RESEARCH PROGRAM ON Livestock

More meat, milk and eggs by and for the poor

Field trial of Lablab (*Lablab purpureus*) genotypes under rain fed conditions in Ethiopia

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December 2021

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The Program thanks all donors and organizations which globally support its work through their contributions to the CGIAR Trust Fund

Editing, design and layout—ILRI Editorial and Publishing Services, Addis Ababa, Ethiopia.

Photo credit: ILRI/Godfrey Manyawu.

Citation: Habte, E., Gari, A., Lire, H. and Jones, C. 2021. *Field trial of Lablab* (Lablab purpureus) *genotypes under rain fed conditions in Ethiopia.* Nairobi, Kenya: ILRI.

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Contents

Table

Figure

Acknowledgments

This project is co-funded by a Royal Society Global Challenges Research Fund (GCRF) FLAIR Collaboration Grant, 'Sustainable intensification of the smallholder livestock sector in SSA/Ethiopia by unlocking the potential of indigenous forage, lablab' a collaboration with the International Livestock Research Institute (ILRI) and the Ethiopian Institute of Agricultural Research (EIAR) which is hosted by the John Innes Centre.

Introduction

Livestock play a key role in food security and incomes, and the farming systems of millions of smallholder farmers in sub–Saharan Africa (SSA) (Moyo and Swanepoel, 2010). However, the livestock sector in SSA is generally underperforming due to various reasons of which limited access to improved feeds and forages is the main one. Access to forage-based feed resources is not adequate in SSA, particularly during the dry seasons, and the situation is worse in lowland areas where pastoralists commonly dwell. Furthermore, adverse effects of climate change and dwindling arable land are making the situation worse, forcing livestock farmers to give up their herds. Thus, developing feed and forage resources is imperative in order to support already under performing small-scale livestock systems in the region and to develop forage varieties that are resilient to climate change. The identification, improvement and, ultimately, utilization of more productive, resilient and locally adapted forages is the first step forward to improve livestock performance in the region.

Lablab (*Lablab purpureus*) is one of the traditionally grown forage legume species in SSA, known for its resilience to drought and heat stress conditions and demanding a minimum amount of inputs during production (Maass et al., 2010). Because of the aforementioned attributes of lablab, a study has been initiated and conducted to evaluate lablab accessions sourced from the International Livestock Research Institute (ILRI) forage genebank, Addis Ababa, Ethiopia, under different agroecological conditions. In addition, the accessions will be genotyped, using the whole genome sequence (WGS) approach, to develop genomic tools for improved selection accuracies and enhanced genetic gains for the traits of interest by plant breeders. A comprehensive reference genome for lablab has also recently been assembled (C Jones 2021, pers. comm., 02 April) which will provide a useful tool for the application of modern breeding approaches for lablab in the future.

Field trial establishment and data collection

An extensive phenotyping and agronomic evaluation of the lablab accessions grown under field conditions has been carried out at three different agroecological locations in Ethiopia, in collaboration with the Ethiopian Institute of Agricultural Research (EIAR). The locations were the ILRI Bishoftu field site, a mid-altitude (1,800 metres above sea level (masl)) location with 800 mm annual rainfall in a bimodal pattern and alfisol/vertisol soils, located 50 kilometres (km) away from Addis Ababa, and the EIAR agricultural research centres at Melkasa, (1,550 masl with 760 mm annual rainfall in a bimodal pattern and clay/loam and sandy loam soils) and Mi'eso (1,470 masl with 740 mm annual rainfall in a bimodal pattern and clay loam soils), 120 and 300 km away from Addis Ababa, respectively. No fertilizer was applied during the course of the trials but manual weeding was carried out regularly. Furthermore, no pesticides or fungicides were applied. The field trials were carried out under rainfed conditions, with minimal input, in order to develop varieties that can perform under farmer's field conditions.

The accessions used in this study were obtained from the ILRI forage genebank collection in Addis Ababa, Ethiopia. One hundred and forty-three (143) lablab accessions were used for the study and the trials were laid out in 13 X 13 simple lattice design, where 26 accessions from the 143 were replicated as internal checks in each incomplete block to minimize the field heterogeneity effect. Each incomplete block has 13 rows 2.5 metres (m) in length with 0.75 m spacing between the rows. The seeds were direct sown in each row (plot), at a depth of 5 centimetres (cm), in July 2021 (03/07/2021 in Melkassa, 06/07/2021 in Bishoftu and 10/07/2021 in Mi'eso). After the seedlings established, the number of plants per plot were thinned to 12 whenever the number of plants exceed this number (Figure 1). Thinning was carried out two weeks after planting. Based on emergence data, all experimental accessions were successfully established and grown in the field except the lablab accessions shaded in Table 1.

The phenotype data was collected using standard lablab descriptors (Byregowda et al., 2015) which include: days to emergence; days to 50% flowering; plant height; fresh and dry stem and leaf weights; leaf, stem, and flower colour. The collected data from all three trial sites will be used for further genomic analyses and to support breeding new varieties. Furthermore, to collect true to type seeds from the studied accessions, the flower buds of selected plants from the trial were covered with pollination bags.

After 50 % of the accessions flowered, plant samples were harvested and dried in an oven at 60 ^{0}C overnight, then taken for the analysis of feed quality parameters, including: dry matter; organic matter; acid detergent fibre; neutral detergent fibre; acid detergent lignin; crude protein; ash; fat; digestibility (*in vitro* gas production) and; metabolizable energy, at the ILRI Nutrition Laboratory in Addis Ababa, Ethiopia.

Figure 1. Field establishment, emergence and mature plots of lablab accessions in the trial sites.

Photo credit Ermias/ILRI.

Table 1. List of lablab accessions used in the trial

DOI	Accession No.	DOI	Accession No.	DOI	Accession No.
10.18730/FT38T	147*	10.18730/FSVTA	14431	10.18730/FXD6C	18611
10.18730/G5TZR	6528	10.18730/FSVXD	14434*	10.18730/FXDBH	18617
10.18730/G5V0S	6529*	10.18730/FSVYE	14435	10.18730/FXDDK	18619
10.18730/G5V2V	6533*	10.18730/FSW1H	14438	10.18730/FXDFN	18622
10.18730/G5V3W	6534	10.18730/FSW2J	14439	10.18730/FXDMT	18627
10.18730/G5V4X	6535	10.18730/FSW3K	14440	10.18730/FXDNV	18628
10.18730/G5V5Y	6536*	10.18730/FSW4M	14441*	10.18730/FXDPW	18629
10.18730/G63A*	6930*	10.18730/FSW5N	14442*	10.18730/FXDRY	18632
10.18730/G66DM	7072*	10.18730/FSW6P	14443	10.18730/FXDV~	18635
10.18730/G6AYH	7278	10.18730/FSW7Q	14444	10.18730/FXDW$	18636
10.18730/G6DS$	7403	10.18730/FSW8R	14445	10.18730/FXDX=	18637
10.18730/FPYDJ	10953	10.18730/FSW9S	14446	10.18730/FZVWE	21029
10.18730/FPYX$	10979(	10.18730/FSWAT	14447	10.18730/FZVZH	21033*
10.18730/FQGD2	11610	10.18730/FSWCW	14449	10.18730/FZW0J	21034*
10.18730/FQGE3	11611	10.18730/FSWH~	14454	10.18730/FZW6R	21042
10.18730/FQGF4	11612	10.18730/FSWK=	14456	10.18730/FZW7S	21043*
10.18730/FQGG5	11613*	10.18730/FSWP1	14459	10.18730/FZW8T	21044*
10.18730/FQGH6	11614	10.18730/FSWT5	14463	10.18730/FZW9V	21045
10.18730/FQGJ7	11615*	10.18730/FSWX8	14466	10.18730/FZWBX	21047
10.18730/FQGM9	11617	10.18730/FSX2D	14471	10.18730/FZWCY	21048
10.18730/FQGNA	11618	10.18730/FSX4F	14474	10.18730/FZWDZ	21049*
10.18730/FQGPB	11619	10.18730/FSX5G	14475	10.18730/FZWK0	21055
10.18730/FQGRD	11620	10.18730/FSX6H	14476	10.18730/FZWM1	21056
10.18730/FQGZM	11630*	10.18730/FSX7J	14477	10.18730/FZWQ4	21059
10.18730/FQH0N	11631	10.18730/FSX8K	14478	10.18730/FZWS6	21060
10.18730/FQH1P	11634	10.18730/FSX9M	14479	10.18730/FZWT7	21061
10.18730/FQH8X	11640	10.18730/FSXAN	14480	10.18730/FZWYB	21065
10.18730/FQHAZ	11642	10.18730/FSXBP	14481	10.18730/FZWZC	21066
10.18730/FSC3S	13685	10.18730/FSXES	14484	10.18730/FZX5J	21071
10.18730/FSCK4	13700	10.18730/FSXFT	14485	10.18730/FZX6K	21072
10.18730/FSCM5	13701*	10.18730/FSXGV	14486	10.18730/FZXAQ	21076

DOI	Accession No.	DOI	Accession No.	DOI	Accession No.
10.18730/FSCN6	13702	10.18730/FSXJX	14488	10.18730/FZXGX	21081*
10.18730/FSV5T	14410	10.18730/FSXKY	14489	10.18730/FZXHY	21082*
10.18730/FSV7W	14412	10.18730/FSXMZ	14490	10.18730/FZXJZ	21083*
10.18730/FSV8X	14413	10.18730/FSXQ$	14493	10.18730/FZXK*	21084*
10.18730/FSVAZ	14415	10.18730/FT8E7	14901	10.18730/FZXM~	21085*
10.18730/FSVB*	14416	10.18730/FT8F8	14902	10.18730/FZXN$	21086
10.18730/FSVC~	14417	10.18730/FT8HA	14904	10.18730/FZXP=	21087*
10.18730/FSVD$	14418	10.18730/FT8KC	14906	10.18730/FZXQU	21088
10.18730/FSVE=	14419	10.18730/FT8MD	14907	10.18730/FZXR0	21089*
10.18730/FSVFU	14420	10.18730/FTPRN	15436	10.18730/G3P55	24747
10.18730/FSVH1	14422	10.18730/FXCR=	18595	10.18730/G3PTT	24768
10.18730/FSVJ2	14423	10.18730/FXCSU	18596	10.18730/G3Q3=	24777
10.18730/FSVK3	14424	10.18730/FXCT0	18597	10.18730/G3Q4U	24778
10.18730/FSVM4	14425	10.18730/FXCW2	18599	10.18730/G3Q94	24783
10.18730/FSVQ7	14428	10.18730/FXCX3	18600	10.18730/G3QPH	24796
10.18730/FSVR8	14429	10.18730/FXD39	18607	10.18730/G3QVP	24800
10.18730/FSVS9	14430	10.18730/FXD4A	18609		

*Indicate internal checks, the shaded accessions did not establish in the Bishoftu field.

Genotyping

Leaf samples were collected from each accession during the seedling establishment stage for whole genome sequencing (WGS). The DNA of these accessions is currently being sequenced. Once the sequence data is ready, it will be used to understand the polymorphisms among the accessions and carry out association mapping studies in order to identify SNPs/Indels for the application of markers-assisted selection or genomic selection.

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