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# Recent developments in *Lablab purpureus* genomics: A focus on drought stress tolerance and use of genomic resources to develop stress-resilient varieties

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## Abstract

Drought is a major climatic challenge that contributes significantly to the decline of food productivity. One of the strategies to overcome this challenge is the use of drought-tolerant crops with a wide range of benefits. *Lablab* is a leguminous crop that has been showing high promise to drought tolerance. It is reported to have higher drought resilience compared with the commonly cultivated legumes such as common beans and cowpeas. Because of its great genetic diversity, *Lablab* can withstand high temperature and low rainfall, unlike other related crops. On top of that, it is grown for multitudes of purposes including food, forages, conservation agriculture, and improved soil fertility. To enhance its production and benefits during the present effects of climate change, it is crucial to develop improved varieties that would overcome the challenge of drought stress. In the past years, there have been several reviews on *Lablab* based on origin, domestication, characterization, utilization, germplasm conservation, some cultivation constraints, and conventional breeding with limitations on the genomic exploitation of the crop for drought tolerance. Conventional breeding is the major breeding technique for many *Lablab* cultivars. The integration of genomic, physiological, biochemical, and molecular approaches would be required to develop drought-tolerant cultivars of *Lablab*. In this review, we discuss recent developments in *Lablab* genomics with a focus on drought stress tolerance and the use of genomic resources to develop stress-resilient varieties.

## KEYWORDS

drought tolerance, genome sequence, genomic exploitation, *Lablab purpureus*, omics technology

## 1 | INTRODUCTION

Global agricultural production will need to double by 2050 to meet the ever-increasing food demand especially in Africa which constitutes the fastest growing population and the second-highest growth rate in the world (AfDB, 2014; United Nations, 2019).

A rise in food demand is likewise predicted due to a rise in drought stress in many parts of the world (FAO, 2017). Approximately 40% of the production land and about 50% of failures of crops have been reported due to drought stress (Fahad et al., 2017; Kapoor et al., 2020). Such an effect on agricultural production is projected in many areas especially in sub-Saharan Africa (SSA) due to

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the effect of climate change (FAO, 2009; Muchuru & Nhamo, 2019; Shiferaw et al., 2014).

Maintaining production in drylands is most likely the major challenge in modern agriculture that deserves immediate intervention. Because we have some crops that perform well in drought-prone environments, the solution can involve an identification of the best cultivars and the knowledge of their drought-tolerance capability (Zandalinas et al., 2018).

Lablab (*Lablab purpureus* L. Sweet) is a drought-resilient crop with multiple benefits (Guretzki & Papenbrock, 2014; Naeem et al., 2020). It is popularly regarded as grain legume, vegetable, and fodder which is rich in protein (comparable with soybean), nutrients, and vitamins (Minde et al., 2020). In the sustainability of conserved agriculture and enhanced soil fertility, farmers have been intercropping Lablab with their major crops or utilizing it as a cover crop and green manure (Chakoma et al., 2016; Mkonda & He, 2017). The crop is a good source of rare pharmaceuticals used to cure diseases in humans and animals. It has been established recently that a carbohydrate-binding protein from Lablab can efficiently block SARS-CoV-2 and influenza viruses, thus providing room for a cure of infections (Liu et al., 2020). Insulin-like protein has also been isolated from the crop (Sachin et al., 2020). The crop also plays a great role in ensuring income security among smallholder farmers especially in dryland and semi-dryland ecosystems (Raghu et al., 2018).

The broad genetic diversity of Lablab has supported adaptation and distribution of the crop over a broad range of environmental and climatic conditions (Ewansiha et al., 2007; Venkatesha et al., 2013; Vidigal et al., 2018). It spreads along the tropical and subtropical region between 30°N and 30°S at an elevation of about 0–2000 m above sea level. Lablab also adapts to a wide range of temperature (18°C to 50°C) and annual rainfall (200–2500 mm). This is different from other related species whose favorable growth temperature ranges only between 18°C and 30°C while unable to survive in the little amount of rainfall compared with Lablab (Bhandari et al., 2017; Maass et al., 2010). Its ability to grow vigorously when rainfall resumes after drought has led to its greater resilience compared with other legumes such as common beans (*Phaseolus vulgaris*), soybeans (*Glycine max*), cowpeas (*Vigna unguiculata*), and pigeon peas (*Cajanus cajan*) (Ewansiha & Singh, 2006; Miller et al., 2018).

To enhance economic productivity and associated benefits of Lablab in the present era of frequent drought spells, there is a need of developing drought-tolerant varieties. In the past 10–15 years, detailed studies and reviews on Lablab origin, domestication, dispersal, utilization, germplasm conservation, characterization, cultivation, some production constraints, and conventional breeding have been written. The conventional breeding of many Lablab varieties was focused on improvement in soil fertility, forage, high yield, and photosensitivity while neglecting stress tolerance. The drought-tolerant traits are polygenic and possess complex nature of inheritance that would require integration of genomic, physiological, biochemical, and molecular approaches for their manipulation. Until presently, there is limited genomic information on Lablab (Rai et al., 2018b; Wang et al., 2018). In this review, we discuss recent

developments in the genomics of the crop with a focus on drought stress tolerance and the use of genomic resources to develop stress-resilient varieties. This would help in improving the economic production of the crop and its associated benefits to the farming community.

## 2 | A BRIEF INTRODUCTION ON LABLAB GENOME

Lablab, which is also known as Dolichos Lablab (in English) and Fiwi or Ngwara (in Swahili), is a leguminous crop in the Fabaceae family. Its genome has recently been sequenced, assembled, and compared with related species (Chang et al., 2018; Iwata et al., 2013) (Table 1). The comparison shows that Lablab with chromosome numbers  $2n = 2x = 20, 22, \text{ and } 24$  is less complex, has a smaller genome size (367 Mb), scaffold assembly (395.47 Mb), and protein-coding genes (20,946) compared with other related species. However, these genes possess tremendous characteristics in functionality such as gene length and coding sequence which are longer compared with other species. Lablab has also longer exons and introns.

Lablab and Bambara nut were compared based on their plastid genome. While their genomes have a quadripartite structure with two inverted repeats (IRs), a large and a small single-copy region, the lengths of their plastomes are 151,753 and 152,015 bp, respectively. Each of these plastomes has four rRNAs and 71 protein-coding genes. However, their tRNA genes were not consistent in each plastome. The plastome in Lablab has 32 tRNA genes, whereas that of Bambara nut has 33 tRNA genes. Phylogenetically, Lablab was noted to relate closely with common beans (Liao et al., 2019; Wang et al., 2017). Sequenced and assembled transcriptome from Lablab was also compared with other three legumes, that is, Bambara nut, winged bean, and grass peas. The comparison revealed that the number of reads (16,190,774), transcripts (52,019), and assembled bases (51,997,858) in Lablab exceeded most of the legumes in the study. N50 of all transcripts was also higher (1570 bp) in Lablab than other legumes and thus formed a more complete assembly. This corresponded also to the highest percentage of putative orthologs in both Lablab and Bambara nut (Chapman, 2015).

## 3 | DROUGHT TOLERANCE IN LABLAB

### 3.1 | Drought-adaptive mechanisms

Crops adapt three resistance mechanisms to cope with drought, that is, drought escape, drought avoidance, and drought tolerance. For plants to escape drought conditions, they have to opt for rapid growth and development which will lead to completion of the growth cycle before drought events (Shavrukov et al., 2017). Few numbers of seeds and reduced biomass are parameters associated with *drought escape*. In *drought avoidance*, plants increase root growth while limiting their vegetative growth and transpiration rates.

**TABLE 1** Genomic features (de novo sequenced genome) of Lablab and other related species

No.	Common name	Chromosome number (2n)	Genome size (Mb)	Scaffold assembled lengths (Mb)	Number of protein-coding genes	Average gene length (bp)	Average length in coding sequence (bp)	Exon length (bp)	Intron length (bp)	Reference
1	Lablab ( <i>Lablab purpureus</i> )	20, 22, 24	367	395.47	20,946	3696	1276	239	557	Iwata et al. (2013); Chang et al. (2018)
2	Common bean ( <i>Phaseolus vulgaris</i> )	22	587	473	27,197	-	-	-	-	Schmutz et al. (2014)
3	Cowpea ( <i>Vigna unguiculata</i> )	22	613	519	29,773	3881	-	313	-	Lonardi et al. (2019)
4	Soybean ( <i>Glycine max</i> )	40	1115	950	55,137	3144	1169	232	488	Valliyodan et al. (2017); Chang et al. (2018)
5	Adzuki beans ( <i>Vigna angularis</i> )	22	542	466.7	34,183	-	-	-	-	Kang et al. (2015); Yang et al. (2015)
6	Mung beans ( <i>Vigna radiata</i> )	22	579	~431	22,427	-	-	-	-	Kang et al. (2014)
7	Bambara nut ( <i>Vigna subterranean</i> )	22	864	535.05	31,707	3287	1163	222	501	Chang et al. (2018)
8	Pigeon pea ( <i>Cajanus cajan</i> )	22	833	605.78	48,680	2348	959.35	-	-	Singh et al. (2017)
9	Groundnut ( <i>Arachis hypogaea</i> )	20, 40	2552	2530	83,709	4275	226	233.21	578	Pandey et al. (2020)
10	B. trefoil ( <i>Lotus japonicus</i> )	12	480	554.08	29,598	-	-	417.54	527.12	Kamal et al. (2020)
11	Acacia ( <i>Faidherbia albida</i> )	26	-	653.73	28,979	3396	1207	226	504	Chang et al. (2018)
12	Marula ( <i>Sclerocarya birrea</i> )	28	-	330.98	18,937	3561	1343	239	479	Bationo-kando et al. (2016); Chang et al. (2018)
13	Drumstick tree ( <i>Moringa oleifera</i> )	28	-	216.76	18,451	3308	1238	232	478	Tian et al. (2015); Chang et al. (2018)
14	Barrel medic ( <i>Medicago truncatula</i> )	16	390	388	50,358	2334	986	243	440	Chang et al. (2018); Young and Zhou (2020)

Note: Lablab has a smaller genome size, scaffold assembly, and protein-coding genes compared with other related species. Gene length, coding sequence, exons, and introns are longer in Lablab than in other species. This points out that Lablab has higher gene expression compared with other related species and thus suitable for genomic exploitation.

The ability of the plant to produce abundantly even under optimal water conditions is known as *drought tolerance* (Abobatta, 2019; Basu et al., 2016). Early plant vigor, fast ground cover, large seed size, long and deep root system, high root biomass, small leaflets, and high leaf water potential are some of the attributes for drought tolerance (Yadav & Sharma, 2016). This type of drought-adaptive mechanism has been noted in Lablab (Robotham & Chapman, 2015) through early or late maturing varieties. For instance, early maturing varieties can escape terminal drought, but if they are exposed to intermittent

stress, they perform very poorly (Mai-Kodomi et al., 1999; Shavrukov et al., 2017). For late-maturing varieties, the sensitivity of the crop to drought stress is more during the flowering stage (Nadeem et al., 2019). These challenges can be taken care of, first by introgression of drought-tolerant attributes to the early maturing varieties, second by identifying late-maturing cultivars with drought tolerance, and third by the use of a computational model to resolve various drought scenarios influenced by climate change. Because some agro-ecological zones are not well defined in many places (Batiemo, 2016),

the model should be simulated based on crop features such as growth development and yield, meteorological data, for example, temperature and rainfall and soil characteristics. Finally it can be through promoting intensified research based on the genomic potential of the selected lines.

### 3.2 | The basis for drought tolerance

Phenotypic plasticity in plants refers to the changes in physiological responses that contribute to their adaptability to the new environment (Alpert & Simms, 2002). The basis for such changes involves *morphological*, *biochemical*, and *molecular* mechanisms (Farooq et al., 2009). Lablab utilizes these three mechanisms to protect itself from drought stress (D'Souza & Devaraj, 2011; Guretzki & Papenbrock, 2014; Maass et al., 2010; Rangaiah & D'Souza, 2016).

*Morphologically*, the mechanisms include glabrous and trailing stems, a vigorous extension of shoots, shifting of leaf inclinations to reduce sun rays, decreasing in leaf sizes and structures, changing in chlorophyll contents and greenness of the crop, alterations in stomatal behavior, and their distribution to control evapotranspiration as well as deep root penetration (2 m) to the soil (Chakoma et al., 2016; USDA, 2012). There have been some “traditional (conventional)” and “improved (modern)” ways of evaluating the phenotyping effect of drought stress on Lablab (Guretzki & Papenbrock, 2013). The traditional method quantifies the effects on few accessions by analyzing their easily measurable parameters such as root parameters (e.g., length, width, and density), leaf parameters (e.g., size, number, greenish, and waxiness), plant height, stem size, and weight of fresh and dry biomass through destructive methods. The improved method can screen many accessions very efficiently without destruction. It computes the effects based on physiological processes. Some parameters that are easily computed through this method are stomatal conductivity (Grant et al., 2006), transpiration rate (Chaerle et al., 2009), and chlorophyll content (Sperdoui & Moustakas, 2012). As it demands more time and labor, the traditional method is thus regarded as less effective compared with the improved method (Golzarian et al., 2011; Honsdorf et al., 2014).

Despite many findings reported on morphological characteristics in Lablab, little has been done to correlate them with drought stress in various stages of crop development. However, there have been some drought-tolerance studies on seedlings in Lablab (D'Souza & Devaraj, 2011; Devaraj et al., 2014a, 2014b) and cowpeas (Agbicodo et al., 2009; Ajayi et al., 2017; Alidu et al., 2019; Bolarinwa et al., 2013; Muchero et al., 2008) with a limited number of accessions. Legumes are highly susceptible to drought during flowering and pod filling stages (Farooq et al., 2016; Nadeem et al., 2019). Hence, correlation studies between reproduction efficiency and drought in Lablab based on floral structure, pollination mechanisms, stigma receptivity, and grain formation are recommended.

High temperature increases reactive oxygen species (ROS) mainly hydroxyl radicals (OH<sup>•</sup>), singlet oxygen (<sup>1</sup>O<sub>2</sub>), and hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) that can damage physiological precursors of the crop (Foyer &

Noctor, 2012; Gill & Tuteja, 2010). However, Lablab can defend against ROS biochemically via enzymatic and nonenzymatic actions (D'Souza & Devaraj, 2011). Antioxidant enzymes such as peroxidase (POX), catalase (CAT), polyphenol oxidase (PPO), glutathione reductase (GR), guaiacol peroxidase (GP), superoxide dismutase (SOD), nitric oxide, salicylic acid, and acid phosphatase (APs) play a great role in transforming ROS into less harmful chemical species (Devaraj et al., 2014a, 2014b). Non-enzymatic compounds from secondary metabolites such as flavonols, flavones, polyols, phenols, proline, glutathione (GSH), malondialdehyde (MDA), ascorbate (ASC), glycine betaines (GB), sugars, and organic solutes accumulate in the crop to regulate and protect its cellular and defense responses against drought (Rangaiah & D'Souza, 2016). Some of these enzymes have also been studied to relate them to drought tolerance in Lablab (Suzuki et al., 2012).

Molecular mechanisms of Lablab against drought stress involve upregulation and downregulation of drought-tolerant genes (Wang et al., 2018; Yao et al., 2013). This phenomenon of gene regulation has been formerly studied through molecular markers. However, the development of marker technology has been slower in Lablab and some other legumes than in cereal crops to the point of recognizing them as “orphan crops” (Dhaliwal et al., 2020; Vijayanthi et al., 2018). In their steps of advancement, the first group of markers, amplified fragment length polymorphism (AFLP), restriction fragment length polymorphism (RFLP), and random amplification of polymorphic DNA (RAPD), was employed to understand the diversity and genetic characterization. The second group, namely, sequence-based markers including single nucleotide polymorphism (SNPs), microsatellite or simple sequence repeats (SSRs), and expressed sequence tags (ESTs), was utilized in mapping studies (Dholakia et al., 2019; Kamocho et al., 2016; Keerthi et al., 2018; Kimani et al., 2012; Konduri et al., 2000; Rai et al., 2018a; Sserumaga et al., 2021; Vijayanthi et al., 2018). Despite their applications in Lablab, there has been little utilization of these markers to improve drought tolerance.

Based on few studies on screening for drought tolerance and utilization of markers for drought tolerance, we are evaluating seedling drought tolerance among 300 Lablab accessions at the Nelson Mandela African Institution of Science and Technology (NM-AIST), Arusha, Tanzania (Figure 1).

To offer useful knowledge in the development and transferability of markers in Lablab (Cheng et al., 2017; Jha et al., 2020; Lepcha et al., 2019), some quantitative trait loci (QTLs) for drought tolerance identified in other legumes has been presented in Table 2. This information would increase comparative knowledge, analysis, and genomic improvement of drought tolerance in Lablab.

## 4 | OMICS TECHNOLOGY AND RECENT GENOMIC DEVELOPMENTS

“Omics technology” is a modern molecular tool useful in recognizing functional genomic systems in an organism (Banerjee et al., 2019; Hu et al., 2018). It involves sequencing and profiling of the expressed transcripts and translated protein. Through this technology, it is easier





**FIGURE 1** (a–f) Drought-tolerance evaluation of about 300 Lablab accessions at seedling stage is being carried out by the Nelson Mandela African Institution of Science and Technology (NM-AIST), Arusha, Tanzania, in a two repeating experiment. Polythene cover noted in the picture is used to induce high temperature inside the house

to expand our knowledge on various genetic processes in Lablab (Jamnadass et al., 2020; Yssel et al., 2019) and related species. Robotham and Chapman (2015) demonstrated drought-tolerance variation among Lablab germplasm through microsatellite genotyping by sequencing. Established genomic resources in Lablab by African Orphan Crops Consortium (AOCC), World Agroforestry Centre (ICRAF), Nairobi, Kenya (Chang et al., 2018), could be utilized to understand drought-tolerance mechanisms and their application in crop improvement. Some of these resources include forward and reverse Suppression Subtraction Hybridization (SSH) libraries generated from root tissues of drought-stressed Lablab accessions. This study identified 1287 unigenes from 1400 drought-induced ESTs and BhGRP1 drought-tolerant gene (Yao et al., 2013). A similar library was also developed by Wang et al. (2018) where 2792 unigenes were gathered from 4064 drought-induced ESTs. Two drought-tolerant microRNAs (miRNAs), that is, miRNA 156 and miRNA 172, were isolated from Lablab (Thilagavathy & Devaraj, 2016). As part of transcriptomic regulation for drought tolerance, the  $\gamma$ ECS gene was noted to influence the free radical system and antioxidant activities during fruit ripening in Lablab (Rai et al., 2017).

There have been also some genes, E, Dt1, GmFT2, GmGla, PvTFLY1, and GmPhyA3, studied to relate high temperature and photoperiodic sensitivity in Lablab (Ramtekey et al., 2019). As temperature increases in many areas, flower dropping is becoming a major problem faced by farmers growing Lablab in Tanzania. It is also a common problem in other Lablab-growing areas in Africa. Although in India HA3 and HA4 Lablab varieties have been developed to overcome this challenge of flower dropping (Ramesh & Byre Gowda, 2016), genomic improvement of our cultivars based on

already available resources (Ramtekey et al., 2019) would create a permanent solution (Rai et al., 2018b; Vaijayanthi et al., 2018).

## 5 | PROMOTING EXPLOITATION OF GENOMIC RESOURCES IN LABLAB FOR STRESS TOLERANCE

Lablab is increasingly becoming a popular crop in the community due to its multitude of values. The crop has therefore been engaged in several research programs, many of them taking place in Asia rather than Africa where the crop originates (Maass, 2016; Maass et al., 2010). Among research happening in Africa, it is only little or none that has been directed to the genomic development affecting the release of varieties for commercial purposes. So far, many of the world-known commercial varieties in Lablab, for example, Koala, HA3, and HA4 for grains and Rongai, Endurance, and Highworth for forage, come from Asia and Australia (Gopalakrishnan, 2007; Maass et al., 2010; Ramesh & Byre Gowda, 2016). In Africa, only Kenya has commercialized its varieties: Eldo-KT Black 1 and 2 (Eldoret Kirkhouse Trust black), Eldo-KT cream, and Eldo-KT Maridadi (KEPHIS, 2017; Kirkhouse Trust, 2015). Evaluation performance of the promising cultivars has also been taking place in Northern Tanzania towards their commercialization (Miller et al., 2018; Nord et al., 2020). The reason behind these few recommended varieties was research focusing more on morphological characterization, forage, and soil properties especially in Africa.

Making genomic information of Lablab easily available such as the AOCC (Hendre et al., 2019) will provide inputs for translational

**TABLE 2** Molecular markers and QTLs for drought tolerance in some other legumes

No.	Crop	Molecular markers/QTLs	Mapping population	Features in drought tolerance	Reference
1	Common beans	SSR; AFLP markers; 49 QTLs	82 recombinant inbred lines (RILs)	Drought-responsive agronomic traits	Sedlar et al. (2020)
		SNP markers; 18 QTLs	97 RIL from parent lines: Portillo × red hawk	Drought-tolerance parameters	Onziga et al. (2019)
		SSR and SNP markers; 12 QTLs	F8; SEA 5 × AND 277	Drought (stress) conditions	Briñez et al. (2017)
		SSR; 69 QTLs SSR; 15 putative QTLs	DOR364 × BAT477	Drought-tolerance parameters; root-drought-related traits	Asfaw and Blair (2012)
		AFLP, RAPD, SSR markers; 143 QTLs	100 RILs	Drought-tolerance and drought-related traits	Diaz et al. (2018)
		SNP markers; 14 QTLs	RILs; SEA5 × CAL96	Phenology-yield-drought	Mukeshimana et al. (2014)
		53 SNP markers; 11 QTLs	128-F8 RILs	Drought stress conditions	Nabateregga et al. (2019)
		SNP markers; genes functioning	Pinto-Villa × Pinto Saltillo, F3:5 (289 genotypes)	Drought tolerance	Villordo-Pineda et al. (2015)
2	Cowpeas	184 genome-wide EST-derived SNP markers; drought-tolerance QTLs	2 drought-tolerant lines (IT93K-503-1 and IT97K-499-35)	Green abilities and yield under water stress conditions	Batieno et al. (2016)
		412 DaRT, 80 AFLP, 28 microsatellite markers; 2 QTLs	72-F1 derived double haploid (DH)	Stress tolerance (drought)	Fan et al. (2015)
		35 SNP markers; tolerance index ranged between 69.19 and 142.01	305-F8 RILs	Tolerance to water-deficit conditions	Ravelombola et al. (2021)
3	Chickpeas	SNP markers and 21 major QTLs	232 RILs; ICC 4958 × ICC 1882	Drought-tolerance parameters	Sivasakthi et al. (2018)
		828 SNPs; DREB and CAPS from QTL-hotspot region	264 RILs	Drought tolerance	Jaganathan et al. (2015)
		47, 53, and 46 SSR markers in selection; QTL-hotspot region	3 elite cultivars	Drought tolerance and grain yield	Bharadwaj et al. (2021)
4	Soybeans	368 SSR including Satt277; QTLs	F2 mapping population (PK1180, SL 46 × UPSL 298, PK 1169)	Seedling survivability under drought conditions	Sreenivasa et al. (2020)
		8078 specific locus amplified fragments (SLAF) markers; 23 QTLs	RILs	Drought-tolerance traits	Ren et al. (2020)
5	Mung bean	3690 SSR; 58 QTLs for plant parameters and 5 for drought tolerance	256 RIL population	Plant tolerance and associated parameters	Liu et al. (2017)
6	Asparagus bean	39 SNPs markers from GWAS	95 accessions	Tolerance to soil water stress	Xu et al. (2015)

Note: Some QTLs and molecular markers from some commonly grown legumes that could provide useful knowledge in their transferability in Lablab. Abbreviations: AFLP, amplified fragment length polymorphism; QTLs, quantitative trait loci; RAPD, random amplification of polymorphic DNA; SNP, single nucleotide polymorphism; SSR, simple sequence repeat.

research on its sustainable development. However, we need further bioinformatics training among researchers for the efficient use of genomic databases. Moreover, the adoption of high-throughput technologies such as next-generation, genome-wide association studies (GWAS), transcript profiling, and gene and genomic editing (CRISPR/cas9) will bring discovery of more drought-tolerant genes and their expressed quantitative loci (eQTLs). Increased deployment of these

genomic tools with an increase of research collaboration will also bring a new revolution in farming systems of drylands (Njarui & Mureithi, 2010; Sennhenn et al., 2017). One of the benefits of using new drought-tolerant varieties is to protect their productivity in dry environments against increased aridity and semiaridity conditions especially in SSA where desertification is highly concerned. As already predicted that desertification will increase as noted in the Saharan

desert that keeps spreading to the south, sensitization of Lablab production to the region would be an important opportunity to minimize the effects of drought stress on the region. In return, production will get improved to make it more commercialized.

Genomic exploitations of Lablab cannot become successful if there is a limitation of genetic resources. This is because, useful resources for exploitation come from a wide range of genetic materials (Azeez et al., 2018). Collections of genetic resources have been the role of the National Plant Genetic Resource Centers (NPGRCs) and local and international research institutions. Whereas the largest world collections of Lablab accessions (650) have been held at the University of Agricultural Sciences (UAS), Bengaluru, India (Ramesh & Byre Gowda, 2016), the NM-AIST, Arusha, Tanzania, has the largest collections (450) of Lablab in Africa (Kirkhouse Trust, 2019). This shows that Africa has fewer collections of resources compared with Asia.

These resources could be enhanced through an exchange of exotic materials and collections of local farmers' landraces. Because they are the populations of historical origin with distinct identities, farmers' landraces have been preferred in genomic exploitation for drought tolerance as they are more adapted to abiotic challenges and well connected to farming practices. Despite their roles in stress resilience, their collections have not been sufficiently exhausted in many countries. Several NPGRCs still lack them to a high extent. Little collections available at the centers are neither comprehensive nor representative of the genetic diversity available from their local context. This is because their collection missions are donor driven with many of them influenced by external needs. Even when collections are done by local personnel for research purposes, there has been a tendency to introduce them from international gene banks. These local resources have also been lost in developing countries due to urbanization and abandonment of farming activities for the farmers' interest of moving to towns and cities for small jobs and business. To handle this challenge, we need a strong collaboration among all stakeholders; farmers, researchers, government, and international agencies that will efficiently control in situ and ex situ conservation of the resources.

## 6 | CONCLUSION

Lablab is exhibiting an increased research interest due to its wide range of benefits. It has shown a great ability to withstand drought stress compared with other related species. Despite this advantage, there has been very little effort in exploitation of genomic resources in Lablab for drought tolerance. As a result, the crop has been underutilized in many areas. However, because of this genomic potential, the development of the crop through an application of "omics" technology is proposed so that we can convert it into a commercialized crop. The challenge behind this mission is the high cost for most of the tools in "omics technology." Additionally, the methods are time consuming, requiring very expensive consumables, and not feasible for a quick response. Reducing their running cost while deploying

cheap and simple tools such as Nanopore MinION field sequencer would lead to the best findings. With sustainable utilization of genomic resources in Lablab, the crop can be transformed from an orphan legume into an industrial crop.

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## CONFLICT OF INTEREST

None.

## ETHICS STATEMENT

This manuscript does not contain any studies with human or animal subjects.

## DATA AVAILABILITY STATEMENT

No new data were created or analyzed in this study.

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