

Table S1. The multilocus genotype (MLG) diversity of nipa populations in Indo-West Pacific^z.

Pop	N	MLG	eMLG	SE	H	G	lambda	E.5	Hexp	Ia	p.Ia	rbarD	p.rD
WP	22	22	11	4.45e-07	3.09	22	0.955	1	0.413	3.529	0.000999	0.11199	0.000999
GPb	13	13	11	0.00e+00	2.56	13	0.923	1	0.276	0.961	0.001998	0.04771	0.001998
GPa	11	11	11	0.00e+00	2.40	11	0.909	1	0.284	0.166	0.269730	0.00712	0.269730
GPn	16	16	11	0.00e+00	2.77	16	0.938	1	0.395	0.944	0.000999	0.02730	0.000999
Total	62	62	11	0.00e+00	4.13	62	0.984	1	0.416	1.646	0.000999	0.04518	0.000999

^zPop = population

N = census population size

MLG = number of unique multilocus genotype (MLG) observed

eMLG = number of expected MLG based on rarefaction at smallest $N \geq 10$

SE = standard error of rarefaction analysis

H = Shannon-Wiener Index of MLG diversity

G = Stoddart and Taylor's Index of MLG diversity

lambda = Simpson's Index

E.5 = Evenness

Hexp = Nei's (1978) expected heterozygosity

Ia = Index of association

p.Ia = p-value for Ia

rbarD = standardized index of association

p,rD = p-value for rbarD

Table S2. Statistical analysis results of Mantel correlogram.

Distance class (W)	Class index	Number of distances	Mantel correlation	<i>p</i> values (Mantel)	<i>p</i> values (corrected)
1	41.451486	1254	0.444921	0.0010	0.0010***
2	124.354458	0	NA	NA	NA
3	207.257430	0	NA	NA	NA
4	290.160402	0	NA	NA	NA
5	373.063374	0	NA	NA	NA
6	455.966346	1056	-0.300587	0.0010	NA
7	538.869318	416	0.059146	0.2139	NA
8	621.772291	0	NA	NA	NA
9	704.675263	0	NA	NA	NA
10	787.578235	0	NA	NA	NA
11	870.481207	0	NA	NA	NA
12	953.384179	1056	-0.207566	0.0010	NA

Significance codes: *** 0.001

Table S3. The list of first-generation (F₀) immigrants detected among *N. shimadai* populations in the northern Taiwan based on multilocus genotypes^a.

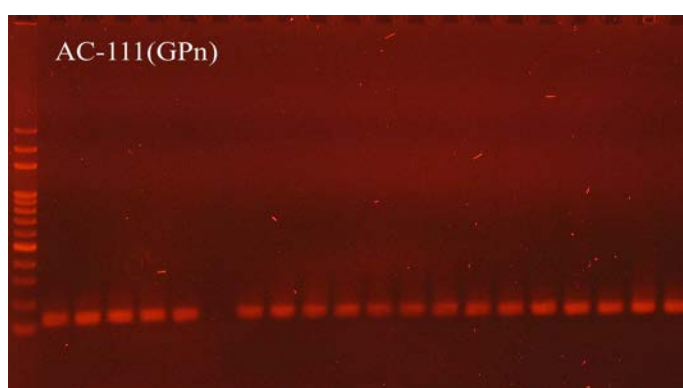
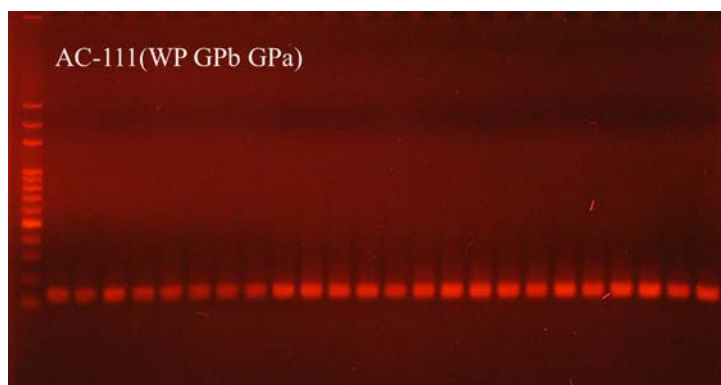
Sample	Home population	-log (L _{home} /L _{max})	Probability	-log(L)	Reference population
ns39	GPb	2.802	0.0006	11.759	GPa
ns41	GPa	1.498	0.0077	15.412	GPb
ns50	GPa	1.307	0.0037	22.204	GPb

^a log(L_{home}/L_{max}) (likelihood ratio); probability, significant at p<0.01; -log(L) (genetic distance); reference population (population of origin) with population codes found in Table 5.

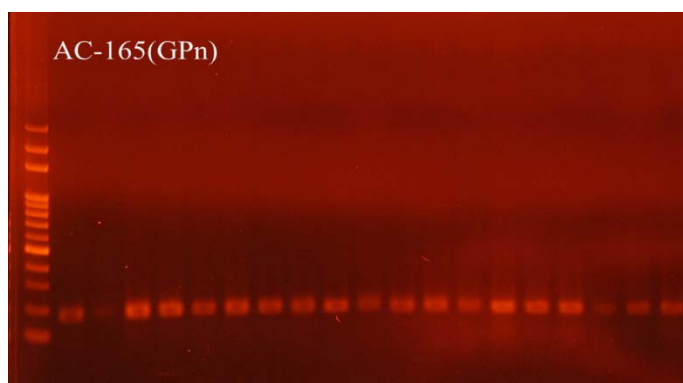
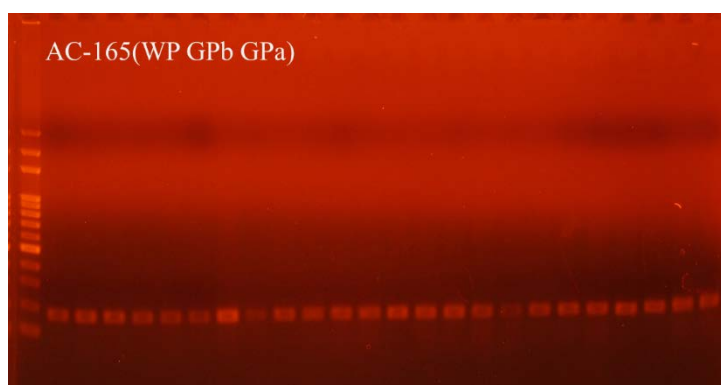
Table S4. Number of migrants (Nm) using private alleles.

Sample size	Nm
Mean N = 10	0.451128
Mean N = 25	0.269447
Mean N = 50	0.199791
Corrected value for sample size	0.291291
Mean sample size: 15.4872	
Mean frequency of private alleles, p (1): 0.165214	

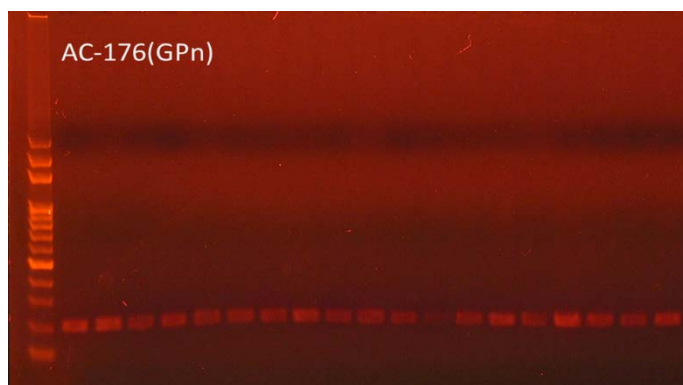
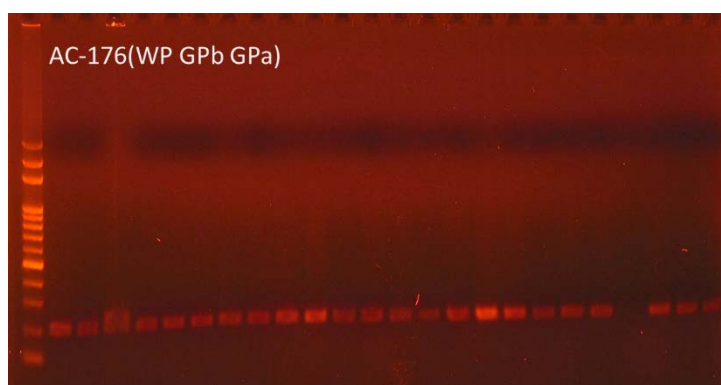
Figure S1. PCR amplicons of the selected 10 primers
ACC-111



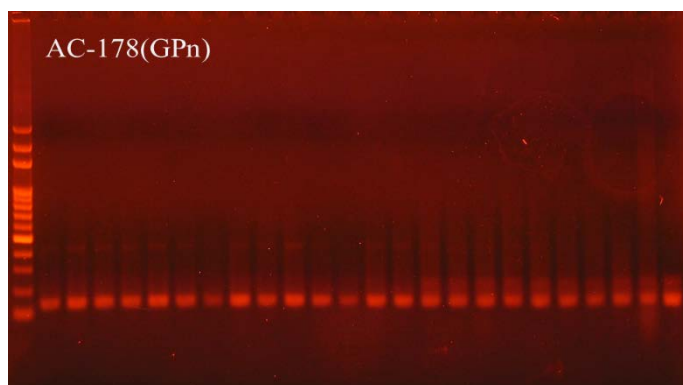
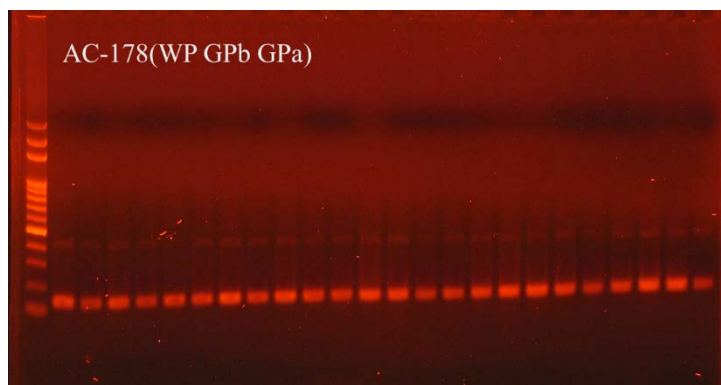
AC165



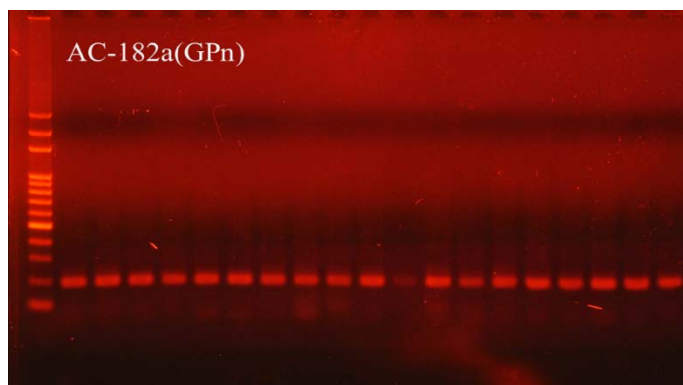
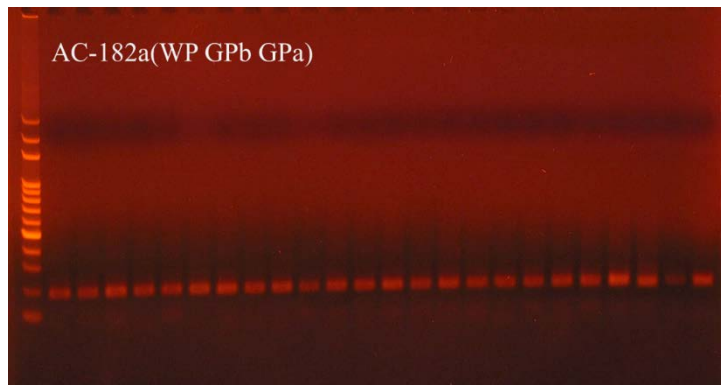
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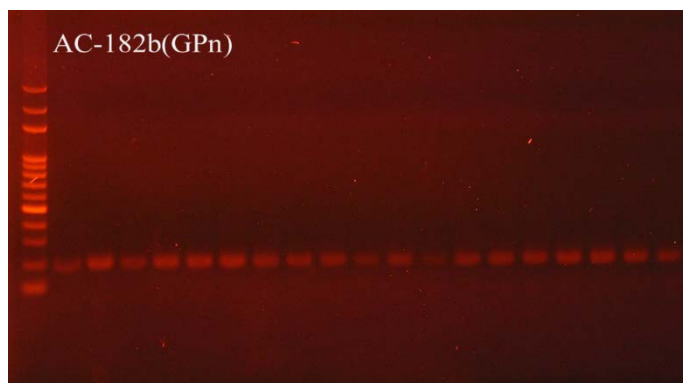
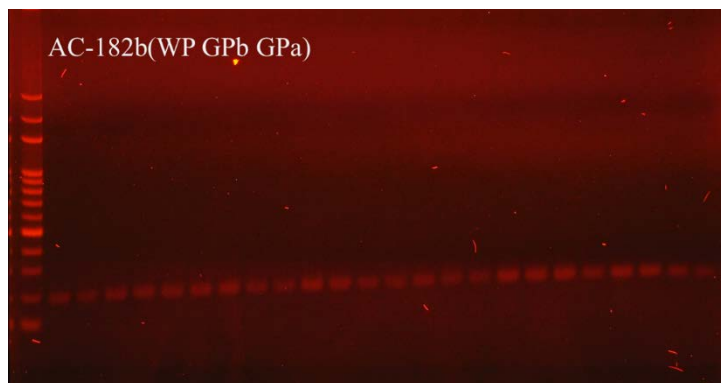
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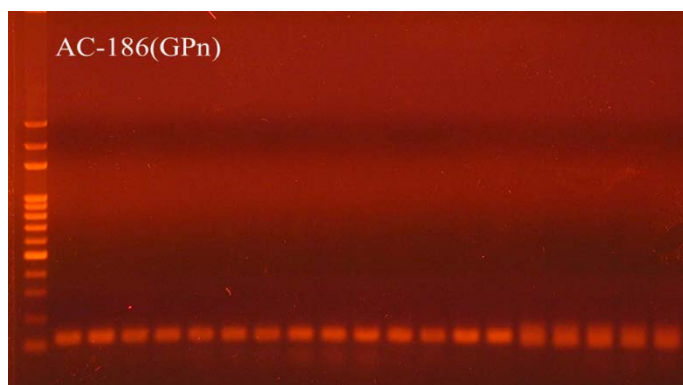
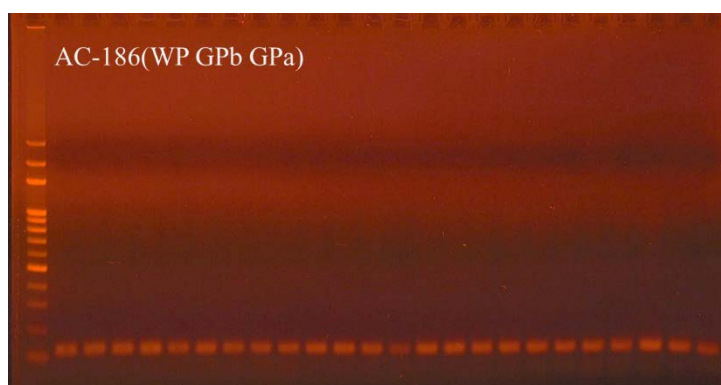
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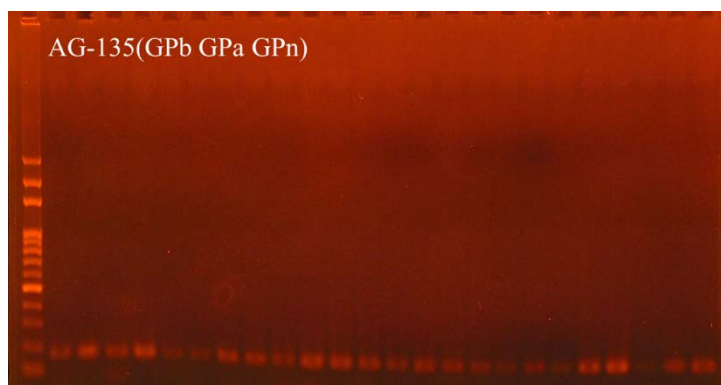
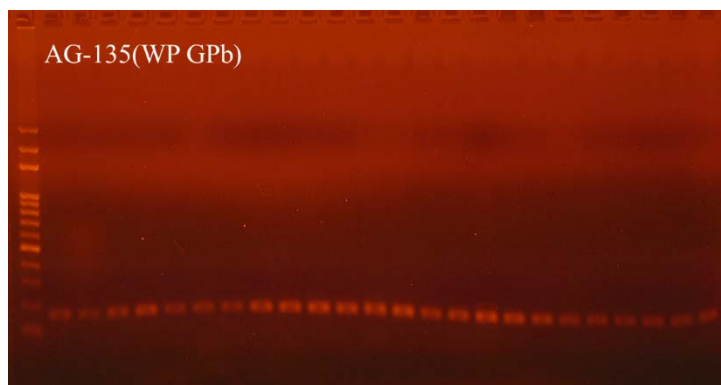
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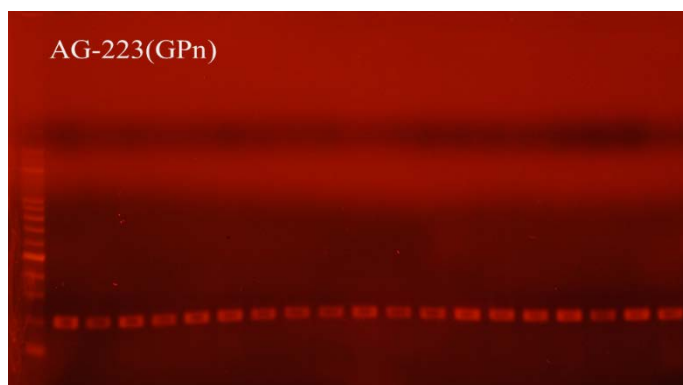
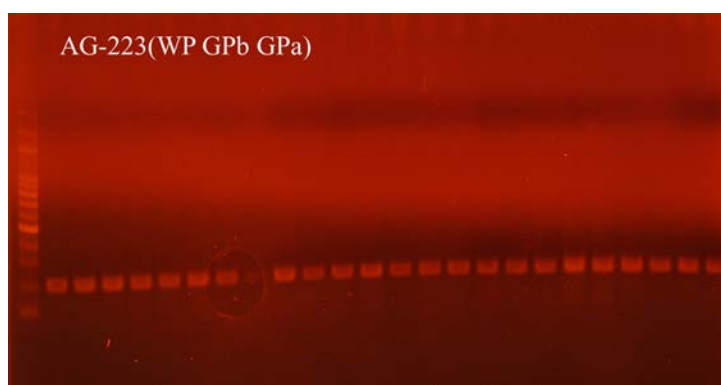
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