

ELECTRONIC SUPPLEMENTARY MATERIAL

Table S1. BLAST analysis of non-microsatellite nucleotide sequences retrieved from archaeological maize specimens (last update January 2005).

Primers used	Samples			Amplification products							
	ID	Type of remain	Race	Size (bp)	No. of clones	BLASTN	E-value	BLASTX	E-value	TBLASTX	E-value
<u><i>Phi127</i></u>											
	T.C.54	cob	NA	226	2	NS		NM	-	NS	
	T.C.54	cob	NA	92	3	NS		<i>Bacillus halodurans</i> C-125/ alpha-L-arabinosidase NP_242740	4exp-6	<i>Bacillus halodurans</i> BA000004	7exp-8
	LH38	kernel	Morocho	128	1	Zea mays clone C9 retrotransposon Huck1 gag/pol gene AF464767	5exp-33	<i>Zea mays</i> gag/pol protein AAM22642	9exp-10	Zea mays unknown AY530950.	8e-13
	LH40	kernel	Chaucha	128	2	Zea mays clone C9 retrotransposon Huck1 gag/pol gene AF464767	8exp-38	<i>Zea mays</i> gag/pol protein AAM22642	9exp-10	<i>Zea mays</i> chromosome 4 clone BAC 072 AF528565	1exp-15
	LH20	kernel	Pisingallo	128	1	Zea mays clone C9 retrotransposon	3exp-35	<i>Zea mays</i> gag/pol protein	9exp-10	<i>Zea mays</i> chromosome 4	1exp-15

LH20	kernel	Pisingallo	110	2	Huck1 gag/pol gene AF464767 <i>Zea mays</i> Zeon-1 retroelement AF090447	6exp-26	NM	AAM22642	clone BAC 072 AF528565 <i>Zea mays</i> Zeon-1 retroelement AF090447	8exp-6
LH39	kernel	Chaucha	95	1	NS		NM		NS	
LH20	kernel	Pisingallo	111	1	Hawaiian green turtle herpesvirus AF035003	1exp-9	NM		NM	
LH20	kernel	Pisingallo	85	1	NS		NM		NM	
LH22	kernel	Capia	110	6	NS		NM		NS	
P.C.15	cob	Pisingallo	129	1	NS		<i>Aspergillus</i> <i>nidulans</i> hypothetical protein EAA57997 .	4exp-6	<i>Aspergillus</i> <i>nidulans</i> predicted mRNA XM 410348	7e-08
P.C.15	cob	Pisingallo	134	6	NS		NM		NS	
P.C.15	cob	Pisingallo	136	2	NS		NS		NS	
P.C.13	cob	Capia	116	1	NS		NS		NS	
P.C.13	cob	Capia	111	7	NS		NM		NS	
<u>Phi029</u>										
T.C.7	cob	NA	207	7	NS		<i>Cytophaga</i> <i>hutchinsonii</i> Predicted epimerase ZP_00311149	7exp-11	<i>Pseudomonas</i> <i>putida</i> arylsulfonate desulfonation gene	3exp-11

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T.C. 7	cob	NA	157	5	NS		NM		NS	
T.C. 27	cob	NA	119	1	NS		NM		NS	
T.C. 27	cob	NA	128	8	NS		<i>Mannheimia succiniciproducens</i> secA protein YP_087519	1exp-4	<i>Mannheimia succiniciproducens</i> complete genome AE016827	6exp-6
P.C. 13B	cob	Capia	248	2	NS		NS		NS	
P.C. 14	cob	Capia	131	7	NS		NM		<i>Zea mays</i> triosephosphate isomerase 1 gene L29431	2exp-3
P.C. 15	cob	Pisingallo	98		D.S.	<i>Leishmania brasiliensis</i> Genomic clone BX905934		4exp-4	NM	NS
<u>Phi059</u>										
T.C. 56	cob	NA	156	1	NS		NM		NS	
T.C. 56	cob	NA	167	10	NS		<i>Dechloromonas aromatica</i> Methylmalonyl-CoA mutase ZP_00152997	2exp-5	<i>Nocardia farcinica</i> complete genome AP006618	2exp-5
T.C. 55	cob	Blanco y ocho rayas	167	7	NS		<i>Dechloromonas aromatica</i> Methylmalonyl-CoA mutase ZP_00152997	6exp-6	<i>Nocardia farcinica</i> complete genome AP006618	6exp-6

T.C. 27Bcob	NA		104	D.S.	<i>Streptomyces coelicolor</i> complete genome AL939115	1exp-17	NS		NS
T.C. 27Bcob	NA		154	1	NS		NS	<i>Z. mays</i> PCO147721 mRNA AY104598	5exp-3
T.C. 27Bcob	NA		146	6	NS		<i>Streptomyces avermitilis</i> putative GTP-binding protein BAC73307	4 exp-5 <i>Streptomyces avermitilis</i> complete genome BA000030	9exp-7
T.C. 27Bcob	NA		149	1	NS		<i>Leifsonia xyli</i> cell division membrane protein YP_061233	6exp-6 <i>Leifsonia xyli</i> cell division membrane protein YP_061233	1exp-7
T.C. 7D cob	NA		126	D.S.	<i>Streptomyces viridochromogenes</i> Avilamycin A biosynthetic gene cluster AF333038	5exp-6	<i>Streptomyces viridochromogenes</i> putative NDP-glucose 4,6-dehydratase AAK83183	2exp-8 <i>Streptomyces viridichromogenes</i> Avilamycin A biosynthetic gene cluster AF333038	1exp-10
LH38	kernel	Morocho	169	1	NS		NS	NS	
LH35	kernel	Capia	207	D.S.	NS		NS	NS	
P.C.13B	cob	Capia	156	D.S.	NS		NS	NS	
P.C.52	cob	NI	160	D.S.	NS		NS	NS	

Figure S1. Allele sequences of locus *phi127* from archaeological and extant maize specimens. Clones (c) and direct sequencing (ds) products corresponding to archaeological specimens are highlighted in gray. *Z.m.p.*: *Zea mays ssp parviglumis*; *Z.m.m.*: *Zea mays ssp mexicana*.

Figure S2. Allele sequences of locus *phi029* from archaeological and extant maize specimens. Clones (c) and direct sequencing (ds) products corresponding to archaeological specimens are highlighted in gray. *Z.m.p.*: *Zea mays ssp parviglumis*; *Z.m.m.*: *Zea mays ssp mexicana*.