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Cassavabase, an advantage for IITA Cassava breeding program

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Introduction

Cassava (*Manihot esculenta* Crantz) storage roots are a staple source of calories that is indispensable to food security in Africa. Unlocking the potential of genetic improvement in cassava has not been possible due to the slow rate of genetic gain achieved through conventional breeding approaches and the long duration of breeding cycle. Phase I of Nextgen Cassava Breeding Project (http://www.nextgencassava.org/) using genomic selection has successfully shortened the breeding cycle for new cassava varieties through improved flowering and other genomic tools and also making cassava genomic information publicly accessible as an open database(https://cassavabase.org). Emphasis in the phase 2 is laid on improving the quality of data uploaded to Cassavabase.

Materials and Methods

➢ Cassavabase is being developed in Boyce Thompson Institute (BTI) for Plant Research in New York in collaboration with Nextgen Cassava partners.

➢ Access is open to all through creation of individual user accounts.

➢ Cassavabase mirror site (https://iita-mirror.cassavabase.org) is hosted at IITA HQ, Ibadan Nigeria. The software and database are updated weekly.

➢ Cassavabase is implemented by IITA along with 13 other breeding programs

➢ The fieldbook application with an user friendly interface and compatible with most android phones and tablets has been adapted for electronic phenotype data collection.

➢ The cassava ontology is dynamic with capacity to add new traits from any breeding program facilitated by the cassava ontology curator at IITA.

➢ High throughput phenotyping applications like fieldbook, inventory, coordinate, onekk, verify etc., have been deployed.

➢ Digital inputs like barcode labels for both phenotype and genotype stocks improve data quality.

➢ Genotyping trials keep track of the content of a genotyping plate sent to a genotyping facility.

Inventory · Coordinate · Fieldbook · White fly counter · www.cassavabase.org · Label Designer: Interactive design tool for creating labels

Graphical filtering: filter down accessions based on combinations of trait performance.

Statistical Analysis : ANOVA, Heritability, PCA, Genomic Selection (solGS), trial comparison, Selection Index, etc.,

Results

➢ Currently cassavabase has data for more than 1300 phenotyping trials from the IITA breeding program starting from year 1998 to 2017.

Years/Locations	Ibadan	Mokwa	Zaria	Ubiaja	Ikenne	Onne	Warri	Malam Madori	Ilorin	Abuja	Kano	Jos	Others	Total
1998-99	13	17												30
1999-00	8	11	8	5		3	6	9			1	4		55
2000-01	21	17	1					8			1			48
2001-02	18	20	8	2	1	3	2	11			1			66
2002-03	19	11	4	1										35
2003-04	20	12	5	2		2							39	80
2004-05	21	13	11	1	5	3	3	6	3	4			21	91
2005-06	14	10	2	8	4	2	2	1						43
2006-07	12	10	5	11	3	4		1		2			2	50
2007-08	7	8	5	1	2	5					1	1	7	37
2008-09	14	5	6	4									1	36
2009-10	12	7	8	10	5								1	43
2010-11	22	9	8	12	6		2		1					60
2011-12	17	5	4	6	4		6		3					45
2012-13	23	10	8	12	8		7		1					69
2013-14	29	8	11	15	14	2			1				2	82
2014-15	34	6	8	16	14				1				1	80
2015-16	41	11	5	23	27				1					108
2016-17	55	13	4	22	18								1	113
2017-18	79	8	2	18	17	2							5	131
	466	194	113	171	132	26	28	36	11	7	4	4	80	1302

➢ Successfully Implemented electronic phenotype data collection using the field book application and barcodes using more than 120 tablets & android phones.

➢ Cassavabase usage increased with help of in-house trainings
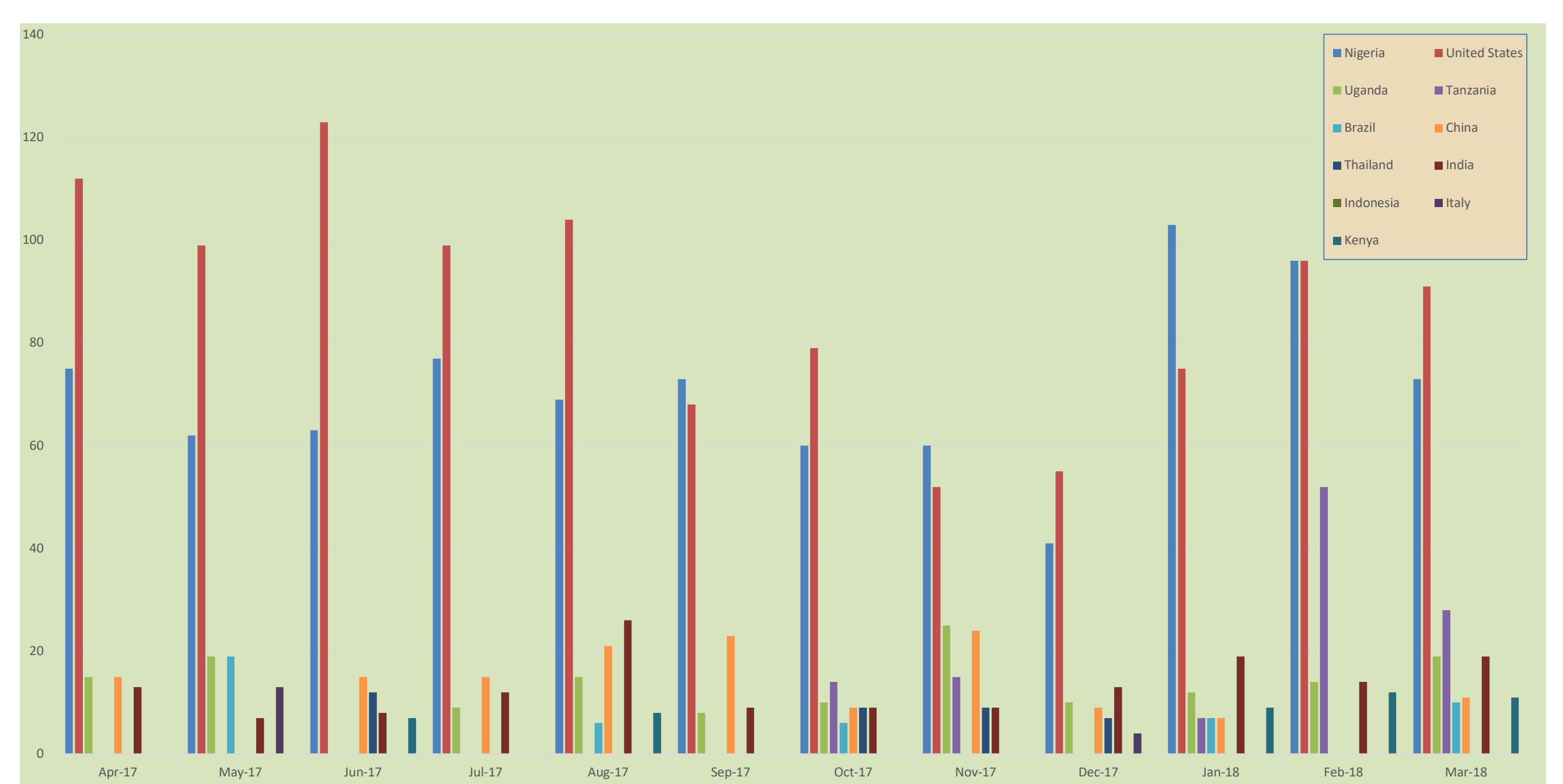
Conclusions

➢ Cassavabase supports the breeders and researchers with up to date phenotypic and genotypic information along with user friendly web based tools to perform genomic selection.

➢ Data quality is ensured by using barcode labels, pheno apps, quality verification tools.

➢ Facilitates rapid decision making by performing Statistical analysis like ANOVA, heritability, and trial comparisons.

➢ All members of the cassava breeding community are encouraged to use cassavabase and contribute data to strengthen international cooperation in cassava.