Genomics of natural and restored populations of *Acropora palmata*

Alvarado-Cerón V.1, Prada C.2* Gómez-Corrales M.2, Padilla-Souza A. C.3, León-Pech M. G.2, Rivera-Madrid R.4, & Arias-González J. E.1

Alvarado-Ceron et al. Genomics Acropora_Formato SR.docx

Supplementary Information

Table S 1. Distance between sampling sites in kilometers.

Site	Ixlache	Cadenita	Farito	Cuevones	Bajito Nizuc	Limones
Cadenita	20.22					
Farito	21.53	1.68				
Cuevones	30.74	10.55	9.22			
Bajito Nizuc	51.96	27.97	26.16	17.80		
Limones	54.49	31.14	29.89	21.50	3.65	
Akumal	142.92	117.56	116.73	106.40	89.36	85.20

Quality filtering on the VCF files was performed using dDocent's SNP filtering workflow (Puritz et al., 2014).

Table S 2. SNPFiltering criteria and results.

	Acropora palmata		
Filtro	**Ind.**	**Sites**	**Kept sites**
remove-indels	128	1899459	1776533
max-missing 0.5	128	1776533	629216
mac 3	128	629216	84961
minQ 30	128	84961	84961
min-meanDP 3	128	84961	41884
missing indv 0.5	115	41884	41884
max-missing 0.7	115	41884	32338
maf 0.03	115	32338	25248
hwe 0.01:	115	25248	15420
PCAdapt*	115	15420	14271
thin 1000	115	14271	6580
remove clones	**107**	**6580**	**6580**

***PCAAdapt: 1198 SNPs under selection**

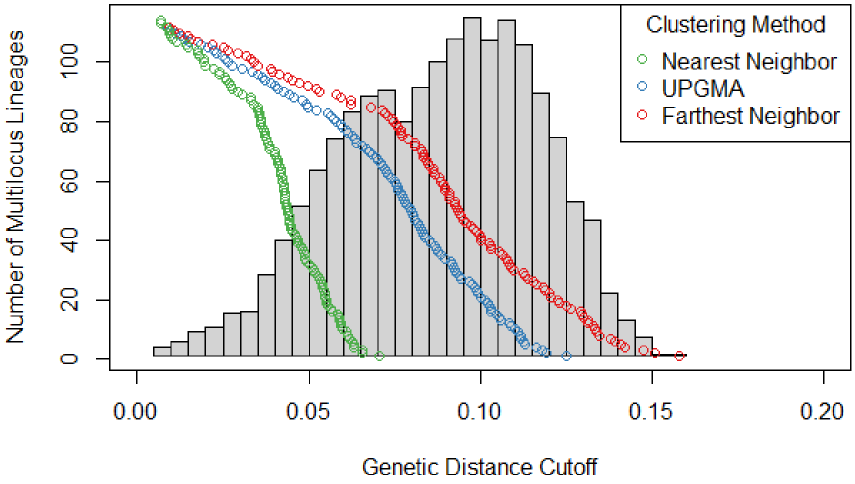
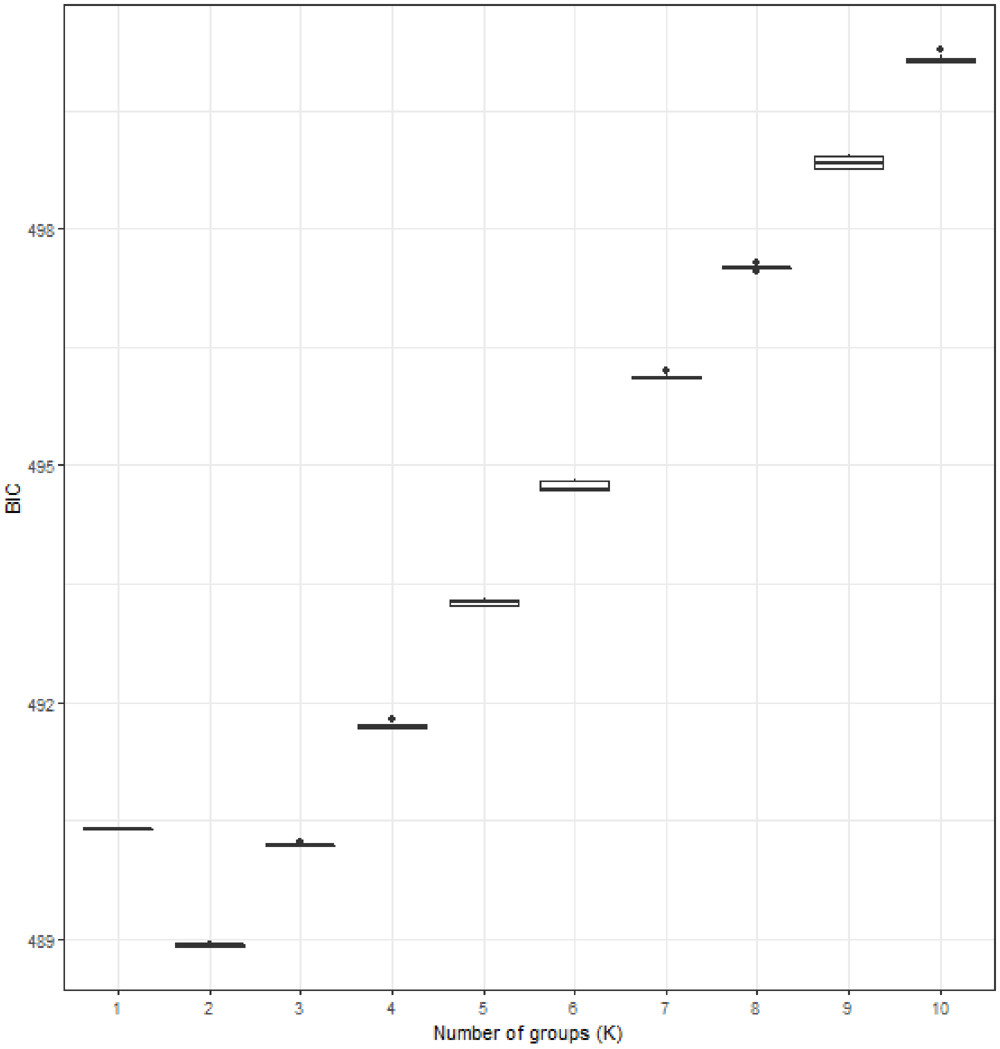


Figure S 1. Histogram of pairwise genetic distances used to determine the threshold for defining genotypes. The plot includes three clustering algorithms that group multilocus genotypes for Acropora palmata. The horizontal axis indicates the Bruvo genetic distance, while the vertical axis represents the number of multilocus lineages observed. Each point marks the threshold at which a certain number of multilocus genotypes are observed.

Table S 3. MSN and percentage of individual for group

Sites-Reefs	Number of individuals Upper group	Percent (%)	Number of individuals Lower group	Percent (%)	Number of individuals Lower-left group	Percent (%)
Akumal	1	50.00	1	50.00	0	0.00
Bajito Nizuc	10	37.03	16	59.25	1	3.70
Cadenita	3	23.07	9	69.23	1	8.00
Cuevones	14	45.16	17	54.93	0	0.00
Farito	1	50.00	0	0.00	1	50.00
Ixlache	0	0.00	5	83.33	1	16.66
Limones	16	61.53	6	23.07	4	15.38



K=1	**K=2**	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10
490.4032	**488.9202**	490.1973	491.6732	493.2999	494.6899	496.1450	497.4809	498.7668	500.0782

Figure S 2. K-means clustering analysis and Bayesian Information Criterion (BIC). The values of k are observed, with lowest value indicating the optimal number of clusters.

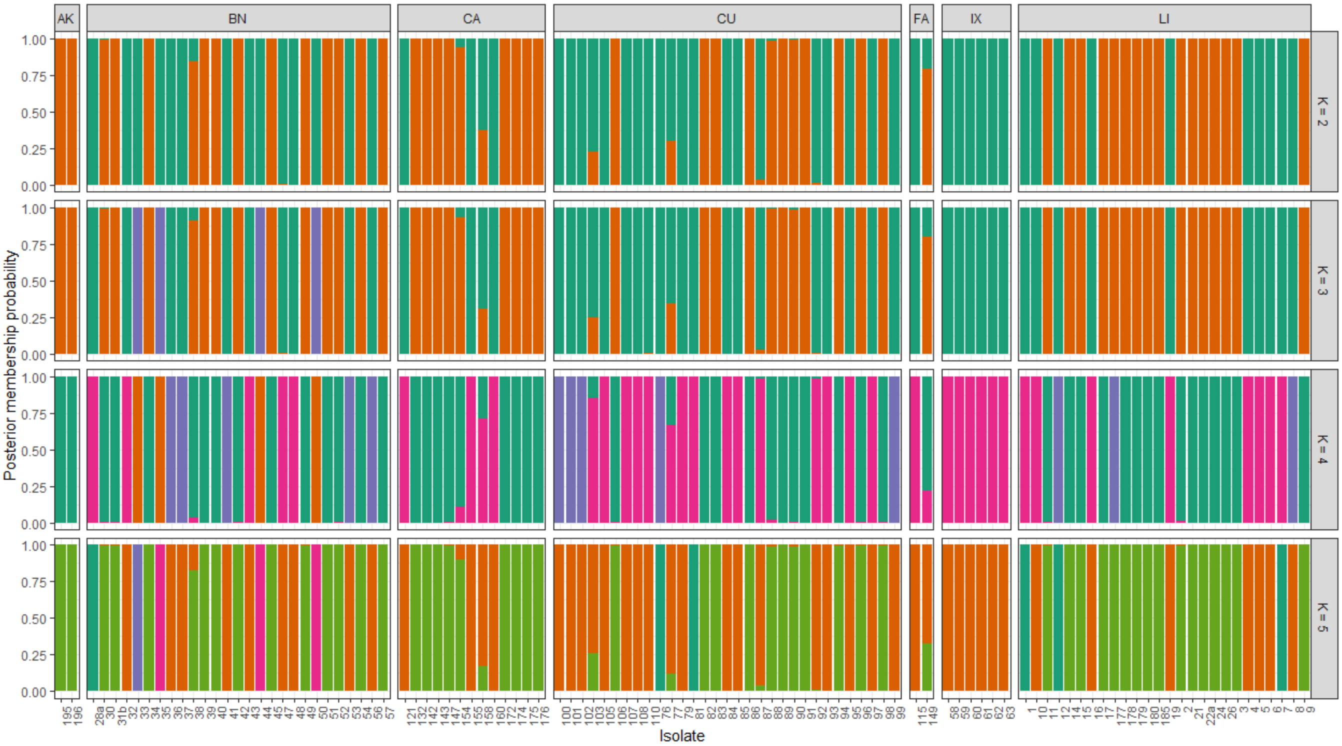


Figure S 3. The DPCA composite barplot shows the genetic difference between populations with different k values. Ixlache and Akumal show genetic structure.in all cases.