

Supplementary Table S1. Description of clusters for 8 quantitative traits of *D. alata* genotypes.

Variables	Cluster 1-C1 (80)		Cluster 2-C2 (115)		Cluster 3-C3 (90)	
	Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range
YAD	244.91 ± 35.9 ^a	133.75-362.92	228.49 ± 28.99 ^b	174.58-339.62	226.56 ± 27.45 ^b	163.33-311.67
Pvig	1.91 ± 0.29 ^a	1.00-2.5	1.85 ± 0.31 ^a	1.17-2.5	1.86 ± 0.29 ^a	1.00-2.5
NTPP	2.20 ± 0.87 ^a	1.00-7.33	1.58 ± 0.38 ^b	1.00-2.67	1.74 ± 0.41 ^b	1.00-2.83
YPP	1.40 ± 0.32 ^b	0.77-2.14	1.71 ± 0.54 ^a	0.76-3.16	1.49 ± 0.38 ^b	0.65-2.54
TOxB	15.57 ± 4.2 ^b	4.72-26.26	18.94 ± 3.79 ^a	9.15-29.76	12.32 ± 5.00 ^c	2.15-23.01
DMC	29.37 ± 2.69 ^a	22.33-37.17	25.37 ± 2.67 ^b	19.00-32.83	28.54 ± 2.52 ^a	23.83-36.17
BldT	3.22 ± 0.7 ^a	1.48-4.84	3.26 ± 0.54 ^a	1.91-4.49	2.46 ± 0.62 ^b	1.08-4.14
PndT	4.90 ± 0.57 ^a	3.36-6.17	4.35 ± 0.54 ^b	2.87-5.71	3.97 ± 053^c	2.26-5.19

YAD: yam anthracnose disease; Pvig: plant vigour; NTPP: number of tubers per plant; YPP: yield per plant; TOxB: tuber oxidation browning; DMC: dry matter content; BldT: boiled tuber quality; PndT: pounded tuber quality.

Supplementary Table S2. Factorial loadings, communalities, uniqueness, and predicted genetic gains based on the multi-trait genotype–ideotype distance index for each family (Bold values represent traits with high contribution to each component).

Variables	FA1	FA2	FA3	FA4	Communality	Uniqueness	Genetic Gain (%)	sense	goal
F1									
YAD	-0.08	0	-0.03	0.96	0.93	0.07	-11.67	decrease	100
Pvig	-0.15	-0.75	-0.1	-0.21	0.64	0.36	8.95	increase	100
NTPP	-0.45	-0.44	0.12	0.15	0.43	0.57	23.24	increase	100
YPP	0.23	-0.82	-0.02	0.16	0.76	0.24	14.56	increase	100
TOxB	-0.74	0.09	-0.11	-0.08	0.57	0.43	-14.45	decrease	100
DMC	-0.86	-0.05	-0.05	0.13	0.76	0.24	9.55	increase	100
BldT	-0.32	-0.05	-0.83	-0.03	0.79	0.21	-17.84	decrease	100
PndT	0.14	-0.02	-0.88	0.06	0.8	0.2	-8.5	decrease	100
Total decrease	-52.46		average communality		0.71				
Total increase	56.3								
F2									
YAD	-0.53	-0.08	-0.13	-0.7	0.79	0.21	-0.15	decrease	100
Pvig	-0.79	-0.01	-0.25	0.1	0.71	0.29	14.39	increase	100
NTPP	-0.38	-0.18	-0.14	0.79	0.82	0.18	48.62	increase	100
YPP	-0.88	0.13	0.14	-0.01	0.81	0.19	17.26	increase	100
TOxB	-0.15	0.35	-0.79	0.08	0.78	0.22	-41.02	decrease	100
DMC	0.01	-0.16	-0.89	-0.03	0.81	0.19	5.28	increase	100
BldT	-0.09	0.86	-0.24	-0.14	0.83	0.17	-23.58	decrease	100
PndT	0.01	0.89	0.13	0.03	0.82	0.18	-8.21	decrease	100
Total decrease	-72.96		average communality		0.80				
Total increase	85.55								

Supplementary Table S2 cont. Factorial loadings, communalities, uniqueness, and predicted genetic gains based on the multi-trait genotype–ideotype distance index for each family (Bold values represent traits with high contribution to each component).

Variables	FA1	FA2	FA3	FA4	Communality	Uniqueness	Genetic Gain (%)	sense	goal
F3									
YAD	0.9	-0.02	0.28	0.1	0.91	0.09	-5.11	decrease	100
Pvig	0.17	0.17	0.79	0.23	0.74	0.26	13.26	increase	100
NTPP	-0.64	-0.21	0.37	0.49	0.84	0.16	12.67	increase	100
YPP	0	-0.03	0.91	-0.07	0.83	0.17	7.74	increase	100
TOxB	0.19	0.1	-0.1	0.9	0.87	0.13	-28.14	decrease	100
DMC	-0.21	0.14	0.22	0.71	0.61	0.39	9.76	increase	100
BldT	-0.1	0.94	0	0.01	0.89	0.11	-22.47	decrease	100
PndT	0.19	0.88	0.11	0.19	0.85	0.15	-29.39	decrease	100
Total decrease	-85.11			average communality	0.82				
Total increase	43.43								
F4									
YAD	-0.74	0.09	0.45	-0.23	0.81	0.19	-6.76	decrease	100
Pvig	-0.8	-0.17	-0.34	-0.04	0.78	0.22	11.49	increase	100
NTPP	0.02	0.25	-0.9	-0.18	0.91	0.09	28.87	increase	100
YPP	-0.81	-0.06	0.02	0.38	0.81	0.19	-1.44	increase	0
TOxB	0.17	0.42	0.52	-0.33	0.58	0.42	-8.31	decrease	100
DMC	0.04	-0.1	-0.05	-0.93	0.88	0.12	6.28	increase	100
BldT	0.01	0.9	0	0	0.81	0.19	-19.57	decrease	100
PndT	0.09	0.85	-0.1	0.1	0.76	0.24	-10.52	decrease	100
Total decrease	-45.16			average communality	0.79				
Total increase	45.2								

YAD: yam anthracnose disease; Pvig: plant vigour; NTPP: number of tubers per plant; YPP: yield per plant; TOxB: tuber oxidation browning; DMC: dry matter content; BldT: boiled tuber quality; PndT: pounded tuber quality.

Supplementary Table S3. Factorial loadings, communalities, and uniqueness of genotypes selected per family based on the multi-trait genotype–ideotype index (MGDI). (Bold values represent traits with high contribution to each factor).

VAR	FA1	FA2	FA3	FA4	Communality	Uniqueness
F1						
YAD	0.472479	0.36136	0.748787	0.157797	0.939399	0.060601
Pvig	0.914766	0.062093	-0.02652	0.263624	0.910853	0.089147
NTPP	-0.82748	0.166941	0.04794	0.380208	0.859446	0.140554
YPP	0.354493	0.185885	-0.85744	-0.00038	0.895427	0.104573
TOxB	-0.03346	-0.04285	-0.07936	-0.96776	0.945805	0.054195
DMC	-0.57935	0.525892	0.170796	-0.38126	0.786739	0.213261
BldT	-0.13898	-0.81629	-0.12428	-0.06315	0.705073	0.294927
PndT	0.208733	-0.7247	0.14952	-0.0249	0.59174	0.40826
F2						
VAR	FA1	FA2	FA3	Communality	Uniqueness	
YAD	0.3009	0.859417	-0.09742	0.838629	0.161371	
Pvig	-0.3571	0.12296	-0.76418	0.726608	0.273392	
NTPP	-0.81627	-0.092	-0.12544	0.69049	0.30951	
YPP	-0.46407	0.767377	0.049046	0.806638	0.193362	
TOxB	0.902742	0.003872	0.050531	0.817511	0.182489	
DMC	-0.03112	-0.04289	-0.92522	0.858848	0.141152	
BldT	0.858744	-0.10623	0.348878	0.870441	0.129559	
PndT	0.849969	-0.05348	0.135731	0.743731	0.256269	
F3						
VAR	FA1	FA2	Communality	Uniqueness		
YAD	0.932074	-0.36067	0.998842	0.001158		
Pvig	0.046656	0.998669	0.999517	0.000483		
NTPP	-0.82484	0.53428	0.965818	0.034182		
YPP	-0.58452	0.591748	0.69183	0.30817		
TOxB	0.973493	-0.21769	0.99508	0.00492		
DMC	0.378255	-0.62442	0.532977	0.467023		
BldT	0.894611	-0.44044	0.994321	0.005679		
PndT	0.986215	0.118907	0.98676	0.01324		
F4						
VAR	FA1	FA2	FA3	Communality	Uniqueness	
YAD	-0.94021	-0.0804	0.265971	0.961199	0.038801	
Pvig	-0.97986	-0.14695	-0.11868	0.995807	0.004193	
NTPP	0.220728	-0.77817	-0.17635	0.685364	0.314636	
YPP	0.007131	-0.41156	-0.81509	0.833805	0.166195	
TOxB	0.437181	0.892651	-0.1052	0.99902	0.00098	
DMC	0.343666	0.083771	-0.92203	0.975262	0.024738	
BldT	0.956082	-0.27508	-0.10118	0.999999	8.83E-07	
PndT	0.383507	-0.46787	0.594406	0.719302	0.280698	

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