

Runs of homozygosity reveal past bottlenecks and contemporary inbreeding across diverging island populations of a bird

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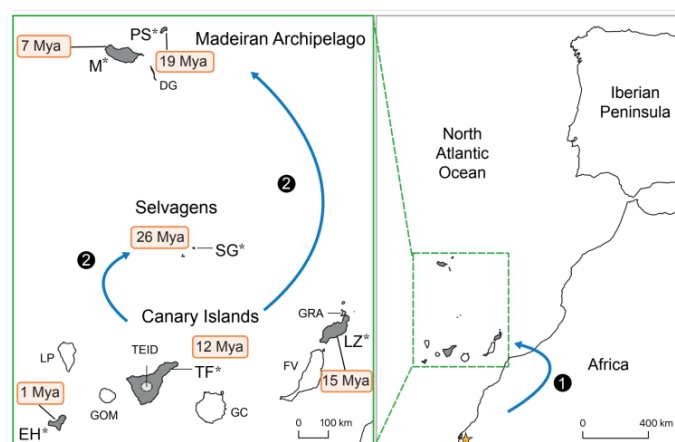
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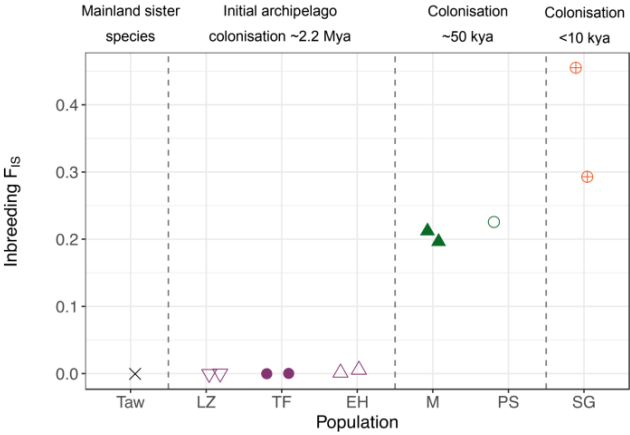
Abstract

Genomes retain evidence of the demographic history and evolutionary forces that have shaped populations. Across island systems, contemporary patterns of genetic diversity reflect complex population demography, including colonisation events, bottlenecks, gene flow and genetic drift. Here, we investigate whether island founder events have prolonged effects on genome-wide diversity and runs of homozygosity (ROH) distributions, using whole genome resequencing from six populations across three archipelagos of Berthelot's pipit (*Anthus berthelotii*) - a passerine which has undergone island speciation relatively recently. Pairwise sequential Markovian coalescent (PSMC) analyses estimated divergence from its sister species approximately two million years ago. Results indicate that all Berthelot's pipit populations had shared ancestry until approximately 50,000 years ago, when the Madeiran archipelago populations were founded, while the Selvagens were colonised within the last 8,000 years. We identify extensive long ROH (>1 Mb) in genomes in the most recently colonised populations of Madeira and Selvagens which have experienced sequential island founder events and population crashes. Population expansion within the last 100 years may have eroded long ROH in the Madeiran archipelago, resulting in a prevalence of short ROH (<1 Mb). Extensive long and short ROH in the Selvagens reflects strong recent inbreeding, small contemporary effective population size and past bottleneck effects, with as much as 37.7% of the autosomes comprised of ROH >250 kb in length. These findings highlight the importance of demographic history, as well as selection and genetic drift, in shaping contemporary patterns of genomic diversity across diverging populations.

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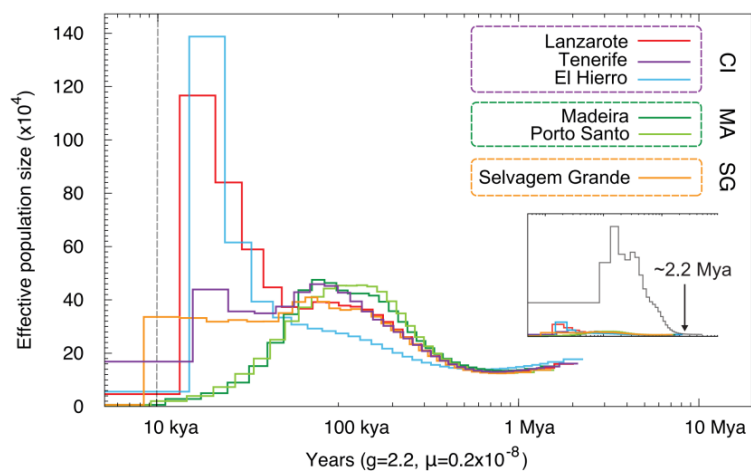
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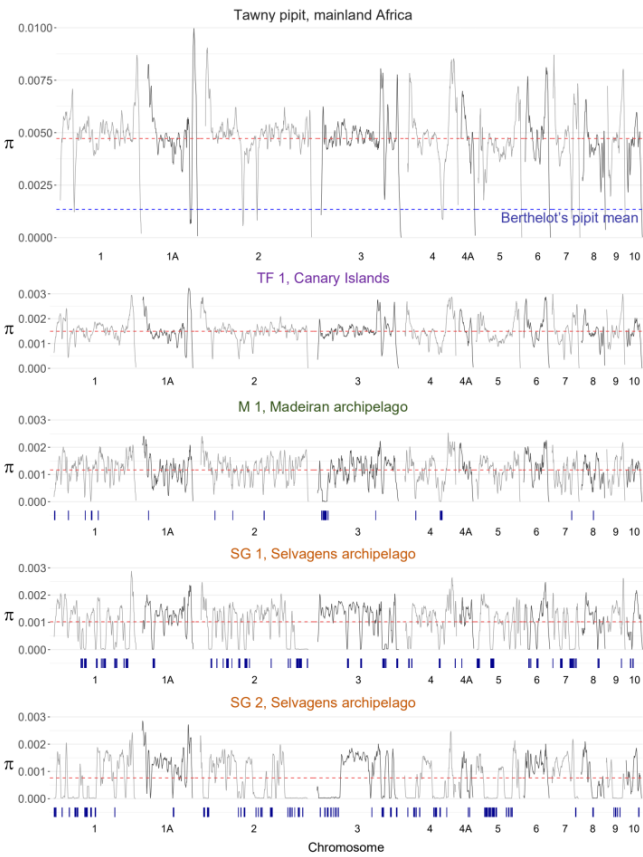


Archipelago / Location	Pop. Code	Sex (Individual)	Mean π	95% CI π	Ho	$F_{ROH} > 250 \text{ kb}$ / F_{IS}
Mauritania, Mainland Africa	TAW	M	0.0047	+/- 0.0010	0.405	0.002/0.000
Canary Islands	LZ	M (1) F (2)	0.0015 0.0015	+/- 0.0003 +/- 0.0003	0.135 0.133	0.015/ 0.019 0.016/ 0.010
Canary Islands	TF	M (1)* F (2)	0.0015 0.0014	+/- 0.0004 +/- 0.0001	0.134 0.130	0.008/ 0.001 0.039/ 0.044
Canary Islands	EH	M (1) F (2)	0.0014 0.0014	+/- 0.0000 +/- 0.0002	0.127 0.132	0.039/ 0.051 0.032/ 0.047
Madeiran	M	M (1)* F (2)	0.0011 0.0012	+/- 0.0000 +/- 0.0000	0.101 0.107	0.138/ 0.248 0.130/ 0.233
Madeiran	PS	F	0.0011	+/- 0.0000	0.101	0.136/ 0.261
Selvagens	SG	M (1)* F (2)*	0.0010 0.0008	+/- 0.0000 +/- 0.0000	0.092 0.082	0.248/ 0.325 0.377/ 0.480

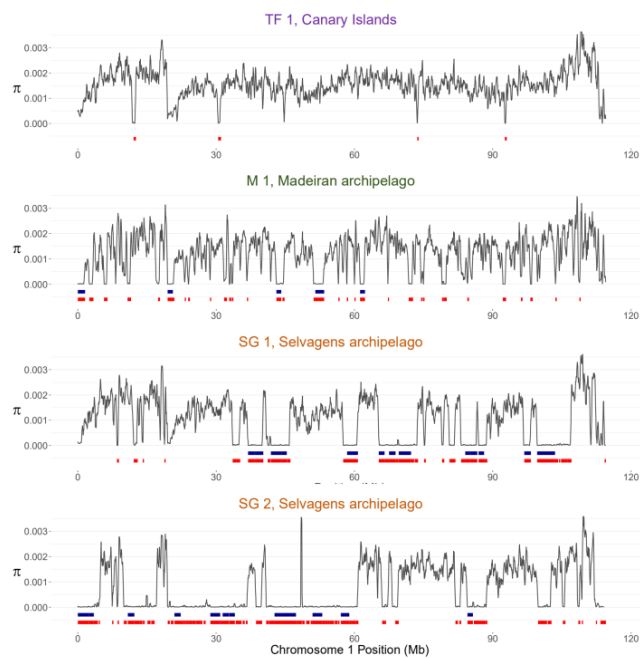
	TAW	TF	LZ	EH	SG	M	PS
TAW	-	0.424	0.431	0.438	0.538	0.516	0.368
TF	2.2 Mya	-	0.019	0.026	0.106	0.096	0.033
LZ	2.2 Mya	45 kya	-	0.026	0.106	0.098	0.037
EH	2.2 Mya	35 kya	<10 kya	-	0.119	0.109	0.054
SG	2.2 Mya	15-25 kya	45 kya	40 kya	-	0.214	0.261
M	2.2 Mya	50 kya	50 kya	40 kya	40 kya	-	0.088
PS	2.2 Mya	50 kya	50 kya	40 kya	40 kya	<10 kya	-



Archipelago / Location	Population (Individual)	No. All ROH (>250 kb)*	Total length All ROH (kb)	No. Short ROH (250 kb – 1 Mb)	Total length Short ROH (kb)	No. Long ROH >1 Mb	Total length long ROH (kb)
Mauritania, Mainland Africa	Taw*	5	1,749	5	1,749	0	0
Canary Islands	LZ (1) LZ (2)	27 33	16,331 16,537	24 30	11,549 12,863	3 3	4,781 3,673
Canary Islands	TF (1)* TF (2)	19 65	8,808 41,552	19 54	8,808 26,993	0 11	0 14,559
Canary Islands	EH (1) EH (2)	70 63	41,381 33,398	63 58	27,102 26,726	7 5	14,278 6,672
Madeiran	M (1)* M (2)	286 285	146,339 137,354	266 264	118,311 110,350	20 21	28,028 27,004
Madeiran	PS	296	143,844	280	122,945	16	20,899
Selvagens	SG (1)* SG (2)*	327 594	262,107 398,181	254 280	131,667 253,352	73 94	130,440 144,829



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