



Zones of maximum discontinuity in the western house mouse (*M. m. domesticus*) genetic landscape: a computational geometry method

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Abstract

To represent the zones of maximum genetic discontinuity in a network of geographically located populations of western house mouse from the previously published mitochondrial DNA D-loop sequence datasets which we acquired from the NCBI GenBank database, we applied a computational geometry approach using the Monmonier's maximum difference algorithm implemented in the BARRIER 2.2 software. We defined ten zones where genetic change among populations is locally increased, three of them occur within the Middle East, while seven occur in Europe. Analysis of molecular variance among post-hoc defined regions using the pattern generated by the BARRIER analysis showed that a significant portion of the genetic diversity was because of among groups component.

Introduction

The zones of maximum genetic discontinuity between adjacent populations are very often strongly stabilized and associated in inhospitable regions which act as natural obstacles to gene flow or dispersal [1]. In continental regions physiographic or climatic barriers produce discontinuities between populations. Mountain ranges can constitute significant barriers, especially if they simultaneously separating climatic zones. Darwin and all the pioneers of evolution have accepted the competence of the oceans and aquatic habitats as barriers to dispersal for majority of terrestrial species [2].

The western house mouse (*M. musculus domesticus*) occupies the Middle East and Western Europe regions. It lives almost solely on agricultural lands and human populated areas. Despite of very limited natural dispersal power, it has dispersed into much of rest of the world with humans [3, 4]. Its dispersal and expansion power is sorely tied to human movements. Authentic zoo-archaeological remains [5-7] along with molecular phylogeography [8] have suggested that the precise dispersion of the western house mouse happened in two stage, the first one limited to the east Mediterranean part while the Western Europe was colonized by the most recent waves during the Bronze and Iron ages. This delay in the westward dispersion is considered to be related to the extensive improvement in marine transportation and the stability of the commensal niche in the west Mediterranean parts [6]. Molecular phylogeography and genetic diversity data have proved that the current pattern of differentiation among populations in this subspecies acquired through these historical demographic events [21].

Whenever sampling coordinates are known, the relation of geographic and genetic distances can be evaluated by spatial autocorrelation or regression tests. These methods give some information about the

possible structure of the genetic landscape. For example, the low mantel index values reported for commensal house mouse [8-10], suggest that the geographic distance only weakly influenced the pattern of genetic variability or differentiation. However, correlation tests fail when trying to define where genetic barriers exist [11]. The correlation can be high in one zone and low in another zone, and these discrepancies can be difficult to see in a regression diagram since it never defines the areas of genomic discontinuity. Thus, the computational geometry methods are more convenient since they provide the locations and the directions of discontinuities. In order to provide a realistic representation of the genetic discontinuities in *M. m. domesticus* genetic landscape (within the Middle East and western Europe), we reanalyzed the previously published mtDNA D-loop sequence datasets using a computational geometry method, the Monmonier's [12] maximum difference algorithm implemented in the BARRIER 2.2 software [11], which created to infer putative genomic boundaries— i.e. zones of increased change in maps of genomic variation— from genome diversity data.

Materials and Methods

Published mtDNA D-Loop Sequences

Previously published mtDNA D-loop sequence datasets (N = 387; nucleotide positions 15444 to 16253; 809 bp length) of *M. m. domesticus* were acquired from the National Center for Biotechnology Information (NCBI) GenBank (<http://www.ncbi.nlm.nih.gov/>). Then, according to the reported information from literature and also geographic proximity of samples we classified them to 29 major populations (Fig. 1A). The GenBank accession numbers, references, geographical coordinates, sample sizes, and additional data about populations and samples were acquired from the NCBI GenBank database (Table 1).

Statistical Analysis

DNA sequences were aligned using the MAFFT version 5 [13] and the probabilistic model of sequence evolution was determined by JmodelTest 2.1.3 [14] using the corrected Akaike information criterion (AICc). The pairwise F_{ST} genetic distances among populations were calculated based on the number of pairwise differences between sequences using the ARLEQUIN 3.5 [15] and the statistical significance of all pairwise F_{ST} values was assessed with permutation method, under 10,000 random permutations. A user friendly graphical approach known as Monmonier's [12] maximum-difference which performed in the software BARRIER version 2.2 [11], was applied to investigate potential genetic discontinuities between adjacent populations. Complete details on the procedure are given in Manni et al. (2004), so that only a brief description of the methodology is presented here. The first stage of the approach is to map the sampled populations according to their geographical coordinates and draw the corresponding Delaunay [16] triangulation network. The resulting Voronoi [17] tessellation is then superimposed over the Delaunay network in order to apply Monmonier's algorithm. The first putative genomic boundary is initiated by drawing a line along the edge of a Voronoi polygon. This line separates the pair of neighboring populations (i.e. populations located on the same Delaunay triangle) for which genetic distance is maximal. The Monmonier's algorithm continues to segregate adjacent pairs of populations on the basis of higher pairwise F_{ST} genetic distances, following the edges of Voronoi polygons. This process is extended until the genetic boundary being traced reaches either the outer limits of the Delaunay network (edge of the map) or a previously established barrier (including itself). Subsequent boundaries can be delimited using the largest remaining pairwise F_{ST} genetic distance among adjacent populations as a starting point. There is no criterion to define the number of genomic boundaries to be recognized in this way, thus we decided to stop at ten. Since there are no specific statistical tests to evaluate the statistical significance of the detected putative genomic boundaries with BARRIER, we ran an algorithmic analysis of molecular variance (AMOVA) [18] using the ARLEQUIN. Testing was accomplished among post hoc defined areas isolated by the software.

Results

By analyzing 809 bp of 387 previously published *M. m. domesticus* mtDNA D-loop sequences, the nucleotide substitution model obtained was HKY [19] coupled with the discrete gamma model [20] of site-specific rate heterogeneity (denoted as the HKY + G model; G = 0.55). The F_{ST} values among population pairs were calculated (Table 2). The ten high-ranking genetic discontinuities identified from BARRIER analysis (Fig. 1B). The number attributed to each barrier indicates its ranking, with 1 being the sharpest. Three of them occur within or near to the Fertile Crescent, one positioned between populations in the eastern arm (boundary No.6), while two positioned between populations in the western arm (boundary No.8 and No.9). The other seven genetic discontinuities (including the sharpest ones) positioned between adjacent populations around the northern shore of Mediterranean Sea (boundaries No.1, No.3 and No.7) and Western Europe (boundaries No.2, No.4, No.5 and No.10). AMOVA— as a test to assess the statistical significance of discontinuities— among post-hoc defined regions using the pattern generated with BARRIER analysis showed that a significant portion (21.57% of total variation) of the total mtDNA diversity was because of among groups component (Table 3).

Discussion

When populations fit the Isolation by Distance (IBD) model, the chances of defining genomic discontinuities dwindle [11]. The low mantel index values reported for commensal house mouse in the literature [8-10] imply the presence of numerous discontinuities in its genetic landscape. Here, the genetic discontinuities statistic in BARRIER analysis graphically defined ten zones where genetic change among adjacent western house mouse populations was locally increased, three of them occur in the Middle East, while seven occur around the Mediterranean basin and Western Europe. AMOVA between post hoc detected areas using the structure obtained in BARRIER analysis confirmed that a significant portion of the total diversity was because of between groups component.

Table-1: Details of the previously published mtDNA D-loop sequences used in this study

Samples					Populations		
No.	Country: City of Origin	GenBank Acc. No.	Reference	Coordinates	Classified as Pop. No.*	Size	Mean Coordinates
1	Italy: Aeolian Islands	JQ646044	[24]	38°82'N14°94'E	1	15	38°82'N14°94'E
2	Italy: Aeolian Islands	JQ646043		"			
3	Italy: Aeolian Islands	JQ646042		"			
4	Italy: Aeolian Islands	JQ646041		"			
5	Italy: Aeolian Islands	JQ646040		"			
6	Italy: Aeolian Islands	JQ646039		"			
7	Italy: Aeolian Islands	JQ646038		"			
8	Italy: Aeolian Islands	JQ646037		"			
9	Italy: Aeolian Islands	JQ646036		"			
10	Italy: Aeolian Islands	JQ646035		"			
11	Italy: Aeolian Islands	JQ646034		"			
12	Italy: Aeolian Islands	JQ646033		"			
13	Italy: Aeolian Islands	JQ646032		"			
14	Italy: Aeolian Islands	JQ646031		"			
15	Italy: Aeolian Islands	JQ646030		"			
16	Iran: Ahvaz	EU194640	[8]	31°32'N48°66'E	2	16	31°32'N48°66'E
17	Iran: Ahvaz	EU194639		"			
18	Iran: Ahvaz	EU194631		"			
19	Iran: Ahvaz	EU194629		"			
20	Iran: Ahvaz	EU194628		"			
21	Iran: Ahvaz	EU194627		"			
22	Iran: Ahvaz	EU194626		"			
23	Iran: Ahvaz	EU194625		"			
24	Iran: Ahvaz	EU194624		"			
25	Iran: Ahvaz	EU194623		"			
26	Iran: Ahvaz	EU194622		"			
27	Iran: Ahvaz	EU194621		"			
28	Iran: Ahvaz	EU194620		"			

Samples					Populations		
No.	Country: City of Origin	GenBank Acc. No.	Reference	Coordinates	Classified as Pop. No.*	Size	Mean Coordinates
29	Iran: Ahvaz	EU194619		"			
30	Iran: Ahvaz	EU194618		"			
31	Iran: Ahvaz	AB649593	[25]	"			
32	Iran: Kalat-Bala	EU194645		27°32'N56°09' E			
33	Iran: Bandar-Abbas	EU194644		27°18'N56°26' E			
34	Iran: Bandar-Abbas	EU194643	[8]	"	3	4	27°18'N56°26'E
35	Iran: Bandar-Abbas	EU194637		"			
36	Bulgaria: Zhitarivo	EU194657		42°60'N27°38' E			
37	Bulgaria: Zhitarivo	EU194655		"			
38	Bulgaria: Zhitarivo	EU194651		"			
39	Bulgaria: Zhitarivo	EU194656		41°38'N24°43' E			
40	Bulgaria: Zhitarivo	EU194654		43°24'N27°55' E			
41	Bulgaria: Zhitarivo	EU194653	[8]	42°43'N27°46' E			
42	Bulgaria: Zhitarivo	EU194648		"			
43	Bulgaria: Zhitarivo	EU194652		42°48'N27°32' E	4	15	42°48'N27°32'E
44	Bulgaria: Zhitarivo	EU194650		42°39'N26°59' E			
45	Bulgaria: Zhitarivo	EU194649		"			
46	Turkey: Kırklareli	AJ843856		41°41'N27°36' E			
47	Turkey: Kırklareli	AJ843855		"			
48	Turkey: Edirne	AJ843848	[10]	41°27'N26°69' E			
49	Turkey: Edirne	AJ843822		40°86'N26°63' E			
50	Bulgaria: Vlas	AB649605	[25]	42°71'N27°75' E			
51	Azerbaijan	JX889726		39°20'N45°41' E			
52	Azerbaijan	JX889725		"			
53	Azerbaijan	JX889724	[26]	"			
54	Azerbaijan	JX889723		"			
55	Azerbaijan	JX889722		"	5	9	39°41'N45°43'E
56	Iran: Mahabad	JN416768		36°76'N45°72' E			
57	Iran: Jolfa	JN416767	[27]	38°95'N45°63' E			
58	Georgia: Alazani	JX658122	[28]	41°56'N45°95' E			
59	Georgia: Chirakskaya	AF506184	[29]	41°70'N44°79' E			
60	Italy	AY560817		42°36'N14°14' E			
61	Italy	AY560808		42°35'N13°74' E			
62	Italy	AY560829		41°87'N12°87' E			
63	Italy	AY560819		42°04'N13°23' E			
64	Italy	AY560821		42°09'N13°30' E			
65	Italy	AY560820		42°17'N13°05' E			
66	Italy	AY560830		42°28'N13°33' E			
67	Italy	AY560805	[30]	42°48'N13°16' E	6	14	42°28'N13°33'E
68	Italy	AY560807		42°93'N12°99' E			
69	Italy	AY560828		43°06'N13°00' E			
70	Italy	AY560804		42°48'N13°16' E			
71	Italy	AY560806		42°28'N13°33' E			
72	Italy	AY560822		41°87'N12°87' E			
73	Italy	AY560809		41°89'N12°48' E			
74	Italy	AY560826		41°63'N14°25' E			
75	Italy	AY560812		41°49'N14°95' E			
76	Italy	AY560815	[30]	41°52'N15°38' E			
77	Italy	AY560827		41°63'N15°83' E			
78	Italy	AY560814		41°24'N15°44' E			
79	Italy	EU194661	[8]	41°08'N14°25' E	7	10	41°49'N14°95'E
80	Italy	AY560825		41°63'N15°83' E			
81	Italy	AY560813		41°63'N14°25' E			
82	Italy	AY560810	[30]	"			
83	Italy	AY560811		"			
84	Italy	AY560816		40°03'N15°86' E			
85	Italy	AY560818	[30]	39°22'N16°09' E			
86	Italy: Calabria	GU384342		39°14'N16°04' E	8	5	39° 22'N16°09'E
87	Italy: Calabria	GU384341		"			
88	Italy: Calabria	JQ646045	[24]	39°00'N16°83' E			
89	Iran: Famenin	EU194617	[8]	35°11'N48°97' E	9	9	35°11'N48°97'E

Samples					Populations		
No.	Country: City of Origin	GenBank Acc. No.	Reference	Coordinates	Classified as Pop. No.*	Size	Mean Coordinates
90	Iran: Famenin	EU194616		"			
91	Iran: Famenin	EU194615		"			
92	Iran: Famenin	EU194614		"			
93	Iran: Famenin	EU194613		"			
94	Iran: Famenin	EU194612		"			
95	Iran: Famenin	EU194609		"			
96	Iran: Hamadan	EU194611		34°80'N48°51' E			
97	Iran: Hamadan	EU194610		34°80'N48°51' E			
98	France	KC139188		48°66'N06°99' E			
99	France	KC139189		"			
100	France	KC139190		"			
101	France	KC139191		"			
102	France	KC139192		"			
103	France	KC139193		"			
104	France	KC139194	[31]	"	10	12	48°66'N06°99'E
105	France	KC139195		"			
106	France	KC139196		"			
107	France	KC139197		"			
108	France	KC139198		"			
109	France	KC139199		"			
110	France	KC139170		44°31'N03°51' E			
111	France	KC139171		"			
112	France	KC139172		"			
113	France	KC139173		"			
114	France	KC139174		"			
115	France	KC139175		"			
116	France	KC139176	[31]	"			
117	France	KC139177		"			
118	France	KC139178		"			
119	France	KC139179		"	11	19	44°31'N03°51'E
120	France	KC139180		"			
121	France	KC139181		"			
122	France	KC139182		"			
123	France	KC139183		"			
124	France	KC139184		"			
125	France	KC139185		"			
126	France	KC139186		"			
127	France	KC139187		"			
128	France: Montpellier	AB649592	[25]	43°61'N03°87' E			
129	France	KC139158		48°64'N03°49' E			
130	France	KC139159		"			
131	France	KC139160		"			
132	France	KC139161		"			
133	France	KC139162		"			
134	France	KC139163		"			
135	France	KC139164	[31]	"	12	13	48°64'N03°49'E
136	France	KC139165		"			
137	France	KC139166		"			
138	France	KC139167		"			
139	France	KC139168		"			
140	France	KC139169		"			
141	France: Paris	HQ185282	[32]	48°85'N02°35' E			
142	France	KC139136		43°34'N01°42' E			
143	France	KC139137		"			
144	France	KC139138		"			
145	France	KC139139		"			
146	France	KC139140	[31]	"	13	23	43°34'N01°42'E
147	France	KC139141		"			
148	France	KC139142		"			
149	France	KC139143		"			
150	France	KC139144		"			

Samples					Populations		
No.	Country: City of Origin	GenBank Acc. No.	Reference	Coordinates	Classified as Pop. No.*	Size	Mean Coordinates
151	France	KC139145		"			
152	France	KC139146		"			
153	France	KC139147		"			
154	France	KC139148		"			
155	France	KC139149		"			
156	France	KC139150		"			
157	France	KC139151		"			
158	France	KC139152		"			
159	France	KC139153		"			
160	France	KC139154		"			
161	France	KC139155		"			
162	France	KC139156		"			
163	France	KC139157		"			
164	France: Toulouse	AB649591	[25]	43°60'N01°44' E	14	12	46°35'N06°13' E
165	France	KC139124	[31]	46°37'N07°00' E			
166	France	KC139125		"			
167	France	KC139126		"			
168	France	KC139127		"			
169	France	KC139128		"			
170	France	KC139129		"			
171	France	KC139130		"			
172	France	KC139131		"			
173	France	KC139132		"			
174	France	KC139133		"			
175	France	KC139134		"			
176	France	KC139135		"			
177	France	KC139091	[31]	47°47'N00°56' W	15	18	47°47'N00°56' W
178	France	KC139092		"			
179	France	KC139093		"			
180	France	KC139094		"			
181	France	KC139095		"			
182	France	KC139096		"			
183	France	KC139097		"			
184	France	KC139098		"			
185	France	KC139099		"			
186	France	KC139100		"			
187	France	KC139101		"			
188	France	KC139102		"			
189	France	KC139103		"			
190	France	KC139104	"				
191	France	KC139105	"				
192	France	KC139106	"				
193	France	KC139107	"				
194	France	KC139108	"				
195	Germany	KC139200	[31]	48°78'N8°645' E	16	12	48°78'N08°64' E
196	Germany	KC139201		"			
197	Germany	KC139202		"			
198	Germany	KC139203		"			
199	Germany	KC139204		"			
200	Germany	KC139205		"			
201	Germany	KC139206		"			
202	Germany	KC139207		"			
203	Germany	KC139208		"			
204	Germany	KC139209		"			
205	Germany	KC139210		"			
206	Germany	KC139211	"				
207	Germany	KC139109	[31]	51°12'N7°374' E	17	15	51°12'N07°37' E
208	Germany	KC139110		"			
209	Germany	KC139111		"			
210	Germany	KC139112		"			

Samples					Populations					
No.	Country: City of Origin	GenBank Acc. No.	Reference	Coordinates	Classified as Pop. No.*	Size	Mean Coordinates			
211	Germany	KC139113		"						
212	Germany	KC139114		"						
213	Germany	KC139115		"						
214	Germany	KC139116		"						
215	Germany	KC139117		"						
216	Germany	KC139118		"						
217	Germany	KC139119		"						
218	Germany	KC139120		"						
219	Germany	KC139121		"						
220	Germany	KC139122		"						
221	Germany	KC139123		"						
222	Israel	EU938924	[33]	31°04'N34°85' E	18	16	31°04'N34°85' E			
223	Israel	EU938923		"						
224	Israel	EU938922		"						
225	Israel	EU938921		"						
226	Israel	EU938920		"						
227	Israel	EU938919		"						
228	Israel	EU938918		"						
229	Israel	EU938917		"						
230	Israel	EU938916		"						
231	Israel	EU938915		"						
232	Israel	EU938914		"						
233	Israel: Ortal	AF506187	[29]	33°08'N35°75' E	19	7	31°26'N49°65' E			
234	Israel: Ortal	AF506186		33°08'N35°75' E						
235	Israel: Jerusalem	AF506185		31°76'N35°21' E						
236	Israel: Keshet	AF506183		32°98'N35°80' E						
237	Israel: Kursi Beach	JX658105	[28]	32°82'N35°66' E				20	9	45°22'N10°35' E
238	Iran: Kuli Alireza	JX658120	[28]	31°26'N49°65' E						
239	Iran: Kuli Alireza	JX658119		31°26'N49°65' E						
240	Iran: Ize	JX658118		31°83'N49°87' E						
241	Iran: Ize	JX658117		"						
242	Iran: Simili	JX658116		31°69'N49°42' E						
243	Iran: Simili	JX658115		"						
244	Iran: Simili	JX658114		"						
245	Italy: Bassa	EU194663	[8]	43°72'N10°87' E	21	12	45°28'N09°08' E			
246	Italy: Costa	EU194660		45°91'N11°69' E						
247	Italy: San Georgio	EU194675		45°32'N11°54' E						
248	Italy: Reggiolo	EU194659		44°91'N10°80' E						
249	Italy: Cadimarco	EU194674		45°22'N10°35' E						
250	Italy: Aselli	EU194673		45°08'N10°01' E						
251	Italy: Cascina Speranza	EU194670		45°62'N09°83' E						
252	Italy: Zanica	EU194671		45°99'N9°998' E						
253	Italy: Aselli	EU194666	45°08'N10°01' E							
254	Italy: Mezzanino	EU194658	[8]	45°20'N09°33' E				22	12	41°12'N37°28' E
255	Italy: Corbesate	EU194667		45°23'N09°25' E						
256	Italy: Corazza	EU194662		44°99'N09°01' E						
257	Italy: Cascina Verdura	EU194676		45°41'N09°19' E						
258	Italy: Binasco	AB649587	[25]	45°33'N09°09' E	22	12	41°12'N37°28' E			
259	Italy: Trovo	EU194672	[8]	45°28'N09°08' E						
260	Italy: Cislago	AB649586	[25]	45°66'N8°974' E						
261	Italy: Nosate	EU194668	[8]	45°55'N8°719' E						
262	Italy: Invotio	EU194669		45°78'N8°503' E						
263	Italy: Arioti	EU194665		45°30'N8°026' E						
264	Italy: Arioti	EU194664		"						
265	Italy: Aosta	AB649589	[25]	45°73'N7°313' E				22	12	41°12'N37°28' E
266	Turkey: Rize	AJ843836	[10]	41°02'N40°52' E						
267	Turkey: Trabzon	AJ843834		41°00'N39°71' E						
268	Turkey: Trabzon	AJ843867		41°05'N39°33' E						
269	Turkey: Ordu	AJ843866		41°12'N37°28' E						

Samples					Populations		
No.	Country: City of Origin	GenBank Acc. No.	Reference	Coordinates	Classified as Pop. No.*	Size	Mean Coordinates
270	Turkey: Samsun	AJ843865		41°25'N36°54' E			
271	Turkey: Samsun	AJ843851		41°43'N36°14' E			
272	Turkey: Sinop	AJ843861		42°02'N35°15' E			
273	Turkey: Sivas	AJ843838		39°74'N37°01' E			
274	Turkey: Samsun	AJ843864		41°62'N35°63' E			
275	Turkey: Samsun	AJ843863		41°61'N35°56' E			
276	Turkey: Sinop	AJ843860		42°02'N35°15' E			
277	Turkey: Samsun	AJ843862		41°61'N35°56' E			
278	Portugal: lisbon	GQ242020		38°72'N09°15' W			
279	Portugal: Sines	GQ242019		37°95'N08°86' W			
280	Portugal: Sines	GQ242018		"			
281	Portugal: Vila Nova Mil Fontes	GQ242017		37°75'N08°76' W			
282	Portugal: Lagos	GQ242016		37°10'N08°67' W			
283	Portugal: Porto	GQ242015		41°15'N08°62' W			
284	Portugal: faro	GQ242014		37°01'N07°93' W			
285	Portugal: lisbon	GQ242013	[34]	38°72'N09°15' W	23	14	38°17'N08°56'W
286	Portugal: Vila Franca de Xira	GQ242012		38°95'N08°98' W			
287	Portugal: Vila Franca de Xira	GQ242011		"			
288	Portugal: Peniche	GQ242010		39°36'N09°38' W			
289	Portugal: Setubal	GQ242009		38°52'N08°89' W			
290	Portugal: Grandola	GQ242008		38°17'N08°56' W			
291	Portugal: Grandola	GQ242007		"			
292	Italy: Sardinia	JQ646051		40°11'N09°01' E			
293	Italy: Sardinia	JQ646050	[24]	"	24	4	40°11'N09°01' E
294	Italy: Sardinia	JQ646049		"			
295	France: Corse	AB649590	[25]	42°30'N9°149' E			
296	Iran: Shavour	EU194642		31°87'N48°34' E			
297	Iran: Shavour	EU194641		"			
298	Iran: Shavour	EU194638		"			
299	Iran: Shavour	EU194636		"			
300	Iran: Shavour	EU194635	[8]	"	25	10	31°87'N48°34' E
301	Iran: Shavour	EU194634		"			
302	Iran: Shavour	EU194633		"			
303	Iran: Shavour	EU194632		"			
304	Iran: Shavour	EU194630		"			
305	Iran: Choqa Zambil	JX658113	[28]	32°02'N48°51' E			
306	Turkey: Harran	JX658109	[28]	36°86'N39°03' E			
307	Turkey: Urfa	AJ843842		37°15'N38°79' E			
308	Turkey: Adiyaman	AJ843826		37°70'N37°86' E			
309	Turkey: Gaziantep	AJ843827		37°06'N37°38' E			
310	Turkey: Adana	AJ843871	[10]	38°26'N36°22' E	26	10	37°06'N37°38' E
311	Turkey: Mersin	AJ843833		36°80'N34°63' E			
312	Turkey: Hatay	AJ843837		36°03'N36°15' E			
313	Turkey: Adana	JX658108		37°00'N35°32' E			
314	Turkey: Harran	JX658109	[28]	36°86'N39°03' E			
315	Turkey: Hatay	AJ843837	[10]	36°03'N36°15' E			
316	Spain: Barcelona	GU384360		42°20'N03°13' E			
317	Spain: Barcelona	GU384359		41°25'N01°47' E			
318	Spain: Barcelona	GU384358	[35]	41°32'N01°23' E	27	16	41°05'N00°87' E
319	Spain: Barcelona	GU384357		41°18'N02°01' E			

Samples					Populations		
No.	Country: City of Origin	GenBank Acc. No.	Reference	Coordinates	Classified as Pop. No.*	Size	Mean Coordinates
320	Spain: Barcelona	GU384355		43°48'N05°28' E			
321	Spain: Barcelona	GU384356		41°19'N01°49' E			
322	Spain: Barcelona	GU384354		41°10'N01°01' E			
323	Spain: Barcelona	GU384353		41°31'N01°42' E			
324	Spain: Barcelona	GU384352		43°48'N05°28' E			
325	Spain: Barcelona	GU384351		41°17'N01°33' E			
326	Spain: Barcelona	GU384350		43°48'N05°28' E			
327	Spain: Barcelona	GU384349		41°27'N01°01' E			
328	Spain: Barcelona	GU384348		41°42'N01°32' E			
329	Spain: Barcelona	GU384347		41°21'N01°46' E			
330	Spain: Barcelona	GU384346		41°23'N01°36' E			
331	Spain: Barcelona	GU384345		41°29'N01°00' E			
332	United Kingdom	FM211631		[36]			
333	United Kingdom	FM211630	"				
334	United Kingdom	FM211629	"				
335	United Kingdom	FM211628	"				
336	United Kingdom	FM211627	"				
337	United Kingdom	FM211626	"				
338	United Kingdom	FM211625	"				
339	United Kingdom	FM211624	"				
340	United Kingdom	FM211623	"				
341	United Kingdom	FM211622	"				
342	United Kingdom	FM211621	"				
343	United Kingdom	FM211620	"				
344	United Kingdom	FM211619	"				
345	United Kingdom	FM211618	"				
346	United Kingdom	FM211617	"				
347	United Kingdom	FM211616	"				
348	United Kingdom	FM211615	"				
349	United Kingdom	FM211614	"				
350	United Kingdom	FM211613	"				
351	United Kingdom	FM211612	"				
352	United Kingdom	FM211611	"				
353	United Kingdom	FM211610	"				
354	United Kingdom	FM211609	"				
355	United Kingdom	FM211608	"				
356	United Kingdom	FM211607	"				
357	United Kingdom	FM211606	"				
358	United Kingdom	FM211605	"				
359	United Kingdom	FM211603	"				
360	United Kingdom	FM211604	"				
361	United Kingdom	FM211602	"				
362	United Kingdom	FM211601	"				
363	United Kingdom	FM211600	"				
364	United Kingdom	FM211599	"				
365	United Kingdom	FM211598	"				
366	United Kingdom	FM211597	"				
367	United Kingdom	FM211596	"				
368	Turkey: Denizli	AJ843859	[10]	37°77'N29°08' E	29	20	39°40'N28°13' E
369	Turkey: Denizli	AJ843858		"			
370	Turkey: Denizli	AJ843857		"			
371	Turkey: Mu la	AJ843870		37°04'N27°38' E			
372	Turkey: Manisa	AJ843845		38°61'N27°42' E			
373	Turkey: Balikesir	AJ843840		39°40'N28°13' E			
374	Turkey: Balikesir	AJ843844		39°64'N27°88' E			
375	Turkey: Balikesir	AJ843853		39°69'N27°95' E			
376	Turkey: Balikesir	AJ843841		40°35'N27°97' E			
377	Turkey: Bursa	AJ843849		40°08'N29°51' E			
378	Turkey: Sakarya	AJ843835		40°77'N30°40' E			
379	Turkey: Zonguldak	AJ843868		41°17'N31°39' E			

Samples					Populations		
No.	Country: City of Origin	GenBank Acc. No.	Reference	Coordinates	Classified as Pop. No.*	Size	Mean Coordinates
380	Turkey: <i>Stanbul</i>	AJ843824		41°17'N29°61' E			
381	Turkey: <i>Stanbul</i>	AJ843823		"			
382	Turkey: <i>Manisa</i>	AJ843839		38°61'N27°42' E			
383	Turkey: <i>Denizli</i>	AJ843843		37°77'N29°08' E			
384	Turkey: <i>Denizli</i>	AJ843831		"			
385	Turkey: <i>Balikesir</i>	AJ843830		39°64'N27°88' E			
386	Turkey: <i>Balikesir</i>	AJ843829		40°35'N27°97' E			
387	Turkey: <i>Bursa</i>	AJ843849		40°08'N29°51' E			

* Population numbers on Fig. 1A.

Table-2: Pairwise F_{ST} distances between 29 *M. m. domesticus* populations from the Middle East and Europe. Above diagonal: the pairwise F_{ST} values based on mtDNA D-loop sequences; and below diagonal: the statistical significance of F_{ST} values (threshold was $p \leq 0.05$)

	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Pop.	
.206	.287	.152	.149	.207	.178	.137	.364	.148	.182	.131	.428	.243	.243	.597	.420	.261	.147	.626	.515	.433	.430	.321	.160	.181	.226	.212	.235	.221	.000	1	
.131	.251	.210	.171	-.01	.253	.202	.240	.155	.169	.044	.312	.217	.217	.599	.361	.243	.180	.549	.530	.375	.304	.403	.152	.166	.155	.128	-.05	.000	+	2	
.092	.233	.204	.218	.063	.265	.158	.253	.123	.139	.097	.291	.145	.145	.688	.374	.200	.148	.778	.600	.365	.466	.737	.228	.170	.149	.088	.000	-	+	3	
.030	.248	.160	.114	.114	.208	.159	.087	.089	.104	.138	.297	.215	.215	.554	.347	.218	.163	.511	.503	.342	.073	.335	.204	.168	.119	.000	-	+	+	4	
.108	.234	.204	.195	.151	.237	.170	.215	.143	.170	.110	.362	.236	.236	.616	.413	.251	.171	.623	.553	.403	.230	.425	.246	.151	.000	+	-	+	+	5	
.105	.238	.162	.158	.161	.045	.166	.273	.101	.093	.155	.359	.197	.197	.572	.368	.231	.143	.591	.472	.381	.343	.370	.187	.000	+	+	+	+	+	6	
.199	.311	.208	.136	.109	.327	.249	.348	.226	.269	.127	.407	.267	.267	.699	.434	.302	.198	.700	.645	.465	.473	.481	.000	+	+	+	+	+	+	+	7
.366	.429	.185	.286	.411	.509	.417	.492	.403	.446	.464	.477	.409	.409	.817	.602	.450	.252	.939	.767	.631	.728	.000	+	+	+	+	+	+	+	+	8
.107	.353	.367	.395	.323	.481	.332	.134	.237	.284	.370	.478	.401	.401	.754	.566	.431	.316	.806	.701	.568	.000	+	+	+	+	+	+	+	+	+	9
.363	.349	.429	.452	.348	.403	.310	.452	.318	.313	.409	.505	.087	.087	.534	.067	.035	.313	.108	.539	.000	+	+	+	+	+	+	+	+	+	+	10
.449	.528	.546	.628	.514	.422	.330	.588	.282	.284	.595	.602	.425	.425	.485	.614	.490	.464	.783	.000	+	+	+	+	+	+	+	+	+	+	+	11
.526	.456	.597	.704	.564	.747	.524	.629	.560	.592	.679	.634	.251	.809	.108	.186	.454	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	12
.169	.137	.098	.105	.170	.116	.178	.287	.142	.179	.121	.358	.150	.150	.522	.290	.179	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	13
.248	.237	.232	.289	.226	.268	.178	.344	.203	.188	.241	.403	.008	.008	.523	.011	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	14
.372	.319	.383	.434	.346	.465	.342	.463	.364	.368	.403	.503	.077	.077	.630	.000	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	15
.533	.598	.603	.676	.583	.539	.437	.626	.453	.467	.650	.630	.492	.492	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	16
.217	.233	.231	.256	.184	.208	.179	.331	.146	.151	.211	.402	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	17
.355	.441	.339	.352	.28	.365	.354	.411	.366	.364	.326	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	18
.145	.24	.158	.120	.051	.211	.190	.287	.137	.190	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	19
.031	.295	.196	.215	.147	.021	.053	.191	-.05	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	20
.031	.273	.182	.190	.119	.042	.050	.182	.000	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	21
.091	.359	.302	.286	.245	.312	.257	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	22
.127	.277	.190	.256	.175	.102	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	23
.127	.310	.180	.231	.218	.000	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	24
.110	.263	.200	.176	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	25
.154	.263	.090	0.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	26
.168	.291	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	27
.268	.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	28
.000	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	29

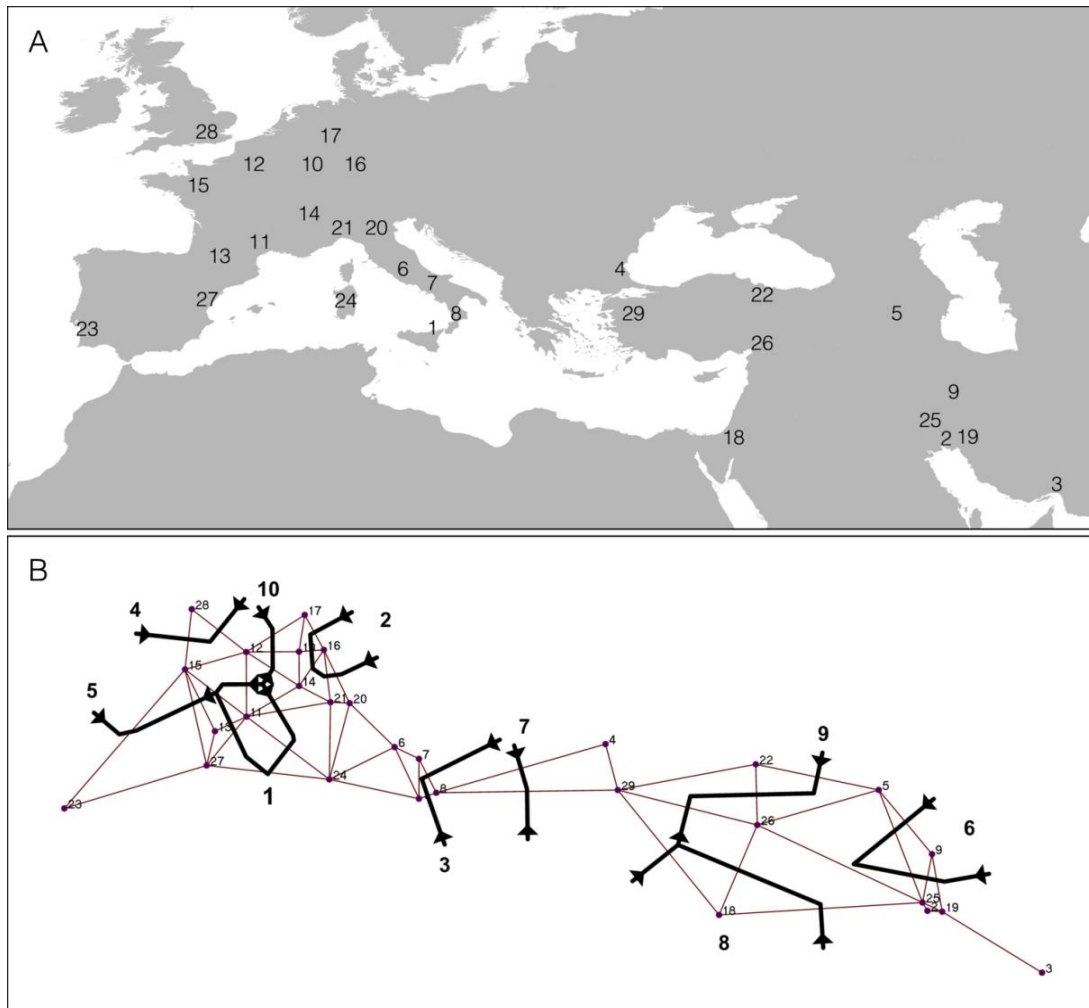


Figure-1: (A) Map of populations; and (B) genetic boundaries obtained with Monmonier’s algorithm. Genetic discontinuity zones are represented by numbered thick black lines and localities are connected by a Delaunay triangulation network (thin lines).

Table-3: AMOVA among *M. m. domesticus* populations, according to the BARRIER analysis

Source of variation	d.f.	Variance components	% variation	Fixation indices	p-values
Among groups	10	0.912	21.57	$F_{CT} = 0.2157$	0.0000
Among populations within groups	18	0.5595	13.23	$F_{SC} = 0.1687$	0.0000
Within populations	353	2.7563	65.19	$F_{ST} = 0.348$	0.0000
Total	381	4.2278	100		

Note: Genetic partition was tested among groups across the identified barriers: [Group I: 9]; [Group II: 2, 3, 5, 19, 25, 26]; [Group III: 18]; [Group IV: 4, 22, 29]; [Group V: 8]; [Group VI: 1, 6, 7, 10, 14, 17, 20, 21, 24]; [Group VII: 16]; [Group VIII: 11]; [Group IX: 12, 15]; [Group X: 28]; [Group XI: 13, 23, 27].

As previously reported [21], owing to man-promoted colonization demographical events, western house mouse populations genetically fell into three degrees of differentiation—the lower one in south Europe, an medium degree between south Europeans and North European populations, and a higher degree between European and the Middle Eastern populations— which has proposed a two-stage process of population expansion [5-8, 21] : the first one (Neolithic stage; starting 10,000 BC) restricted to the eastern Mediterranean basin close to starting location of its commensalism with man, and the second one (Iron Age stage; starting 1,000 BC) continues westwards along the Mediterranean by sea transportation and then to north and western

continent through overland routes. Regardless of geographic distance, these historical demographic events have resulted in the multiple simultaneous founding of populations indwelling the region [21-23]. Monmonier's algorithm in BARRIER analysis identified more barriers in Western Europe region (in comparison to the Middle East) which imply the high genetic heterogeneity resulted from multiple simultaneous founding of populations.

Conclusion

The Monmonier's maximum difference algorithm, a computational geometry method in BARRIER analysis, graphically represented a discontinuity pattern in the western house mouse genetic landscape, which its formation process have been attributed to man-promoted historical migrations since the Neolithic transition.

References

1. A. Banaszek, J. Ziomek, K. A. Jadwyszczak, E. Kaczyńska, and P. Mirski, "Identification of the barrier to gene flow between phylogeographic lineages of the common hamster *Cricetus cricetus*" *Acta. Theriol.* 57(3), pp. 195-204, (2012).
2. E. Mayr, "Populations, species, and evolution: an abridgment of animal species and evolution", Harvard University Press, pp. 297-336, (1970).
3. R. Sage, "Wild mice" *The mouse in biomedical research* 1, pp. 39-90, (1981).
4. E. Schwarz and H. K. Schwarz, "The wild and commensal stocks of the house mouse, *Mus musculus* Linnaeus" *J. Mammal.* 24(1), pp. 59-72, (1943).
5. T. Cucchi, J. D. Vigne, and J. C. Auffray, "First occurrence of the house mouse (*Mus musculus domesticus* Schwarz & Schwarz, 1943) in the Western Mediterranean: a zooarchaeological revision of subfossil occurrences" *Biol. J. Linn. Soc.* 84(3), pp. 429-445, (2005).
6. T. Cucchi, "Uluburun shipwreck stowaway house mouse: molar shape analysis and indirect clues about the vessel's last journey" *J. Archaeol. Sci.* 35(11), pp. 2953-2959, (2008).
7. J.-C. Auffray, E. Tchernov, F. Bonhomme, G. Heth, S. Simson, and E. Nevo, "Presence and ecological distribution of *Mus spretoides* and *Mus musculus domesticus* in Israel Circum-Mediterranean vicariance in the genus *Mus*" *Zeitschrift für Säugetierkunde* 55(1), pp. 1-10, (1990).
8. H. Rajabi-Maham, A. Orth, and F. Bonhomme, "Phylogeography and postglacial expansion of *Mus musculus domesticus* inferred from mitochondrial DNA coalescent, from Iran to Europe" *Mol. Ecol.* 17(2), pp. 627-641, (2008).
9. S. I. Gabriel, M. D. L. Mathias, and J. B. Searle, "Genetic structure of house mouse (*Mus musculus* Linnaeus 1758) populations in the Atlantic archipelago of the Azores: colonization and dispersal" *Biol. J. Linn. Soc.* 108(4), pp. 929-940, (2013).
10. İ. Gündüz, R. V. Rambau, C. Tez, and J. B. Searle, "Mitochondrial DNA variation in the western house mouse (*Mus musculus domesticus*) close to its site of origin: studies in Turkey" *Biol. J. Linn. Soc.* 84(3), pp. 473-485, (2005).
11. F. Manni, E. Guerard, and E. Heyer, "Geographic patterns of (genetic, morphologic, linguistic) variation: how barriers can be detected by using Monmonier's algorithm" *Hum. Biol.* 76(2), pp. 173-190, (2004).
12. M. S. Monmonier, "Maximum-Difference Barriers: An Alternative Numerical Regionalization Method" *Geogr. Anal.* 5(3), pp. 245-261, (1973).
13. K. Katoh, K.-i. Kuma, H. Toh, and T. Miyata, "MAFFT version 5: improvement in accuracy of multiple sequence alignment" *Nucleic. Acids. Res.* 33(2), pp. 511-518, (2005).
14. D. Posada, "jModelTest: phylogenetic model averaging" *Mol. Biol. Evol.* 25(7), pp. 1253-1256, (2008).
15. L. Excoffier and H. E. Lischer, "Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows" *Mol. Ecol. Resour.* 10(3), pp. 564-567, (2010).
16. K. E. Brassel and D. Reif, "A procedure to generate Thiessen polygons" *Geogr. Anal.* 11(3), pp. 289-303, (1979).

17. G. Voronoï, "Nouvelles applications des paramètres continus à la théorie des formes quadratiques. Deuxième mémoire. Recherches sur les paralléloèdres primitifs" *J. Reine. Angew. Math.* 1908(134), pp. 198-287, (1908).
18. L. Excoffier, P. E. Smouse, and J. M. Quattro, "Analysis of molecular variance inferred from metric distances among DNA haplotypes: application to human mitochondrial DNA restriction data" *Genetics* 131(2), pp. 479-491, (1992).
19. M. Hasegawa, H. Kishino, and T.-a. Yano, "Dating of the human-ape splitting by a molecular clock of mitochondrial DNA" *J. Mol. Evol.* 22(2), pp. 160-174, (1985).
20. Z. Yang, "Maximum likelihood phylogenetic estimation from DNA sequences with variable rates over sites: approximate methods" *J. Mol. Evol.* 39(3), pp. 306-314, (1994).
21. J. Britton-Davidian "Genic differentiation in *M. m. domesticus* populations from Europe, the Middle East and North Africa: geographic patterns and colonization events" *Biol. J. Linn. Soc.* 41(1-3), pp. 27-45, (1990).
22. R. D. Sage, E. Prager, H. Tichy, and A. C. Wilson, "Mitochondrial DNA variation in house mice, *Mus domesticus* (Rutty)" *Biol. J. Linn. Soc.* 41(1-3), pp. 105-123, (1990).
23. F. Bonhomme, A. Orth, T. Cucchi, H. Rajabi-Maham, J. Catalan, P. Boursot, J.-C. Auffray, and J. Britton-Davidian, "Genetic differentiation of the house mouse around the Mediterranean basin: matrilineal footprints of early and late colonization" *P. Roy. Soc. B- Biol. Sci.* 278(1708), pp. 1034-1043, (2011).
24. E. Solano, P. Franchini, P. Colangelo, E. Capanna, and R. Castiglia, "Multiple origins of the western European house mouse in the Aeolian Archipelago: clues from mtDNA and chromosomes" *Biol. Invasions* 15(4), pp. 729-739, (2013).
25. H. Suzuki, M. Nunome, G. Kinoshita, K. P. Aplin, P. Vogel, A. P. Kryukov, M.-L. Jin, S.-H. Han, I. Maryanto, and K. Tsuchiya, "Evolutionary and dispersal history of Eurasian house mice *Mus musculus* clarified by more extensive geographic sampling of mitochondrial DNA" *Heredity* 111(5), pp. 375-390, (2013).
26. T. Cucchi, Z. E. Kovács, R. Berthon, A. Orth, F. Bonhomme, A. Evin, R. Siahsarvie, J. Darvish, V. Bakhshaliyev, and C. Marro, "On the trail of Neolithic mice and men towards Transcaucasia: zooarchaeological clues from Nakhchivan (Azerbaijan)" *Biol. J. Linn. Soc.* 108(4), pp. 917-928, (2013).
27. H. Rajabi-Maham, A. Orth, R. Siahsarvie, P. Boursot, J. Darvish, and F. Bonhomme, "The south-eastern house mouse *Mus musculus castaneus* (Rodentia: Muridae) is a polytypic subspecies" *Biol. J. Linn. Soc.* 107(2), pp. 295-306, (2012).
28. M. Macholán, M. M. Vyskočilová, V. Bejček, and K. Šťastný, "Mitochondrial DNA sequence variation and evolution of Old World house mice (*Mus musculus*)" *Folia. Zool.* 61(3-4), pp. 284-307, (2012).
29. A. Orth, J. Auffray, and F. Bonhomme, "Two deeply divergent mitochondrial clades in the wild mouse *Mus macedonicus* reveal multiple glacial refuges south of Caucasus" *Heredity* 89(5), pp. 353-357, (2002).
30. R. Castiglia, F. Annesi, and E. Capanna, "Geographical pattern of genetic variation in the Robertsonian system of *Mus musculus domesticus* in central Italy" *Biol. J. Linn. Soc.* 84(3), pp. 395-405, (2005).
31. M. Linnenbrink, J. Wang, E. A. Hardouin, S. Künzel, D. Metzler, and J. F. Baines, "The role of biogeography in shaping diversity of the intestinal microbiota in house mice" *Mol. Ecol.* 22(7), pp. 1904-1916, (2013).
32. E. A. Hardouin, J.-L. Chapuis, M. I. Stevens, J. B. van Vuuren, P. Quillfeldt, R. J. Scavetta, M. Teschke, and D. Tautz, "House mouse colonization patterns on the sub-Antarctic Kerguelen Archipelago suggest singular primary invasions and resilience against re-invasion" *BMC Evol. Biol.* 10(1), pp. 325, (2010).
33. A. Geraldes, P. Basset, B. Gibson, K. L. Smith, B. Harr, H. T. YU, N. Bulatova, Y. Ziv, and M. W. Nachman, "Inferring the history of speciation in house mice from autosomal, X-linked, Y-linked and mitochondrial genes" *Mol. Ecol.* 17(24), pp. 5349-5363, (2008).
34. D. Förster, I. Gündüz, A. Nunes, S. Gabriel, M. Ramalinho, M. Mathias, J. Britton-Davidian, and J. Searle, "Molecular insights into the colonization and chromosomal diversification of Madeiran house mice" *Mol. Ecol.* 18(21), pp. 4477-4494, (2009).

35. E. P. Jones, F. Jóhannesdóttir, I. Gündüz, M. B. Richards, and J. Searle, "The expansion of the house mouse into north-western Europe" *J. Zool.* 283(4), pp. 257-268, (2011).
36. J. B. Searle, C. S. Jones, Í. Gündüz, M. Scascitelli, E. P. Jones, J. S. Herman, R. V. Rambau, L. R. Noble, R. Berry, and M. D. Giménez, "Of mice and (Viking?) men: phylogeography of British and Irish house mice" *P. Roy. Soc. B- Biol. Sci.* 276(1655), pp. 201-207, (2009).

