
Supplementary material

Exploring the role of within-island ecogeographical factors: insights from the genetic diversity of Cretan trap-door spiders (*Cyrtocarenum cunicularium*, Ctenizidae : Araneae)

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Table S1. Sample ID and locality codes (also given in Figure 1) for each sampling locality of the specimens used in the phylogenetic analyses

GenBank accession numbers of sequence data for both DNA segments are shown. Na, non-amplified

Sample Code	Locality Code	Locality & Prefecture	GenBank Accession Numbers	
			<i>COI</i>	<i>H3</i>
466	Fa	Falasarna, Chania	KY859322	Na
340	Plo	Plokamiana, Chania	KY859314	Na
355	To	Topolia, Chania	KY859312	Na
377			KY859311	Na
382			KY859310	KY859335
397			KY859313	Na
367	Kou	Koustomatados, Chania	KY859308	KY859332
406			KY859309	KY859345
387	Kar	Kares, Chania	KY859307	KY859338
370	Om	Omalos Plateau, Chania	KY859294	KY859334
391			KY859295	KY859342
390	Msk	Meskla, Chania	KY859296	KY859341
400			KY859298	KY859344
408			KY859297	KY859347
356	Fou	Fournes, Chania	KY859301	Na
373			KY859299	Na
380			KY859300	Na
403			KY859323	Na
364	LK	Kournas Lake, Chania	KY859302	KY859330
369			KY859303	Na
345	Sfa	Sfakia, Chania	KY859306	Na
346			KY859305	Na
396			KY859324	KY859343
407			KY859325	KY859346
341	Geo	Georgioupoli, Rethymno	KY859304	KY859329
357	Kas	Kastelo, Rethymno	KY859326	Na
368			KY859327	KY859333
351	Pre	Moni Kato Preveli, Rethymno	KY859328	Na
386	Ape	Apesokari, Irakleio	KY859277	KY859337
416			KY859278	KY859349
352	Ast	Asterousia Mt., Irakleio	KY859275	Na
366			KY859279	KY859331
384			KY859276	Na
388	Fo	Fodele, Irakleio	KY859285	KY859339
389			KY859287	KY859340
399			KY859315	Na
350	Gor	Gorgolaini, Lasithi	KY859270	Na
371			KY859271	Na
374			KY859272	Na
376			KY859273	Na
385			KY859274	KY859336
432	Gou	Moni Gouverniotissa, Lasithi	KY859286	KY859359
437	Dik	Dikteon Andron, Lasithi	KY859316	Na

349	Pin	Pinakiano, Lasithi	KY859288	Na
424			KY859284	KY859354
431			KY859317	KY859358
413	Lmn	Limnakaro, Lasithi	Na	KY859348
422			KY859280	Na
423			KY859282	KY859353
427			KY859283	KY859356
429			KY859281	KY859357
348	AgS	Agioi Saranta, Lasithi	KY859289	Na
430			KY859290	Na
324	Pam	Pachia Ammos, Lasithi	KY859321	Na
419	Bra	Bramiana, Lasithi	KY859269	KY859350
421	Sxi	Sxinokapsala, Lasithi	KY859292	KY859352
412	Zir	Ziros Lake, Lasithi	KY859319	Na
414			KY859320	Na
425			KY859318	KY859355
428			KY859291	Na
420	Vai	Vai, Lasithi	KY859293	KY859351

Table S2. Genetic diversity and summary statistics (Fu's F_s and Ramos-Onsins and Rozas's R_2) of the mismatch distribution analyses under the population expansion model, estimated for each genetic marker and each lineage

COI sequences are grouped in lineages according to the BI tree of Figure 2. *H3* sequences are grouped according to their phylogenetic relationships shown in the respective network of Figure 3.

* $P \leq 0.05$, significant values in bold

	<i>COI</i>		<i>H3</i>	
	" <i>mtWest</i> "	" <i>mtEast</i> "	" <i>nuWest</i> "	" <i>nuEast</i> "
Number of haplotypes	16	17	13	14
Haplotype diversity (<i>Hd</i>)	0.955	0.944	0.971	1.000
Nuclotide diversity (<i>Pi</i>)	0.058	0.053	0.049	0.065
F_s^*	-0.602	0.317	-0.199	-3.228
R_2^*	0.160	0.106	0.181	0.191

Table S3. Genetic divergence (TrN) and the respective standard errors (S.E. in italics) based on the *COI* mitochondrial gene

Sequences were grouped according to their sampling location and the phylogenetic lineages shown in the BI tree of Figure 2

Within divergence (geographical groups)	d	S.E.	
West Crete	0.104	<i>0.019</i>	
Central Crete	0.065	<i>0.013</i>	
East Crete	0.105	<i>0.018</i>	

Net between divergence (geographical groups)	West Crete	Central Crete	East Crete
West Crete		<i>0.066</i>	<i>0.051</i>
Central Crete	0.252		<i>0.010</i>
East Crete	0.191	0.038	

Within divergence (phylogenetic lineages)	d	S.E.	
<i>“mtWest”</i>	0.104	<i>0.018</i>	
<i>“mtEast”</i>	0.108	<i>0.017</i>	

Net between divergence (phylogenetic lineages)	<i>“mtWest”</i>	<i>“mtEast”</i>
<i>“mtWest”</i>		<i>0.055</i>
<i>“mtEast”</i>	0.206	

Table S4. Genetic divergence (TrN) and the respective standard errors (S.E. in italics) based on the *H3* nuclear gene

Sequences were grouped according to their sampling location and their phylogenetic relationships shown in the respective network of Figure 3

Within divergence (geographical groups)	d	S.E.	
West Crete	0.049	<i>0.010</i>	
Central Crete	0.090	<i>0.021</i>	
East Crete	0.116	<i>0.024</i>	
Net between divergence (geographical groups)	West Crete	Central Crete	East Crete
West Crete		<i>0.017</i>	<i>0.010</i>
Central Crete	0.061		<i>0.010</i>
East Crete	0.030	0.033	
Within divergence (phylogenetic lineages)	d	S.E.	
“ <i>nuWest</i> ”	0.079	<i>0.018</i>	
“ <i>nuEast</i> ”	0.106	<i>0.022</i>	
Net between divergence (phylogenetic lineages)	“ <i>nuWest</i> ”	“ <i>nuEast</i> ”	
“ <i>nuWest</i> ”		<i>0.030</i>	
“ <i>nuEast</i> ”	0.131		

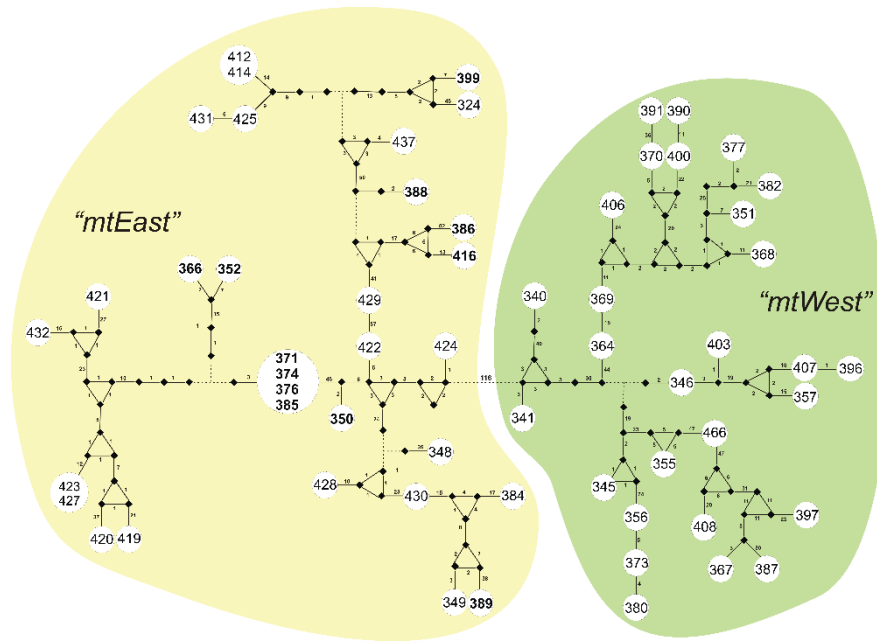


Fig. S1. Simplified representation of the Median-Joining network connecting the haplotypes found for the *COI* mitochondrial marker. Circles represent haplotypes and circle area is proportional to the number of individuals (sample ID codes inside the circle) sharing each haplotype. Black diamonds stand for ancestral/unknown haplotypes, the mutational steps between haplotypes are given as numbers next to their respective connections and dashed lines represent multiple alternative connections.

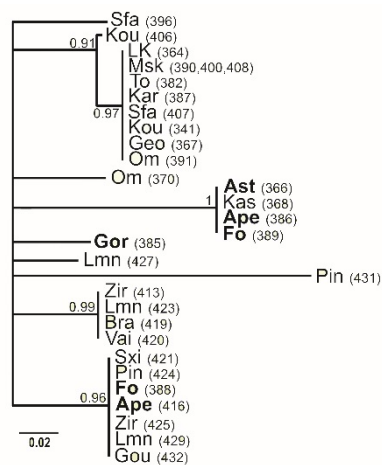


Fig. S2. Bayesian Inference (BI) tree based on the phylogenetic analysis of the *H3* nuclear marker with MrBayes, shown here with final nodes collapsed and tips grouping all sequences per population. BI posterior probability values of the respective node are given above branches, only for nodes with bootstrap support ≥ 90 . Population and sample ID codes are geographically depicted in Figure 1 and the respective information is given in Table S1. Populations/samples from Central Crete are highlighted in bold.

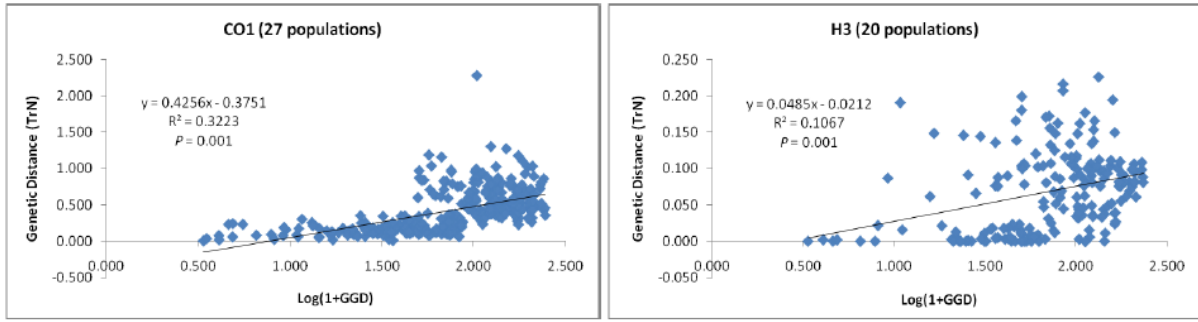


Fig. S3. Mantel-test results for each genetic locus between Tamura-Nei (TrN) genetic distances and Log geographical distances for all pairs of populations.

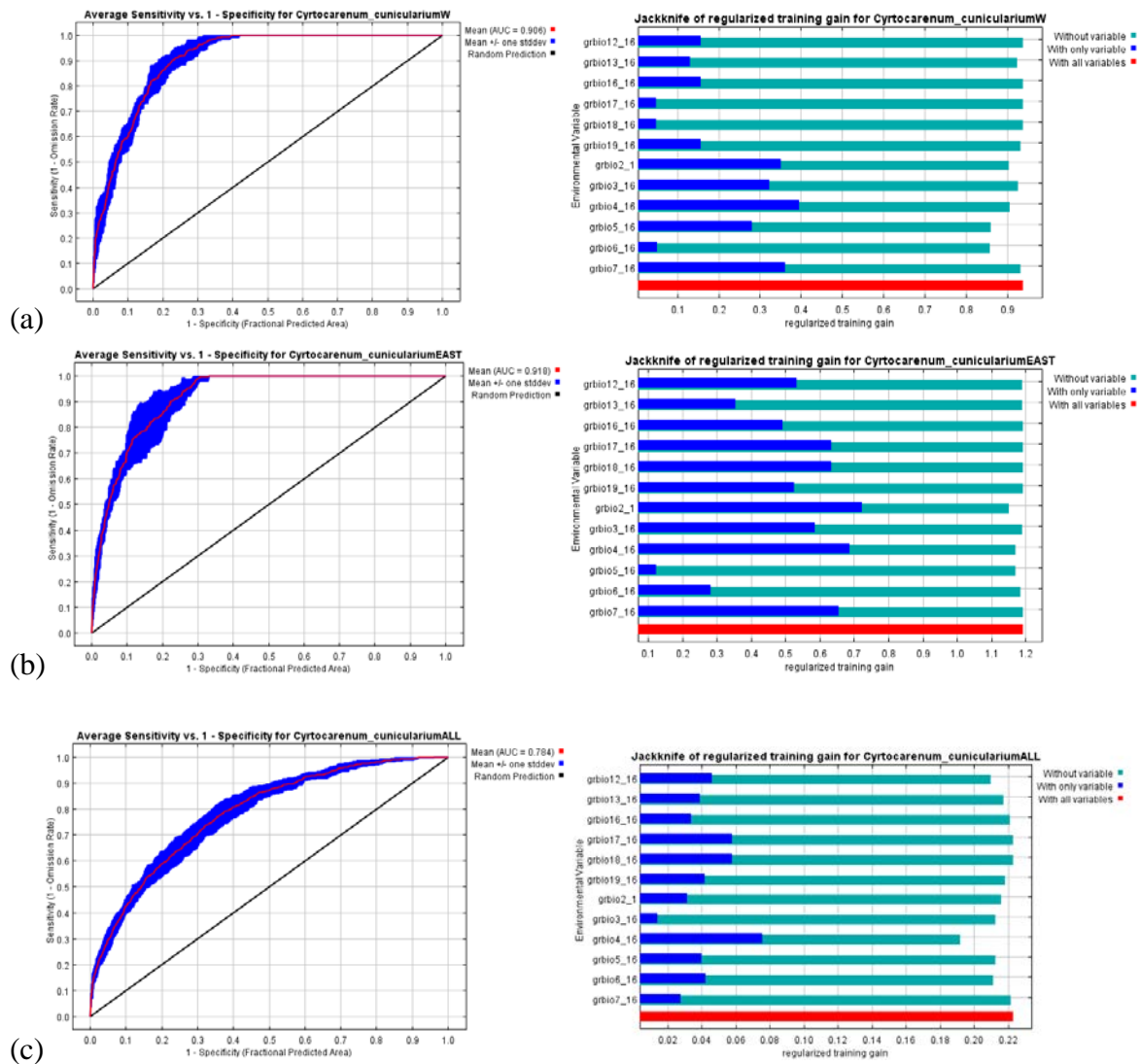


Fig. S4. ROC curves and jackknife test results of the SDM analysis on the (a) “West”, (b) “East” and (c) overall Cretan (“All”) models.