

Urban Ecosystems

Supporting Information

Genetic analysis reveals urban matrix permeability to
Nasutitermes corniger (Isoptera: Termitidae), a native termite
species and pest in the Neotropical region

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Table S1 – Geographic characterization of the ten sampling sites.

Fragment	Coordinates (Lat./Long.)	Size (ha)	Perimeter (ha)	Circularity Index
UFPB	7°08'09"S / 34°50'45"W	22.11 ha	0.27 ha	0.62
RVMB	7°08'20"S / 34°50'45"W	510.86 ha	0.92 ha	0.87
PNMC	7°11'25"S / 34°51'31"W	43.66 ha	0.43 ha	0.54
PEMX	7°10'14"S / 34°55'25"W	437.02 ha	2.77 ha	0.27
PZAC	7°06'50"S / 34°52'37"W	24.92 ha	0.27 ha	0.65
FACS	7°09'33"S / 34°48'05"W	23.61 ha	0.31 ha	0.55
PACB	7°08'46"S / 34°48'19"W	7.99 ha	0.28 ha	0.36
FIGISF	7°06'52"S / 34°52'58"W	6.13 ha	0.11 ha	0.80
PETCR	7°11'25"S / 34°48'46"W	536.2 ha	2.83 ha	0.29
UNIESP	7°05'40"S / 34°51'03"W	25.55 ha	0.30 ha	0.60

Table S2 – Genetic characterization of four microsatellite *loci* for *N. corniger* (Atkinson *et al.*, 2007).

Locus	Motif	Primer sequence (5'-3')	Dye	Na	Allele size range (bp)
<i>Multiplex 1</i>					
<i>Ncor3</i>	(TAA) ₂₆	F: GATCACTGTTGGTTCAAGAGA R: ATGATACACCCAAATGAAATG	NED	6	122–228
<i>Ncor6</i>	(TG) ₂₄	F: GCATTTATGGCTCCTATTGTGAT R: ACCTCGCTGTTTGCCTGCTGC	6' FAM	8	151–210
<i>Ncor7</i>	(TG) ₁₇	F: TATTCTCACATGATTGACAAA R: CACAGATGCTAAGTAAAGTATCC	VIC	7	236–281
<i>Ncor8</i>	(AAT) ₁₁	F: GTAATACCAAGCGAAAGAGGA R: GAGATTATCACACACAATTCTG	PET	7	116–169

Na: Number of alleles; bp: Base pairs.

Table S3 - Genotypes of individuals of *N. corniger* from 10 Atlantic Forest fragments inside João Pessoa's metropolitan urban matrix region (Northeast Brazil).

Colony	Individual	Locus							
		Ncor3		Ncor6		Ncor7		Ncor8	
UF1N	NCOR1	124	130	148	168	174	174	243	243
UF1N	NCOR2	122	130	162	172	172	172	243	249
UF1N	NCOR3	124	124	172	172	174	174	246	246
UF1N	NCOR4	128	128	176	176	172	178	246	246
UF2N	NCOR5	126	132	172	172	170	176	261	264
UF2N	NCOR6	126	132	176	176	176	176	252	252
UF2N	NCOR7	128	134	172	172	172	178	255	255
UF2N	NCOR8	130	134	172	172	180	180	261	261
UF3N	NCOR9	124	124	174	174	174	174	252	252
UF3N	NCOR10	122	122	166	166	172	172	249	249
UF3N	NCOR11	122	128	166	166	170	170	246	261
UF3N	NCOR12	122	122	144	168	170	170	249	249
MB1N	NCOR13	122	128	150	150	170	170	249	261
MB1N	NCOR14	122	130	146	166	172	172	249	264
MB1N	NCOR15	124	124	160	160	174	174	252	264
MB1N	NCOR16	128	128	170	170	178	178	267	282
MB2N	NCOR17	122	128	150	166	164	170	255	261
MB2N	NCOR18	120	120	142	142	170	170	252	261
MB2N	NCOR19	120	126	166	170	168	168	243	249
MB2N	NCOR20	122	122	166	170	170	170	249	252
MB3N	NCOR21	122	128	150	172	170	170	252	258
MB3N	NCOR22	122	122	146	146	172	172	252	255
MB3N	NCOR23	122	128	166	170	170	170	258	264
MB3N	NCOR24	126	132	170	170	174	174	264	270
CU1N	NCOR25	122	122	168	168	172	172	264	270
CU1N	NCOR26	122	128	168	168	170	170	249	261
CU1N	NCOR27	120	126	164	168	168	168	249	267
CU1N	NCOR28	120	128	164	170	170	170	255	261
CU2N	NCOR29	122	122	162	166	164	170	255	261
CU2N	NCOR30	122	122	166	166	170	170	261	264
CU2N	NCOR31	122	128	168	168	170	170	261	264
CU2N	NCOR32	124	130	170	170	168	168	264	267
CU3N	NCOR33	122	128	166	166	170	170	264	267
CU3N	NCOR34	120	130	164	164	164	168	249	249
CU3N	NCOR35	124	124	158	164	170	170	264	267
CU3N	NCOR36	120	126	164	170	168	168	261	267
XX1N	NCOR37	120	126	164	170	168	168	255	258

XX1N	NCOR38	120	126	166	166	170	170	258	261
XX1N	NCOR39	122	130	140	140	172	172	264	264
XX1N	NCOR40	124	124	174	174	168	174	267	267
XX2N	NCOR41	122	128	142	168	172	172	261	273
XX2N	NCOR42	120	126	142	142	168	168	249	270
XX2N	NCOR43	122	126	164	164	162	168	255	255
XX2N	NCOR44	120	120	164	170	170	170	255	255
XX3N	NCOR45	124	126	170	170	168	168	249	264
XX3N	NCOR46	120	126	164	168	168	168	261	270
XX3N	NCOR47	120	126	154	154	170	170	249	264
XX3N	NCOR48	124	130	170	170	168	168	267	276
BI1N	NCOR49	122	128	140	140	172	172	264	267
BI1N	NCOR50	122	128	166	166	170	170	261	261
BI1N	NCOR51	122	128	150	170	170	170	261	261
BI1N	NCOR52	122	122	146	146	170	170	264	267
BI2N	NCOR53	120	126	164	164	168	168	264	264
BI2N	NCOR54	122	128	168	168	166	170	264	267
BI2N	NCOR55	122	128	144	144	162	166	270	270
BI2N	NCOR56	124	130	168	172	168	172	270	270
BI3N	NCOR57	124	124	142	172	172	172	264	264
BI3N	NCOR58	122	128	144	168	170	170	261	264
BI3N	NCOR59	120	120	140	166	168	168	255	255
BI3N	NCOR60	120	120	166	170	168	168	258	261
CS1N	NCOR61	124	130	170	170	172	172	255	255
CS1N	NCOR62	120	126	164	164	168	168	258	261
CS1N	NCOR63	122	128	168	168	170	170	255	255
CS1N	NCOR64	122	130	172	172	166	172	258	261
CS2N	NCOR65	124	130	170	178	174	174	255	261
CS2N	NCOR66	122	128	156	168	170	170	255	258
CS2N	NCOR67	122	128	140	160	172	172	255	261
CS2N	NCOR68	122	128	168	168	170	182	255	258
CS3N	NCOR69	122	122	144	144	170	170	276	282
CS3N	NCOR70	120	128	166	166	170	180	255	255
CS3N	NCOR71	122	128	168	168	172	172	255	276
CS3N	NCOR72	120	126	170	170	174	174	255	258
CB1N	NCOR73	124	132	162	162	174	174	276	282
CB1N	NCOR74	124	130	162	162	174	174	258	261
CB1N	NCOR75	122	128	170	170	170	170	276	276
CB1N	NCOR76	120	128	156	160	176	196	255	255
CB2N	NCOR77	122	128	166	166	170	170	255	258
CB2N	NCOR78	120	128	152	152	170	170	270	276
CB2N	NCOR79	122	128	168	168	172	172	255	261
CB2N	NCOR80	124	130	170	170	174	174	258	261
CB3N	NCOR81	122	128	144	168	178	178	273	276
CB3N	NCOR82	126	126	156	156	174	174	270	270

CB3N	NCOR83	124	132	140	154	174	174	264	264
CB3N	NCOR84	126	132	170	170	174	174	261	264
SF1N	NCOR85	124	130	170	170	174	174	255	255
SF1N	NCOR86	126	132	142	170	174	174	258	261
SF1N	NCOR87	124	132	170	170	174	180	255	255
SF1N	NCOR88	126	134	172	172	170	176	258	261
SF2N	NCOR89	122	132	140	140	178	182	255	255
SF2N	NCOR90	128	134	178	178	174	178	258	261
SF2N	NCOR91	128	128	140	144	170	178	255	261
SF2N	NCOR92	128	128	160	176	164	178	255	258
SF3N	NCOR93	122	128	174	174	172	178	255	261
SF3N	NCOR94	126	132	140	140	170	176	255	258
SF3N	NCOR95	126	126	176	176	172	176	261	261
SF3N	NCOR96	126	132	176	176	176	176	258	261
JA1N	NCOR97	124	124	154	168	178	182	270	270
JA1N	NCOR98	122	122	154	168	174	178	264	264
JA1N	NCOR99	124	124	140	140	174	174	261	264
JA1N	NCOR100	126	126	154	168	176	176	255	255
JA2N	NCOR101	126	126	160	160	174	174	258	261
JA2N	NCOR102	124	124	152	152	174	174	255	255
JA2N	NCOR103	126	126	158	158	174	174	258	261
JA2N	NCOR104	130	130	160	160	170	170	255	255
JA3N	NCOR105	124	124	154	154	176	196	258	261
JA3N	NCOR106	122	122	152	152	170	170	255	261
JA3N	NCOR107	120	120	154	154	170	170	255	258
JA3N	NCOR108	122	122	152	152	190	190	249	249
BE1N	NCOR109	122	122	154	168	174	178	255	258
BE1N	NCOR110	122	122	154	168	174	174	255	261
BE1N	NCOR111	124	124	154	168	176	176	255	258
BE1N	NCOR112	126	126	158	158	154	154	276	282
BE2N	NCOR113	120	120	158	158	174	174	255	255
BE2N	NCOR114	120	120	154	168	178	178	255	276
BE2N	NCOR115	120	120	152	152	174	174	255	258
BE2N	NCOR116	120	120	150	150	174	174	276	282
BE3N	NCOR117	120	120	160	160	174	174	258	261
BE3N	NCOR118	122	122	152	152	174	174	276	276
BE3N	NCOR119	122	122	150	150	174	174	255	255
BE3N	NCOR120	124	124	152	152	174	180	255	258

Table S4 - Linkage Disequilibrium test performed with Genepop v4.8.3 (Rousset, 2008) using 10,000 MCMC repetitions and 5,000 iterations.

Pair of Locus	Chi2	df	<i>p-value</i>
Ncor3 & Ncor6	3.580339	18	0.999895
Ncor3 & Ncor7	9.938468	20	0.969274
Ncor6 & Ncor7	5.023785	18	0.998822
Ncor3 & Ncor8	5.763493	16	0.990455
Ncor6 & Ncor8	3.595137	10	0.963769
Ncor7 & Ncor8	7.169742	16	0.969849

Table S5 - Test for estimating null allele frequency performed with FreeNA (Chapuis and Estoup, 2007).

Locus/ Estimation of null allele frequency				
Colony	Ncor3	Ncor6	Ncor7	Ncor8
1	0.13173	0.13173	0.20190	0.20190
2	0.00000	0.29029	0.13173	0.27832
3	0.19665	0.23625	0.38687	0.23625
4	0.13173	0.30000	0.42857	0.00000
5	0.08334	0.00050	0.19665	0.00000
6	0.00000	0.13173	0.38687	0.00000
7	0.00000	0.00000	0.38687	0.00000
8	0.00000	0.27832	0.19665	0.00000

9	0.00050	0.10733	0.20190	0.00050
10	0.00050	0.30000	0.27832	0.16667
11	0.00000	0.08334	0.27832	0.00071
12	0.00000	0.23625	0.29029	0.00000
13	0.00000	0.30000	0.29029	0.00071
14	0.00000	0.27832	0.00000	0.20190
15	0.23625	0.00000	0.38687	0.13173
16	0.00000	0.42857	0.27832	0.00071
17	0.00000	0.00000	0.27832	0.00000
18	0.00000	0.42857	0.27832	0.00000
19	0.00000	0.23625	0.23625	0.13173
20	0.00000	0.42857	0.38687	0.00000
21	0.00000	0.16667	0.29029	0.13173
22	0.00000	0.19665	0.00000	0.00071
23	0.00000	0.13173	0.00000	0.00000
24	0.00000	0.38687	0.00000	0.00000
25	0.38687	0.00050	0.13173	0.27832
26	0.38687	0.38687	0.29029	0.00071
27	0.38687	0.33333	0.23625	0.00050
28	0.38687	0.00050	0.27832	0.00000

29	0.00100	0.30000	0.29029	0.00000
30	0.38687	0.38687	0.00001	0.00000

Table S6 - Hardy-Weinberg Equilibrium test for heterozygote deficiency and excess (Rousset and Raymond, 1995), performed with Genepop v4.8.3 (Rousset, 2008) using 10,000 MCMC repetitions and 5,000 iterations.

Colony code	Hardy-Weinberg Equilibrium test when H1 = heterozygotes deficit – <i>p</i> -value	SE	Hardy-Weinberg Equilibrium test when H1 = heterozygotes excess – <i>p</i> -value	SE
UF1N	0.0006	0.0002	0.9998	0.0001
UF2N	0.0030	0.0004	0.9982	0.0005
UF3N	0.0000	0.0000	1.0000	0.0000
MB1N	0.0003	0.0002	0.9999	0.0001
MB2N	0.0809*	0.0038	0.9466*	0.0033
MB3N	0.0146	0.0015	0.9906	0.0011
CU1N	0.0514*	0.0032	0.9550*	0.0039
CU2N	0.0067	0.0010	0.9948	0.0007
CU3N	0.0107	0.0010	0.9920	0.0014
XX1N	0.0000	0.0000	1.0000	0.0000
XX2N	0.0029	0.0007	0.9977	0.0005
XX3N	0.0716*	0.0039	0.9352*	0.0041
BI1N	0.0060	0.0006	0.9951	0.0005
BI2N	0.0098	0.0010	0.9937	0.0010
BI3N	0.0007	0.0002	0.9996	0.0001
CS1N	0.0006	0.0002	0.9995	0.0002

CS2N	0.1614*	0.0051	0.8538*	0.0049
CS3N	0.0010	0.0004	0.9998	0.0001
CB1N	0.0013	0.0004	0.9996	0.0002
CB2N	0.0015	0.0006	0.9978	0.0004
CB3N	0.0002	0.0001	0.9999	0.0001
SF1N	0.1675*	0.0071	0.8375*	0.0069
SF2N	0.1940*	0.0079	0.8290*	0.0056
SF3N	0.0836*	0.0030	0.9553*	0.0016
JA1N	0.0003	0.0001	0.9996	0.0002
JA2N	0.0001	0.0000	0.9999	0.0001
JA3N	0.0008	0.0002	0.9999	0.0001
BE1N	0.0029	0.0003	0.9981	0.0003
BE2N	0.0030	0.0006	0.9997	0.0001
BE3N	0.0011	0.0003	0.9991	0.0002

Marked (*) non-significant *p-values* for heterozygotes deficit and excess indicates that these colonies are under HWE. SE: Standard Error.

Table S7 – Similarity scores of genetic clusterings (K) estimated using Clumpak (Kopelman *et al.*, 2015), applying the LargeKGreedy algorithm with 2,000 repetitions.

Cluster	LnProb Mean	Mean Similarity Score
K =1	-2162.190	1.000
K = 2	-1978.925	0.994
K = 3	-1890.159	0.973
K = 4	-1798.644	0.987
K = 5	-1752.915	0.979
K = 6	-1724.928	0.842

K = 7	-1697.521	0.839
K = 8	-1667.824	0.856
K = 9	-1667.995	0.832
K = 10	-1655.170	0.815

Fig. S1 – StructureSelector graphs (Li and Liu, 2018) showing genetic clustering for all colonies based on the ΔK method of Evanno *et al.* (2005).

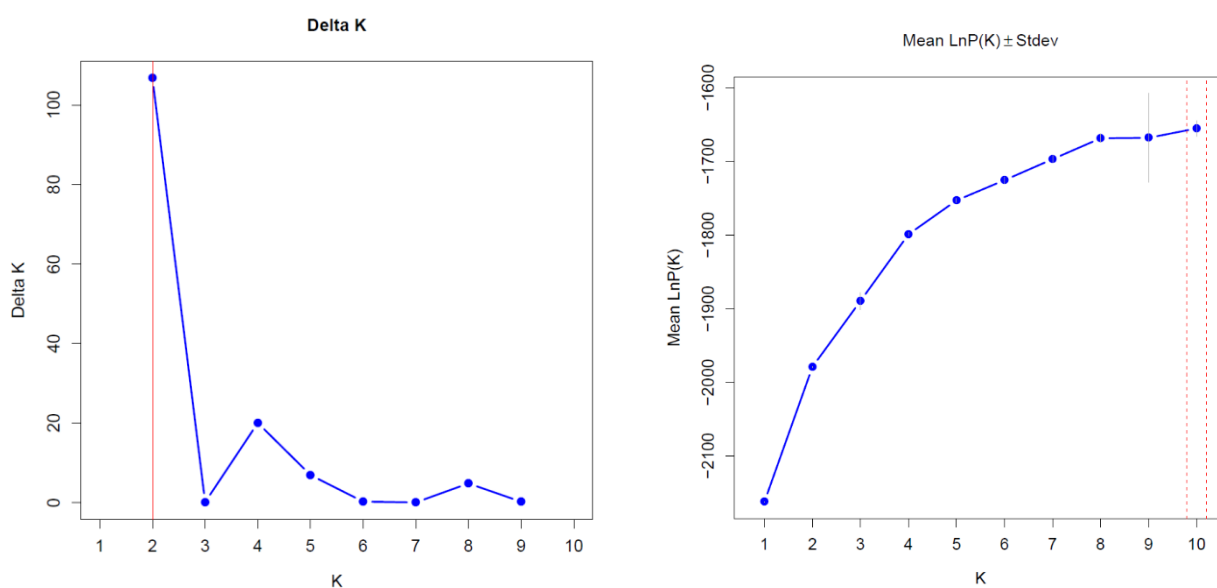


Table S9 - Genetic clustering proportions (Cluster 1 and 2) for all 30 *N. corniger* colonies obtained with STRUCTURE v2.3.4 (Pritchard *et al.*, 2000).

Colonies	Colony code	Cluster 1 (Blue)	Cluster 2 (Red)
1	UF1N	0.580 (58%)	0.420 (42%)
2	UF2N	0.714 (71.4%)	0.286 (28.6%)
3	UF3N	0.258 (25.8%)	0.742 (74.2%)
4	MB1N	0.289 (28.9%)	0.711 (71.1%)
5	MB2N	0.427 (42.7%)	0.573 (57.3%)

6	MB3N	0.273 (27.3%)	0.727 (72.7%)
7	CU1N	0.371 (37.1%)	0.629 (62.9%)
8	CU2N	0.267 (26.7%)	0.733 (73.3%)
9	CU3N	0.709 (70.9%)	0.291 (29.1%)
10	XX1N	0.580 (58%)	0.420 (42%)
11	XX2N	0.671 (67.1%)	0.329 (32.9%)
12	XX3N	0.890 (89%)	0.110 (11%)
13	BI1N	0.024 (2.4%)	0.976 (97.6%)
14	BI2N	0.476 (47.6%)	0.524 (52.4%)
15	BI3N	0.653 (65.3%)	0.347 (34.7%)
16	CS1N	0.485 (48.5%)	0.515 (51.5%)
17	CS2N	0.282 (28.2%)	0.718 (71.8%)
18	CS3N	0.291 (29.1%)	0.709 (70.9%)
19	CB1N	0.720 (72%)	0.280 (28%)
20	CB2N	0.289 (28.9%)	0.711 (71.1%)
21	CB3N	0.734 (73.4%)	0.266 (26.6%)
22	SF1N	0.950 (95%)	0.050 (5%)
23	SF2N	0.241 (24.1%)	0.759 (75.9%)
24	SF3N	0.729 (72.9%)	0.271 (27.1%)
25	JA1N	0.684 (68.4%)	0.316 (31.6%)
26	JA2N	0.873 (87.3%)	0.127 (12.7%)
27	JA3N	0.425 (42.5%)	0.575 (57.5%)
28	BE1N	0.593 (59.3%)	0.407 (40.7%)
29	BE2N	0.732 (73.2%)	0.268 (26.8%)
30	BE3N	0.618 (61.8%)	0.382 (38.2%)

Table S10 – Molecular variance analysis (AMOVA), considering all three colonies from each fragment as subpopulations, performed with Arlequin V. 3.5.2.2 (Excoffier and Lischer, 2005) with 10,000 permutations applied.

Source of Variation	Sum of squares	Variance Components	Percentage Variation
Among subpopulations	41.950	0.08588	4.93105
Among colonies within the subpopulations	52.000	0.03490	2.00366
Among individuals within the colonies	208.875	0.70000	40.19272
Among individuals	110.500	0.92083	52.87257
Total	413.325	1.73569	100%

Fixation indexes: FIS: 0.43188 (p -value = 0.00000), FSC: 0.02108 (p -value = 0.07752), FCT: 0.04931 (p -value = 0.00000) and FIT: 0.47127 (p -value = 0.00000).

Table S11 - Test for landscape influence on allele richness performed with GESTE V. 2.0 (Foll and Gaggiotti, 2006), using 100,000 Monte Carlo–Markov Chain (MCMC) repetitions, followed by a 50,000 burn-in period, identifying the highest-probability model and the posterior probabilities of the variables that best explain the patterns observed in the genetic data.

Variables	Highest-probability model	P (model)	P (G1)	P (G2)	P(G1*G2)
Size	Constant	-	0.0627	-	-
Shape	Constant	-	-	0.0301	-
Size, Shape	Constant	-	-	-	0.000240

Constant	Constant	0.909	-	-	-
Constant, Size	Constant	0.0606	-	-	-
Constant, Shape	Constant	0.0280	-	-	-
Constant, Shape, Size	Constant	0.00212	-	-	-
Constant, Size*Shape, Shape, Size	Constant	0.000240	-	-	-

Table S12 – Descriptive genetic diversity values for all *N. corniger* colonies.

Code	Colony	Locality	N	%PL	Na (SE)	Ne (SE)	PA	He (SE)	Ho (SE)	<i>f</i> (SE)
UF1N	1	UFPB	4	100	3.25 (0.25)	2.68 (0.33)	0	0.61 (0.04)	0.33 (0.00)	0.44 (0.04)
UF2N	2	UFPB	4	100	4.00 (0.70)	3.43 (0.64)	0	0.65 (0.09)	0.43 (0.21)	0.42 (0.27)
UF3N	3	UFPB	4	100	3.50 (0.28)	2.65 (0.18)	0	0.61 (0.03)	0.18 (0.06)	0.69 (0.10)
MB1N	4	RVMB	4	100	4.75 (0.47)	4.36 (0.38)	0	0.76 (0.02)	0.43 (0.21)	0.43 (0.26)
MB2N	5	RVMB	4	100	4.00 (0.40)	3.36 (0.50)	0	0.68 (0.05)	0.62 (0.16)	0.12 (0.17)
MB3N	6	RVMB	4	100	4.25 (0.47)	3.53 (0.45)	0	0.70 (0.03)	0.56 (0.21)	0.22 (0.28)
CU1N	7	PNMC	4	100	4.00 (0.70)	3.42 (0.70)	0	0.67 (0.06)	0.56 (0.21)	0.19 (0.27)

CU2N	8	PNMC	4	100	3.75 (0.25)	2.79 (0.34)	0	0.62 (0.04)	0.50 (0.17)	0.21 (0.25)
CU3N	9	PNMC	4	100	4.25 (0.62)	3.56 (0.63)	0	0.69 (0.04)	0.56 (0.12)	0.21 (0.13)
XX1N	10	PEMX	4	100	4.75 (0.25)	4.31 (0.25)	0	0.76 (0.01)	0.43 (0.12)	0.43 (0.15)
XX2N	11	PEMX	4	100	4.25 (0.25)	3.37 (0.10)	0	0.70 (0.00)	0.50 (0.10)	0.28 (0.14)
XX3N	12	PEMX	4	100	4.00 (0.81)	3.34 (0.77)	0	0.64 (0.09)	0.56 (0.25)	0.24 (0.33)
BI1N	13	PZAC	4	100	3.00 (0.70)	2.68 (0.67)	0	0.56 (0.08)	0.37 (0.16)	0.32 (0.34)
BI2N	14	PZAC	4	100	4.50 (0.64)	3.88 (0.59)	0	0.71 (0.04)	0.56 (0.18)	0.25 (0.21)
BI3N	15	PZAC	4	100	4.50 (0.86)	3.88 (0.86)	0	0.71 (0.04)	0.43 (0.21)	0.43 (0.25)
CS1N	16	FACS	4	100	4.25 (0.62)	3.88 (0.55)	0	0.72 (0.03)	0.43 (0.21)	0.40 (0.26)

CS2N	17	FACS	4	100	4.00 (0.00)	3.49 (0.40)	0	0.70 (0.03)	0.75 (0.17)	-0.09 (0.28)
CS3N	18	FACS	4	100	4.75 (0.47)	3.50 (0.22)	0	0.71 (0.02)	0.43 (0.18)	0.36 (0.27)
CB1N	19	PACB	4	100	4.25 (0.47)	3.78 (0.57)	0	0.71 (0.03)	0.50 (0.17)	0.33 (0.20)
CB2N	20	PACB	4	100	4.25 (0.47)	3.81 (0.40)	0	0.72 (0.03)	0.50 (0.28)	0.34 (0.37)
CB3N	21	PACB	4	100	4.50 (0.86)	3.73 (0.77)	0	0.67 (0.10)	0.43 (0.15)	0.42 (0.20)
SF1N	22	FIGISF	4	100	3.75 (0.47)	2.91 (0.56)	0	0.62 (0.05)	0.56 (0.15)	0.14 (0.16)
SF2N	23	FIGISF	4	100	4.25 (0.47)	3.03 (0.37)	0	0.65 (0.04)	0.68 (0.12)	-0.05 (0.17)
SF3N	24	FIGISF	4	100	3.50 (0.28)	2.78 (0.07)	0	0.64 (0.00)	0.56 (0.18)	0.12 (0.29)
JA1N	25	PETCR	4	100	3.50 (0.28)	3.17 (0.22)	0	0.68 (0.02)	0.37 (0.16)	0.45 (0.24)

JA2N	26	PETCR	4	100	2.75 (0.25)	2.40 (0.26)	0	0.56 (0.06)	0.12 (0.12)	0.80 (0.20)
JA3N	27	PETCR	4	100	3.25 (0.47)	2.89 (0.41)	0.25	0.63 (0.05)	0.25 (0.17)	0.65 (0.23)
BE1N	28	UNIESP	4	100	3.75 (0.47)	3.28 (0.30)	0.25	0.68 (0.02)	0.50 (0.22)	0.29 (0.31)
BE2N	29	UNIESP	4	75	3.00 (0.91)	2.52 (0.79)	0	0.45 (0.17)	0.25 (0.17)	0.51 (0.29)
BE3N	30	UNIESP	4	100	3.00 (0.40)	2.54 (0.47)	0	0.54 (0.11)	0.18 (0.12)	0.54 (0.28)
Total Mean	-	-	-	99.17	3.91 (0.10)	3.30 (0.09)	-	0.66 (0.01)	0.45 (0.03)	0.33 (0.04)

N: Number of individuals; %PL: Percentage of polymorphic loci; Na: Number of alleles; Ne: Number of effective alleles; PA: Frequency of private alleles; He: Expected heterozygosity; Ho: Observed heterozygosity; *f*: Fixation index; SE: Standard error.

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