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Supplementary materials

Genetic diversity in *Colocasia esculenta* and *Xanthosoma mafaffa* in Togo, West Africa

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All relevant data are within the paper and its Supporting Information files.

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The authors declare no competing interests.

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Abstract: Taro and new cocoyam are root and leaf crops commonly grown in tropical to warm temperate regions. In Togo, they are neglected and underutilized. Here we report the genetic and morphological diversity of 26 accessions of taro and 101 accessions of new cocoyam. Analysis of simple sequence repeats revealed low polymorphic information content of 0.43 and 0.25 in taro and new cocoyam, respectively. PCA scatterplots and Neighbour Joining dendrograms based on the SSR data clustered accessions into groups that more-or-less correspond to morphological diversity in both species. AMOVA within and between morphological groups revealed greater variances within groups than between. This indicates weak genetic differentiation between morphological groups, particularly for taro. Genetic diversity was greater among taro cultivars. Taro has a longer history of introduction and dispersal in Africa, and has had more opportunity for multiple introduction and local cultivar development. Different strategies are suggested for future development of these crops in Togo and Africa. For taro, further studies of existing diversity and recent experimental introductions to Africa are likely to be rewarding. For new cocoyam, a modern historical introduction, has spread widely in Africa with little genetic diversity. International collaboration is needed to clarify taxonomy, to select and introduce further cultivars for evaluation under local conditions in Africa.

Table S1 - Annotated bibliography of simple sequence repeat (SSR) studies in Araceae. Reference details are provided at the end of supplementary materials

References	Target taxa	Primers developed/used
Amorphophallus		
Santosa *et al.*, 2007	*A. paeoniifolius*, cultivars	***Ampa*** primer series first reported
Santosa *et al.*, 2010	*A. paeoniifolius,* cultivars	Used *Ampa* primers; geographical survey
Pan *et al.*, 2012	*A. konjac*	***Amor*** primer series first reported
Colocasia esculenta		
Mace and Godwin, 2002	Cultivars; Asia and Pacific	***uQ*** primer series first reported (later authors refer to these with *Xqutem* prefix)
Noyer *et al.,* 2003	Cultivated and wild; Asia and Pacific	***Ces*** primer series first reported (did not amplify *X. sagittifolium*)
Mace *et al*., 2006	Cultivars; Pacific	*Xqutem (uQ)* primer series used to reduce duplication in large regional collection
Singh *et al.,* 2007	Cultivars; Papua New Guinea	*Xqutem (uQ)* primers used to reduce duplication in living cultivar collection
Hu *et al.,* 2009	Cultivars; China	***AC-HK*** primer series first reported, used for geographical survey
Quain *et al.*, 2010	Cultivars; Ghana	First report: **Sweet potato EST-SSR** primers successful in test with taro cultivars
Mace *et al.*, 2010	Cultivars; Pacific	*Xqutem (uQ)* primer series used to reduce duplication in large regional collection
Lu *et al.,* 2011	Cultivars; China	***Taro*** series first reported; geographical survey
Sardos *et al.,* 2012	Cultivars; Asia and Pacific	*Ces* primers used for geographical survey
Hunt *et al.,* 2013	Wild; Papua New Guinea and northern Australia	*uQ* and *AC-HK* primers used to survey wild breeding populations
Mabhaudhi and Modi, 2013	Cultivars; South Africa	*uQ* primers used to test dasheen and eddoe morphotypes; geographical survey
Traore, 2013	Cultivars; Burkina Faso	Results later published in Chaïr *et al.,* 2016 (see below)
Macharia *et al.,* 2014	Cultivars; Kenya, Tanzania, Uganda	*Xqutem (uQ)* primers used for Lake Victoria regional survey
You *et al.*, 2015	Wild and cultivated; China (36% of primer pairs succeeded with *Alocasia macrorrhizos)*	Thousands of EST-SSR loci detected, ***CE-EST-SSR*** primer series first reported; wild taro in Jiangxi a distinct clade
Chaïr *et al.,* 2016	Mostly cultivars; Asia, Africa, Oceania, America	*Ces*, *uQ*, and *HK* primers used; geographical survey, 19 countries
Dai *et al.,* 2016	Cultivars; China	*Ces* and *Taro* primers used to develop cultivar-specific SSR-SCAR test; coupled with chloroplast DNA
Palapala and Akwee, 2016	Cultivars; Kenya	*Xqutem (uQ)* primers used; geographical survey
Rasco *et al*, 2016	Cultivars, Philippines	Used *uQ* primers, ***CT*** primers from cassava (Moyib *et al.*, 2007), and ***SSRY*** primers from citrus (no
Mezhii *et al.*, 2017	Cultivars, India	***COL*** primer series first reported here (designed by GCC Biotech, Kolkata); geographical survey
Soulard *et al.*, 2017	Experimental crosses (cultivar breeding lines), Vanuatu	Loci detected by *uQ, Ces, HK,* and *Taro* (FJ895341) primers mapped (alongside SNP loci) in 14 linka-
Khatemenla *et al.*, 2019	Cultivars, India	*uQ*, and ***Ce1*** primers used; geographical survey (no ref. cited for Ce1)
Xanthosoma spp.		
Traore, 2013	*X. sagittifolium*, *X. robustum*, *X. mafaffa*, *X. dealbatum, X. mexicanum,* from Costa Rica and India	*Ces*, *uQ*, and *HK* primer series used, with some success (part of the study with Chaïr *et al.,* 2016); taxonomic survey
Cathebras *et al.,* 2014	*X. atrovirens, X. blandum, X. brasiliense, X. ceronii, X. granvillei, X. harlingii, X. hylaeae, X. mexicanum, X. piquambiense, X. poeppigii, X. pubescens, X. robustum, X. sagittifolium, X. violaceum, X. viviparum*, from central and South America	***Xs*** primer series first reported; taxonomic survey

Table S2 - List of 127 accessions of taro and new cocoyam in the Togo collection

Sample ID	Morphological groups	Species	Local name	Village
TGULT047	G3	*X. mafaffa*	Mancani Djin	Kouma konda
TGULT047 bis	G1	*X. mafaffa*	Mancani Djin	Kouma konda
TGULT048	G1	*X. mafaffa*	Mancani Hé	Koudzravi
TGULT050	G1	*X. mafaffa*	Mancani Hé	Dzédramégan
TGULT052	G3	*X. mafaffa*	Mancani Hé	Dzédramégan
TGULT053	G3	*X. mafaffa*	Mancani Djin	Dzédramégan
TGULT055	G3	*X. mafaffa*	Mancani Djin	Dzédramégan
TGULT059	G3	*X. mafaffa*	Manguélé moédé	Vhé N'Kougna
TGULT062	G3	*X. mafaffa*	Manguélé moédé	Vhé N'Kougna
TGULT064	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT065	G1	*X. mafaffa*	manguélé kpèlè	Dakan
TGULT066	G1	*X. mafaffa*	manguélé kpèlè	Dakan
TGULT067	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT068	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT069	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT074	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT075	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT076	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT078	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT080	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT081	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT082	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT083	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT085	G1	*X. mafaffa*	manguélé kpèlè	Dakan
TGULT086	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT088	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT089	G2	*X. mafaffa*	manguélé kpèlè	Dakan
TGULT090	G3	*X. mafaffa*	manguélé kpèlè	Dakan
TGULT093	G1	*X. mafaffa*	manguélé kpèlè	Dakan
TGULT095	G3	*X. mafaffa*	Mancani Djin	Kpélé Elémé
TGULT097	G3	*X. mafaffa*	Manguélé moédé	Aka
TGULT098	G1	*X. mafaffa*	Manguélé kpèlè	Aka
TGULT100	G3	*X. mafaffa*	Mancani Djin	Kpélé Elé
TGULT101	G1	*X. mafaffa*	Mancani Hé	Kpélé Elé
TGULT104	G2	*X. mafaffa*	Manguélé kpèlè	Danyigan
TGULT105	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT106	G3	*X. mafaffa*	Manguélé kpèlè	Danyigan
TGULT107	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT108	G2	*X. mafaffa*	Manguélé kpèlè	Danyigan
TGULT109	G2	*X. mafaffa*	Manguélé kpèlè	Danyigan
TGULT110	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT111	G2	*X. mafaffa*	Manguélé kpèlè	Danyigan
TGULT112	G2	*X. mafaffa*	Manguélé kpèlè	Danyigan
TGULT113	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT114	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT116	G2	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT117	G3	*X. mafaffa*	manguélé kpèlè	Danyigan
TGULT118	G2	*X. mafaffa*	manguélé kpèlè	Danyigan
TGULT119	G3	*X. mafaffa*	Manguélé moédé	Danyigan

to be continued..

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Sample ID	Morphological groups	Species	Local name	Village
TGULT047	G3	*X. mafaffa*	Mancani Djin	Kouma konda
TGULT047bis	G1	*X. mafaffa*	Mancani Djin	Kouma konda
TGULT048	G1	*X. mafaffa*	Mancani Hé	Koudzravi
TGULT050	G1	*X. mafaffa*	Mancani Hé	Dzédramégan
TGULT052	G3	*X. mafaffa*	Mancani Hé	Dzédramégan
TGULT053	G3	*X. mafaffa*	Mancani Djin	Dzédramégan
TGULT055	G3	*X. mafaffa*	Mancani Djin	Dzédramégan
TGULT059	G3	*X. mafaffa*	Manguélé moédé	Vhé N’Kougna
TGULT062	G3	*X. mafaffa*	Manguélé moédé	Vhé N’Kougna
TGULT064	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT065	G1	*X. mafaffa*	manguélé kpèlè	Dakan
TGULT066	G1	*X. mafaffa*	manguélé kpèlè	Dakan
TGULT067	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT068	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT069	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT074	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT075	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT076	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT078	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT080	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT081	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT082	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT083	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT085	G1	*X. mafaffa*	manguélé kpèlè	Dakan
TGULT086	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT088	G3	*X. mafaffa*	Manguélé moédé	Dakan
TGULT089	G2	*X. mafaffa*	manguélé kpèlè	Dakan
TGULT090	G3	*X. mafaffa*	manguélé kpèlè	Dakan
TGULT093	G1	*X. mafaffa*	manguélé kpèlè	Dakan
TGULT095	G3	*X. mafaffa*	Mancani Djin	Kpélé Elémé
TGULT097	G3	*X. mafaffa*	Manguélé moédé	Aka
TGULT098	G1	*X. mafaffa*	Manguélé kpèlè	Aka
TGULT100	G3	*X. mafaffa*	Mancani Djin	Kpélé Elé
TGULT101	G1	*X. mafaffa*	Mancani Hé	Kpélé Elé
TGULT104	G2	*X. mafaffa*	Manguélé kpèlè	Danyigan
TGULT105	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT106	G3	*X. mafaffa*	Manguélé kpèlè	Danyigan
TGULT107	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT108	G2	*X. mafaffa*	Manguélé kpèlè	Danyigan
TGULT109	G2	*X. mafaffa*	Manguélé kpèlè	Danyigan
TGULT110	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT111	G2	*X. mafaffa*	Manguélé kpèlè	Danyigan
TGULT112	G2	*X. mafaffa*	Manguélé kpèlè	Danyigan
TGULT113	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT114	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT116	G2	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT117	G3	*X. mafaffa*	manguélé kpèlè	Danyigan
TGULT118	G2	*X. mafaffa*	manguélé kpèlè	Danyigan
TGULT119	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT120	G3	*X. mafaffa*	Manguélé moédé	Danyigan

to be continued..

Table S2 - List of 127 accessions of taro and new cocoyam in the Togo List of 127 accessions of taro and new cocoyam in the Togo collection

Sample ID	Morphological groups	Species	Local name	Village
TGULT120	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT121	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT122	G3	*X. mafaffa*	Manguélé moédé	Danyigan
TGULT123	G3	*X. mafaffa*	Mancani Djin	Ayomé
TGULT124	G3	*X. mafaffa*	Mancani Djin	Ayomé
TGULT127	G3	*X. mafaffa*	mancani	Guégué
TGULT128	G1	*X. mafaffa*	Mancani koulomo	Kpélé Elémé
TGULT129	G1	*X. mafaffa*	Mancani koussèmo	Kpélé Elémé
TGULT131	G3	*X. mafaffa*	Mancana	Kpégodo
TGULT133	G3	*X. mafaffa*	Mancani Djin	Kpové Atikpo
TGULT136	G3	*X. mafaffa*	Bancani	Dalanda
TGULT139	G3	*X. mafaffa*	Bancani	Dalanda
TGULT140	G3	*X. mafaffa*	Bancani	Bonangana
TGULT146	G3	*X. mafaffa*	Bancani	Welou
TGULT147	G2	*X. mafaffa*	Bancani	Welou
TGULT149	G3	*X. mafaffa*	Bancani	Asséré
TGULT156	G3	*X. mafaffa*	Mancani Djin	Atchintsè
TGULT158	G3	*X. mafaffa*	Mancani	Atchintsè
TGULT159	G3	*X. mafaffa*	Mancani pibal	Diguina Anamagnè
TGULT160	G3	*X. mafaffa*	Mancani pibal	Diguina Anamagnè
TGULT164	G1	*X. mafaffa*	Bancani	Warkambou
TGULT164bis	G3	*X. mafaffa*	Bancani	Warkambou
TGULT165	G1	*X. mafaffa*	Bancani	Warkambou
TGULT166	G3	*X. mafaffa*	Bancani	Goundoga
TGULT168	G3	*X. mafaffa*	Bancani	Kpalgou
TGULT169	G3	*X. mafaffa*	Bancani	Kpalgou
TGULT171	G3	*X. mafaffa*	Bancani	Yadè Bohou
TGULT175	G3	*X. mafaffa*	Bancani	Yadè Bohou
TGULT180	G3	*X. mafaffa*	Bancani	Yadè Bohou

Table S3 - Characteristics of 47 SSR primers tested and recommended annealing temperatures. Sources for the primer sequences were: Ampa series = *Amorphophallus paeonifolius* (Santosa *et al*., 2007), AC-HK series = *Colocasia esculenta* (Hu *et al*., 2009), Xs series = *Xanthosoma sagittifolium* (Cathebras *et al*., 2014)

#	Primer pair ID	Repeat motif	Forward (F) and reverse (R) primer sequences	Average annealing T °C	*Used/not used
1	Ampa01	(CT)5(GT)10	F: GAGTCTACGATCTGCGACTTC R: CACCAATACAACATATGTGTG	52.1	ns
2	Ampa02	(CT)13(GT)7 (CT)7(CA)9	F: CACCCGATTGCGTTGTGCACT R: TCTCCCTTCCTACTCATCCAC	58.2	ns
3	Ampa03	(TG)16	F: GATTTAGAAAGCTGGCTAGGG R: CCAGCATCCAGATGATCATC	53	ns
4	Ampa04	(CT)7(GT)10	F: CCTCTGTCACAGGTTTAGTAC R: AGCCCCAAGTACAAAGCTGG	55	ns
5	Ampa05	(TC)19(TG)10	F: CCTCCCTCTAAGTGATCAAGG R: GAGATATAAGGGTTGAAGTTC	51	ns
6	Ampa06	(TG)18(AG)9	F: GAACCTACACCGTGAGGAAAATGTTGG R: GGTGTTGAGCTAGGCCAATAC	57.6	ns
7	Ampa07	(TG)11(AG)15	F: GCTTTCAAGAGTCTCCTACTATCTAAC R: CTCTCCGTCCAGAGATGCAAC	55.9	ns
8	Ampa08	(TG)18(AG)7	F: GCGTTCTCTCAGGATAAATCCACCAAC R: GAAGCCGTAGCCCTAAGAAG	57.2	ns
9	Ampa09	(TG)11(AG)14	F: CCAAACCAATCACGCCTCAG R: GACCAAAATACCCTCATTGAC	54	Ce+ Xm+
10	Ampa10	(TG)13(AG)15	F: CGAGTCCAATCTGAACCTAATTCATTG	55	ns

Primers were (a) used, or (b) not used as follows. (a) used to test all samples in full survey (30 primer pairs): Yellow highlight, Ce+, Xm+ = polymorphic in taro and new cocoyam (2 pairs) (scorable in both species). Green highlight, Ce+ = polymorphic in taro (11 pairs); not scorable in new cocoyam. Grey highlight, Xm+ = polymorphic in nex cocoyam (14 pairs); not scorable in taro. No highlight, mmXm= monomorphic in new cocoyam (3 pairs); not scorable in taro.(b) No used in full survey (17 primer pairs): not scorable (ns) in taro or new cocoyam.

to be continued..

Table S3 - Characteristics of 47 SSR primers tested and recommended annealing temperatures. Sources for the primer sequences were: Ampa series = *Amorphophallus paeonifolius* (Santosa *et al*., 2007), AC-HK series = *Colocasia esculenta* (Hu *et al*., 2009), Xs series = *Xanthosoma sagittifolium* (Cathebras *et al*., 2014)

#	Primer pair ID	Repeat motif	Forward (F) and reverse (R) primer sequences	Average annealing T °C	*Used/not used
11	Ampa11	(TC)6(TG)14	F: CATGCGCCTTGTGGCACTCAC R: CACCATAGCCATTCACCTTG	57.7	ns
12	Ampa12	(TG)11(AG)10	F: GAGATAGAGAGAGATAAGAGTG R: CTTGAAAATCCTTACAATAGT	47.1	ns
13	Ampa13	(TG)7 … (TG)24(AG)13	F: CACTATGTGCCTTTGTAAATGGGGCAG R: CCGTCTACTCGTATGTATAC	54.45	ns
14	Ampa14	(CT)20	F: CTGTACACATCTCTTTCCACTTTATAG R: CCTGACTAAATAAATCCAGTG	50.75	ns
15	Ampa15	(GA)7(GT)11	F: CACCTTGACCGTACGAGAGAC R: CAAGCTGTAGCTAGAGAGTG	54.55	Ce+ Xm+
16	Ampa16	(AG)10(TG)7	F: CGAGTGTGGCATAGCATAGCA R: GGACTTTGCGTTCCTCACGAC	57.9	ns
17	Ampa17	(AG)12(TG)9(AG)3	F: GAAAGAAAGGCAAATAGCAGG R: CTCATCAGTTACCCCCTCCCT	55	ns
18	Ampa18	(CT)17	F: GCATTTTATGACATTGAATCCATTAAG R: GCGATCGCTCACGCGTGAG	56.65	ns
19	Ampa19	(GA)7(GT)8 (CG)6 … (CT)11	F: GCTCGCACGCACAGAAAGAG R: CTCACCGGTATACGAGTGAC	56.75	ns
20	AC3	(GT)8(AG)9	F: AGTGGCATCAATGGAGGA R: CCACTAAACGACGACCCAC	54.55	Ce+
21	HK5	(AG)28	F: CCCACCTCTTCCCATTCGCTT R: CGATCCTTCCAGCTCCGACAT	59.3	Ce+
22	HK7	(CT)14TTCTT(CT)4	F: GTTGTCCGCCTGTGCGTTCT R: CTCTTGGGAATTCTCCGGGTG	59.2	Ce+
23	HK22	(AG)18	F: ACATCAAACCTCTGGTGGGC R: AGCAATCCTAGCCGAGGTG	57.4	Ce+
24	HK25	(AC)22	F: TGACTAGGCAGGAAGGTAA R: CAAGCATTCTCTGAACTATG	50.5	Ce+
25	HK26	(CT)15	F: GGGTGTTATCGCCATAGTCAT R: GAAACACCACAACGGAGAAAC	54.5	Ce+
26	HK29	(CT)42	F: GTCTGTGGAACCCTCAAGC R: ATTGTGGGAGCGATAGGG	55	Ce+
27	HK31	(GT)6(GA)11	F: TACCGCCGAGTGCTTATC R: TACGGCTGGAATCAAAGC	53.5	Ce+
28	HK34	(AG)29	F: TTACTCCAAACGAGGCAAAC R: CCTTCAAGATGTTACCAAATGC	52.7	Ce+
29	HK35	(CT)15L(CT)9	F: TACTAGAACCCCGTCAGTCT R: CGTCGATTTATCAGTGAGC	52.5	Ce+
30	HK38	(AG)12	F: AAACGCGGCCAGAAGATC R: GAATAGCGGAACAAGGTAGA	53.7	Ce+
31	mXsCIR05	(CA) 8 (CACA) 3	F: GCGCATTATTAACGAATATC R: GTCATCTATGGCTATCACCT	49	Xm+
32	mXsCIR07	(TG) 7 (AG) 19	F: GGACTGGGAGTCTGAGTAG R: CCTTTCCCCTCACTATAAA	51	Xm+
33	mXsCIR10	(AG) 22	F: GATGTCTGTAGTGGCCTAGT R: AATTAAGTTGGGTGGTAGAT	51	Xm+
34	mXsCIR11	(TG) 10 (GA) 16	F: AATTCTTAGCAGCATTGTTA R: CATTCGTATCAACTTCCTTT	47.6	Xm+
35	mXsCIR12	(TC) 17 (TTC) 7 (TCCC) 3 (TTCTTG) 3	F: TACATTTCCATTGCCATC R: CAAATTAAAGAGGGAGACAG	47.7	Xm+

Primers were (a) used, or (b) not used as follows.
(a) used to test all samples in full survey (30 primer pairs): Yellow highlight, Ce+, Xm+ = polymorphic in taro and new cocoyam (2 pairs) (scorable in both species). Green highlight, Ce+ = polymorphic in taro (11 pairs); not scorable in new cocoyam. Grey highlight, Xm+ = polymorphic in nex cocoyam (14 pairs); not scorable in taro. No highlight, mmXm= monomorphic in new cocoyam (3 pairs); not scorable in taro.
(b) No used in full survey (17 primer pairs): not scorable (ns) in taro or new cocoyam.

to be continued..

Table S3 - Characteristics of 47 SSR primers tested and recommended annealing temperatures. Sources for the primer sequences were: Ampa series = *Amorphophallus paeonifolius* (Santosa *et al*., 2007), AC-HK series = *Colocasia esculenta* (Hu *et al*., 2009), Xs series = *Xanthosoma sagittifolium* (Cathebras *et al*., 2014)

#	Primer pair ID	Repeat motif	Forward (F) and reverse (R) primer sequences	Average annealing T °C	*Used/not used
36	mXsCIR13	(CA) 8 (AG) 16	F: GTTTCCTTTATTCGTTGATG R: GTAGTGGCTGAGAATTGAAA	48.6	Xm+
37	mXsCIR14	(AG) 20	F: TACCCTACATTTGGGATCT R: TTTTGGCTTTAGGTCTATTC	48.7	Xm+
38	mXsCIR16	(AG) 15	F: CTTATTGATGCCGAGAATAC R: TTCCTCACAATATGTTCTCAT	48.6	Xm+
39	mXsCIR19	(AC) 8 (AC) 24 (AC) 8	F: CAACTTGTGTATCCTACATCC R: GCGTGGTTTATGTGTATCTT	50.5	Xm+
40	mXsCIR20	(CT) 11 (TC) 15 (TCTA) 3	F: CCCTTATTGCTGTTTTCA R: CATATCTCTTCCTCTCACCA	49	Xm+
41	mXsCIR21	(AG) 30	F: CTTAACCTTGTCAGCCTCT R: GAGCGGTATAACAATTCATC	50.1	Xm+
42	mXsCIR22	(AG) 22	F: CGTGAGAAACACCTGAATTA R: AATTTGCTCTGTCATTGTG	49.3	Xm+
43	mXsCIR23	(GA) 23	F: TGTAGGTATGGACACATGG R: TTAAGACAAACCCTCAGC	50.2	mmXm
44	mXsCIR24	(AG) 23	F: AATTTGAAGTGAAACGATCA R: TTCCTGTCATCAGAATTGTA	48.1	Xm+
45	mXsCIR26	(TC) 9 (TC) 9	F: TTCACCATTACTTGTCCACT R: TTAACATGGGAACGTATCTT	50	mmXm
46	mXsCIR27	(AG) 15 (GAA) 6	F: TGCATGAATTGAAGAAAT R: AACAAAGAGTCTCACCACAT	47.9	Xm+
47	mXsCIR28	(GA) 9	F: ACAGAAGTTGACATGGAGAG R: AATGTTAAAGAGCAAAAGGA	49.7	mmXm

Primers were (a) used, or (b) not used as follows.
(a) used to test all samples in full survey (30 primer pairs): Yellow highlight, Ce+, Xm+ = polymorphic in taro and new cocoyam (2 pairs) (scorable in both species). Green highlight, Ce+ = polymorphic in taro (11 pairs); not scorable in new cocoyam. Grey highlight, Xm+ = polymorphic in nex cocoyam (14 pairs); not scorable in taro. No highlight, mmXm= monomorphic in new cocoyam (3 pairs); not scorable in taro.
(b) No used in full survey (17 primer pairs): not scorable (ns) in taro or new cocoyam.

Table S4 - Mapped locations of taro SSR loci detected by the HK primer series1. HK7 and HK26 (highlighted) were found in the same linkage group (LG032). HK7 was also found by us in one of the chromosome sequences reported 3 , but other HK loci (including HK26) were not found in the reported chromosome sequences, presumably because the sequences are not complete, or because the SSR loci are null in the sequenced genome. Reference details are provided in footnote

SSR primer pair ID (z)	SSR primer target sequence		Major linkage group (LG) (y)	cv. Jiangsu chromosome (x)	
	Genebank ID (z)	length (bp)		Genbank ID(x)	1st base position for primer target
HK5	EU532198.1	246	-	CM024753.1	45,720,051
HK7	EU532199.1	228	LG03	CM024760.1	67,924,214
HK22	EU532200.1	256	-	CM024757.1	165,875,866
HK25	EU532201.1	159	-	CM024759.1	75,888,016
HK26	EU532202.1	210	LG03	-	-
HK34	EU581819.1	304	-	CM024753.1	156,550,046
HK35	EU581820.1	304	minor linkage group	-	-

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