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The puzzling taxonomic rank of *Pijnackeria hispanica*, a chimerical hybrid androgen (Insecta, Phasmida)

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1 **The puzzling taxonomic rank of *Pijnackeria hispanica*, a chimerical**
2 **hybrid androgen (Insecta, Phasmida)**

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35

36 **Abstract**

37

38 The stick-insect genus *Pijnackeria* includes four diploid bisexual and two polyploid (3n,
39 4n) parthenogenetic species. Earlier analyses of the tetraploid parthenogen *P. hispanica*
40 using mitochondrial markers allowed to trace its maternal ancestry to *Pijnackeria*
41 *originis*, while no maternal nuclear contribution was found, thus suggesting an
42 androgenetic and hybrid origin. The recently described *Pijnackeria recondita*—
43 showing, among other features, a specific antennal structure linking it to the tetraploid
44 parthenogen—prompted us to check whether the new species could be *P. hispanica*
45 unknown paternal ancestor. In this work we use karyology and of molecular analysis of
46 the mitochondrial gene cytochrome c oxidase subunit 2 (*cox2*), and the nuclear gene
47 elongation factor 1 subunit α (*efl- α*) to investigate the origin of such a complex
48 tetraploid hybrid parthenogen.

49 The molecular analysis supported *P. recondita* as being a paternal ancestor of the *P.*
50 *hispanica*, but also suggested that two more fathering species have to be taken into
51 account: *P. barbarae* and the unknown paternal ancestor of the triploid hybrid *P.*
52 *masettii*. Therefore, *P. hispanica* is apparently a polyphyletic chimeric androgen, which
53 we propose to indicate as an *androgenetic complex*. Our data also revealed that *P.*
54 *hispanica* is between 1.96 Myr and 3.31 Myr old, making it the oldest parthenogenetic
55 taxon discovered among insects.

56

57 Keywords: androgenesis, hybridization, parthenogenesis, *Pijnackeria hispanica*,
58 *Pijnackeria recondita*, reticulate evolution.

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60

61 **Introduction**

62

63 The phasmid genus *Pijnackeria* Scali, 2009 is a Spanish monophyletic taxon
64 embodying four diploid bisexual and two polyploid parthenogenetic species (3n, 4n), all
65 sharing the same haploid chromosome set with $n = 19$ (Brock 1991, 1993 for reviews;
66 Bianchi, 1992, Bianchi and Meliado, 1998; Scali, 2009a; Scali et al. 2013).
67 *P. hispanica* (Pantel, 1890) (Fig. 1), the nominal species of the genus, appears to be a
68 very successful tetraploid hybrid parthenogen, ranging from the Sierra Nevada

69 (southern Spain) up to the Sistema Central Mountains, northwestwards and to the
70 Serrania de Cuenca, northeastwards. Here, its distribution area overlaps that of the
71 similarly successful triploid hybrid parthenogen *P. masettii* Scali et al., 2013 which is
72 also distributed up to the southern French districts of Var, Herault and Basses Alps
73 (Bianchi, 1992; Ghiselli et al. 2007, Scali, 2009; Scali et al. 2013) (Fig. 2). The
74 remaining four taxa, namely *P. lucianae* (Scali et al. 2013), *P. barbarae* (Scali et al.
75 2013), *P. lelongi* (Scali et al. 2013) and *P. originis* (Scali et al. 2013) are diploid and
76 show much more limited distribution areas in the south-eastern Iberian Peninsula,
77 clearly suggestive of relict distribution (Fig. 2).

78 Molecular genetic analyses, carried out using both the mitochondrial gene cytochrome c
79 oxidase subunit 2 (*cox2*) and the nuclear gene elongation factor 1 subunit α (*efl- α*) as
80 markers, suggested the bisexual diploid *P. lelongi* Scali et al., 2013 as the maternal
81 ancestor of *P. masettii*, and the diploid bisexual *P. originis* Scali et al., 2013 of Tiscar
82 (Sierra de Cazorla) as the maternal ancestor of the tetraploid *P. hispanica* (Ghiselli et al.
83 2007; Scali, 2009a). On the other hand, quite surprisingly, while *P. masettii* showed the
84 *efl- α* allele of maternal derivation, as it could be expected, *P. hispanica* did not, so that
85 its *efl- α* gene ought to be of only paternal derivation (Ghiselli et al. 2007). In order to
86 explain such finding, three different hypotheses were considered: *i*) the effect of gene
87 conversion; *ii*) the outcome of a non-equivalent gene silencing in the hybrid; *iii*) the
88 clear-cut consequence of the maternal genome exclusion within an androgenesis
89 scenario (Ghiselli et al. 2007; Milani et al. 2010, 2013). At any rate, the available data
90 greatly stimulated us to trace the paternal ancestor(s) of *P. hispanica* and to try to shed
91 light on its puzzling genetic structure, without forgetting that even the paternal ancestor
92 of *P. masettii* was actually unknown.

93 Recently, a new *Pijnackeria* species, *P. recondita* Valero and Ortiz, 2015 was found in
94 a very small area of the Sierra Nevada, right at the border of *P. hispanica* southernmost
95 range (Fig. 2; Valero and Ortiz, 2015). Its general morphology differs from *P. hispanica*
96 only in the lower amount of body granulation and chorionic egg sculpturing. All other
97 morphological and morphometric characters are shared with the tetraploid hybrid,
98 including a very similar structure and number of antennae articles (Scali et al. 2013). All
99 these features point to the possibility to consider *P. recondita* as a candidate paternal
100 ancestor of *P. hispanica*. We therefore decided to test the supposed paternal role of *P.*
101 *recondita* by investigating its chromosome set—which obviously had to be congruent

102 with the tetraploid karyotype—and, more importantly, by comparing the *cox2* and the
103 *efl- α* gene sequences of the newly described species with those of *P. hispanica*.

104

105 **Material and Methods**

106

107 On the second half of July 2016, 14 adult specimens (8 males and 6 females) were
108 found in the tiny area of the Sierra Nevada, 2,000 meters a.s.l., as precisely indicated by
109 Valero and Ortiz (2015) (Fig. 2). Owing to the very small size of the population, four
110 males and two females were released on the spot to keep the population as steady as
111 possible. At collection, few specimens were found on the common broom, *Cytisus*
112 (*Sarothamnus*) *scoparius*, but most of them were caught resting on, or actually eating, a
113 different leguminous plant, here tentatively referred to as *Cytisus sp.* (Fig. 3); no
114 *Dorycnium pentaphyllum* was recorded in the collecting area, although it was easily
115 accepted as lab feed, as stated by Valero and Ortiz (2015). The insects were therefore
116 kept on their original food plants added with *D. pentaphyllum*, until their utilization for
117 cytogenetic and molecular analyses.

118 During the same sampling campaign, two adult females of *P. hispanica*, also feeding on
119 *Cytisus sp.*, were collected 15 kilometers away, along the route to El Purche, about 2
120 Km from the A395 junction.

121 Chromosome plates of *P. recondita* were obtained from anaesthetized specimens by
122 manual dissection of the gonads soaked in Ringer solution for insects. After a short
123 hypotonic shock (5-10 min), testes or ovariole tips were put in an 1% sodium citrate
124 solution, fixed for 30 min in a simplified Carnoy solution (3:1, absolute ethanol:acetic
125 acid), and then gently pinched in drops of 45% acetic acid and dried on a hot plate (60°
126 C). Finally, a post-fixation treatment with the same fixative was applied to the slides
127 and then the Giemsa staining was performed. Dry stained slides were eventually
128 mounted in some drops of Canadian balm. Later on, chromosome observations were
129 carried out with a Zeiss photomicroscope, which also allowed picture recording on
130 Ilford film or direct recording from the microscope camera.

131 Total genomic DNA was obtained according to the method described in Preiss *et al.*
132 (1988). Total RNA was obtained with TRIzol reagent (ThermoFisher) according to
133 manufacturer instructions, then the cDNA was reverse transcribed as indicated in
134 Ghiselli *et al.* (2007). The partial sequences of mitochondrial gene *cox2* and of the
135 nuclear gene *efl- α* were PCR-amplified as described in Ghiselli *et al.* (2007). Obtained

136 PCR product were purified using the Wizard PCR Preps DNA Purification System
137 (Promega), and Sanger-sequenced at Macrogen Europe Lab.
138 Sequence chromatograms checking and multiple sequence alignments with ClustalW
139 algorithm were carried out using Mega v.7 (Kumar et al. 2016). New sequences were
140 elaborated together with previously obtained ones (Fig. 4; Table 1 and Table 2;
141 Supplementary material 1-3 for Genbank accession numbers and sequences) in order to
142 get a more comprehensive analysis.
143 Maximum Likelihood tree searches were performed with RAxML v. 8.2 (Stamatakis
144 2014), using the GTR+G substitution model and 500 rapid bootstrap replicates for both
145 genes. Bayesian inferences were conducted with Mr Bayes v3.2.6 (Ronquist et al.
146 2012): two runs were launched, each with 1,000,000 generations, sampled every 500th
147 generation, and using the GTR+G substitution model. Convergence was assessed
148 through the variance of split frequencies (<0.01), PSRF (=1.00) and ESS (>200). Age
149 estimates of cladogenetic event were calculated using a bayesian framework with
150 BEAST v. 1.8 (Drummond and Rambaut, 2007) on the *cox2* dataset. Two independent
151 searches were run, each 10,000,000 generations long, sampled every 1,000th generation,
152 and using the GTR+G substitution model. Convergence was assessed through ESS
153 values >200. Following Mantovani et al., 2000, time calibration was set to the split
154 between *Bacillus rossius tripolitanus* and *B. rossius rossius/B. rossius redtenbacheri*:
155 the separation of this two clades would date back to the end of Messinian salinity crisis,
156 when the Mediterranean basin was filled up, separating North Africa, hosting *B. r.*
157 *tripolitanus* only, and Southern Italy, where only *B. rossius rossius/B. rossius*
158 *redtenbacheri* can be found. Calibration time was, therefore, set to 5.33 ± 0.5 Myr ago
159 and implemented with a normal distribution. Searches were run with an uncorrelated,
160 log-normal relaxed molecular clock and the birth-death speciation process. Haplotype
161 parsimony networks were calculated through TCS v. 1.21 (Clement et al. 2000).

163 **Results**

165 *Karyotype analysis*

166
167 The chromosome set of *P. recondita* fully matched to expectations, for both number and
168 structure, being $2n=37,X0$ male / $38,XX$ female (Fig. 5), and showing similarities to the
169 *P. hispanica* quartets (Fig. 6). The main features of *P. recondita* karyotype are three

170 large pairs of metacentrics (1, 2, 4), and a smoothly decreasing series of acro- and
171 subacrocentric pairs; the last four pairs, owing to their minute size, could also be
172 envisaged as small metacentrics.
173 The *P. recondita* karyotype shows an overall good correspondence with the *P.*
174 *hispanica* chromosome set (Figs 5, 6), the main differences being the different
175 centromere position in the 4th and 6th pairs of the former when compared to the
176 corresponding quartets of the latter. It could also be noted that the first and 13th quartets
177 have two chromosomes bearing small satellites, lacking in the corresponding positions
178 of *P. recondita*, which, in turn, presents satellites on the 2nd and 4th pairs.

179 The peculiar features of *P. masettii* (3n = 57) can be summarized as follows: *P. masettii*
180 is a triploid hybrid with one chromosome set derived from *P. lelongi* and the other two
181 from an unknown heterospecific paternal ancestor, as both the structure of several
182 chromosome triplets and the cytological satellite features clearly support (Fig. 6, triplets
183 1-4, 6, 12, 17-19) (Ghiselli et al. 2007; Scali et al. 2013). Its link to *P. hispanica* will be
184 commented in the Discussion section.

185

186 *Molecular analysis*

187

188 Maximum Likelihood and Bayesian inference phylogenetic analyses carried out on the
189 *cox2* mitochondrial gene are congruent (Fig. 7a) and cluster *Pijnackeria* and *Leptynia*
190 species in a monophyletic clade (bootstrap = 64%; posterior probability = 0.99).
191 However, relationships within this clade are not fully resolved. Overall, taxa are split in
192 a polytomy where it is possible to recognize four well-supported clades: *i*) the *L.*
193 *annaepaulae* clade, *ii*) a clade including *L. attenuata*, *L. caprai*, and *L. montana*, *iii*) the
194 *P. recondita* clade, which embodies also the newly obtained sequences, and *iv*) a cluster
195 comprising *P. lucianae* in sister relationship with the group of the remaining
196 *Pijnackeria* species. In this latter group, *P. masettii* and *P. lelongi* cluster together with
197 high support; on the other hand, the cluster including *P. hispanica* and *P. originis* is
198 weakly supported (bootstrap = 71%; posterior probability < 0.9). The same analyses
199 performed on the *ef-1 α* nuclear gene are congruent as well (Fig. 7b), and place the *P.*
200 *recondita* clade in sister relationship with the remaining *Pijnackeria* species. *P.*
201 *hispanica* and *P. originis* are not included in the same cluster, while three *P. masettii ef-*
202 *1 α* sequences cluster with that of *P. lelongi*.

203 Parsimony network on *Pijnackeria cox2* sequences (Fig. 8) is consistent with the
204 phylogenetic analyses. Three separate networks can be observed: i) one formed by *P.*
205 *recondita* haplotypes, ii) one made by *P. lucianae* haplotypes, and iii) another one
206 including sequences from *P. barbarae*, *P. lelongi*+*P. masettii*, and *P. hispanica*+*P.*
207 *originis*.

208 The parsimony network of *ef-1α* (Fig. 9), though, shows a quite different pattern. The *P.*
209 *hispanica* subnetwork is connected with two different subnetworks, one including *P.*
210 *barbarae* and one including *P. masettii* and *P. lelongi*. *P. recondita*, and *P. originis* are
211 included in two different networks. Interestingly, when the network connection limit is
212 relaxed (< 90%), the three networks become connected and *P. recondita* appears more
213 related to the *P. hispanica* sub-network. On the other hand, the *P. originis* sub-network
214 results connected to that of *P. masettii* (Fig. 9).

215 The Bayesian time tree analysis (Supplementary Figure 1) produced a tree topology that
216 is fully compatible with that obtained through Maximum Likelihood and Bayesian
217 inference analyses. Age estimates of the main *Pijnackeria* clades are included between
218 0.14 Mya (*P. barbarae*) and 3.25 Mya (*P. lucianae*) (Table 3; Supplementary Figure 1).
219 The *P. hispanica*+*P. originis* clade resulted to be 1.96 Myr old and diverged from the
220 sister clade (*P. masettii*+*P. lelongii*) 3.31 Mya (Supplementary Figure 1). The
221 divergence of the *Leptynia-Pijnackeria* clade dates back to 29.73 Mya (Table 3;
222 Supplementary Figure 1)

223

224 Discussion

225

226 *The origin of P. hispanica genome*

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228 Our results suggest a quite complex scenario for the composition of *P. hispanica*
229 genome and the possible role of *P. recondita* as a fathering species.

230 From a chromosome analysis standpoint, the karyotypes of *P. recondita* and *P.*
231 *hispanica* are highly similar, especially the relative size and centromere positioning of
232 most chromosomes. However, there are also differences such as the centromere position
233 in the 4th and 6th pairs, and the position of cytological satellites. The karyotype of *P.*
234 *recondita* shows the same basic haploid set of 19 elements consistently found in all
235 other diploid species of the genus (Scali, 2009a; Scali et al. 2013), and also keeps the
236 metacentric X chromosome as the largest. This finding clearly follows from the male

237 mitotic divisions which, being the male sex-chromosome formula X0, allow the
238 identification of the unique X chromosome: therefore, we could reasonably assign the
239 same role of sex-chromosomes to the first quartet in the karyotype of the
240 parthenogenetic *P. hispanica*.
241 The combined analysis of *cox2* mitochondrial sequences and of *efl-a* nuclear genes
242 suggests a quite intriguing origin of *P. hispanica* hybrid genome. *P. originis* and *P.*
243 *hispanica* *cox2* haplotypes always cluster together, indicating a clear genetic
244 homogeneity. Therefore, in line with previous analyses (Ghiselli et al. 2007), the
245 maternal ancestor would have been *P. originis*, as *P. hispanica* clearly incorporates its
246 mitochondrial marker. On the other hand, the paternal contributions are less clear.
247 Based on the *efl-a* phylogenetic and network analyses, *P. hispanica* is more related to
248 *P. barbarae*, *P. masettii*, and *P. lelongi* than to *P. recondita* and *P. originis*. However,
249 less stringent parameters for network construction allowed the connection of *P.*
250 *recondita* and *P. hispanica* sub-networks. This suggests a common ancestry of the two
251 nuclear sequences, but it also indicates a wide differentiation between *P. recondita* and
252 *P. hispanica*. The time tree analysis clearly supports such distant relationship, dating the
253 divergence of mitochondrial *cox2* sequences back to the Mid-Oligocene (29.73 Mya).
254 Overall, the results are not in contrast with a possible contribution of *P. recondita* to the
255 genome of *P. hispanica*, although the level of genetic divergence observed in both
256 mitochondrial and nuclear markers would suggest caution. In summary, we can say that
257 the data are compatible with the hypothesis of an ancestral contribution followed by
258 diversification. It is worth noting that the *P. recondita* and the *P. hispanica* subnetworks
259 are connected through the sample from El Purche (PUR), which has been collected very
260 close to the distribution area of *P. recondita* (Sierra Nevada, SNE) (Fig. 8). Therefore, it
261 is possible that widening the sampling in the area of sympatry would shed light on this
262 issue.
263 *P. hispanica* is a very unusual hybrid since it incorporates the mitochondrial marker of
264 *P. originis* but it includes the nuclear sequences of different species. The tetraploid
265 constitution of *P. hispanica* genome and the close similarity of chromosome sets shared
266 by all *Pijnackeria* taxa suggest the possibility of polyploidization. On the other hand,
267 some minute differences among specific chromosome complements indicate a
268 heterogeneous structure, supporting a complex chromosome set with heterospecific
269 genomes. Among these, at least one of *P. recondita* origin. However, further inspection
270 of *P. hispanica* karyotype with heteromorphic quartets points to just a double *P.*

271 *recondita* chromosome set contribution—also in view of a diploid structure of the initial
272 hybrid—with two paternal chromosome sets derived each from the unknown paternal
273 ancestor of *P. masettii* and *P. barbarae*. Overall, *P. hispanica* genetic structure points to
274 a complex, unusual derivation.

275 The occurrence of a mitochondrial genome from one species and the nuclear genome
276 from a different species inherited by an individual of a third species was observed for
277 the first time through allozyme analysis and cytological investigations of both field-
278 collected and lab-reared specimens of the hybridogenetic *Bacillus rossius-grandii*
279 strains (Mantovani and Scali, 1992; Tinti and Scali, 1996), thus providing clear
280 evidence for androgenesis in stick insects. Afterwards, natural androgenesis was also
281 discovered in several species of the freshwater clam *Corbicula* (Komaru et al. 1998;
282 Byrne et al. 2000; Qiu et al. 2001) and in the cypress tree *Cupressus dupreziana* (Pichot
283 et al. 2001). Our analysis with a mitochondrial gene and a single nuclear marker cannot
284 be conclusive but, all considered, it is reasonable to suggest an androgenetic origin also
285 for *P. hispanica*, which could date back to between 2 Mya (the estimated age of the
286 clade) and 3.3 Mya (the estimate split age from the closest relative).

287 Because of the clonal structure of parthenogenetic taxa, with consequent loss of genetic
288 variability, the causes and consequences of their longevity are debated (see Bell, 1982;
289 Wrijenhoek and Lerman, 1982; Wrijenhoek, 1998; Normark et al. 2003). Data on stick
290 insects obtained so far indicated that *Bacillus* hybrid taxa originated around 1 Mya
291 (Mantovani et al. 2001), whereas parthenogenetic *Timema* lineages have evolved
292 between 500,000 and 2 Mya (Schwander et al. 2011). In this view, *P. hispanica* may
293 represent the oldest parthenogenetic taxon discovered so far among insects.

294

295 *The Pijnackeria karyotype and the evolution of egg maturation modes*

296

297 A great stability for chromosome number and structure within a cluster of related
298 species is quite a rare finding among Phasmida: all species-rich genera investigated so
299 far actually showed a marked karyotype plasticity for both number and structure of
300 chromosomes, particularly when parthenogens are involved. Striking instances of this
301 feature are the Australian *Didymuria* (Craddock, 1972, 1975) and *Sipyloidea* (John et al.
302 1987), as well as the circum-Mediterranean *Bacillus* and *Clonopsis* (Scali, 2009b;
303 Milani et al. 2010). Also the Iberian genus *Leptynia*—defined on both morphology and
304 genetic basis, and encompassing only four species—revealed diploid chromosome sets

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305 ranging from 36 to 40, and a very significant structural variation, even entailing the sex-
306 chromosome formula with a shift from the usual XX/X0, to the rarer XX/XY one (Scali,
307 2009c; Scali et al. 2016). In addition, the karyotype stability of *Pijnackeria* species is
308 mirrored by the number and localization of cytological NOR-bearing satellites (Ghiselli
309 et al. 2007; Scali et al. 2016): taking into account the tens of specimens analyzed
310 belonging to the seven *Pijnackeria* species, we were able to score 10 different satellite
311 positions, but each species possesses a maximum of two different locations. This is a
312 quite different scenario from that observed for NOR-bearing satellites of *Bacillus*,
313 where a single species may encompass as much as 12 different locations for cytological
314 satellites (Manaresi et al. 1991, 1992, 1993; Salvadori et al. 2018; Scali et al.
315 submitted). Frequent changes in location and number of satellites are a common finding
316 in stick insects, and it has been suggested that they could be an outcome of transposon
317 activity (Meyne et al. 1990; Zhdanova et al. 2007; Ruiz Herrera et al. 2008; Ocalewicz,
318 2013; Satovic et al. 2016). For example, R2 non-LTR transposons have been reported to
319 be active in *Bacillus* species and even particularly prone to accumulate in
320 parthenogenetic taxa (Bonandin et al. 2014, 2017; Scavariello et al. 2017).

321 The cytological satellite features are not just a trait of inter- and intra-specific
322 variability, since in all investigated phasmatodean species—13 all together up to now—
323 chromosomal satellites have been always found to be sites of highly enriched and co-
324 localized rDNA/telomeric sequences (Scali et al. 2016; Liher et al. 2017; Salvadori et al.
325 2018): therefore, this trait appears to have a biological and evolutionary bearing.

326 Actually, it has been already possible to observe that in the di-hybrid *Bacillus whitei*
327 and the three-hybrid *B. lynceorum*, active NORs derive from all ancestors, although that
328 of maternal *B. rossius* derivation appears as the most conserved (Manaresi et al.
329 1991, 1992, 1993). However, owing to the androgenetic structure of *P. hispanica*, such a
330 feature cannot be verified.

331 A careful karyotype analysis of *Pijnackeria* polyploids gives us some indirect clues
332 about their egg maturation mechanisms, since a direct investigation has not been
333 possible. In stick insects, egg meiosis is blocked at pachytene during the first instar
334 larva, to be resumed in adults at laying. Consequently, eggs can be collected at precisely
335 scheduled times and investigated. Unfortunately, in *Pijnackeria* such a direct analysis of
336 oocyte maturation is not feasible, because the few laid eggs are firmly glued to the
337 substratum and their chorionic capsule is too fragile to be handled and cut for fixation as
338 it has been done in *Bacillus* and *Clonopsis* (Marescalchi et al. 1991; Scali et al. 2010).

339 Owing to such limitations, we can propose only conjectural hypotheses for *P. hispanica*,
340 and considering its complex hybrid structure, an apomictic mechanism maintaining a
341 steady karyotype structure appears the most likely. In this connection, we can observe
342 that *P. masettii* is a triploid hybrid with one chromosome set derived from *P. lelongi*
343 and the other two from an unknown heterospecific paternal ancestor, as both the
344 structure of several chromosome triplets and the cytological satellite features clearly
345 support (Fig. 6, triplets 1-4, 6, 12, 17-19; see also Ghiselli et al. 2007; Scali et al. 2013).
346 At the time of its formation, such a hybrid certainly suffered from a diffuse imbalance in
347 pairing and segregation of the trivalents during the first meiotic division, as actually
348 observed in triploid specimens of *Bacillus atticus* (Marescalchi and Scali 1997, 2003);
349 therefore, a modified meiosis escaping such constraints is likely to have been evolved
350 by selecting an apomictic egg-maturation mechanism. A similar meiotic pathway could
351 have been evolved in the tetraploid *P. hispanica* androgenetic parthenogen with a high
352 (76) chromosome number.

353 Gathering all relevant observations on the issue, the most parsimonious series of
354 gains/losses of whole chromosome sets leading to the extant structure of *P. hispanica*
355 can be envisaged as follows: a seminal parthenogenetic *P. originis*/*P. recondita* hybrid
356 with an apomictic reproduction owing to the marked genetic differentiation of the
357 parental taxa was produced. Pre-mating isolating mechanisms were easily overcome,
358 since in phasmids they are rather ineffective even between utterly differentiated species
359 (Scali et al. 1995). Back-crosses to *P. recondita* males were still possible (see Tinti and
360 Scali, 1996) and, thanks to the physiological egg-polyspermy (Scali, 1972), an all-
361 paternal progeny was originated when syngamy with the hybrid egg nucleus failed and
362 two spermatozoa fused to originate a 2n androgen, which only kept the mitochondrial
363 DNA of the mother but continued an apomictic reproduction (Mantovani and Scali,
364 1992). The 4n ploidy of *P. hispanica* could then be reached through a two-step
365 acquisition of additional *Pijnackeria* genomes by the androgen. After the original
366 hybridization of *P. recondita* with *P. originis* leading to an early diploid androgen, an
367 additional fathering taxon, providing the third haploset, should have been different from
368 *P. recondita* and likely similar to the unknown paternal ancestor of *P. masettii*. The last
369 contribution of a fourth genome could have been provided by a *P. barbarae*-like
370 paternal ancestor: the heterozygous structure of several quartets of *P. hispanica* (Fig. 6)
371 and the high variability of its *efl-α* sequences (Fig. 9) are consistent with the above
372 outlined assumptions. Being these correct, *P. hispanica* could be then envisaged as a

1 373 polyphyletic hybrid-complex endowed with a high colonizing potential. Moreover, it is
2 374 tempting to speculate that such kind of multi-hybrid origin could be the reason behind
3 375 the long evolutionary persistence (1.96-3.31 Myr) of this parthenogenetic taxon. The
4 376 high variability produced by multiple hybridizations events might have compensated for
5 377 the absence of sexual recombination (Ghiselli et al 2007 and references therein).
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7 378 On the issue, we would like mentioning that androgenetic stick-insect strains of *Bacillus*
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9 379 and *Clonopsis* contributed to the formation of a complex network among parental and
10 380 derived taxa, so that their reproductive and micro-evolutionary features were defined as
11 381 “reticulate evolution” (reviewed in Scali, 2009a), and, within it, androgenesis has been
12 382 proposed as a short-cut pathway for speciation (Ghiselli et al. 2007; Milani et al. 2010;
13 383 2015). To better envisage the cladogenetic potential of androgenesis, a simple model of
14 384 hybrid eggs maturation and genome transmission has been worked out for *Clonopsis*
15 385 hybrids, which would even explain the ascertained diploid structure of polyploid
16 386 karyotypes (Milani et al. 2009; 2010): the *Clonopsis* model also accommodates quite
17 387 easily the otherwise inexplicable chromosomal findings reported in the Australian
18 388 *Sipyloidea nelida* species complex by John et al. (1987).
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20 389 On the whole, the targeted cytogenetic insight and transmission analysis of genomes,
21 390 although rather limited, appears an effective tool to reveal the exploitation of a wide
22 391 array of reproductive modes and evolutionary pathways in stick insects: these insights
23 392 seem to really add to the routinely accepted ideas about reproductive features,
24 393 evolutionary modes and phylogenetic relationships in animals.
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40 395 *Taxonomic implications*

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43 397 Following the above described scenario of “reticulate” backcrosses, multiple tetraploid
44 398 populations arose in different areas of the *Pijnackeria* range, stepwise embodying
45 399 additional sets of fathering taxa, some of which can also be missing from the sampling.
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47 400 These 4n populations are now spread and mixed in the region indicated in Figure 2.
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49 401 According to this phylogeographic pattern, *P. hispanica* would then represent the
50 402 ensemble of many subpopulations of 4n parthenogenetic androgens in which the
51 403 multiple contributions from diverse diploid species can be appreciated in the *efl*-
52 404 α network (Fig. 9). Each *P. hispanica* specimen within the different subpopulations
53 405 appears to possess a chimerical genetic structure, even more strengthened by the
54 406 occurrence of the “foreign” mitochondrial DNA of the maternal ancestor. All this points
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407 to a composite, polyphyletic structure of the tetraploid hybrid, which we propose to
408 indicate as an *androgenetic complex*.
409 Finally, we would like to point out that, if in *cox2* network the recently described Sierra
410 Nevada (SNE) *P. recondita* taxon does not actually cluster together with the previously
411 described *Pijnackeria* species (Fig. 7a,b), and Valero and Ortiz (2015) obtained the same
412 tree topology from *cox1* and *cox 2* analyses. Although this topology does not fully resolve
413 the relationships within the genus *Pijnackeria*, it clearly indicates a high degree of
414 differentiation between *P. recondita* and the other conspecific species. Further molecular
415 investigation may help to shed light on the evolution of this genus and its relationship
416 with the closely related genus *Leptynia*.

417

418 **Data availability:** The datasets generated during and/or analyzed during the current
419 study are available in the GenBank repository (see corresponding GenBank numbers in
420 Supplementary Material 1). The sequences generated during this study are also available
421 as Supplementary Material 2 and 3 in FASTA format.

422

423 **Conflict of Interest:** The authors declare that they have no conflict of interest.

424

425 **Ethical approval:** All applicable international, national, and/or institutional guidelines
426 for the care and use of animals were followed.

427

428 **Figure Captions**

429

430 **Fig. 1** Specimen of *Pijnackeria hispanica*: the nominal species of the new genus
431 (corresponding to the originally described *Leptynia hispanica* species by Pantel
432 1890). Note the very short antennae and the pointed abdomen end peculiar to the taxon.
433 Additional information and images of this tetraploid parthenogen and of all other
434 congeneric species are to be found in Scali 2009, Scali et al. 2012, Scali et al.
435 2013; Valero and Ortiz 2015.

436

437 **Fig. 2** Ranges of *Pijnackeria* taxa. **2n**: **A**, *P. lucianae*; **B**, *P. barbarae*; **C**, *P. lelongi*; **D**,
438 *P. originis*; **3n**, *P. masettii*; **4n**, *P. hispanica*. Sample acronyms as in Ghiselli *et al*,
439 2007. The area of *P. recondita* (Sierra Nevada) and *P. hispanica* (El Purche) samples is

440 represented by a single dot south-east of PRA (Puerto La Ragua). Acronyms as in Table
441 1 and Table 2

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443 **Fig. 3** *Pijnackeria recondita* food plants: *Cytisus scoparius* on the right and *Cytisus sp.*,
444 on the left

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446 **Fig. 4** Geographical distribution of the haplotypes obtained both by sampling and from
447 literature contributing to the molecular analysis. A) *cox2*. B) *efl-α*. For the exact
448 coordinates of the sampling sites, refer to Table 1 and Table 2

449

450 **Fig. 5** Karyotype of *Pijnackeria recondita*. The karyotype is very similar to those of all
451 other *Pijnackeria* species. A) Female: 1st pair, heterochromosomes; the 2nd and
452 4th pairs bear a heterozygous satellite; B) Male: its unique sex chromosome (X0) allows
453 to indicate the first female pair as the heterochromosome pair in both *P. recondita* and,
454 as a consequence, in *P. hispanica*

455

456 **Fig. 6** Karyotype of the triploid *Pijnackeria masettii* (on the top), and of the tetraploid
457 *Pijnackeria hispanica* (on the bottom) modified from Scali et al. (2013). *P. hispanica*
458 appears either a 2+2 structure, or, better, a 2+1+1 structure. *P. masettii* triplets 1-4, 6,
459 12, 17-19 clearly support a 2+1 structure; 1st, 2nd, 13th, 15th and 19th quartets of *P.*
460 *hispanica* seem to suggest either a 2+2 structure, or better a 2+1+1 structure

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462 **Fig. 7** Schematic drawing of Maximum Likelihood/Bayesian Inference on *cox2* (A; $-\ln L$
463 = 3431.06/3503.44) and *efl-α* (B; $-\ln L$ = 1958.30/20072.49) datasets. Number at nodes
464 are bootstrap/posterior probabilities support values. Outgroup(s) have been omitted for
465 graphical purposes

466

467 **Fig. 8** Parsimony network of the *cox2* gene sequences. Circles size is proportional to
468 haplotype frequency; black dots represent missing/ideal haplotypes. Connections
469 obtained with relaxed parameters are indicated with dashed, grey lines; grey numbers in
470 parentheses are the number of missing/ideal haplotypes along the connection

471

472 **Fig. 9** Templeton network of the *efl-α* gene sequences. Circles size is proportional to
473 haplotype frequency; black dots represent missing/ideal haplotypes. Connections

1 474 obtained with relaxed parameters are indicated with dashed, grey lines; grey numbers in
2 475 parentheses are the number of missing/ideal haplotypes along the connection

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5 478 **Legends to tables**

6 479

7 480 Table 1. Analyzed species for *cox2*, with collecting place with acronyms and geographic
8 481 coordinates.

9 482

10 483 Table 2. Analyzed species for *efl- α* , with collecting place with acronyms and
11 484 geographic coordinates.

12 485

13 486 Table 3. Age estimates of the main *Pijnackeria* clades.

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16 489 **Supplementary material**

17 490

18 491 Supplementary Figure 1. Time calibrated tree obtained on *cox2* gene sequence.

19 492 Numbers on branches represent the posterior probability nodal support; bars at nodes
20 493 indicate the 95% high posterior density (HPD).

21 494

22 495 Supplementary Material 1. Genbank accession numbers of the analyzed sequences.

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24 497 Supplementary Material 2. *cox2* sequences.

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26 499 Supplementary Material 3. *efl- α* sequences.

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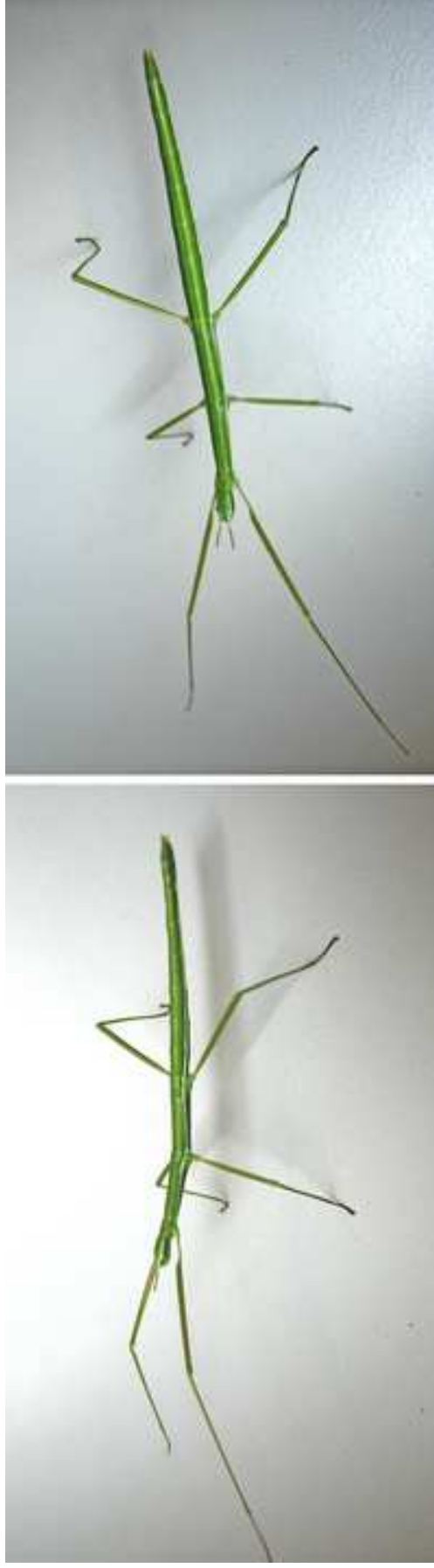
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FIGURE 1

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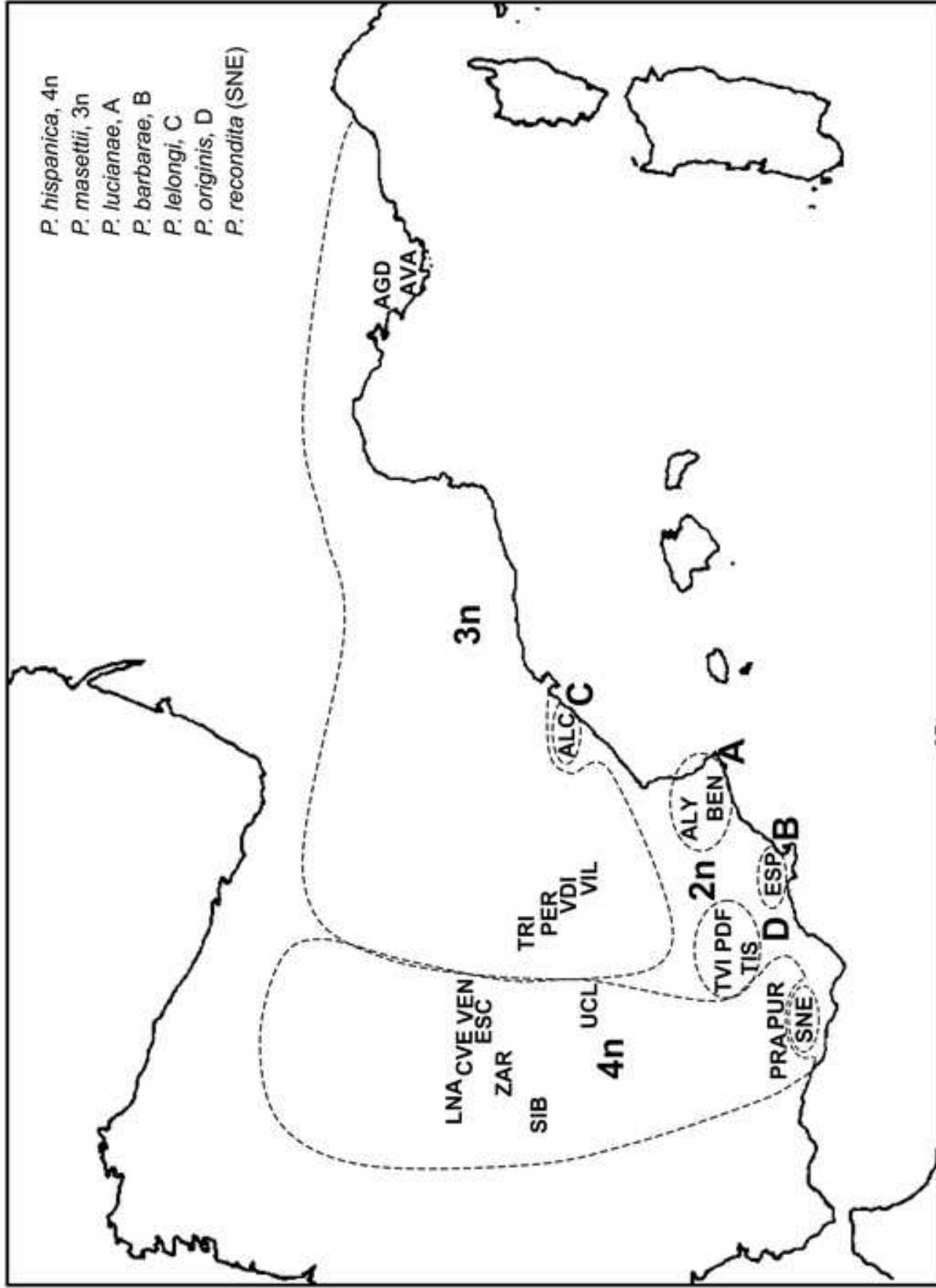


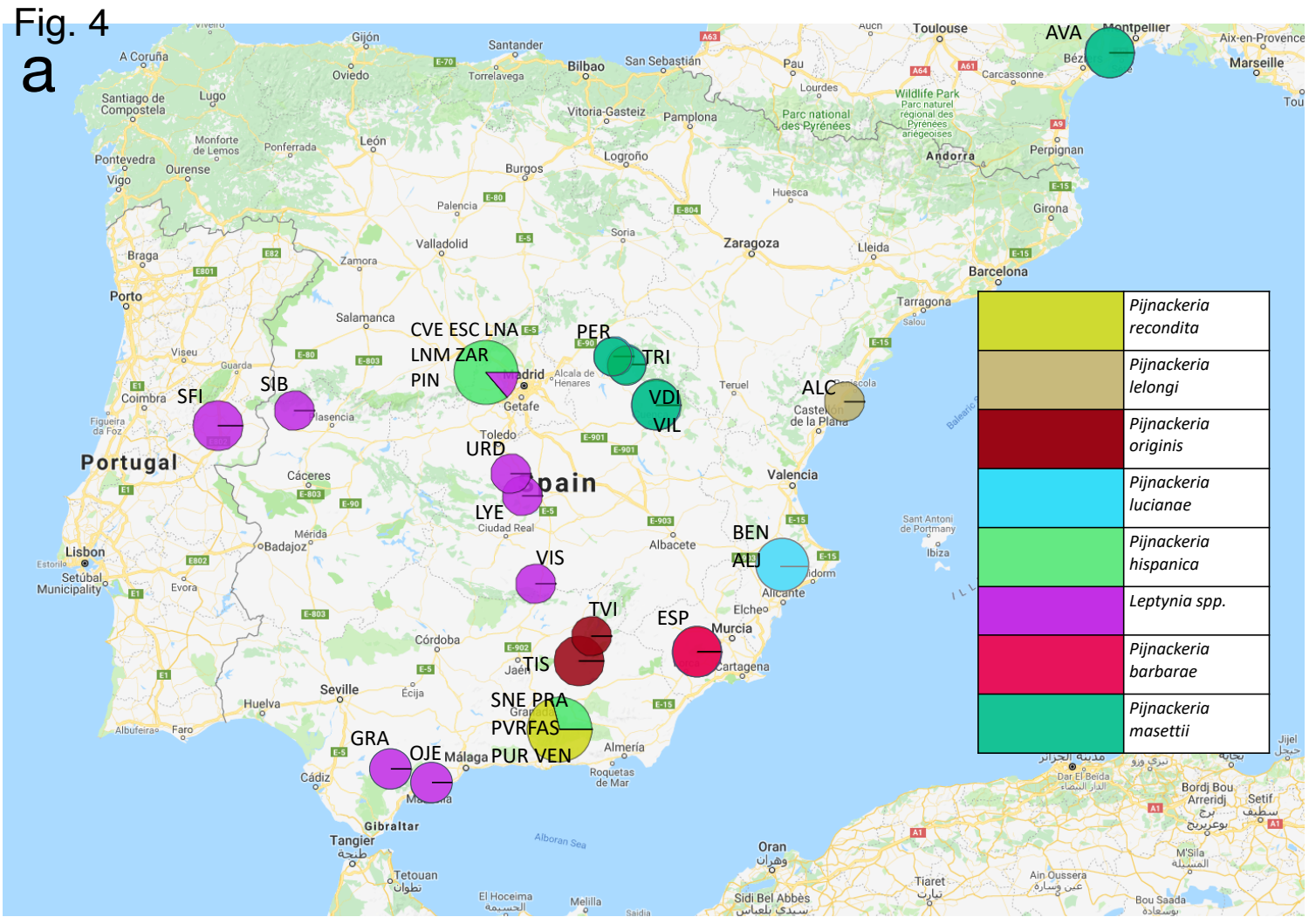
FIGURE 2

FIGURE 3

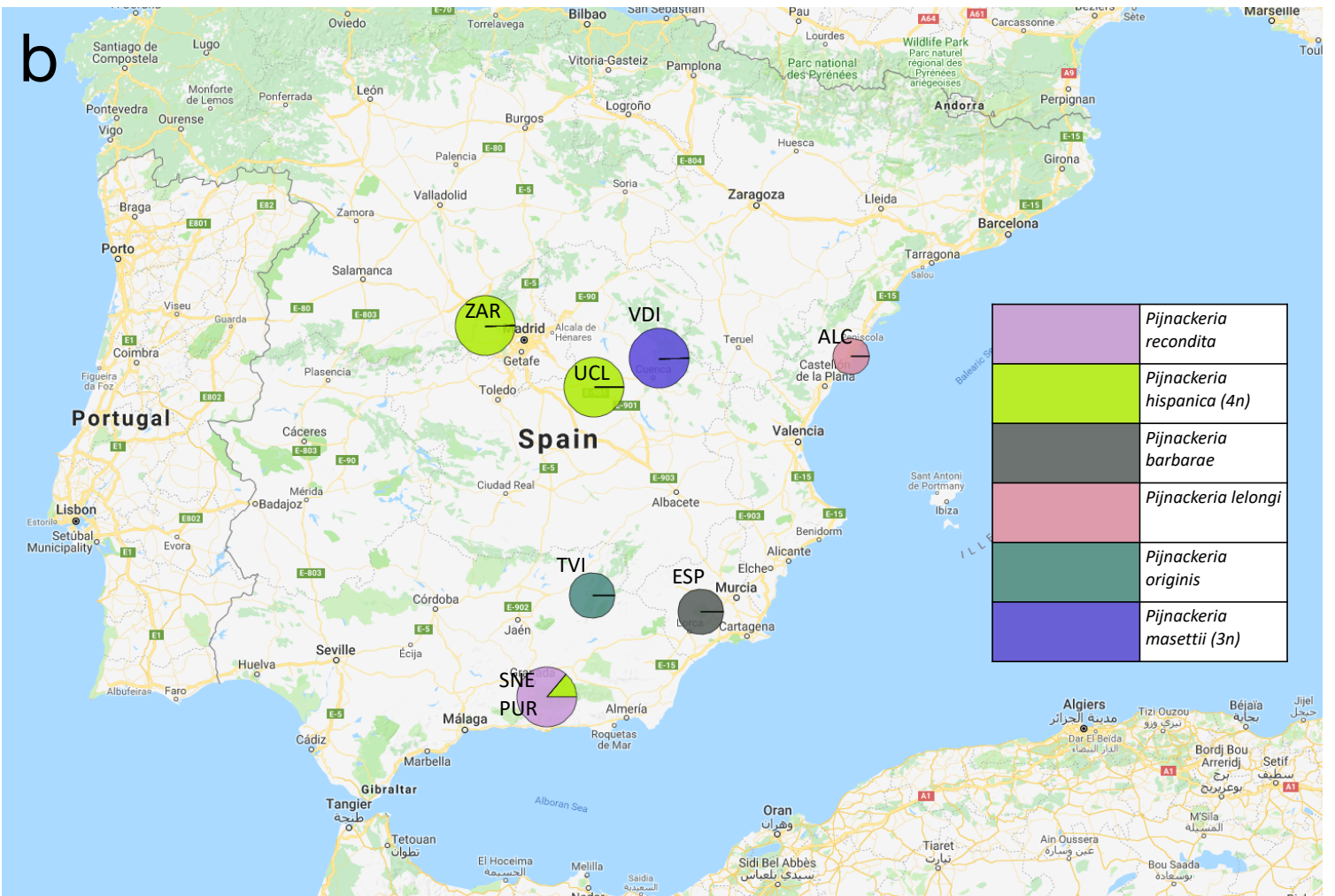
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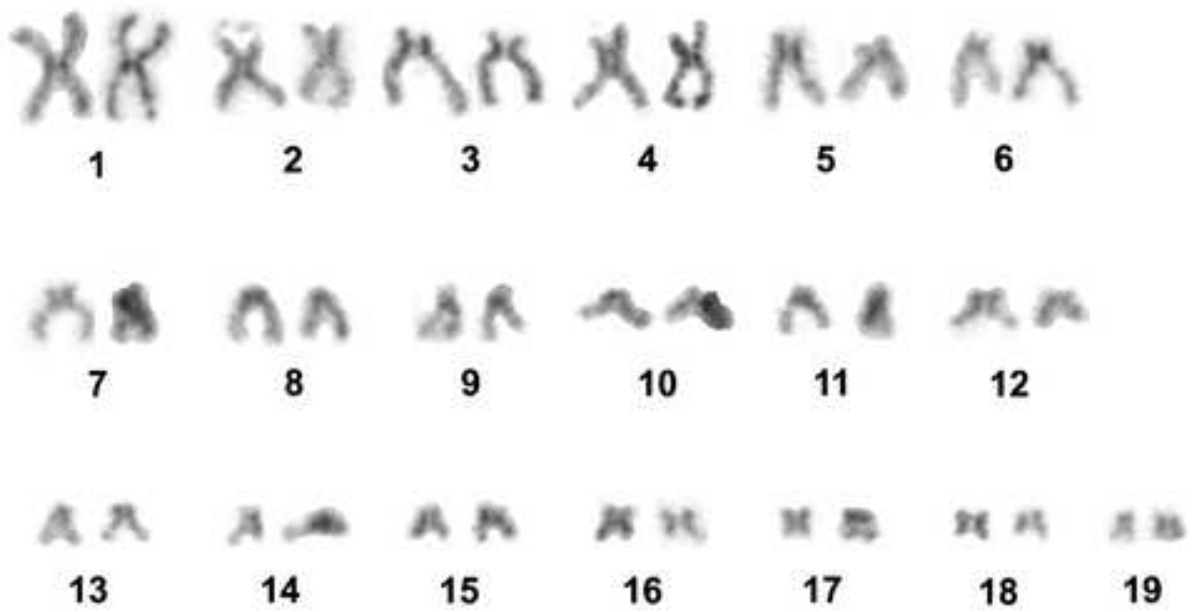
Fig. 4
a



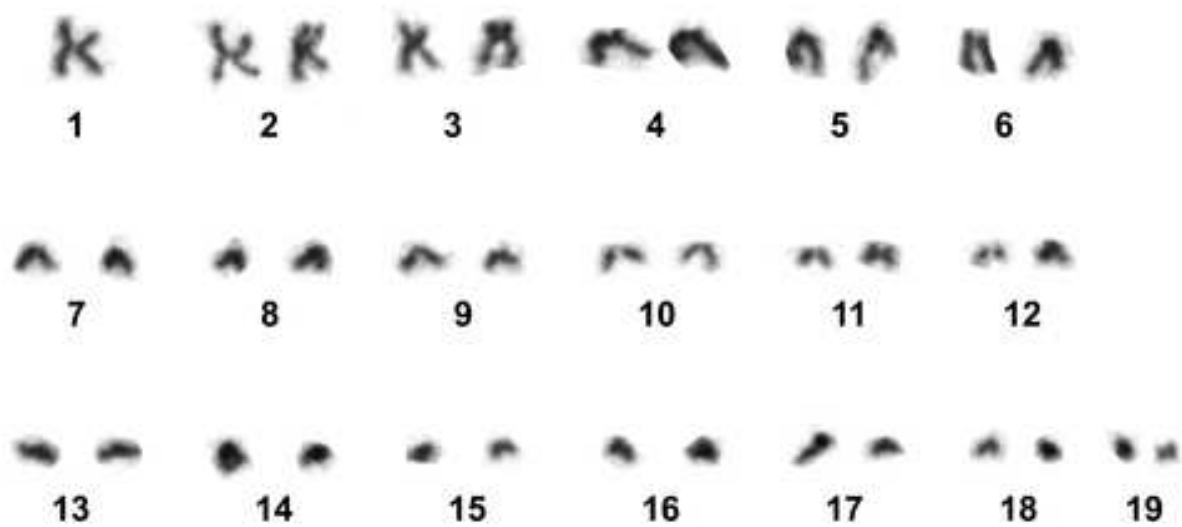
b



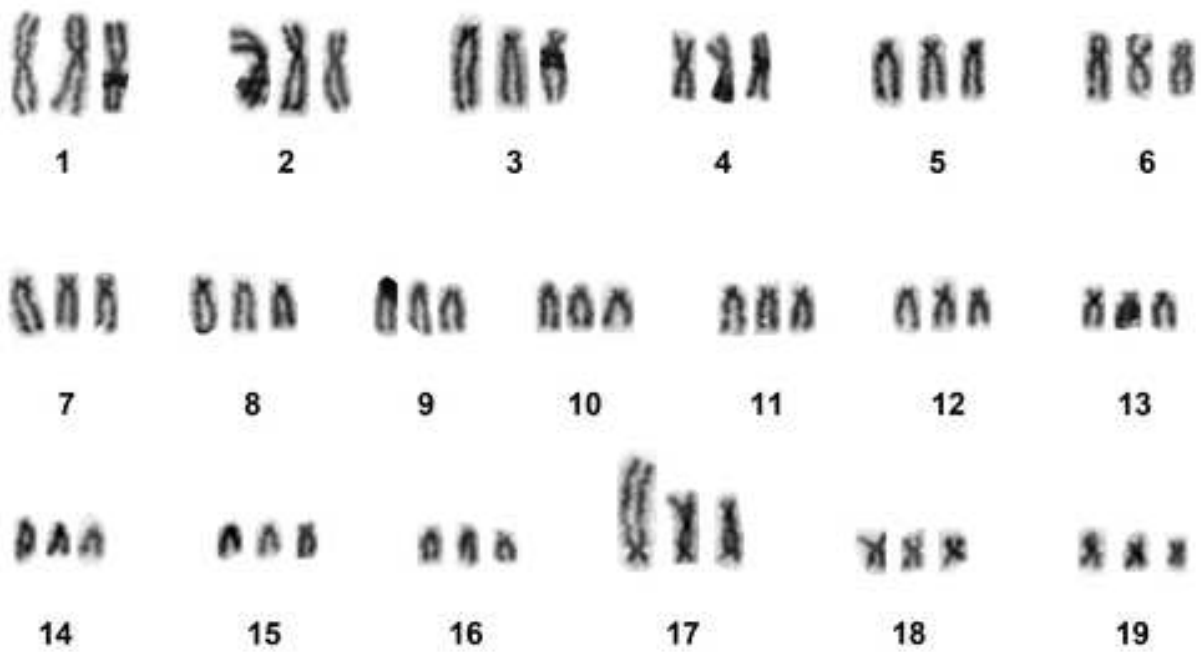
A



B



A



B

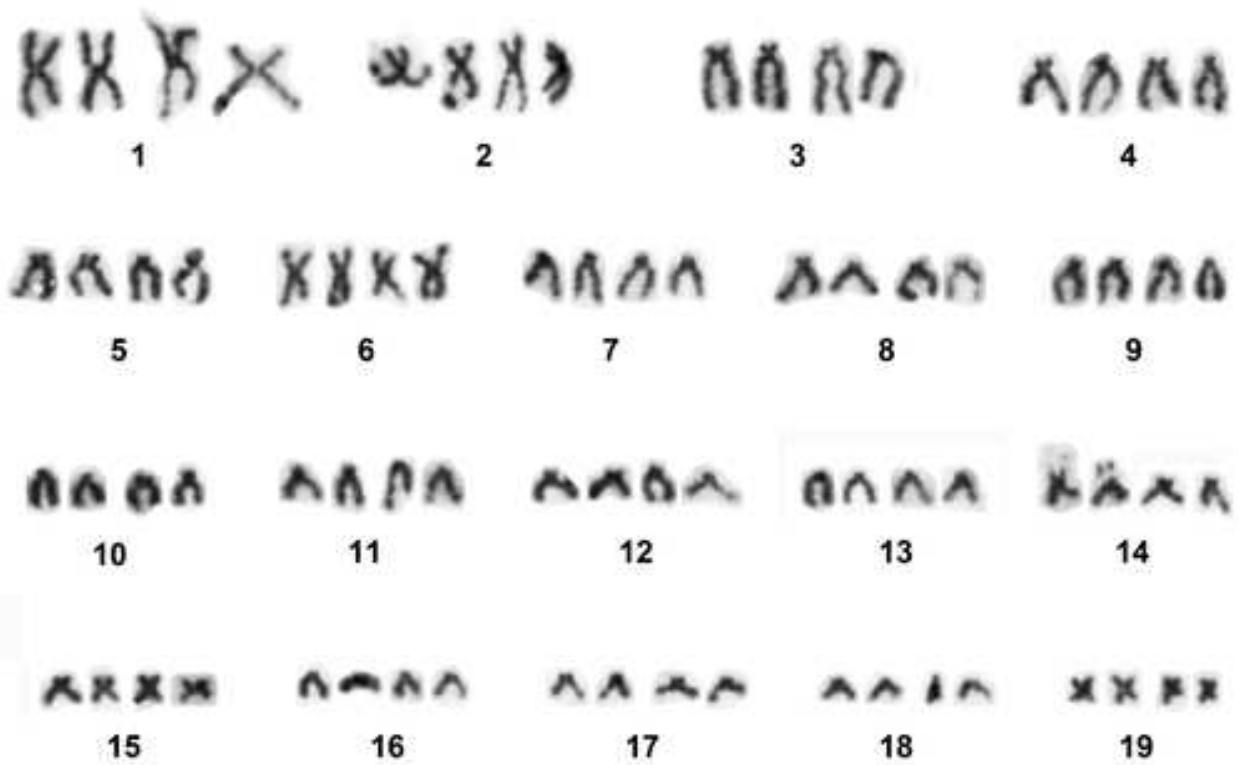


Fig. 8

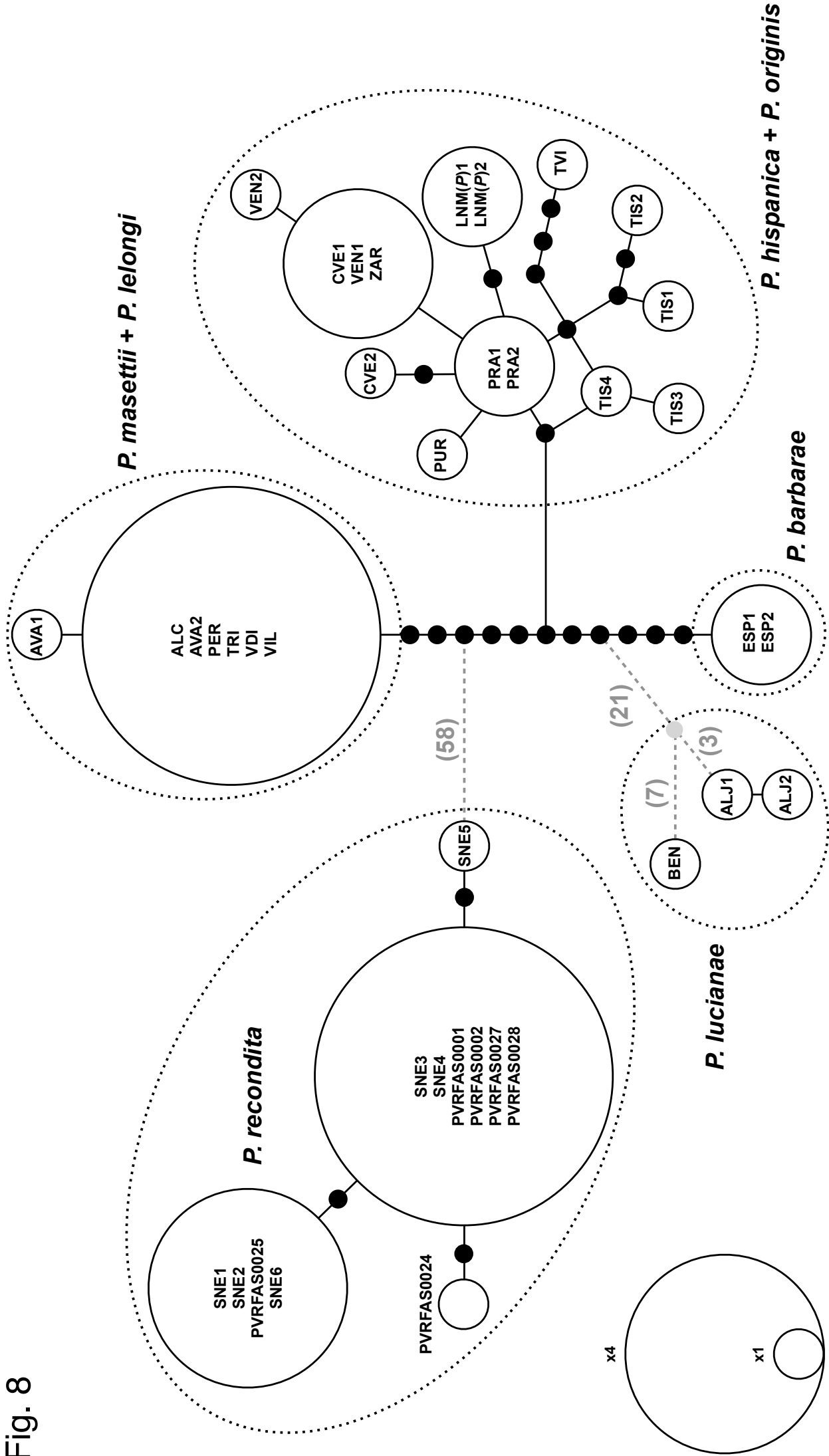


Fig. 9

