Supplementary Information

Genetic diversity of Italian greater horseshoe bats (*Rhinolophus ferrumequinum*) and distinction of the Sardinian colonies

N. Mucci, A. Palladini, M. Mucedda, E. Pidinchedda, A. Martinoli, D. Russo, G. Bogliani

Table S1: Haplotype distribution across colonies: heatmap of the percent coverage of the haplotypes present in each colony. Growing intensity of green indicates a higher proportion of the bats sampled in the colony exhibited that haplotype. Percent values are calculated by dividing the number of individuals with a given haplotype in a colony by the total number of bats sampled in that colony.

	AO	**CN_A**	**CN_B**	**SV**	**CO**	**GO**	**FC**	**MO_SC**	**MO_T**	**PC_A**	**PC_T**	**MC**	**PG**	**MT_A**	**MT_J**	**FG_C**	**FG_I**	**FG_F**	**S_OG**	**S_OR**	**S_CC**	**S_CA**
IT1	100%	91%	36%	38%		50%	8%	52%		26%	21%	64%	63%			82%	9%	64%	29%			
IT2						25%	8%	30%	100%	21%	13%	9%										
IT3							23%															
IT4	9%	45%	36%																			
IT5	9%																					
IT6																9%	36%					
IT7				19%						21%	17%	9%										
IT8				6%			3%	4%				9%	13%									
IT9												9%	13%									
IT10			45%				8%	13%			25%											
IT11							18%						13%									
IT12		9%								5%												
IT13			9%	13%							13%											
IT14			9%	6%																		
IT15				13%																		
IT16						25%																
IT17										11%	8%											
IT18										5%												
IT19										5%												
IT20										5%												
IT21											4%											
IT22																			29%			20%
IT23																			2929%	83%	90%	20%
IT24																			14%			
IT25																				17%		60%
IT26																					10%	
IT27							5%															
IT28							3%															
IT29					80%																	
IT30					20%																	
IT31														94%	100%							
IT32														6%								

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Table S2: Pairwise analysis for F_{st} (A), and G_{st} (B). F_{st} and G_{st} indicate the genetic differentiation between two colonies. Their values are below the diagonal, while their respective p-values are above the diagonal. Probability, p(rand >= data) is based on 999 permutations. Significance threshold is 0.0042 after applying the Bonferroni correction (0.05/12). Significant adjusted p-values are shown in **bold**.

A) pairwise F_{st}

	AO	CN_A	CN_B	SV	CO	GO	FC	MO_SC	MO_T	PC_A	PC_T	MC	PG	MT_A	MT_J	FG_C	FG_F	FG_I	CA	OG	OR	SS	
AO		0.391	0.019	0.012	0.005	**0.002**	0.005	0.049	0.186	0.009	0.028	0.075	0.067	0.076	0.259	0.001	0.015	0.005	**0.001**	**0.001**	**0.001**	**0.001**	**AO**
CN_A	0.012		0.655	0.847	0.014	0.055	0.876	0.853	0.562	0.198	0.905	0.51	0.83	0.819	0.847	0.075	0.216	0.112	**0.001**	**0.001**	**0.001**	**0.001**	**CN_A**
CN_B	0.021	0.014		0.705	0.086	0.334	0.187	0.122	0.12	0.252	0.51	0.344	0.109	0.08	0.226	0.024	0.201	0.009	**0.001**	**0.001**	**0.001**	**0.001**	**CN_B**
SV	0.02	0.012	0.015		0.103	0.046	0.541	0.528	0.372	0.335	0.96	0.585	0.586	0.26	0.535	0.33	0.245	0.047	**0.001**	**0.001**	**0.001**	**0.001**	**SV**
CO	0.055	0.044	0.039	0.039		0.008	0.045	**0.003**	0.019	0.013	0.015	0.005	0.005	**0.004**	0.007	**0.002**	**0.002**	**0.001**	**0.001**	**0.001**	**0.002**	**0.001**	**CO**
GO	0.03	0.021	0.019	0.023	0.055		0.041	**0.004**	0.046	0.06	0.022	0.053	0.145	**0.004**	0.068	**0.003**	0.008	**0.001**	**0.001**	**0.001**	**0.001**	**0.001**	**GO**
FC	0.019	0.011	0.018	0.014	0.04	0.022		0.417	0.255	0.041	0.327	0.068	0.556	0.537	0.186	0.273	0.22	0.018	**0.001**	**0.001**	**0.001**	**0.001**	**FC**
MO_SC	0.015	0.01	0.017	0.013	0.048	0.023	0.012		0.458	0.408	0.622	0.318	0.653	0.093	0.316	0.049	0.232	0.172	**0.001**	**0.001**	**0.001**	**0.001**	**MO_SC**
MO_T	0.028	0.024	0.033	0.029	0.06	0.04	0.029	0.024		0.389	0.13	0.108	0.443	0.178	0.522	0.117	0.043	0.314	**0.001**	**0.002**	**0.001**	**0.001**	**MO_T**
PC_A	0.017	0.015	0.017	0.015	0.044	0.02	0.017	0.012	0.027		0.551	0.392	0.412	0.048	0.481	0.004	0.014	0.011	**0.001**	**0.001**	**0.001**	**0.001**	**PC_A**
PC_T	0.018	0.01	0.015	0.01	0.042	0.022	0.014	0.011	0.031	0.012		0.579	0.389	0.059	0.362	0.028	0.285	0.018	**0.001**	**0.001**	**0.001**	**0.001**	**PC_T**
MC	0.023	0.018	0.021	0.019	0.055	0.028	0.024	0.019	0.037	0.019	0.017		0.49	0.134	0.629	0.093	0.127	0.01	**0.001**	**0.001**	**0.001**	**0.001**	**MC**
PG	0.03	0.019	0.031	0.024	0.062	0.032	0.022	0.02	0.036	0.024	0.024	0.028		0.626	0.886	0.368	0.159	0.2	**0.001**	**0.002**	**0.001**	**0.001**	**PG**
MT_A	0.017	0.012	0.021	0.017	0.053	0.027	0.013	0.016	0.03	0.018	0.019	0.023	0.022		0.943	0.093	0.08	0.449	**0.001**	**0.001**	**0.001**	**0.001**	**MT_A**
MT_J	0.021	0.017	0.026	0.021	0.061	0.031	0.024	0.021	0.033	0.019	0.022	0.024	0.024	0.016		0.347	0.339	0.326	**0.001**	**0.001**	**0.001**	**0.001**	**MT_J**
FG_C	0.031	0.022	0.027	0.02	0.062	0.035	0.018	0.021	0.035	0.029	0.024	0.027	0.028	0.022	0.026		0.683	0.194	**0.001**	**0.001**	**0.001**	**0.001**	**FG_C**
FG_F	0.028	0.021	0.024	0.023	0.057	0.032	0.021	0.02	0.04	0.027	0.021	0.028	0.033	0.025	0.028	0.02		0.208	**0.001**	**0.001**	**0.001**	**0.001**	**FG_F**
FG_I	0.027	0.019	0.027	0.023	0.06	0.038	0.021	0.017	0.029	0.022	0.022	0.031	0.028	0.016	0.024	0.021	0.023		**0.001**	**0.001**	**0.001**	**0.001**	**FG_I**
CA	0.058	0.042	0.059	0.052	0.098	0.063	0.044	0.048	0.057	0.059	0.053	0.061	0.055	0.046	0.061	0.063	0.071	0.05		0.327	0.788	0.417	**CA**
OG	0.076	0.06	0.066	0.062	0.116	0.076	0.061	0.06	0.077	0.069	0.066	0.07	0.076	0.06	0.077	0.076	0.082	0.056	0.032		0.82	0.152	**OG**
OR	0.00075	0.054	0.061	0.059	0.1	0.068	0.053	0.057	0.073	0.069	0.062	0.067	0.069	0.059	0.077	0.074	0.081	0.061	0.026	0.028		0.812	**OR**
SS	0.058	0.042	0.051	0.047	0.088	0.062	0.04	0.044	0.063	0.059	0.049	0.052	0.055	0.046	0.055	0.059	0.066	0.047	0.024	0.033	0.024		**SS**
	AO	**CN_A**	**CN_B**	**SV**	**CO**	**GO**	**FC**	**MO_SC**	**MO_T**	**PC_A**	**PC_T**	**MC**	**PG**	**MT_A**	**MT_J**	**FG_C**	**FG_F**	**FG_I**	**CA**	**OG**	**OR**	**SS**	

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Table S2: (*continued*) Pairwise analysis for F_{st} (A), and G_{st} (B). F_{st} and G_{st} indicate the genetic differentiation between two colonies. Their values are below the diagonal, while their respective p-values are above the diagonal. Probability, p(rand >= data) is based on 999 permutations. Significance threshold is 0.0042 after applying the Bonferroni correction (0.05/12). Significant adjusted p-values are shown in **bold**.

B) pairwise G_{st}

	AO	**CN_A**	**CN_B**	**SV**	**CO**	**GO**	**FC**	**MO_SC**	**MO_T**	**PC_A**	**PC_T**	**MC**	**PG**	**MT_A**	**MT_J**	**FG_C**	**FG_F**	**FG_I**	**CA**	**OG**	**OR**	**SS**	
AO		0.391	0.019	0.012	0.005	**0.002**	0.005	0.049	0.186	0.009	0.028	0.075	0.067	0.076	0.259	**0.001**	0.015	0.005	**0.001**	**0.001**	**0.001**	**0.001**	**AO**
CN_A	0.012		0.655	0.847	0.014	0.055	0.876	0.853	0.562	0.198	0.905	0.51	0.83	0.819	0.847	0.075		0.112	**0.001**	**0.001**	**0.001**	**0.001**	**CN_A**
CN_B	0.021	0.014		0.705	0.086	0.334	0.187	0.122	0.12	0.252	0.51	0.344	0.109	0.08	0.226	0.024	0.201	0.009	**0.001**	**0.001**	**0.001**	**0.001**	**CN_B**
SV	0.02	0.012	0.015		0.103	0.046	0.541	0.528	0.372	0.335	0.96	0.585	0.586	0.26	0.535	0.33	0.245	0.047	**0.001**	**0.001**	**0.001**	**0.001**	**SV**
CO	0.055	0.044	0.039	0.039		0.008	0.045	**0.003**	0.019	0.013	0.015	0.005	0.005	**0.004**	0.007	**0.002**	**0.002**	**0.001**	**0.001**	**0.001**	**0.002**	**0.001**	**CO**
GO	0.03	0.021	0.019	0.023	0.055		0.041	**0.004**	0.046	0.06	0.022	0.053	0.145	**0.004**	0.068	**0.003**	0.008	**0.001**	**0.001**	**0.001**	**0.001**	**0.001**	**GO**
FC	0.019	0.011	0.018	0.014	0.04	0.022		0.417	0.255	0.041	0.327	0.068	0.556	0.537	0.186	0.273	0.22	0.018	**0.001**	**0.001**	**0.001**	**0.001**	**FC**
MO_SC	0.015	0.01	0.017	0.013	0.048	0.023	0.012		0.458	0.408	0.622	0.318	0.653	0.093	0.316	0.049	0.232	0.172	**0.001**	**0.001**	**0.001**	**0.001**	**MO_SC**
MO_T	0.028	0.024	0.033	0.029	0.06	0.04	0.029	0.024		0.389	0.13	0.108	0.443	0.178	0.522	0.117	0.043	0.314	**0.001**	**0.002**	**0.001**	**0.001**	**MO_T**
PC_A	0.017	0.015	0.017	0.015	0.044	0.02	0.017	0.012	0.027		0.551	0.392	0.412	0.048	0.481	0.004	0.014	0.011	**0.001**	**0.001**	**0.001**	**0.001**	**PC_A**
PC_T	0.018	0.01	0.015	0.01	0.042	0.022	0.014	0.011	0.031	0.012		0.579	0.389	0.059	0.362	0.028	0.285	0.018	**0.001**	**0.001**	**0.001**	**0.001**	**PC_T**
MC	0.023	0.018	0.021	0.019	0.055	0.028	0.024	0.019	0.037	0.019	0.017		0.49	0.134	0.629	0.093	0.127	0.01	**0.001**	**0.001**	**0.001**	**0.001**	**MC**
PG	0.03	0.019	0.031	0.024	0.062	0.032	0.022	0.02	0.036	0.024	0.024	0.028		0.626	0.886	0.368	0.159	0.2	**0.001**	**0.002**	**0.001**	**0.001**	**PG**
MT_A	0.017	0.012	0.021	0.017	0.053	0.027	0.013	0.016	0.03	0.018	0.019	0.023	0.022		0.943	0.093	0.08	0.449	**0.001**	**0.001**	**0.001**	**0.001**	**MT_A**
MT_J	0.021	0.017	0.026	0.021	0.061	0.031	0.024	0.021	0.033	0.019	0.022	0.024	0.024	0.016		0.347	0.339	0.326	**0.001**	**0.001**	**0.001**	**0.001**	**MT_J**
FG_C	0.031	0.022	0.027	0.02	0.062	0.035	0.018	0.021	0.035	0.029	0.024	0.027	0.028	0.022	0.026		0.683	0.194	**0.001**	**0.001**	**0.001**	**0.001**	**FG_C**
FG_F	0.028	0.021	0.024	0.023	0.057	0.032	0.021	0.02	0.04	0.027	0.021	0.028	0.033	0.025	0.028	0.02		0.208	**0.001**	**0.001**	**0.001**	**0.001**	**FG_F**
FG_I	0.027	0.019	0.027	0.023	0.06	0.038	0.021	0.017	0.029	0.022	0.022	0.031	0.028	0.016	0.024	0.021	0.023		**0.001**	**0.001**	**0.001**	**0.001**	**FG_I**
CA	0.058	0.042	0.059	0.052	0.098	0.063	0.044	0.048	0.057	0.059	0.053	0.061	0.055	0.046	0.061	0.063	0.071	0.05		0.327	0.788	0.417	**CA**
OG	0.076	0.06	0.066	0.062	0.116	0.076	0.061	0.06	0.077	0.069	0.066	0.07	0.076	0.06	0.077	0.076	0.082	0.056	0.032		0.82	0.152	**OG**
OR	0.075	0.054	0.061	0.059	0.1	0.068	0.053	0.057	0.073	0.069	0.062	0.067	0.069	0.059	0.077	0.074	0.081	0.061	0.026	0.028		0.812	**OR**
SS	0.058	0.042	0.051	0.047	0.088	0.062	0.04	0.044	0.063	0.059	0.049	0.052	0.055	0.046	0.055	0.059	0.066	0.047	0.024	0.033	0.024		**SS**
	AO	**CN_A**	**CN_B**	**SV**	**CO**	**GO**	**FC**	**MO_SC**	**MO_T**	**PC_A**	**PC_T**	**MC**	**PG**	**MT_A**	**MT_J**	**FG_C**	**FG_F**	**FG_I**	**CA**	**OG**	**OR**	**SS**	

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Figure S3: Analysis of the molecular variance (AMOVA) performed on the haplotypes of A) all colonies, B) peninsular colonies, C) Sardinian against peninsular colonies.

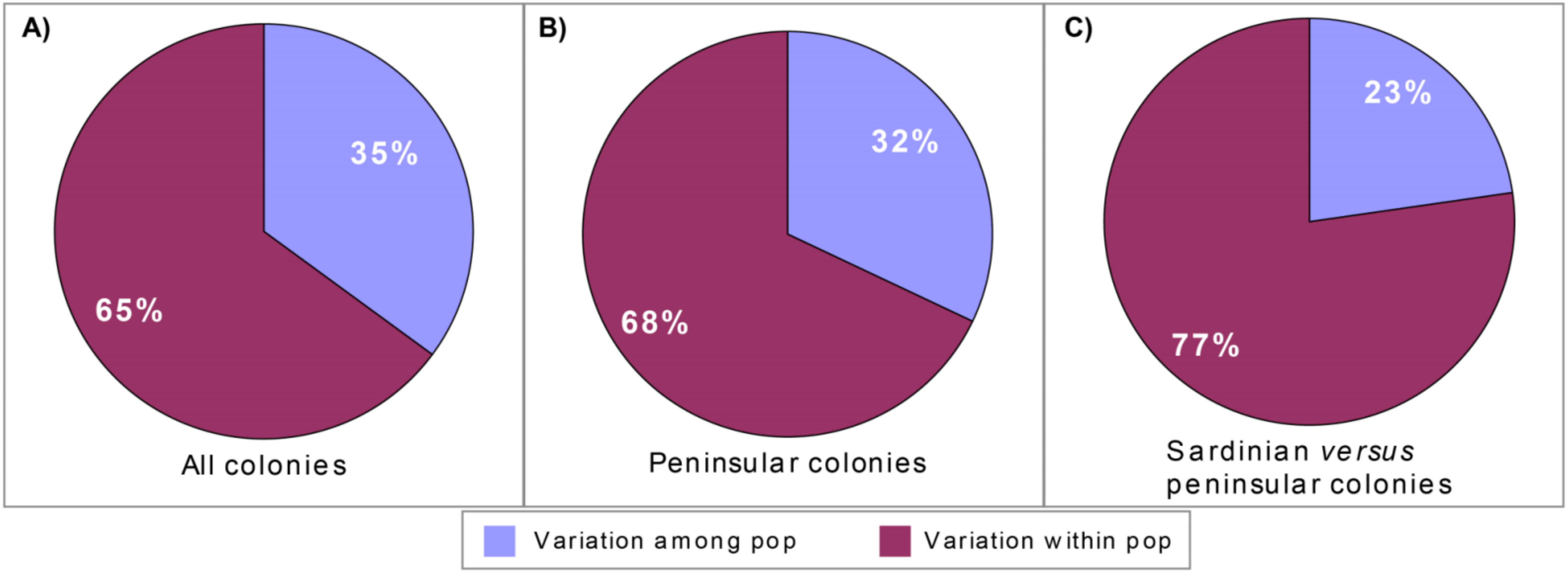

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Figure S4: Analysis of the molecular variance (AMOVA) performed on the microsatellite loci of A) all colonies, B) peninsular colonies, C) Sardinian against peninsular colonies.