研　究　集　会

Application of Predictive Breeding in Yam Improvement for West Africa

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Introduction

Yam (*Dioscorea* spp.) is a highly prized tuber crop in West African agriculture and food systems. The yam crop provides an important source of dietary carbohydrate and other nutrients for millions of people in West Africa where over 95% of the global yam production comes from. Yams cultivation in West Africa is not only attached with a highly esteemed food source but also associated as a significant source of household income and a deep-rooted socio-cultural relevance (Coursey and Coursey, 1971; Zannou *et al.*, 2004). However, the crop's tremendous potential for food security, wealth creation, and socio-cultural value has not yet been fully exploited. A number of endemic and emerging constraints hinder the African farmers from exploiting the yam's potential for food security and economic welfare. These constraints extend from the range of biotic and abiotic factors (fungal disease, virus, nematodes, and low soil fertility) to underdeveloped seed system, agronomic and post-harvest practices limiting yield potential and reducing end-use quality. Fortunately, some of these challenges can be mitigated and genetic improvement through breeding can play a great role in unlocking

its potential. Breeding can offer yam farmers better cultivars with improved genetics that help to maximize productivity and minimize quality reducing factors. Yam breeding, however, presents special challenges and heavily relies on the traditional techniques of exploiting the genetic variation. With current advances in science and technology, it is possible for yam breeders to better understand the genetic makeup of the plants and efficiently link it with the phenotypic features they intend to breed for. This process entails parent trait profiling, smart crossing to recombine underlying traits responsible for phenotype, selection of individuals with superior attributes, and confirmation of the observed trait superiority in target environments for commercial deployment in production and consumption system. The yam breeding teams in West Africa with the support of AfricaYam project, are integrating predictive platforms in population and clonal development to accelerate genetic gain and optimize the breeding process. The prediction platform targets trait-packages including both core and desirable traits that are important for the success of the breeding program. The programs also carry out genetic value determination in parents, prediction of future progeny performance in crosses, and prediction of cultivar performance across a target set of production environments. Here we describe the potential prediction models being implemented in yam breeding in West Africa to optimize the yam population and clonal devel-

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opment process.

Parental and clonal value determination

Choice of right parents for hybridization that effectively yield heterotic progenies and the identification of superior plants/individuals with the potential as candidate cultivar for commercial deployment are the most critical and challenging aspects of the yam breeding. Best parent choice and superior progeny selection require a technique that predicts the genetic potential genotypes for traits of economic and social interest. In order to optimize the parent choice and clonal selection in yam breeding, early generation yam breeding population represented by over 381 progenies derived from full-sib families involving crosses from 12 female and 10 male parents were assessed based on the predicted genetic potential for key traits. The progeny trial was conducted at Ibadan in 2016 cropping season using an augmented row and column experimental design along with four check varieties replicated six times. The trial was established using a single row plot of three plants at a spacing of one meter between plants in a plot size of 3 m². The ridges were about 0.3 - 0.35 meters high and 3 meters long. Multiple traits related with above ground plant performance and below ground tuber yield and quality were measured using yam trait ontology (http://www.cropontology.org/ontology/CO_343/Yam) and yam standard operation protocol (Asfaw, 2015). Univariate restricted maximum likelihood (REML) analysis was performed to estimate genetic parameters and predict

the genetic potential of parents and clonal values of progenies for different economic traits using various statistical packages in R software. The following linear mixed model was used:

Model= lmer(y ~ row + colmon + entrycheck + (1|block) + (1|entry:new), data = mydata). where y is trait value and mydata is a data file used for the analysis. Row and column effects were added to the model as fixed whereas block effect as a random variable when significant for a trait. Sett weight (weight of seed tubers used for planting) and the number of plants at harvest were added to the model as the covariate for tuber yield characteristics whenever significant. Different selection models were applied based on the results of genetic variability, heritability and genetic value estimates (Tables 1 and 2) in current breeding materials. Backward selection for parental choice based on their progeny performance and forward selection to identify best progenies with high genetic value for the measured traits using best linear unbiased prediction (BLUP) method were employed. Predicted breeding values, the accuracy of prediction and future progeny performance forecast were calculated for the different traits and an index was constructed to rank the parents (Table 2). The top-ranking parents were crossed as best founders to generate new progenies for further selection. Back selection for best founder parents in crossing program would help to achieve genetic gain for those traits with low to intermediate heritability (<50%) such as yam anthracnose disease severity, a number of stems per

Table 1.　Genetic parameter estimates for different traits in white yam early generation clones evaluated at Ibadan, Nigeria in 2016 cropping season.

Trait	Mean	CV	P value	σ^2_g	σ^2_e	σ^2_p	H²	GCV	PCV	GA	GAM
YMV (AUDPC)	200.6	12.4	0.09	764.64	614.06	1378.70	0.55	13.78	18.51	43.28	21.57
YAD (AUDPC)	130.5	26.3	0.38	305.34	1181.25	1486.59	0.21	13.39	29.55	18.04	13.82
Dry matter	35.0	6.2	0.01	16.30	4.77	21.07	0.77	11.54	13.12	7.27	20.77
Tuber weight per plant	3.0	24.5	0.04	1.02	0.55	1.57	0.65	33.46	41.44	1.74	57.59
Ware tuber yield (tha⁻¹)	24.9	31.3	0.06	94.39	60.73	155.12	0.61	39.05	50.06	15.99	64.25
Average tuber weight (kg)	2.3	28.9	0.03	1.02	0.44	1.45	0.70	44.07	52.72	1.83	79.82
Number of stems per plant	1.4	39.2	0.45	0.04	0.28	0.33	0.13	15.36	42.13	0.16	11.66
Vine diameter (mm)	4.5	18.7	0.46	0.10	0.71	0.81	0.12	6.91	19.97	0.23	5.03
Total fresh tuber yield (tha⁻¹)	26.1	25.1	0.03	114.99	42.99	157.98	0.73	41.04	48.11	16.72	63.99
Number of tubers per plant	0.7	25.5	<0.0001	0.40	0.03	0.43	0.93	93.76	97.16	1.27	188.64
Tuber surface texture (TR)	1.9	7.5	0.458	0.00	0.01	0.01	0.12	1.97	5.72	0.06	3.34
Tuber thorniness (scale)	0.6	52.0	0.122	0.11	0.11	0.22	0.51	52.62	73.99	0.50	77.74
Senescence class (TR)	1.1	28.6	0.389	0.02	0.10	0.12	0.19	14.07	31.89	0.49	45.44
Tuber length (cm)	25.5	24.7	0.190	28.21	39.67	67.88	0.42	20.84	32.33	7.84	30.75

CV = Coefficient of variation, σ^2_g = genetic variance; σ^2_e = random error variance; σ^2_p = Phenotypic variance; H² = Heritability (broad sense); GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation; GA = genetic advance; GAM = predicted genetic advance over population mean. YMV = yam mosaic virus severity; YAD = yam anthracnose disease severity; AUDPC = area under disease progression curve. TR = analysis done for transformed value.

Table 2. Parental predicted breeding value, prediction accuracy, predicted future progeny performance and index breeding value calculated on early generation white yam clonal trial evaluated at Ibadan, Nigeria in 2016.

Parents	Sex	N	Vine diameter (mm)			Tuber No. per plant			Tuber yield (t ha⁻¹)			Average tuber weight (kg)			Dry matter (%)			AUDPC-YMV			Index BV
			BV	rIH	Predicted FPP	BV	rIH	Predicted FPP	BV	rIH	Predicted FPP	BV	rIH	Predicted FPP	BV	rIH	Predicted FPP	BV	rIH	Predicted FPP	
TDr04-219	F	14	-0.34	0.35	4.32	2.30	0.84	2.66	-1.72	0.75	25.72	-1.09	0.61	1.78	-0.35	1.01	34.75	1.42	0.72	201.64	-0.15
TDr9518544	F	6	-0.03	0.24	4.47	0.31	0.71	1.67	-0.63	0.60	26.26	-0.38	0.45	2.13	0.89	0.93	35.37	0.45	0.56	201.16	0.48
TDr8902475	F	25	0.06	0.44	4.52	0.85	0.90	1.93	-0.26	0.84	26.45	-0.66	0.72	1.99	1.57	0.97	35.70	-1.89	0.81	199.98	2.10
TDr9700205	F	70	0.14	0.64	4.56	-0.89	0.96	1.07	-0.46	0.93	26.35	-0.08	0.87	2.28	0.24	1.00	35.04	0.70	0.92	201.28	-0.68
TDr9700917	F	59	-1.09	0.61	3.95	0.44	0.95	1.73	-1.31	0.92	25.92	-1.48	0.85	1.58	-2.64	1.02	33.60	-1.20	0.91	200.33	-2.24
TDr9519156	F	28	0.20	0.46	4.59	1.19	0.91	2.11	-0.21	0.85	26.48	0.01	0.74	2.32	-0.04	1.00	34.90	2.34	0.83	202.10	-0.09
TDr9700632	F	47	0.15	0.56	4.57	-1.30	0.94	0.86	2.00	0.90	27.58	1.91	0.82	3.27	-1.44	1.02	34.20	-0.98	0.89	200.44	-0.62
TDr9700840	F	41	0.53	0.54	4.75	0.02	0.93	1.52	-0.44	0.89	26.36	0.01	0.80	2.33	-0.44	1.01	34.70	0.69	0.87	201.28	-0.67
Agbanwobe	F	54	0.54	0.59	4.76	-1.06	0.95	0.98	2.46	0.91	27.81	1.74	0.84	3.19	-0.87	1.01	34.48	-0.68	0.90	200.59	0.03
Ufenyi	F	8	0.05	0.27	4.52	-0.25	0.75	1.39	-0.29	0.65	26.44	-0.14	0.50	2.25	3.27	0.84	36.56	-0.62	0.62	200.62	2.54
TDr8902665	F	4	0.17	0.19	4.57	0.12	0.63	1.57	0.78	0.52	26.97	0.08	0.38	2.36	1.33	0.87	35.58	-0.26	0.49	200.80	1.49
TDr06-4	F	5	-0.03	0.22	4.47	-0.58	0.67	1.22	-0.50	0.56	26.33	-0.08	0.42	2.28	1.15	0.90	35.50	-0.01	0.53	200.92	0.41
TDr9902789	M	44	0.07	0.55	4.53	0.20	0.94	1.61	-0.79	0.90	26.19	-0.47	0.81	2.09	-0.89	1.01	34.48	0.31	0.88	201.09	-1.02
TDr 9902626	M	4	-0.07	0.19	4.45	1.16	0.63	2.09	-0.54	0.52	26.31	-0.36	0.38	2.14	-0.73	1.11	34.56	0.76	0.49	201.31	-0.39
TDr9600629	M	6	-0.25	0.24	4.37	3.65	0.71	3.33	-1.45	0.60	25.85	-0.81	0.45	1.91	1.54	0.89	35.69	1.47	0.56	201.66	2.25
TDr06-15	M	8	-0.06	0.27	4.46	-0.16	0.75	1.43	0.29	0.65	26.73	-0.07	0.50	2.29	-0.40	1.03	34.72	-0.78	0.62	200.54	-0.10
TDr9501932	M	80	0.75	0.66	4.87	-0.69	0.96	1.17	1.53	0.94	27.34	1.22	0.88	2.93	-0.07	1.00	34.89	-0.76	0.93	200.55	0.52
TDr9902607	M	95	0.61	0.70	4.80	-1.18	0.97	0.92	0.56	0.95	26.86	1.03	0.90	2.83	0.12	1.00	34.98	0.30	0.94	201.08	-0.29
TDr8902677	M	57	-1.15	0.60	3.91	0.32	0.95	1.67	-1.61	0.92	25.78	-1.59	0.84	1.52	-2.58	1.02	33.63	-1.31	0.90	200.28	-2.35
TDr9700777	M	64	0.14	0.62	4.56	1.10	0.96	2.06	-0.20	0.93	26.48	-0.55	0.86	2.05	0.57	1.00	35.21	0.88	0.91	201.37	0.68
TDr04-219	M	12	-0.15	0.33	4.42	-0.29	0.82	1.36	1.44	0.73	27.30	0.46	0.58	2.55	-0.67	1.03	34.59	-0.52	0.69	200.67	0.01
TDr 9600582	M	5	0.01	0.22	4.49	-0.51	0.67	1.25	0.81	0.56	26.99	0.75	0.42	2.70	-1.94	1.28	33.95	-0.51	0.53	200.67	-1.30

BV= predicted breeding value, rIH= Breeding value prediction accuracy (correlation between true and predicted breeding value), predicted FPP= predicted future progeny performance for the traits for any future cross involving the parent and any other parent not been used for current analysis.

Table 3. Cultivar performance prediction at target set of environments.

Growing State	Target environment Statistical production yield (t ha⁻¹)	TDr1100163			TDr1100421			TDr1100497		
		On-station yield (t ha⁻¹)	On-farm predicted yield (t ha⁻¹)	Confidence interval (95%)	On-station yield (t ha⁻¹)	On-farm predicted yield (t ha⁻¹)	Confidence interval (95%)	On-station yield (t ha⁻¹)	On-farm predicted yield (t ha⁻¹)	Confidence interval (95%)
FCT	7.25	10.44	6.58	(6.40,6.76)	9.58	5.20	(4.45,5.95)	9.58	3.93	(3.18,4.68)
Ebonyi	11.80	23.28	8.57	(8.39,8.75)	19.15	6.77	(6.02,7.52)	17.79	7.74	(6.99,8.49)
Oyo	15.26	20.90	15.21	(15.03,15.39)	16.97	12.01	(11.26,12.76)	22.47	15.43	(14.68,16.18)
Benue	11.75	6.78	9.12	(8.94,9.30)	4.20	7.20	(6.45,7.95)	8.53	8.22	(7.47,8.97)
Edo	11.37	5.92	23.91	(23.16,24.09)	6.35	18.88	(18.13,19.63)	4.15	21.15	(20.40,21.90)
Abia	14.37	21.81	16.71	(16.53,16.89)	15.03	13.19	(12.44,13.94)	19.66	16.55	(15.80,17.30)

plant, vine diameter, vine senescence and tuber length in a current set of materials. The best individual clones identified with BLUP method were forward selected to advanced stage multi-location and multi-year trials to confirm their per se genetic superiority for the assessed traits in the target set of environments as well as used as a seed parents by collecting open-pollinated botanical seeds and generate half-sib progenies for another cycle of progeny testing. For traits with higher heritability (>50%) such as yam mosaic virus severity, dry matter, tuber yield per plant, total fresh tuber yield, tuber number per plant, tuber surface texture and tuber thorniness score (Table 1), fast improvement with current set of materials could be achieved in few cycles using forward selection for progenies with higher clonal values. Our result showed developing predictive platform is highly relevant to optimize the parental choice and increase the efficiency for development of improved varieties in yams for West Africa.

Prediction of cultivar performance

Prediction of cultivar performance at target set of production environments was performed using the regression method as specified by Mi *et al.*, (2011). Top three advanced white yam clones identified from the multi-environment trials in Nigeria were used for this analysis (Table 3). Based on the on-farm tuber yield prediction, TDr1100163 is best-adapted cultivar for yam growing states in Nigeria. TDr1100497 is the second-best choice for on-farm recommendation except for the federal capital territory. This exercise suggests in addition to trial site-based yam cultivar stability and adaptability analysis, prediction of on-farm performance in the target set of production environments would facilitate the recommendation of suitable variety for the target environment.

Conclusion

Genetic improvement of crops requires better understanding of genetic parameters such as the level and pattern of variation, heritability and relatedness for the traits of economic importance, and expected occurrence of the desired progeny within the breeding population for selection (Asfaw *et al.*, 2017). Such genetic parameter assessment has extensively been utilized and determined in crop breeding programs to improve breeding strategy and facilitate a choice of breeding method use in genetic improvement (Falconer and Mackay, 1996). Genetic parameters have rarely been utilized and determined in yam breeding population to devise a reliable and efficient genetic improvement methods for the crop. The current attempt of integrating predictive platforms in population and clonal development would accelerate genetic gain and optimize the breeding process in yams for West Africa.

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