SNP variants (A) Manhattan and quantile-quantile (Q-Q) plots of SNPs in linkage groups 7, 8 & 11 showed significant associations with fresh weight (B)

Perspective

If the livestock production system is supported with sufficient quality and quantity of feed, then it can begin to reach the potential contribution to socio-economic development and minimize health loss, even death, arising from protein malnutrition. Therefore, key tropical forages such as lablab should get much needed research attention in terms of developing genomics tools capable of accelerating breeding projects in Africa and worldwide.

Reference

Chromosome-scale assembly of the lablab genome - A model for inclusive orphan crop genomics. Isaac Njaci, Bernice Waweru, Nadia Kamal, Meki Shehabu Muktar, David Fisher, Heidrun Gundlach, Collins Muli, Lucy Muthui, Mary Maranga, Davies Kiambi, Brigitte L Maass, Peter MF Emmrich, Jean-Baka Domelevo Entfellner, Manuel Spannagl, Mark A Chapman, Oluwaseyi Shorinola, Chris S Jones. bioRxiv 2022.05.08.491073; doi: <https://doi.org/10.1101/2022.05.08.491073>