

Analysis of Genetic Diversity and Population Structure in Yam (*Dioscorea* species) Germplasm Using Start Codon Targeted (SCoT) Molecular Markers

Anne Owiti^{1,2}, Joel L. Bargul^{2,3} and George O. Obiero¹, Evans N. Nyaboga^{1*}

¹Department of Biochemistry, University of Nairobi, Nairobi, Kenya

²Department of Biochemistry, Jomo Kenyatta University of Agriculture and Technology (JKUAT), Nairobi, Kenya

³International Centre of Insect Physiology and Ecology (ICIPE), Nairobi, Kenya

*Author to whom correspondence should be addressed.

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Supplementary Table S1: List of SCoT primer sequences used for PCR amplification and genetic diversity of 20 yam accessions

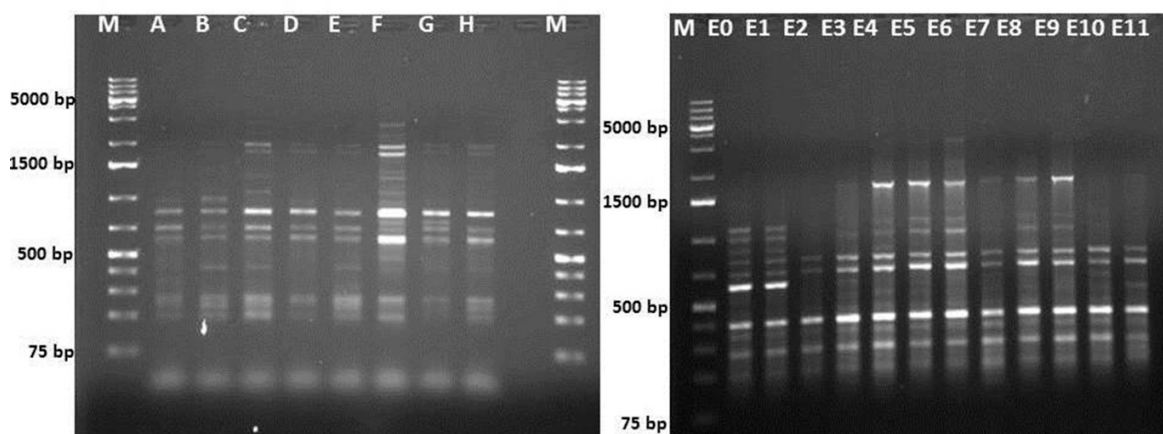
No	Name	Sequences	%G/C	Annealing temperature (°C)	Size of amplified products ranges (bp)
1	SCoT2	CAACAATGGCTACCACCC	56	50	200 - 2500
2	SCoT3	CAACAATGGCTACCACCG	56	53	200 - 2500
3	SCoT6	CAACAATGGCTACCACGC	56	50	200 - 3000
4	SCoT7	CAACAATGGCTACCACGG	56	48	350 - 3000
5	SCoT9	CAACAATGGCTACCAGCA	50	56	200 - 3000
6	SCoT10	CAACAATGGCTACCAGCC	56	56	500 - 3000

7	SCoT11	AAGCAATGGCTACCACCA	50	51	300 - 3000
8	SCoT12	ACGACATGGCGACCAACG	61	52	350 - 3000
9	SCoT14	ACGACATGGCGACCACGC	56	60	350 - 1300
10	SCoT16	ACCATGGCTACCACCGAC	56	52	100 - 3000
11	SCoT17	ACCATGGCTACCACCGAG	67	54	350 - 3000
12	SCoT19	ACCATGGCTACCACCGGC	67	56	200 - 3000
13	SCoT20	ACCATGGCTACCACCGCG	67	60	200 - 2500
14	SCoT21	ACGACATGGCGACCCACA	61	60	200 - 2000
15	SCoT23	CACCATGGCTACCACCAG	61	52	1300 - 3000
16	SCoT25	ACCATGGCTACCACCGGG	67	56	200 - 3000
17	SCoT26	ACCATGGCTACCACCGTC	61	52	200 - 4000
18	SCoT27	ACCATGGCTACCACCGTG	61	56	400 - 1500
19	SCoT29	CCATGGCTACCACCGGCC	72	58	250 - 3000
20	SCoT30	CCATGGCTACCACCGGCG	72	60	200 - 2000
21	SCoT32	CCATGGCTACCACCGCAC	67	60	100 - 3000
22	SCoT33	CCATGGCTACCACCGCAG	67	58	200 - 5000
23	SCoT34	ACCATGGCTACCACCGCA	61	60	200 - 3000
24	SCoT35	CATGGCTACCACCGGCCC	72	58	200 - 3000
25	SCoT36	GCAACAATGGCTACCACC	56	51	200 - 4000

Supplementary Table S2: Jaccard's similarity coefficient generated from the binary data.

	A	B	C	D	E	F	G	H	E7	E10	E0	E1	E2	E3	E4	E5	E6	E9	E8	E11
A	1																			
B	0.36	1																		
C	0.57	0.29	1																	
D	0.51	0.36	0.45	1																
E	0.61	0.31	0.59	0.59	1															
F	0.53	0.33	0.57	0.48	0.57	1														
G	0.65	0.33	0.60	0.57	0.68	0.62	1													
H	0.34	0.38	0.32	0.36	0.36	0.32	0.37	1												
E7	0.44	0.22	0.43	0.34	0.47	0.38	0.43	0.22	1											
E10	0.46	0.24	0.50	0.41	0.49	0.45	0.46	0.23	0.65	1										
E0	0.44	0.24	0.44	0.37	0.45	0.37	0.41	0.24	0.66	0.66	1									
E1	0.53	0.24	0.48	0.38	0.50	0.44	0.48	0.27	0.71	0.70	0.74	1								
E2	0.50	0.24	0.50	0.37	0.50	0.43	0.49	0.26	0.72	0.70	0.72	0.83	1							
E3	0.51	0.23	0.50	0.36	0.50	0.43	0.47	0.26	0.73	0.71	0.72	0.79	0.87	1						
E4	0.48	0.21	0.49	0.36	0.49	0.43	0.46	0.24	0.76	0.70	0.68	0.77	0.82	0.82	1					
E5	0.49	0.22	0.49	0.36	0.48	0.40	0.45	0.22	0.76	0.73	0.72	0.80	0.84	0.77	0.85	1				
E6	0.50	0.21	0.48	0.37	0.49	0.40	0.45	0.22	0.71	0.71	0.69	0.76	0.81	0.78	0.79	0.84	1			
E9	0.49	0.23	0.48	0.37	0.49	0.42	0.46	0.24	0.74	0.73	0.68	0.77	0.83	0.83	0.80	0.83	0.81	1		
E8	0.48	0.23	0.48	0.38	0.50	0.44	0.48	0.23	0.74	0.69	0.67	0.74	0.78	0.76	0.80	0.82	0.87	0.81	1	
E11	0.51	0.23	0.49	0.36	0.50	0.43	0.50	0.23	0.73	0.69	0.64	0.70	0.78	0.75	0.70	0.74	0.77	0.76	0.77	1

Supplementary Figures



Supplementary Figure S1: Representative agarose gel electrophoresis showing amplification profile: (A) for marker SCoT33 and (B) SCoT35 in yam accessions, where M: 1 kb plus ladder, Lane A – H and E0 – E11 denoted different accessions.