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1                   **Contrasting genomic and phenotypic outcomes of**  
2                   **hybridization between pairs of mimetic butterfly taxa**  
3                   **across a suture zone**  
4

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26

27 **Abstract.**

28 Hybrid zones, whereby divergent lineages come into contact and eventually hybridize, can  
29 provide insights on the mechanisms involved in population differentiation and reproductive  
30 isolation, and ultimately speciation. Suture zones offer the opportunity to compare these  
31 processes across multiple species. In this paper we use reduced-complexity genomic data to  
32 compare the genetic and phenotypic structure and hybridization patterns of two mimetic  
33 butterfly species, *Ithomia salapia* and *Oleria onega* (Nymphalidae: Ithomiini), each  
34 consisting of a pair of lineages differentiated for their wing colour pattern and that come into  
35 contact in the Andean foothills of Peru. Despite similarities in their life history, we highlight  
36 major differences, both at the genomic and phenotypic level, between the two species. These  
37 differences include the presence of hybrids, variations in wing phenotype, and genomic  
38 patterns of introgression and differentiation. In *I. salapia*, the two lineages appear to hybridize  
39 only rarely, whereas in *O. onega* the hybrids are not only more common, but also genetically  
40 and phenotypically more variable. We also detected loci statistically associated with wing  
41 colour pattern variation, but in both species these loci were not over-represented among the  
42 candidate barrier loci, suggesting that traits other than wing colour pattern may be important  
43 for reproductive isolation. Our results contrast with the genomic patterns observed between  
44 hybridizing lineages in the mimetic *Heliconius* butterflies, and call for a broader investigation  
45 into the genomics of speciation in Ithomiini - the largest radiation of mimetic butterflies.

46

47 **Keywords.** Hybridization, Ithomiini, introgression, differentiation, admixture mapping,  
48 mimicry

49

50 **Introduction**

51           Speciation is the ultimate process responsible for the considerable biological diversity  
52 observed on Earth. Hybrid zones, whereby divergent lineages come into contact and  
53 potentially hybridize, can provide insights into the mechanisms involved in population  
54 differentiation and reproductive isolation, and ultimately speciation (Barton & Hewitt, 1989;  
55 Ravinet et al., 2017; Safran & Nosil, 2012). When hybrid zones span an environmental  
56 transition, populations across the hybrid zone diverge not only because of genetic drift but  
57 also due to local adaptation to different environments. Over time, drift and selection can lead  
58 to the emergence of barriers to gene flow that increase reproductive isolation, resulting in  
59 heterogeneous patterns of differentiation and introgression across the genome (Barton &  
60 Bengtsson, 1986; Ravinet et al., 2017; Safran & Nosil, 2012). Genomic regions with low rates  
61 of introgression are more likely to be associated with divergent selection and reproductive  
62 isolation (Gompert & Buerkle, 2009; *Heliconius* Genome Consortium, 2012; Mallet, 2005;  
63 Mallet & Barton, 1989; Jay et al., 2018). Assessing the genetic structure of hybrid zones can  
64 therefore shed light on the evolutionary processes at play during the early stages of speciation  
65 by revealing the number and distribution of loci presenting deviant patterns of differentiation  
66 and introgression compared to the genome-wide average (Bierne, Welch, Loire, Bonhomme,  
67 & David, 2011). Additionally, while genetic mapping of adaptive traits has classically relied  
68 on controlled crosses, which cannot be performed in many organisms, hybrid zones enable the  
69 application of admixture mapping approaches that take advantage of natural mixing and  
70 recombination to investigate the genetic basis underlying adaptive phenotypic variation  
71 (Buerkle & Lexer, 2008; Gompert & Buerkle, 2013; Pallares, Harr, Turner, & Tautz, 2014).

72

73 Many studies have focused on hybrid zones to unravel the processes generating local  
74 adaptation (e.g. Jones et al., 2012; Larson, Andrés, Bogdanowicz, & Harrison, 2013; Soria-  
75 Carrasco et al., 2014) and reproductive isolation (e.g. Christe et al., 2016; Teeter et al., 2008)

76 and have revealed different patterns (Barton & Hewitt, 1985, 1989; Gompert & Buerkle,  
77 2009; Kronforst et al., 2013; Rieseberg, Whitton, & Gardner, 1999; Teeter et al., 2010; Via &  
78 Hawthorne, 2002). These differences may stem from differences in the organisms studied, but  
79 may also stem from differences in the environmental conditions faced by populations of these  
80 organisms, such that comparative interpretations are rather limited. To investigate the  
81 repeatability of genetic and phenotypic differentiation, reproductive isolation and  
82 introgression patterns across incipient species diverging under similar environmental  
83 conditions are needed. Suture zones are areas where multiple recently diverged pairs of taxa  
84 come into contact and hybridize (Remington, 1968), and typically span a sharp environmental  
85 gradient or a dispersal barrier (Dasmahapatra, Lamas, Simpson, & Mallet, 2010; Endler,  
86 1977; Moritz et al., 2009). With replicated pairs of divergent and hybridizing lineages, suture  
87 zones offer an exceptional opportunity to compare levels and patterns of hybridization and  
88 reproductive isolation in relation to genomic and phenotypic divergence in a common  
89 environmental setting (Moritz et al., 2009; Nosil, Funk, & Ortiz-Barrientos, 2009; Rissler &  
90 Smith, 2010).

91 Müllerian mimicry in butterflies, in which multiple defended species locally converge  
92 on warning wing colour patterns and form mimicry 'rings' (Bates, 1862; Muller, 1879),  
93 provides an excellent system to unravel the mechanisms underlying adaptation and speciation.  
94 Two large neotropical mimetic butterfly tribes, Heliconiini and Ithomiini (Nymphalidae, 77  
95 and 393 species, respectively) are particularly well suited. Heliconiine and ithomiine species  
96 typically comprise multiple geographical subspecies that differ in colour patterns (Brown,  
97 Sheppard, & Turner, 1974). Because warning colour patterns in mimetic butterflies are under  
98 strong positive frequency-dependent selection locally (Kapan, 2001; Mallet & Barton, 1989),  
99 divergent mimetic subspecies are often separated by narrow hybrid zones maintained by  
100 migration-selection balance (Mallet & Barton, 1989). Mimicry generates postzygotic

101 reproductive isolation via higher predation on intermediate-patterned, non-mimetic hybrids  
102 (Merrill et al., 2012) and prezygotic reproductive isolation if there is also assortative mating  
103 for colour pattern among subspecies (Jiggins, Naisbit, Coe, & Mallet, 2001; McClure et al.,  
104 2019; Merrill et al., 2011; 2012). Mimicry is therefore a strong ecological driver of speciation,  
105 and is believed to have triggered the diversification of large radiations of heliconiine and  
106 ithomiine butterflies (Jiggins et al., 2001; Kozak et al., 2015). Studies of genetic  
107 differentiation and the basis of colour pattern variation in mimetic butterflies have almost  
108 exclusively focused on heliconiine butterflies (particularly the genus *Heliconius*), where a few  
109 major-effect genes (dubbed the mimicry ‘toolkit’, (Joron et al., 2006)) have been found to  
110 control wing pattern variation (Martin et al., 2012; Mazo-Vargas et al., 2017; Nadeau et al.,  
111 2016; Reed et al., 2011; Westerman et al., 2018) and to be highly differentiated across hybrid  
112 zones, while the rest of the genome seems highly permeable (Nadeau et al., 2014). By  
113 contrast, because of practical limitations (difficulties in maintaining captive populations and  
114 making controlled crosses), much less is known about population genetics of Ithomiini  
115 species (but see Dasmahapatra, Lamas, Simpson, & Mallet, 2010; McClure & Elias, 2016;  
116 McClure et al., 2019), let alone of the genetics of wing pattern variation. Yet, Ithomiini  
117 numerically dominate forest communities of day-flying Lepidoptera and are believed to be  
118 some of the main drivers of both Müllerian and Batesian mimicry (whereby palatable species  
119 mimic unpalatable aposematic species) among Lepidoptera in the Neotropics (Bates, 1862;  
120 Beccaloni, 1997; Muller, 1879). Because of the ecological importance of Ithomiini, shedding  
121 light on how populations are structured across hybrid zones and elucidating the genetic basis  
122 of wing pattern variation would significantly advance our understanding of adaptation and  
123 speciation in mimetic butterflies.

124

125           The foothills of the Andes in the region of Tarapoto are transitional between lowland  
126 rainforest and mid-elevation mountain forest. This area is a major suture zone for a range of  
127 organisms (Roberts et al., 2006; Smith et al., 2014; Weir, 2006) including heliconiine and  
128 ithomiine mimetic butterflies (Dasmahapatra, Lamas, Simpson, & Mallet, 2010; Nadeau et  
129 al., 2014; Whinnett et al., 2005) that harbour divergent wing colour patterns across the suture  
130 zone. Here we take advantage of the Tarapoto suture zone to assess the patterns of genomic  
131 and phenotypic divergence and infer the extent of reproductive isolation across the hybrid  
132 zone for two widespread ithomiine species, *Ithomia salapia* and *Oleria onega*, that each  
133 harbour divergent wing colour patterns across the Tarapoto suture zone. The two species have  
134 broadly similar life histories (e.g., forest habitats, mimicry, Solanaceae hostplants) and  
135 although they are somewhat differently distributed throughout the Neotropics, in the area of  
136 Tarapoto their populations have similar distributions. In this area, *I. salapia* comprises two  
137 subspecies: *I. salapia aquinia*, on the Amazonian side, which has a transparent yellow colour  
138 pattern surrounded by an orange and black line with small white dots; and *I. salapia derasa*,  
139 on the Andean side above about 500m alt., has a similar yellow pattern but surrounded by a  
140 thick black line with large white dots (Figure 1). In addition to being found on the Amazonian  
141 side of the Escalera mountains, *I. salapia aquinia* is also found on the other side of the  
142 mountains, in the lowlands of the Río Mayo valley near Tarapoto.

143           On the Andean side (including in the lowlands of the Río Mayo) *O. onega* ssp. nov. 2  
144 has translucent white wings with black patterning that splits the apical part of the forewing  
145 into two white ‘windows’, while in the Amazonian subspecies *O. onega janarilla* the  
146 forewing black patterning nearly splits the apical part of the forewing into four windows  
147 (Figure 1).

148           Thus, whereas *I. salapia* has a strictly altitude-based distribution of populations, *O.*  
149 *onega* has populations that differ geographically East-West, independently of altitude. For

150 each species, the two subspecies belong to distinct mimicry rings, which they numerically  
151 dominate. Therefore, *I. salapia* and *O. onega* likely play a major role in divergence and  
152 maintenance of their respective mimicry rings. Individuals with intermediate patterns are  
153 sometimes found in the contact zone, suggesting that occasional interlineage hybrids are  
154 produced.

155

156 In this paper we carry out population genomic analyses and quantify wing colour  
157 pattern variation in samples from Andean, Amazonian and intermediate populations of *I.*  
158 *salapia* and *O. onega* to address the following questions: (1) what are the overall patterns of  
159 differentiation, admixture and introgression between subspecies for each taxon pair? (2) To  
160 what extent does introgression vary across the genome, and are genetic regions associated  
161 with colour pattern among those that exhibit higher differentiation and reduced introgression?  
162 (3) How repeatable are the patterns of differentiation, introgression and genotype-phenotype  
163 association across the two taxon pairs?

164

## 165 **Material and Methods**

### 166 *Sampling*

167 Sampling was performed in five study sites in the region of Tarapoto in Peru (Figure 1a;  
168 details in Supplementary Table 1: gives each site, GPS coordinates and the number of each  
169 sex of *I. salapia* and *O. onega* sampled, before and after filtering). One hundred and twelve  
170 (112) *I. salapia* specimens were sampled from five localities, and 149 *O. onega* specimens  
171 were sampled in five localities.

172

### 173 *Genotyping by sequencing (GBS)*



174 DNA was extracted from ¼ of thorax of each individual using the Qiagen DNeasy blood and  
175 tissue kit, following the manufacturer protocol. We generated reduced genomic complexity  
176 libraries for each specimen using a GBS (genotyping by sequencing) approach (Gompert et  
177 al., 2012; Parchman et al., 2012). Briefly, genomic DNA was digested with the restriction  
178 endonucleases EcoRI and MseI and resulting fragments were ligated to double-stranded  
179 adaptor oligonucleotides. These adaptors consisted of the Illumina sequencing priming sites  
180 followed barcodes that allow for the identification of sequences for each individual. These  
181 barcodes allowed us to multiplex all individuals into one library. Sequencing of the library  
182 was completed by the National Center for Genome Research (Santa Fe, NM, USA) on an  
183 Illumina HiSeq platform; 100 base single-end sequencing reads were generated.

184

#### 185 *SNP calling*

186 First, sequencing primers were removed, sequences were demultiplexed and associated with  
187 each individual based on internal barcode sequences. SNP-calling was performed on samples  
188 from each species separately using `DiscoSnp-RAD`, a *de novo* reference-free and assembly-  
189 free method (Gauthier et al., 2017; Uricaru et al., 2015). SNPs are identified from particular  
190 arrangements in the De Bruijn graph built using a k-mer size of 31 and a minimal coverage of  
191 2 for each allele (Gauthier et al., 2017; Uricaru et al., 2015). Individuals with more than 90%  
192 missing genotypes were excluded (Supplementary Table 1) resulting in a final dataset  
193 consisting of 105 samples for *I. salapia* and 142 for *O. onega*. SNPs scored in at least 80% of  
194 the samples (i.e. sites with < 20% missing data) and with a minor allele frequency above 0.01  
195 were retained using `vcftools` (Danecek et al., 2011) resulting in a dataset of 17,779 SNPs  
196 for *I. salapia* and 15,894 SNPs for *O. onega*.

197

198 *Population structure analyses*

199 Population genetic structure was investigated using a subset of SNPs, where only one SNP  
200 per GBS locus was considered so as to minimize the effects of linkage disequilibrium that  
201 would occur within loci, as often recommended (Falush, Stephens, & Pritchard, 2003). A total  
202 of 8,219 SNP for *I. salapia* and 5,133 SNP for *O. onega* were retained. To investigate genetic  
203 structure, we used principal component analysis implemented for genetic data in the  
204 adegenet R package (Jombart & Ahmed, 2011). We used Bayesian admixture analysis  
205 implemented in Structure (Pritchard, Stephens, & Donnelly, 2000) to estimate admixture  
206 proportions, that is, the proportion of each individual's genome inherited from each of  $K$   
207 hypothetical source populations. We ran analyses with  $K$  from 1 to 6 with 3 independent  
208 Markov chains each, using 200,000 steps and including 10,000 burn-in steps. We checked the  
209 results obtained in each run to verify convergence of the chains to a stable posterior  
210 distribution. The most likely number of clusters was identified using Evanno's method  
211 (Evanno, Regnaut, & Goudet, 2005) implemented in Structure Harvester (Earl &  
212 vonHoldt, 2012).

213

214 *Genome-wide introgression and estimates of differentiation*

215 To investigate introgression among each population pair and to search for loci potentially  
216 associated with reproductive isolation, we used a genomic cline approach using bgc  
217 (Gompert & Buerkle, 2012). Loci acting as barriers to gene flow and linked regions should  
218 exhibit reduced introgression into the foreign genomic background. Locus-specific  
219 introgression is characterized by the probability  $\phi$  of being inherited from a given parental  
220 population (here, the Amazonian lineage; the probability of being inherited from the Andean  
221 lineage is therefore  $1 - \phi$ ). These probabilities are compared to the genome-wide average

222 probability, which corresponds to the hybrid index. Introgression patterns can be summarized  
223 by two locus-specific genomic cline parameters:  $\alpha$ , the genomic center parameter, and  $\beta$ , the  
224 genomic cline rate parameter. The genomic cline center parameter  $\alpha$  specifies an increase  
225 (positive values of  $\alpha$ ) or decrease (negative values of  $\alpha$ ) in the probability of ancestry of the  
226 focal population (here, the Amazonian lineage). Positive or negative  $\alpha$  values denote an  
227 asymmetry in the direction of introgression with hybrids having increased or decreased  
228 ancestry from one or the other ancestral lineage, respectively. The genomic cline rate  
229 parameter  $\beta$  specifies the cline steepness, with an increase (positive values of  $\beta$ ) or decrease  
230 (negative values of  $\beta$ ) in the rate of transition from low to high probability of ancestry  
231 (Gompert & Buerkle, 2011). Positive or negative  $\beta$  values are associated with a high or low  
232 level of gene flow, respectively. We estimated the posterior probability distribution of hybrid  
233 indices and cline parameters with `bgc`. MCMC of 50,000 steps including 10,000 burn-in  
234 steps for *I. salapia* samples and 100,000 with 30,000 burn-in steps for *O. onega* samples were  
235 used to reach mixing, and convergence was verified graphically by plotting log-likelihood  
236 distributions. For a given SNP, outlier introgression from the genome-wide average was  
237 identified as credible when the 95% credible intervals of the cline parameters  $\alpha$  and  $\beta$   
238 excluded zero. These SNPs deviating from global pattern should reflect unusual patterns of  
239 evolution acting on these loci. We used the admixture model implemented in `entropy`  
240 (version 1.2) to estimate admixture proportions and intertaxon ancestry (Gompert et al. 2014).  
241 This model explicitly estimates the proportion of each individuals' genome where the two  
242 allele copies are derived from different source populations (i.e., the proportion of the genome  
243 with intertaxon ancestry). `entropy` also incorporates uncertainty in genotypes due to limited  
244 sequence coverage and sequencing errors. We fit the model using Markov chain Monte Carlo  
245 (MCMC). We ran the MCMC algorithm three times with 15,000 iterations following a 5,000

246 iteration burnin, and with a thinning interval of 5. We assumed the number of source  
247 populations ( $K$ ) was two.

248

249 Genome-wide weighted and per-SNP genetic differentiation  $F_{ST}$  were estimated using  
250 Weir and Cockerham's method (Weir & Cockerham, 1984) implemented in `vcftools`  
251 (Danecek et al., 2011). To do so, only samples from parental lineages, that is, samples from  
252 the initial localities distant from the hybrid zone, were kept. To identify outlier SNPs with  
253 elevated genetic differentiation, the threshold was fixed to the 95th percentile of  $F_{ST}$   
254 distribution obtained by random sampling with replacement of 100,000 values.

255

#### 256 *Wing pattern analyses*

257 Photographs of dorsal and ventral sides of detached wings of 90 and 94 of the  
258 genotyped specimens of *I. salapia* and *O. onega*, respectively, were taken with a Nikon D90  
259 digital camera and a 105 mm lens on a white background with a piece of millimeter paper for  
260 scale. For each specimen, dorsal and ventral patterns of fore- and hindwings were quantified  
261 using Colour Pattern Modeling (CPM, (Le Poul et al., 2014) as follows: wings were first  
262 extracted from their background, resulting in eight images per specimen (2 wings [forewing  
263 and hindwing] x 2 lateral sides [left/right] x 2 vertical sides [ventral/dorsal]); for each image,  
264 wing pattern was described by semi-automatically categorizing wings into a finite number of  
265 colours (yellow, black, orange and white for *I. salapia*; white, black and orange for *O. onega*).  
266 Damaged wings were discarded, and when left and right wings were available only one  
267 randomly chosen side was used in subsequent analyses. Homologous wings were then aligned  
268 according to both shape and pattern (Le Poul et al., 2014), and a binary principal components  
269 analysis based on one-hot encoding of colours (i. e., where each colour is encoded by a string

270 of bits among which only one takes the value 1) was performed on the colour of homologous  
271 pixels shared by all wings. Principal component (PC) scores were used as a quantitative  
272 measure of colour pattern in subsequent analyses.

273

#### 274 *Admixture association mapping*

275 To identify SNPs associated with variation in wing patterns, we performed association  
276 mapping using the Genome-wide Efficient Mixed Model Association tool (GEMMA) (Zhou &  
277 Stephens, 2012, 2014). We used the multivariate linear mixed model (mvLMM) to test  
278 marker associations with multiple phenotypes and to estimate genetic correlations among  
279 complex phenotypes. To do so, we retained all wing pattern PCs that explained more than 1%  
280 of the variation in each species as variables. This included 14 variables accounting for 57.1%  
281 of the variation in wing pattern for *I. salapia* and 18 variables explaining 54.9% of the  
282 variation for *O. onega*. Both the variation linked to sex and the confounding effect of  
283 population structure (Freedman et al., 2004; Price et al., 2006) were integrated into the models  
284 by implementing a relatedness matrix between individuals generated using GEMMA (Zhou &  
285 Stephens, 2012) and the first population structure PC (obtained using *adegenet* R package  
286 (Jombart & Ahmed, 2011)) as a covariate. Analyses were carried out using the option `-lmm 1`  
287 to perform a Wald test evaluating the probability of the null hypothesis that the marker effect  
288 sizes for all phenotypes were zero. For the identification of SNPs significantly associated with  
289 wing pattern, the threshold was fixed to a p-value adjusted using (i) a classical Bonferroni  
290 correction, which divides the significance threshold by the number of multiple comparisons,  
291 that is, the number of molecular markers multiplied by the number of variables, and (ii) using  
292 the false discovery rate (FDR) method (Benjamini & Hochberg 1995). We considered SNPs  
293 identified by both of these correction methods as significantly associated with wing pattern.

294 To test whether outlier SNPs by the three approaches, i.e. differentiation genome-scan,  
295 introgression pattern and admixture mapping, are distributed randomly or if there is  
296 enrichment in shared outlier SNPs, we used two methods: a Pearson's Chi-squared test to  
297 compare shared outlier to a random distribution and a bootstrap of 1,000 random samplings  
298 among SNPs to estimate confidence interval of such shared SNPs.

299

### 300 *Similarities with other Lepidoptera genomes*

301 Loci containing SNPs identified as outliers in the genetic differentiation or the  
302 differential introgression approaches were screened by BLAST against all annotated butterfly  
303 reference genomes in LepBase v4 (Challis, Kumar, Dasmahapatra, Jiggins, & Blaxter, 2016)  
304 to investigate the gene content of homologous genomic regions. This was performed using the  
305 BLASTn tool available on the LepBase platform (Priyam et al., 2019). Best hits, their location  
306 in reference genomes and genes were then investigated manually.

307

## 308 **Results**

309 Our reduced complexity genotype by sequencing approach coupled with Illumina sequencing  
310 produced 77.8 million reads distributed relatively evenly between samples with a mean of  
311 340,940 reads per individual (sd: 157,991) for *I. salapia* samples and a mean of 270,602 reads  
312 per individual (sd: 103,734) for *O. onega*. From this sequencing data, SNP calling and  
313 filtering steps resulted in final datasets of 17,779 SNPs from 6,972 loci for *I. salapia* samples  
314 and 15,894 SNPs from 4,524 loci for *O. onega* samples.

315

### 316 *Population genetic structure*

317 For *I. salapia* we considered two parental lineages, an Amazonian lineage corresponding to  
318 subspecies *aquinia* sampled from two sites, Km-26 Yurimaguas-Tarapoto (1) and San Miguel  
319 de Achinamiza (2), and an Andean lineage corresponding to subspecies *derasa* and sampled  
320 from one site Puente Aguas Verdes (5). Between these sites a zone that is geographically and  
321 altitudinally intermediate and where those lineages are in contact was sampled at two sites  
322 (sites Km-42 Tarapoto-Yurimaguas (i3) and La Florida (i4), hybrid zone) (Figure 1a). The  
323 genetic structure, identified by multivariate analyses on genetic data (Figure 2a) as well as  
324 *Structure* (Figure 2b), highlight that the samples likely segregate in 3, best clustering, or 2  
325 groups (Evanno's method: higher  $\Delta K$  of 5037.42 for  $K=3$  and 718.12 for  $K=2$ ). These results  
326 shows that the two parental lineages are distinct and show a low level of admixture. They  
327 have a weighted genome-wide differentiation  $F_{ST}$  of 0.177 between the two. In the  
328 intermediate populations, we did not find putative F1 hybrids (i.e. individuals with hybrid  
329 index close to 0.5 and high intertaxon ancestry). Rather, four individuals (subpopulation 3.1,  
330 Figure 2b) were genetically similar to individuals from the parental Amazonian *aquinia*  
331 lineage, and the 28 other samples had equal levels of admixture with the majority of their  
332 genetic content associated with the Andean *derasa* population (Figure 2b). Hybrid indices  
333 estimated for these individuals is also indicative of this (Figure 2c).

334 The distribution of *O. onega* hybrids in the study area is somewhat similar to that observed in  
335 *I. salapia*. The genetic structure, identified by multivariate analyses on genetic data (Figure  
336 2a) as well as *Structure* (Figure 2b), highlight the samples likely segregate in 2, best  
337 clustering, or 3 groups (Evanno's method: highest  $\Delta K$  of 9887.07 for  $K=2$  and 7.76 for  $K=3$ ).  
338 This species also consists of two parental lineages corresponding to an Amazonian  
339 subspecies, *O. onega janarilla*, collected from two sites, Km-26 Yurimaguas-Tarapoto (1)  
340 and San Miguel de Achinamiza (2) and an Andean subspecies, *O. onega* ssp. nov. 2  
341 (Gallusser, 2002; Dasmahapatra, Lamas, Simpson, & Mallet, 2010), sampled at Puente

342 Serranoyacu (5). In addition to these sites, a geographically and altitudinally intermediate  
343 zone was also sampled (sites Shapaja-Chazuta (o3) and a site spanning Quebrada Yanayacu to  
344 Laguna del Mundo Perdido (o4), hybrid zone) (Figure 1b). The two parental lineages are  
345 genetically divergent with a weighted genome-wide differentiation  $F_{ST}$  of 0.372, more than  
346 twice as high as between *I. salapia* parental lineages. The samples from the hybrid zone  
347 comprise a mix of individuals with low and intermediate levels of admixture. Most  
348 individuals have a low level of admixture (39 out of 46 had  $q < 0.2$ ), and are genetically  
349 closest to the Amazonian parental lineage. The stronger link with the Amazonian lineage  
350 suggests a directionality in hybridization different from that of the *I. salapia* hybrid zone.  
351 Three individuals show hybrid indices that suggest almost equal contributions from each  
352 parental lineage (Figure 2a,b,c). One of these has a high level of intertaxon ancestry, which  
353 suggests it is an F1 hybrid. The two other individuals have lower heterozygosity, which is  
354 consistent with recent backcrossing. In conclusion, both species show some evidence of gene  
355 flow and introgression, but both also exhibit strongly bimodal phenotypes (sensu Jiggins &  
356 Mallet, 2000) in the region of the hybrid zone, suggesting strong reproductive isolation in  
357 both species. However, *O. onega* displays somewhat more evidence of ongoing hybridization  
358 and gene flow than *I. salapia*.

359

### 360 *Genomic patterns of introgression and differentiation*

361 Introgression varied across the genome for each taxon pair, with distinct patterns of  
362 introgression for the two studied species, *I. salapia* and *O. onega*, as demonstrated by the  
363 distributions of the genomic cline center ( $\alpha$ ) and rate parameters ( $\beta$ ) (Figure 3). In each  
364 species the center parameter ( $\alpha$ ) is highly variable, with point estimates (posterior median)  
365 ranging from -3.067 to 2.864 for *I. salapia* and from -5.785 to 5.907 for *O. onega*. With  
366 respect to  $\alpha$ , many loci show introgression patterns that differ credibly from the genome-wide



367 average. Loci with positive center parameter  $\alpha$  are more likely to be inherited from the  
368 Amazonian parental lineage than the rest of the genome. Conversely, loci with negative  $\alpha$  are  
369 more likely to be inherited from the Andean lineage. For *I. salapia*, 2125 SNPs (11.95 % of  
370 all SNPs) have a center parameter  $\alpha$  that differ from the genome-wide average, consistent  
371 with different levels of introgression than the average of the rest of the genome. Among the  
372 SNPs with credible evidence of differential introgression, most of them (1637 out of 2125, i.  
373 e., 77%) have excess ancestry from the Amazonian populations whereas the genome-wide  
374 average is more closely associated with the Andean population (Figure 2b,c). In *O. onega*,  
375 where intermediate populations are genetically closer to the Amazonian lineage, 2146 SNPs  
376 (13.50 % of all SNPs) have a center parameter  $\alpha$  that significantly deviates from the genome-  
377 wide average. The distribution is reversed compared to *I. salapia*, however, with most of  
378 those SNPs (1406 out of 2146, i. e., 66%) having a lower probability of being inherited from  
379 the Amazonian parental lineage. This is expected, as there is more statistical power to detect  
380 differential introgression of alleles of the less common (i.e., minor) ancestry type.

381 Regarding the genomic cline rate parameter ( $\beta$ ), the profiles for the two species are markedly  
382 different. In *I. salapia* species,  $\beta$  hardly shows any variation, ranging from -0.681 to 0.738,  
383 whereas the variation observed in *O. onega* is higher by tenfold, ranging from -7.710 to 8.440.  
384 Such a large variation in *O. onega* is probably due to the heterogeneity of the hybridization  
385 profiles observed in the hybrid zone (Figure 2b). While in *I. salapia* no SNPs are different  
386 from the genome-wide expectation, in *O. onega*, 1274 SNPs have a genomic cline rate ( $\beta$ )  
387 credibly different from the genome-wide pattern, with 447 and 827 SNPs having higher and  
388 lower values, respectively. These 447 SNPs with steeper introgression patterns than the  
389 genome-wide average are characteristic of SNPs putatively associated with barrier loci (i.e.,  
390 in LD with barrier loci).

391 This difference observed between *I. salapia* and *O. onega* can be explained, at least in part, by  
392 the fact that there is hardly any variation among hybrids in *I. salapia* in our sampling. Perhaps  
393 an even larger sample than at present would show additional variation. In any case, the  
394 absence of variation in the *I. salapia* hybrids is a result in itself but limits the capacity to  
395 detect variation in patterns of introgression.

396 Genetic differentiation ( $F_{ST}$ ) between parental lineages was heterogeneous across the genome,  
397 ranging from ~0 to 1.000 with a weighted mean value of 0.177 for *I. salapia* and from ~0 to  
398 1.000 with a weighted mean value of 0.372 for *O. onega*. The genome scan also identifies  
399 outlier SNPs that deviate from the genome-wide distribution and have unusually high levels  
400 of differentiation. In *I. salapia*, the 95th percentile threshold corresponds to an  $F_{ST}$  value of  
401 0.415, and was exceeded by 890 SNPs. In *O. onega*, the 95th percentile threshold corresponds  
402 to an  $F_{ST}$  value of 0.686, and was exceeded by 795 SNPs.

403

#### 404 *Phenotypic variation*

405 For both species, the first principal component on colour pattern separates Andean from  
406 Amazonian lineages (Fig. 4). However, the two species differ in where along this axis  
407 specimens from intermediate populations fall. For *I. salapia*, most specimens in the hybrid  
408 zone cluster with the Andean *I. salapia derasa*, while only four (with a predominantly  
409 Amazonian genetic background) cluster with Amazonian *I. salapia aquinia* (Figure 4). No  
410 individual in this sample has a markedly intermediate color pattern along this first principal  
411 component. By contrast, most *O. onega* from the hybrid zone have an intermediate position  
412 along the first principal component. For both species, the second axis highlights variation  
413 associated with sex and as a result males and females are segregated along this axis. While  
414 sexual dimorphism is moderate and of the same magnitude in both lineages of *O. onega*, it is  
415 more pronounced in the Andean lineage *I. salapia derasa* and virtually absent in the

416 Amazonian lineage *I. salapia aquinia*. Sex was therefore included as a factor in our  
417 phenotype-genotype analyses, along with genetic structure.

418

#### 419 *Phenotype-genotype relationship and association mapping*

420 Despite the low variability among hybrid individuals from the hybrid zone, especially for *I.*  
421 *salapia*, we attempted to associate genetic variation in specific SNPs to wing pattern  
422 variation. All principal components (PCs) explaining at least 1% of total phenotypic variation  
423 were included in association mapping (i.e. 14 variables for *I. salapia*, jointly explaining  
424 57.1% of the variance, and 18 for *O. onega*, jointly explaining 54.9% of the variance).  
425 Association mapping using GEMMA revealed several PCs for which a large phenotypic  
426 variation is explained, specifically more than 80% phenotypic variation explained (pve) for  
427 7/14 PCs for *I. salapia* and for 4/18 PCs for *O. onega*. When combining all PCs that were  
428 retained (i.e., all those that explained at least 1% of the phenotypic variation), 59.3% of the  
429 phenotypic variation is explained for *I. salapia* and 26.3% for *O. onega* (Supplementary  
430 Figure 2). The PCs explaining most genetic variation are also those harbouring the largest  
431 proportions of wing pattern variation. Specifically, 84.3% of the wing pattern variation is  
432 explained for *I. salapia* and 65.3% for *O. onega*. The multivariate linear mixed model of  
433 GEMMA performs tests to evaluate the probability that SNPs are associated with phenotypic  
434 variation and outputs the corresponding p-value resulting from a Wald test. Retaining  
435 significant SNPs concurrently in Bonferroni p-value correction and FDR approach, 88 SNPs  
436 (0.49% of all SNPs) were significantly associated with wing patterns in *I. salapia* and 109  
437 SNPs (0.69% of all SNPs) in *O. onega* (Figure 5).

438 We then focused on the differentiation and introgression patterns of SNPs associated with  
439 wing pattern. A very small number of SNPs, 17 for *I. salapia* and 4 for *O. onega*, combine

440 strong association with wing pattern and high levels of differentiation, but in *I. salapia* the  
441 SNP with the strongest association with wing pattern is also an outlier in genome scan for  
442 differentiation (Figure 5).

443 With all of these approaches combined, we observe both differences and similarities between  
444 *I. salapia* and *O. onega* in the number of SNPs similarly identified as outliers by multiple  
445 approaches. The proportion of SNPs combining both high differentiation levels ( $F_{ST}$ ) and  
446 differential introgression ( $\alpha$ ), and which are characteristic of loci potentially involved in  
447 adaptation in hybrid samples, are of the same order in *I. salapia* and in *O. onega* (1.81%,  
448 321/17,779, for *I. salapia*, and 1.59%, 253/15,894, for *O. onega*, Figure 6), and higher than  
449 expected at random (Pearson's Chi-squared test, p-value = 1.32e-114 and 95% CI = [103, 135]  
450 for *I. salapia* and Pearson's Chi-squared test, p-value = 2.99e-54 and 95% CI = [92, 123] for  
451 *O. onega*). SNPs previously identified as potentially involved in adaptation and adaptive  
452 introgression, combining high differentiation levels ( $F_{ST}$ ) and differential introgression ( $\alpha$ ), do  
453 not have a specific enrichment in SNPs significantly associated with wing pattern. In *I.*  
454 *salapia* and *O. onega* the numbers of SNPs that fit this description are low, respectively only  
455 two and one SNPs, and do not differ from a random distribution (Pearson's Chi-squared test,  
456 p-value = 0.74 and 95% CI = [0, 4] for *I. salapia* and Pearson's Chi-squared test, p-value =  
457 0.57 and 95% CI = [0, 4] for *O. onega*). The main difference between the two species consists  
458 in the SNPs with differential positive genomic cline rate values ( $\beta$ ) and potentially involved in  
459 reproductive isolation. None of the SNPs in *I. salapia* have positive  $\beta$  while a non-trivial  
460 proportion do in *O. onega*, i.e. 447 SNPs or 2.81%. Among these SNPs only a small fraction  
461 is also significantly associated with wing pattern variation (5) and not enriched compared to a  
462 random distribution (Pearson's Chi-squared test, p-value = 0.26 and 95% CI = [1, 6]).  
463 Moreover, among the SNPs involved in both, high differentiation level and positive  $\beta$  (71)

464 and potentially involved in reproductive isolation, none of them is associated with wing  
465 pattern variations (Figure 6).

466

#### 467 *Similarities with other Lepidoptera genomes*

468 We used BLASTn to investigate the potential functional roles of the loci carrying the SNPs  
469 highlighted by the approaches listed above. We identified homologous regions in the *D.*  
470 *plexippus* genome for loci containing SNPs significantly associated with wing patterns (12/67  
471 loci for *I. salapia* and 21/99 for *O. onega*; Supplementary Table 3). None of the genes known  
472 to control colour pattern variation in Lepidoptera and identified in the *D. plexippus* genome,  
473 i.e. *optix*, *cortex*, *WntA*, *ebony* and *aristaless*, were identified.

474 On the other side the BLASTn of loci with SNPs potentially involved in adaptation and  
475 adaptive introgression or reproductive isolation highlighted candidate genomic region and  
476 gene in the genome of *D. plexippus* (37/277 loci for *I. salapia* and 66/218 for *O. onega*  
477 potentially involved in adaptation and adaptive introgression and 73/389 loci potentially  
478 involved in reproductive isolation for *O. onega*; Supplementary Table 2). We here report the  
479 list of scaffold containing these loci of interest which are potential candidates for genes  
480 involved in local adaptation and reproductive isolation, and on which further functional  
481 analyses could be performed to investigate underlying biological functions (Supplementary  
482 Table 2).

483

#### 484 **Discussion**

485 The comparison of genome-wide patterns of genetic differentiation, introgression and  
486 genotype-phenotype associations in two species, *I. salapia* and *O. onega*, that face similar  
487 environmental transitions revealed some surprisingly large phenotypic and genomic

488 differences. Below, we discuss potential reasons for the differences observed in light of  
489 biological and ecological information.

490

491 *Genomic and phenotypic differentiation patterns across the Tarapoto suture zone: similarities*  
492 *and differences*

493 Both *I. salapia* and *O. onega* are distributed across an important environmental gradient in the  
494 region of Tarapoto in Peru, and both species consist of an Andean and Amazonian lineage.

495 Our analysis of wing pattern variation confirms that Amazonian and Andean lineages of both  
496 species are phenotypically different (as is seen by the human eye) and also reveals a subtle  
497 sexual dimorphism not readily discernible.

498 Phenotypic differentiation between populations of each species is associated with strong  
499 overall genomic differentiation, especially in *O. onega*. These findings are consistent with  
500 those obtained by Dasmahapatra, Lamas, Simpson, & Mallet (2010) using four loci, which  
501 also revealed inter-lineage differentiation for these taxa, with the strongest genetic  
502 differentiation occurring in *O. onega*.

503 However, the genomic and phenotypic population structure of hybrid populations differ  
504 between *I. salapia* and *O. onega*. Firstly, while all but four of the *I. salapia* individuals  
505 sampled in the hybrid zone are genetically closer to the Andean population, most individuals  
506 in the *O. onega* hybrid populations we sampled are genetically closer to Amazonian  
507 populations. Secondly, one individual in *O. onega* is likely a F1, and two other individuals are  
508 recent backcrosses, while no such genetically intermediate individuals were found in our  
509 samples of *I. salapia*. Thirdly, the phenotypic structure of hybrid populations mirrors the  
510 genomic patterns. Along the first PC individuals in intermediate populations of *I. salapia* are  
511 phenotypically closest to the Andean parental lineage (*derasa*), to which they are also closest

512 genetically. In our sample, intermediate color patterns are not observed in these populations,  
513 nor in parental populations. By contrast, individuals in intermediate populations of *O. onega*  
514 have intermediate phenotypes between the two lineages, with a tendency to be closer to the  
515 Amazonian lineage (*janarilla*), to which they are also closest genetically.

516 Overall, the patterns detected suggest past gene flow in both species (most individuals have a  
517 similar, low hybrid index), with potentially more recent (but rare) gene flow in *O. onega* -  
518 although we cannot rule out the fact that we may have missed recent hybrids in *I. salapia*.  
519 Genomic differentiation across hybrid zones in Müllerian mimetic butterflies have mostly  
520 been documented in the genus *Heliconius*. While *Heliconius* sub-specific lineages sometimes  
521 exhibit high genome-wide differentiation across hybrid zones (Martin, Davey, Salazar, &  
522 Jiggins, 2019; Van Belleghem et al., 2018), this appears not to be the case in the Tarapoto  
523 suture zone. In this region, Nadeau *et al.* (2014) found that in phenotypically differentiated  
524 lineages of *H. erato* and *H. melpomene* only loci around pattern gene loci showed genetic  
525 differentiation, while the rest of the genome was highly permeable to gene flow, with  $F_{ST}$   
526 values ranging from 0.0112 to 0.0280 (see also Martin et al., 2013). This stands in stark  
527 contrast to the strong overall differentiation we revealed in ithomiine butterflies from the  
528 Tarapoto suture zone ( $F_{ST} = 0.177$  for *I. salapia* and  $F_{ST} = 0.372$  for *O. onega*).

529 While intermediate populations of *O. onega* show a high extent of genetic heterogeneity, in *I.*  
530 *salapia* all but four individuals from intermediate populations are remarkably similar in their  
531 genetic composition. This suggests that intermediate populations of *I. salapia* are hardly  
532 exchanging genes with Andean and Amazonian populations, and may be in the process of  
533 forming a distinct taxon.

534

535 *Genomic patterns of introgression*

536 Variation in introgression patterns across the genome can help pinpoint loci involved in  
537 adaptation and reproductive isolation (Gompert & Buerkle, 2011; Gompert et al., 2012;  
538 Gompert, Mandeville, & Buerkle, 2017). In particular, highly divergent SNPs with deviant  
539 genomic cline center parameters ( $\alpha$ ) or positive genomic cline rate parameter ( $\beta$ ) (i. e.,  
540 exhibiting a steep cline) should be more common in regions of the genome involved in local  
541 adaptation or reproductive isolation.

542 Here, intermediate populations of both *I. salapia* and *O. onega* present SNPs with outlier  
543 values in their genomic cline center parameters ( $\alpha$ ), meaning that these SNPs have an ancestry  
544 different from that of the average of the genome. The SNPs exhibiting deviant  $\alpha$  should be  
545 enriched for genomic regions involved in adaptation or reproductive isolation. Such SNPs  
546 (77.0%) are shifted towards Amazonian ancestry in *I. salapia*, whereas the majority of SNPs  
547 with deviant  $\alpha$  (65.5%) are shifted towards Andean ancestry in *O. onega*. While this may  
548 indicate introgression from the parental lineage that is least represented in the genomic  
549 background of intermediate populations, in our case such asymmetry may also result from a  
550 lower power to detect introgression from the dominant parental background. . Whether some  
551 of those SNPs result from adaptive introgression, as has been revealed in *Heliconius*  
552 butterflies (*Heliconius* Genome Consortium, 2012; Jay et al., 2018), warrants further study.

553 Patterns of the parameter cline rate  $\beta$  markedly differ between *I. salapia* and *O. onega*. While  
554 in *I. salapia* no SNPs show outlier cline steepness, in *O. onega* many SNPs show narrower or  
555 wider clines compared to the genome average. Overall, in *O. onega*, the distribution of  
556 genomic cline parameters is wider and more heterogeneous than in *I. salapia*, suggesting less  
557 constraints in the hybridization process. Such heterogeneity in *O. onega* allows the  
558 identification of loci with specific introgression levels. Highly divergent genomic regions that  
559 have low levels of introgression are likely associated with reproductive isolation (Gompert &  
560 Buerkle, 2011; Gompert et al., 2012). Low levels of introgression can be the result of several



561 evolutionary processes involving both extrinsic mechanisms, such as divergent selection and  
562 environment-dependent selection against hybrids, and intrinsic mechanisms such as an  
563 environment-independent reduced hybrid fitness caused by Bateson-Dobzhansky-Muller  
564 incompatibilities (Gompert & Buerkle, 2011; Gompert et al., 2012). Correlation of genetic  
565 patterns with other evidence (e. g., candidate traits) may shed light on the mechanisms of  
566 speciation and reproductive isolation (Ravinet et al., 2017).

567

### 568 *Genetic bases of colour pattern variation*

569 Our admixture mapping analysis revealed SNPs associated with color pattern in *I. salapia* (88  
570 SNPs, representing 0.49% of all SNPs) and *O. onega* (109 SNPs, representing less than  
571 0.69% of all SNPs).

572 In nymphalid butterflies, wing pattern variation can be explained by combinations of  
573 conserved pattern elements (Martin & Reed, 2014) and tends to be controlled by small  
574 numbers of loci (Van Belleghem et al., 2017; Zhang et al., 2017). Previous studies, including  
575 studies on mimetic *Heliconius* (Joron et al., 2006; Martin et al., 2012; Nadeau, 2016; Reed et  
576 al. 2011; Westerman et al., 2018) and *Papilio* (Timmermans et al., 2014) identified a list of  
577 candidate genes such as *WntA*, *optix*, *cortex*, *ebony* and *aristaless*. Some of these have been  
578 functionally characterized (Martin & Reed, 2014; Nadeau, 2016; Nadeau et al., 2016). A  
579 recent study on *D. plexippus*, the most closely related species to Ithomiini for which a  
580 reference genome is available, highlighted the role of *WntA* in vein shape (Mazo-Vargas et  
581 al., 2017).

582 None of our candidate loci correspond to genes known to be involved in wing colour pattern  
583 in other butterflies. This is likely due to the relatively low-resolution genotype-by-sequencing

584 approach adopted here, such that we may have missed gene regions that were not covered by  
585 our loci.

586 Moreover, only a small fraction of loci with SNPs associated with wing pattern (23.9% for *I.*  
587 *salapia* and 21.2% for *O. onega*) map to an orthologous region in the *D. plexippus* genome.  
588 This deficit is related to the relatively large divergence time between our focal species and *D.*  
589 *plexippus* (ca. 42 million years ago, Chazot et al., 2019), which limits our ability to find  
590 orthologous regions and more specifically to find regions involved in non-coding regulatory  
591 loci. We may therefore have missed loci that contain known genes involved in wing pattern  
592 development.

593 Finally, the extremely low level of hybridization observed in *I. salapia* reduces the statistical  
594 power of admixture mapping and hampers detection of genomic regions associated with wing  
595 pattern variation. The function of most regions identified in our analyses are unknown and  
596 represent a starting point for further analyses of these regions, as those regions may contain  
597 novel genes in these pathways.

598

#### 599 *Colour pattern and reproductive isolation*

600 Wing colour pattern is known to cause pre- and post-zygotic reproductive isolation in  
601 Müllerian mimetic butterflies (e. g., Chamberlain, Hill, Kapan, Gilbert, & Kronforst, 2009;  
602 Jiggins, Naisbit, Coe, & Mallet, 2001; Mallet & Barton, 1989; Merrill et al., 2012; Merrill et  
603 al., 2011; Naisbit, Jiggins, Linares, Salazar, & Mallet, 2002), including Ithomiini (McClure et  
604 al., 2019).

605 In our admixture mapping analysis, we found that only two and one of the significantly  
606 differentiated introgression outliers were also associated with wing pattern variation in *I.*  
607 *salapia* and *O. onega*, respectively. These figures do not differ from random expectations.

608 These results suggest that wing colour pattern may be moderately involved in reproductive  
609 isolation in both species, but since our genomic data do not cover the entire genome, we  
610 cannot rule out the fact that we may have missed some important loci involved in wing  
611 pattern coloration and with deviant genomic clines.

612 In mimetic butterflies, hybrid individuals with intermediate colour pattern may suffer more  
613 predation because they are not recognized as unpalatable (e. g., Merrill et al., 2012), which  
614 may in turn select for assortative mating for wing colour pattern through reinforcement (e. g.,  
615 Kronforst, Young, & Gilbert, 2007), resulting in reproductive isolation between  
616 phenotypically differentiated lineages. Whether individuals with intermediate phenotype  
617 suffer increased predation has never been tested in *I. salapia* and *O. onega*, but predation  
618 experiments on *Heliconius* species carried out in the same region demonstrated the ability of  
619 predators to discriminate fine phenotypic differences (Arias et al., 2016; Chouteau, Arias, &  
620 Joron, 2016). Assortative mating seems likely in *I. salapia* and *O. onega* (MM and ME, pers.  
621 obs.), and has been documented by genetic and phenotypic characterization of the reared  
622 offspring of females collected in hybrid populations of *O. onega* (De Silva, 2010: chapter 5).

623 There are fewer phenotypically intermediate individuals in *I. salapia* than in *O. onega*. This  
624 difference might be explained by the mimicry rings to which the two species belong. While  
625 the mimicry rings of *I. salapia* lineages are readily discriminated and show little variation  
626 within each mimicry ring, the forms *O. onega* belongs to are more variable with overlapping  
627 phenotypes (ME pers. obs.; Supplementary Figure 1). Because of the greater variation and  
628 overlap of the two *O. onega* mimicry rings in Tarapoto, selection against hybrids with  
629 intermediate phenotypes may be reduced compared with that in *I. salapia*, thereby allowing  
630 the persistence of greater levels of gene flow between lineages. Whether the absence of  
631 intermediate phenotypes in *I. salapia* is due to high mortality of hybrids through predation,

632 strong assortative mating, hybrid incompatibilities or all of these is currently unknown and  
633 deserves further examination.

634

635 *Other putative adaptive traits*

636 In both species, only a small number of SNPs potentially involved in adaptation or  
637 reproductive isolation (i. e., highly differentiated SNPs that show deviant  $\alpha$  or significantly  
638 positive  $\beta$ ) are also associated with wing pattern. This suggests that other traits may play a  
639 role in reproductive isolation. Because interactions with local host plants at the larval stage  
640 and the ability to fully exploit them often impact fitness in phytophagous insects (Simon et  
641 al., 2015), larval hostplant shifts are believed to be an important driver of reproductive  
642 isolation. However, in *O. onega* the two lineages utilize the same larval hostplants, *Solanum*  
643 *mite* and related *Solanum* sect. *Pteroidea* species (de-Silva, Vásquez, & Mallet, 2011;  
644 Gallusser, 2002). Similarly, *I. salapia derasa* larvae commonly feed on *Witheringia*  
645 *solanacea* (Beccaloni, 1997), a plant also used by *I. salapia aquinia* (JM, MM and ME,  
646 unpublished observations). Shifts in hostplant are therefore unlikely to explain divergence  
647 between lineages in either of these species, as is the case in another ithomiine genus,  
648 *Melinaea*, present in the same region (McClure & Elias, 2016).

649 The two lineages of *O. onega* have divergent egg-laying behavior: females of the Amazonian  
650 population (*janarilla*) lay eggs on the hostplants, while females of the Andean population  
651 (ssp. nov. 2) tend to lay eggs off the host plant (Gallusser, 2002). Eggs are typically laid up to  
652 0.5 m away from the nearest host plant individual, on twigs, leaf litter or live non-host plant,  
653 which reduces egg predation ( de-Silva, Vásquez, & Mallet, 2011). Differences in egg-laying  
654 behavior have been shown to cause reduced hybrid fitness in butterflies (McBride & Singer,  
655 2010). This could be the case here, too, if hybrid females lay eggs off the plant, and if first  
656 instar larvae are incapable of locating their host plant.

657 Other putative adaptive traits include adaptations to distinct habitats (higher elevations and  
658 cooler temperatures for Andean lineages) and potentially microhabitats where co-mimics are  
659 most abundant (e. g., Elias, Gompert, Jiggins, & Willmott, 2008).

660 Finally, as many butterfly species, Ithomiini probably rely on sexual pheromones during mate  
661 choice (Schulz et al., 2004), and differences in sexual pheromones may incur discrimination  
662 between lineages. Notably, putative male pheromones have been shown to differ between the  
663 two lineages of *O. onega* (Stamm, Mann, McClure, Elias, & Schulz, 2019).

664 The role of these traits in reproductive isolation remains to be further explored using both  
665 experimental and genomic approaches.

666

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676

677 **Data accessibility.** Sequence reads are archived at the NCBI SRA in the BioProject  
678 PRJNA575968. Scripts describing the whole analytic process have been uploaded to GitHub  
679 ([https://github.com/JeremyLGauthier/Scripts\\_Gauthier\\_et.al\\_2019\\_ME](https://github.com/JeremyLGauthier/Scripts_Gauthier_et.al_2019_ME)).

680

681 **Author contributions :** ME and ZG designed the study. LdS, JM , MM and ME performed  
682 sampling. LdS, AW, ZG and ME performed labwork. JG analysed the molecular data, with  
683 contributions from ZG, AW, CL and FL. ME, JG, CH and YLP analysed phenotypic data. All  
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- 969

970 **Figure captions :**

971

972 **Figure 1.** The study organisms and sites studied in N.E. Peru. a. Photos of representative  
973 specimens from each population of the two studied species (dorsal side shown against a dark  
974 background to highlight transparency and ventral side shown against a white background to  
975 highlight colour pattern). b. Sampling sites for *I. salapia* populations (top) with Amazonian  
976 sites in red (1) Km-26 Yurimaguas-Tarapoto and (2) San Miguel de Achinamiza, the Andean  
977 sites in blue (5) Puente Aguas Verdes and sites within the hybrid zone in purple (i3) Km-42  
978 Tarapoto-Yurimaguas and (i4) La Florida. For *O. onega* populations (bottom), Amazonian  
979 sites are in green (1) Km-26 Yurimaguas-Tarapoto and (2) San Miguel de Achinamiza,  
980 Andean sites are in yellow (5) Puente Serranoyacu and the sites in the hybrid zone are in  
981 apple green (o3) Shapaja-Chazuta (o4) from Quebrada Yanayacu to Laguna del Mundo  
982 Perdido. Color codes are conserved for all other figures. c. Photos of putative hybrid  
983 specimens with intermediate color patterns (ventral side). Photo credits: Céline Houssin

984

985 **Figure 2.** Population structure of pure and hybrid populations of *Ithomia salapia* (top) and  
986 *Oleria onega* (bottom). a. Principal component Analysis (PC1: horizontal axis, PC2: vertical  
987 axis), the percentage of total inertia explained by each axis is indicated in parentheses and the  
988 histograms in the top corners represent the inertia percentages of the first principal  
989 components. b. Structure plot for  $K = 2$  and  $K = 3$ . The number of individuals that were used  
990 is indicated for each site. c. Plot of the hybrid index of each sample from the hybrid  
991 populations. The points represent the mean hybrid index value estimated from the posterior  
992 distribution and black lines indicate 95% credible intervals. d. Plot of intertaxon ancestry and  
993 hybrid index. Population color codes are the same as those in Figure 1b.

994

995 **Figure 3.** Scatterplots representing the relationships between the genomic cline center  
996 parameter ( $\alpha$ ), representing SNP ancestry; the genomic cline rate parameter ( $\beta$ ), representing  
997 the steepness of the cline; and the differentiation level,  $F_{ST}$ , estimated for each SNP. Plots for  
998 *I. salapia* and *O. onega* are on the left and right, respectively. Each data point is colored in grey,  
999 and darkness increases with point density (i. e., darker areas contain more points). Blue lines  
1000 frame sets of SNPs for which the genomic cline center parameters ( $\alpha$ ) significantly deviates  
1001 from the genome-wide pattern. Green lines frame sets of SNPs for which the genomic cline  
1002 rate parameters ( $\beta$ ) significantly deviates from the genome-wide pattern. Note that for *I.*  
1003 *salapia*, no SNPs have genomic cline rate parameters ( $\beta$ ) that deviate from the genome-wide  
1004 pattern. SNPs on the right hand side of the orange lines harbour a significantly higher  
1005 differentiation (high  $F_{ST}$ ) than the genome average.

1006

1007 **Figure 4.** Phenotypic position of 90 *I. salapia* (top) and 94 *O. onega* (bottom) in the wing  
1008 color space consisting of the two main principal components from the colour pattern  
1009 modeling approach. Color indicates sample populations as in Figure 1b. Females and males  
1010 are depicted by circles and triangles, respectively. Representative images of the average  
1011 phenotypes for population and sex are shown on each side of the figure.

1012

1013 **Figure 5.** The relationship between the significance of association with color pattern  
1014 (represented as  $-\log_{10}(p\text{-Wald})$ ) and  $F_{ST}$  for *I. salapia* (left) and *O. onega* (right). Yellow  
1015 points indicate SNPs significantly associated with wing patterns (after both Bonferroni and

1016 FDR corrections). Orange points highlight SNPs with high  $F_{ST}$  values and red points highlight  
1017 SNPs with significant association both to wing pattern and to high  $F_{ST}$ .

1018

1019 **Figure 6.** Venn diagram combining number of SNPs identified as supported by each approach  
1020 (differentiation, introgression and admixture mapping) and shared between them. Note that  
1021 for introgression patterns, no SNP showed deviant genomic cline rate parameters ( $\beta$ ) in *I.*  
1022 *salapia*. This parameter is therefore not represented in the diagram.

1023

1024

1025 **Supplementary material :**

1026

1027 **Supplementary Figure 1.** Mimicry ring example for each studied species and lineages, in  
1028 black frameworks, including various other butterfly species.

1029

1030 **Supplementary Figure 2.** Barplots with error bars of the Phenotypic Variation Explained  
1031 (PVE) by genetic for each variable (PC) explaining more than 1% of the wing pattern  
1032 variation.

1033

1034 **Supplementary Table 1.** Sampling information including species, population, sex, location,  
1035 region, GPS positions, sampling date. For each sample, the number of reads sequenced and  
1036 SNPs called has been given.

1037

1038 **Supplementary Table 2.** BLAST results of locus with outlier SNPs identified as potentially  
1039 involved in local adaptation, adaptive introgression and reproductive isolation, i.e. differential  
1040 genomic cline center ( $\alpha$ ), high differentiation level ( $F_{ST}$ ) and differential positive genomic  
1041 cline rate ( $\beta$ ).

1042

1043 **Supplementary Table 3.** BLAST results of loci with SNPs significantly associated with wing  
1044 pattern variation.

1045

1046

a.

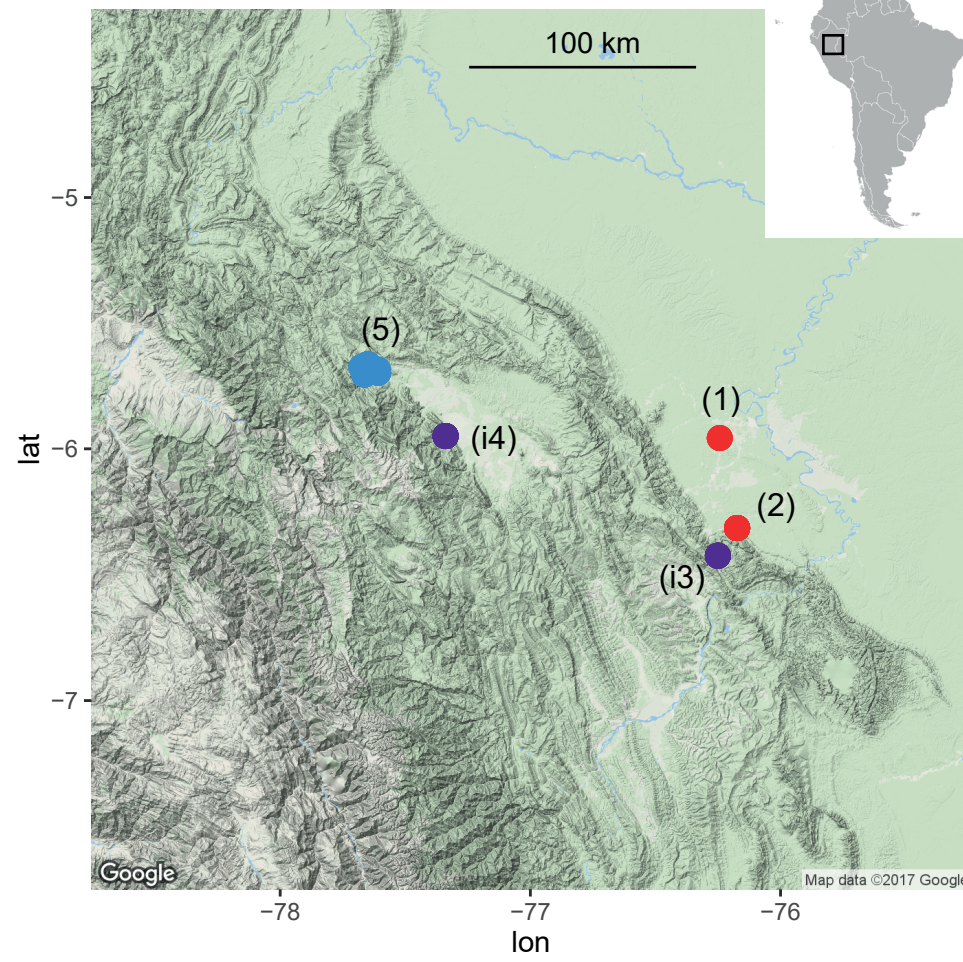
*Ithomia salapia aquinia* (Amazon)



*Ithomia salapia derasa* (Andes)



b.



c.

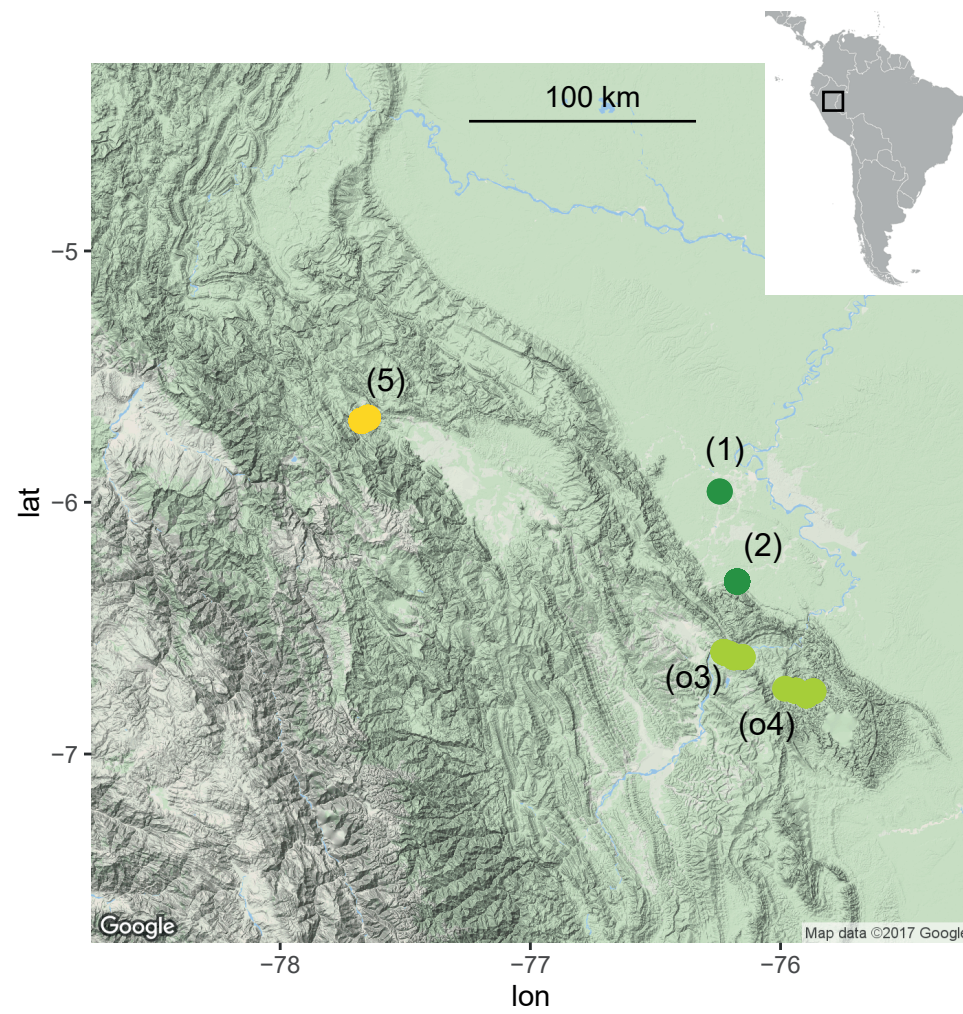
*Ithomia salapia* hybrid



*Oleria onega janarilla* (Amazon)



*Oleria onega* ssp nov 2 (Andes)

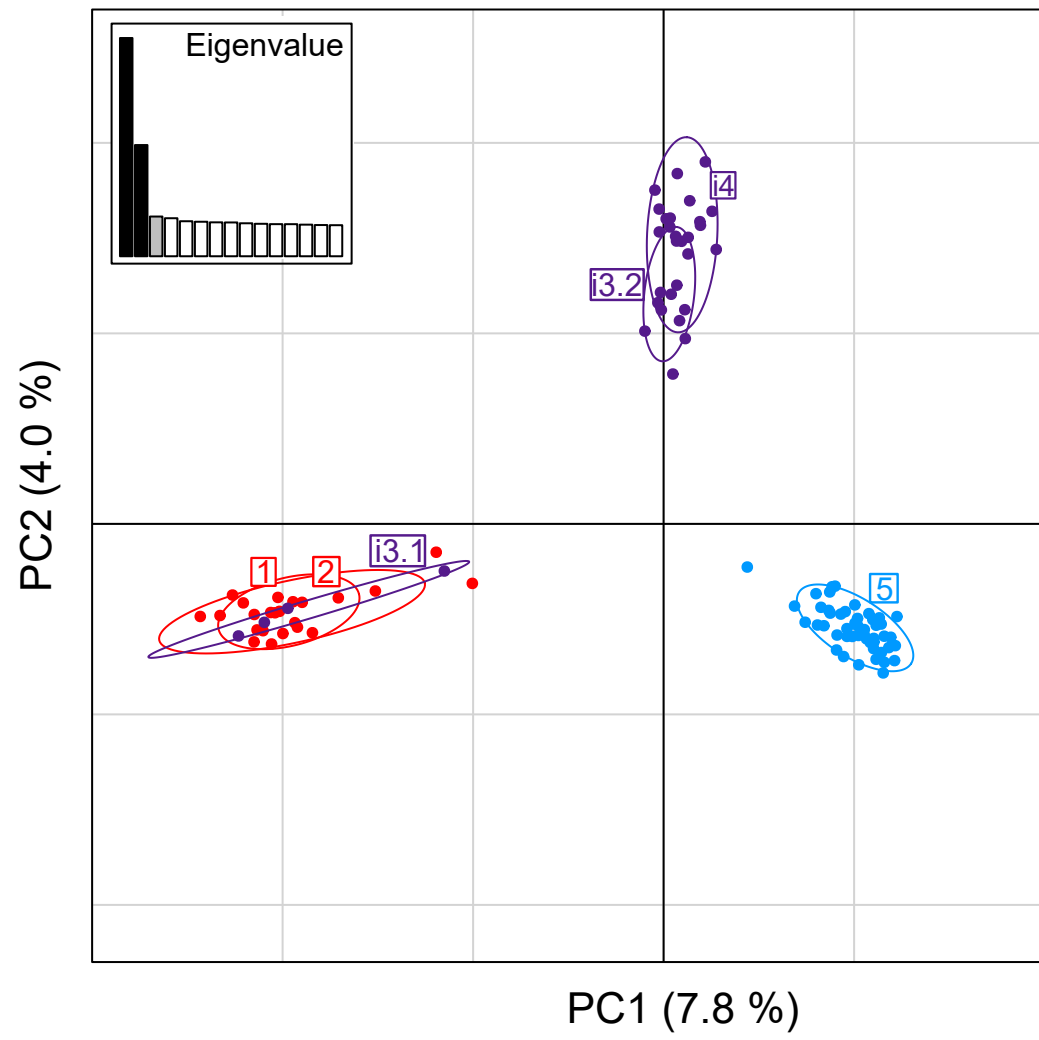


*Oleria onega* hybrid

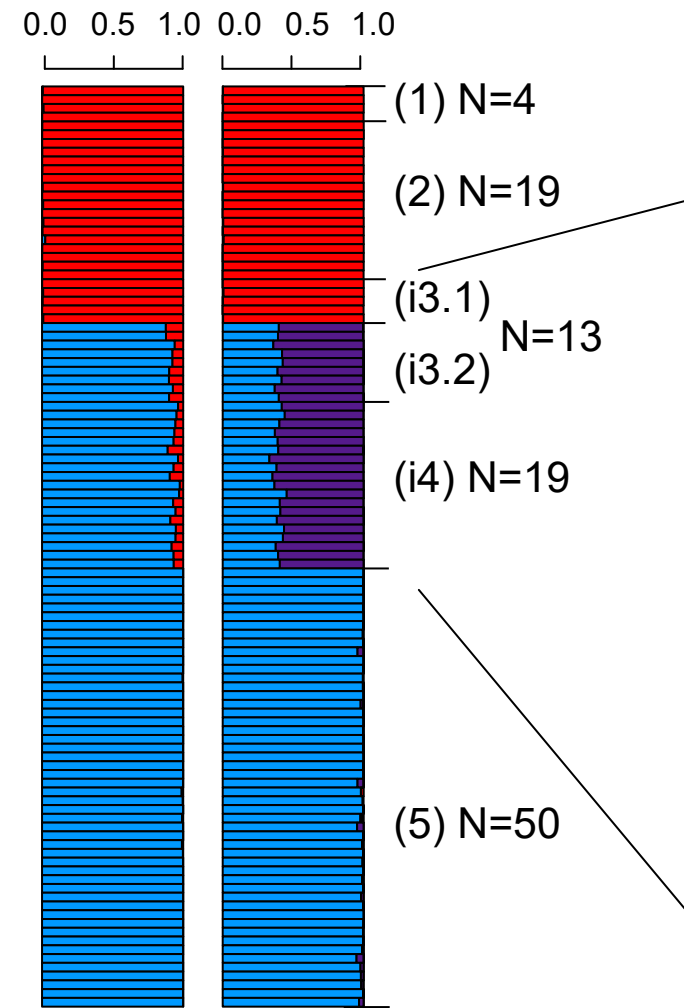




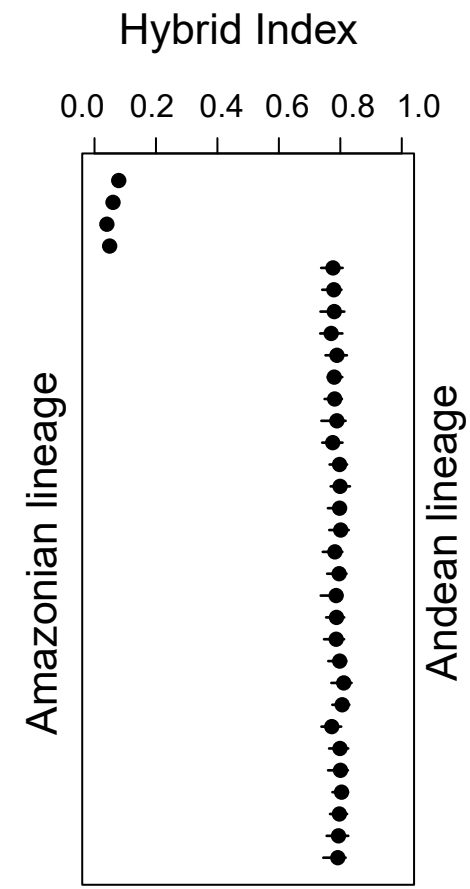
a. *Ithomia salapia*



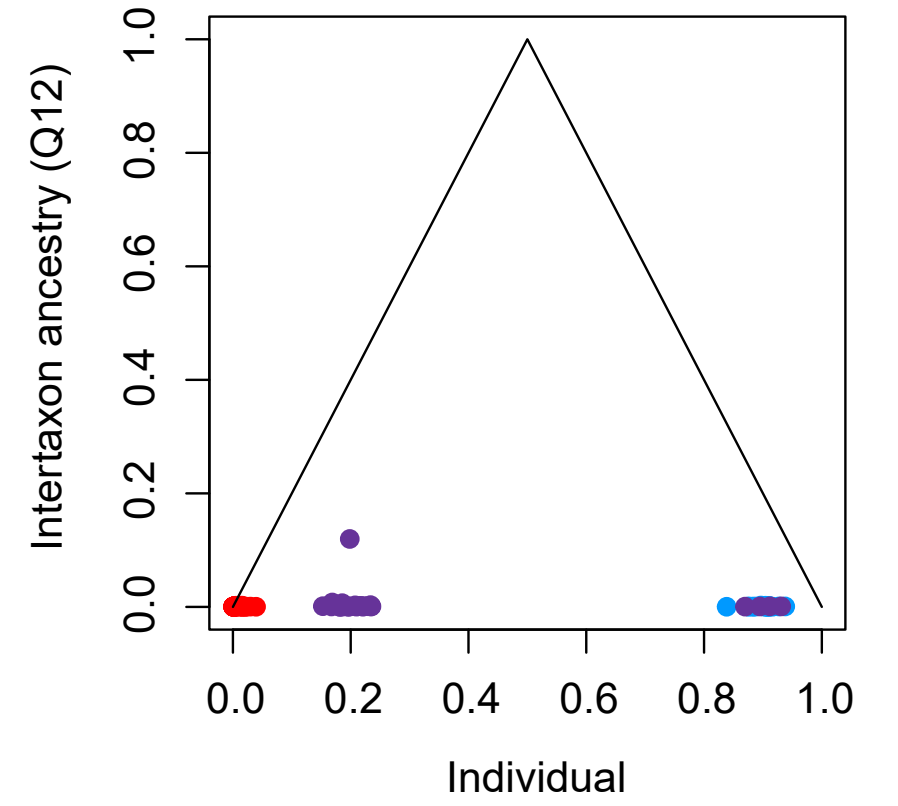
b.



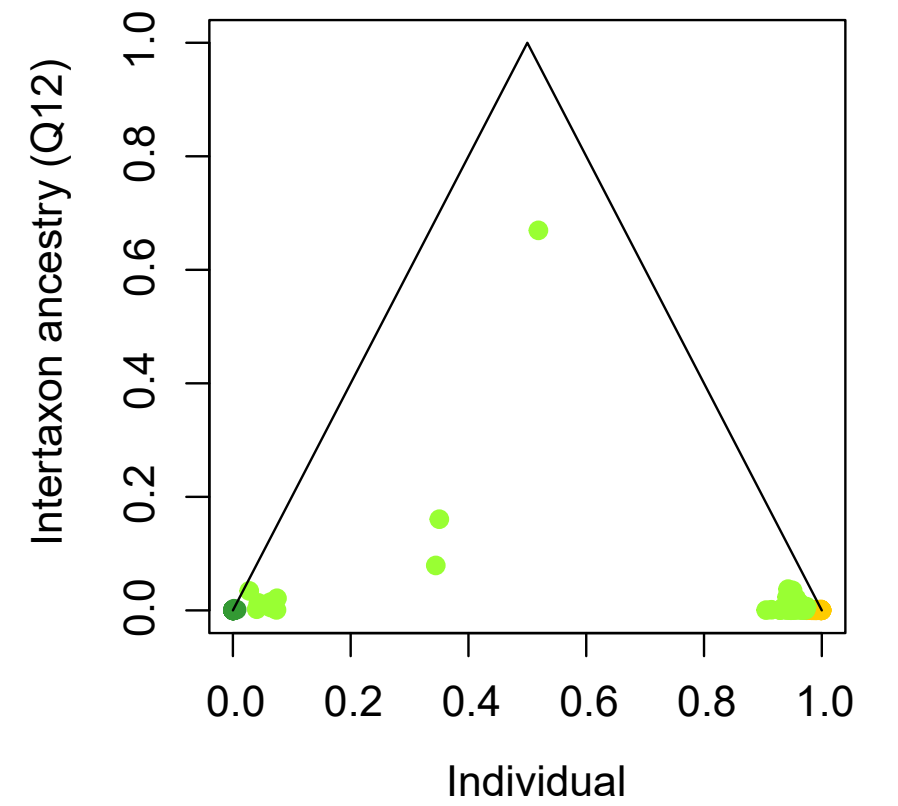
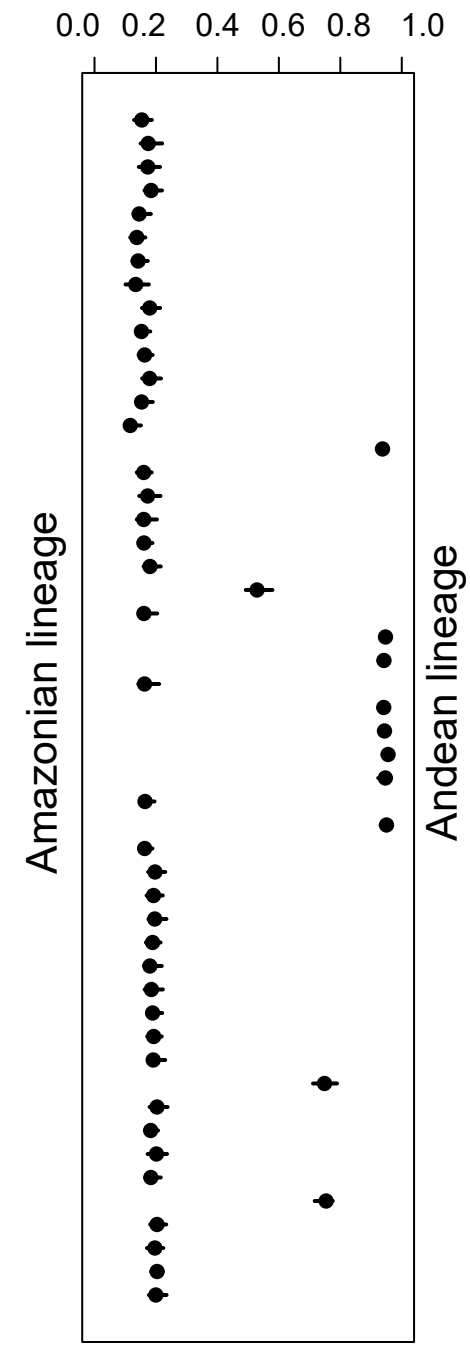
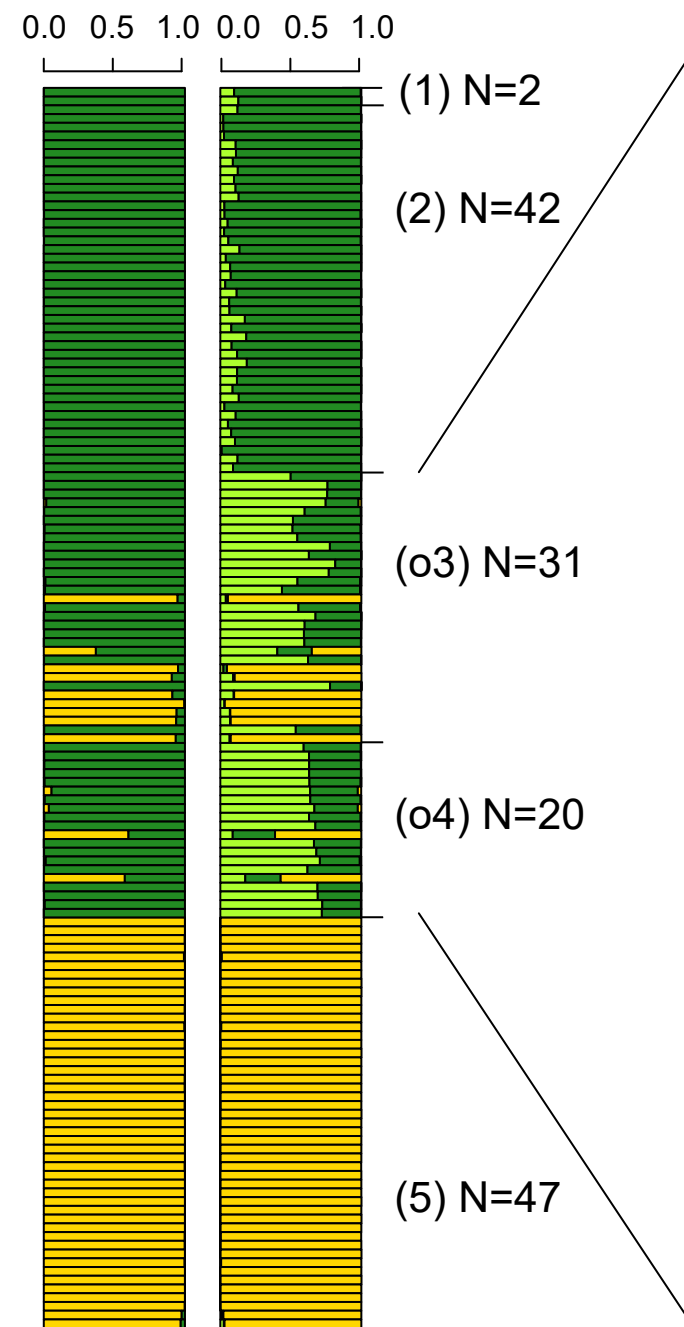
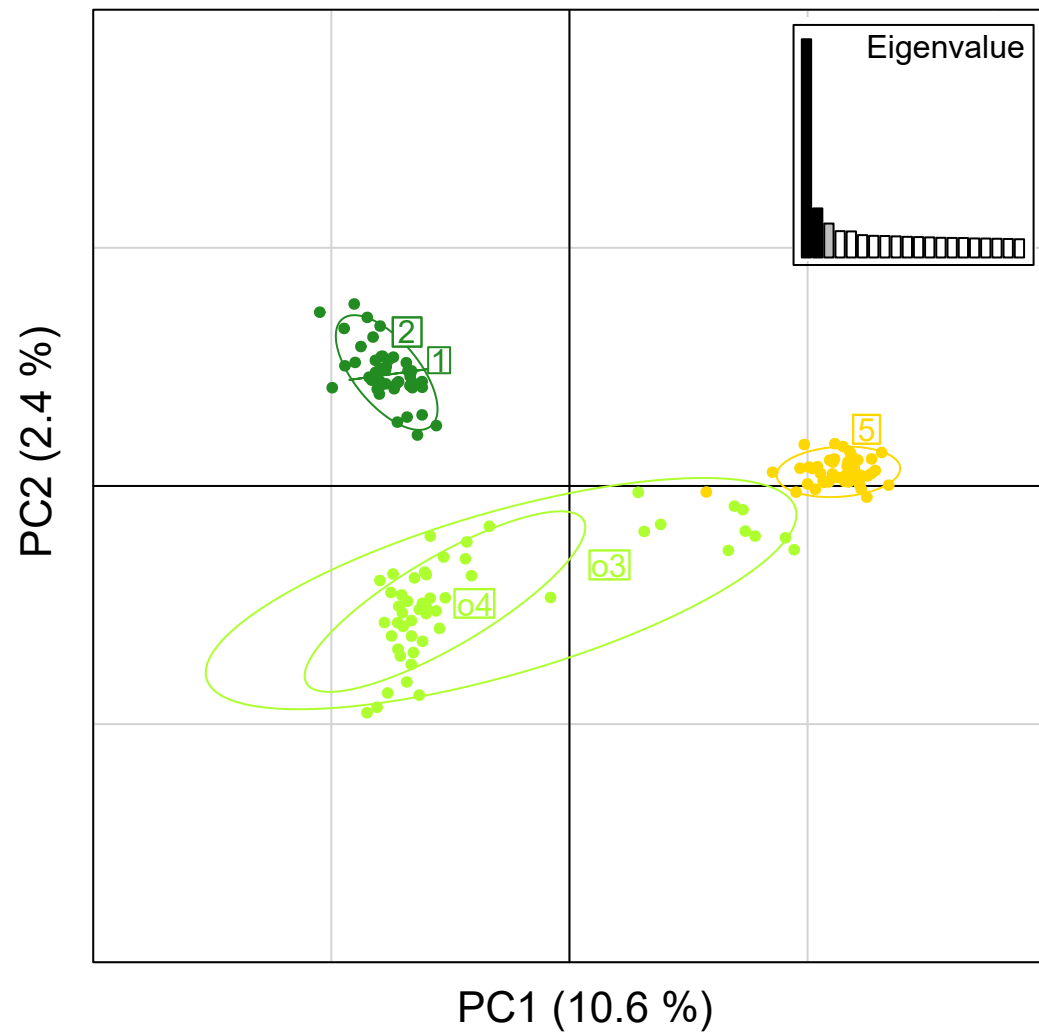
c.



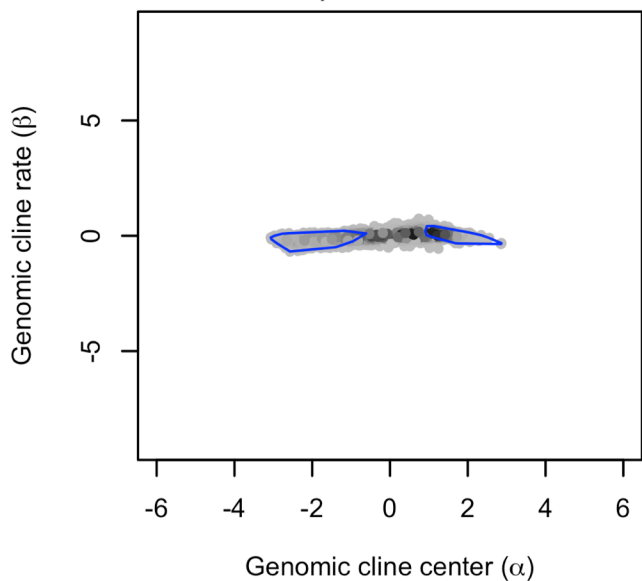
d.



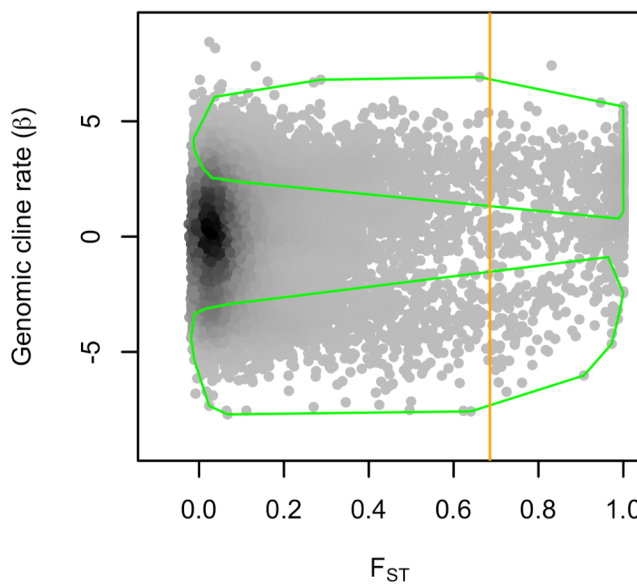
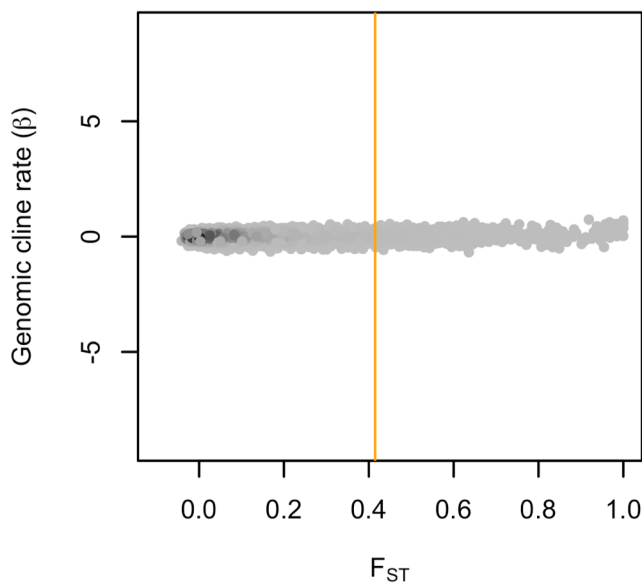
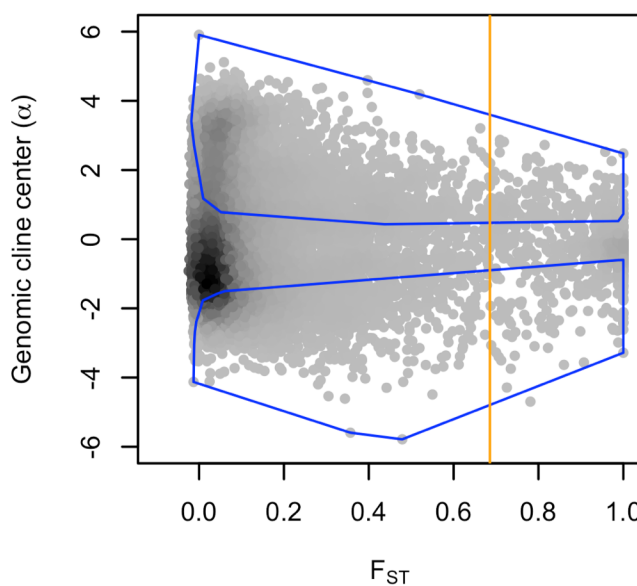
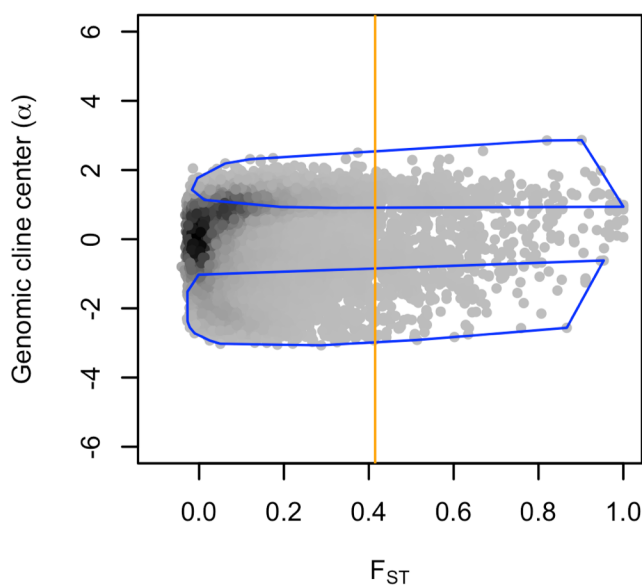
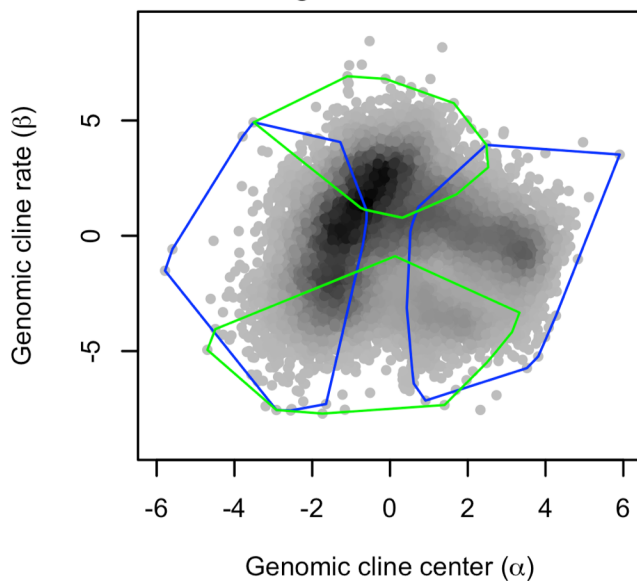
*Oleria onega*



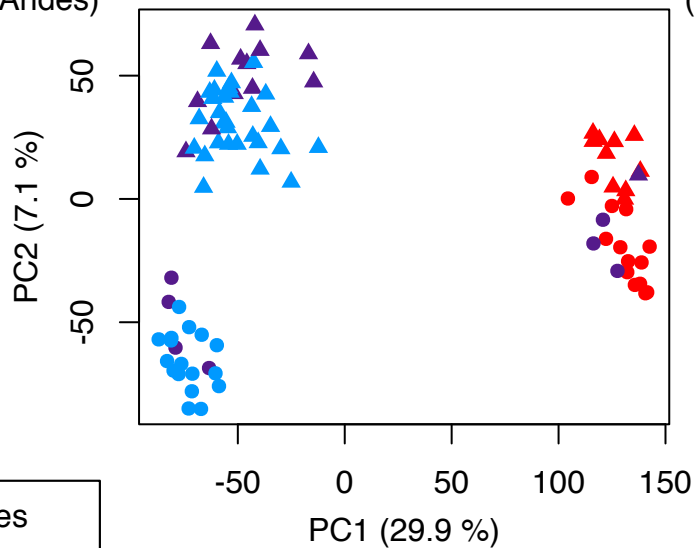
*Ithomia salapia*



*Oleria onega*



*Ithomia salapia derasa*  
(Andes)



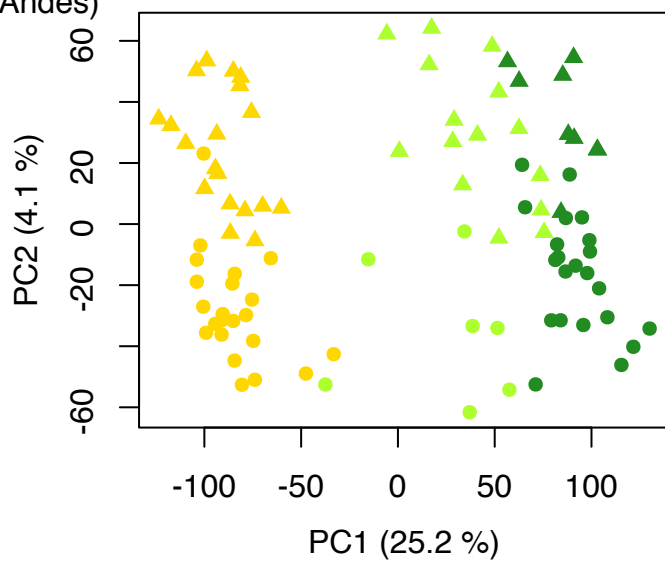
*Ithomia salapia aquinia*  
(Amazon)



△ male  
○ female

Andes  
Hybrids  
Amazon

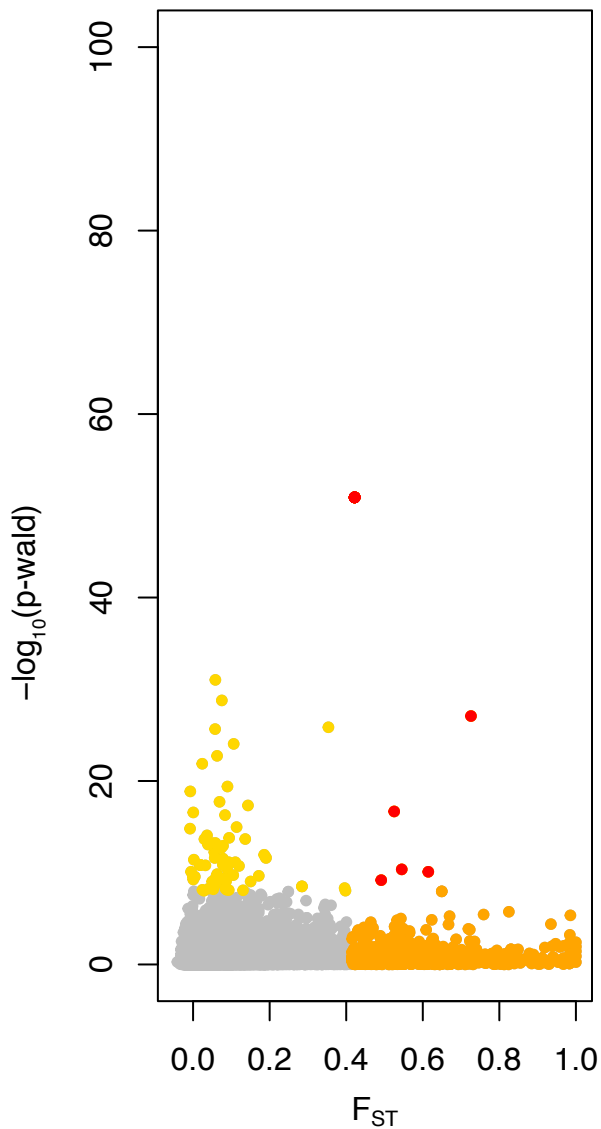
*Oleria onega ssp nov 2*  
(Andes)



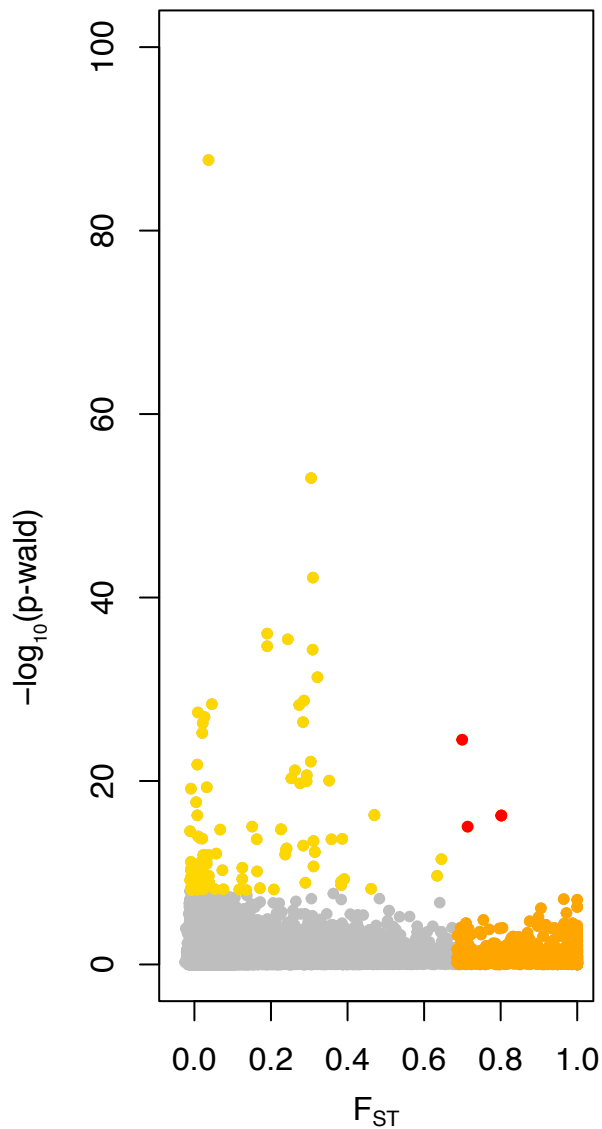
*Oleria onega janarilla*  
(Amazon)



*Ithomia salapia*

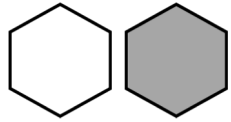


*Oleria onega*

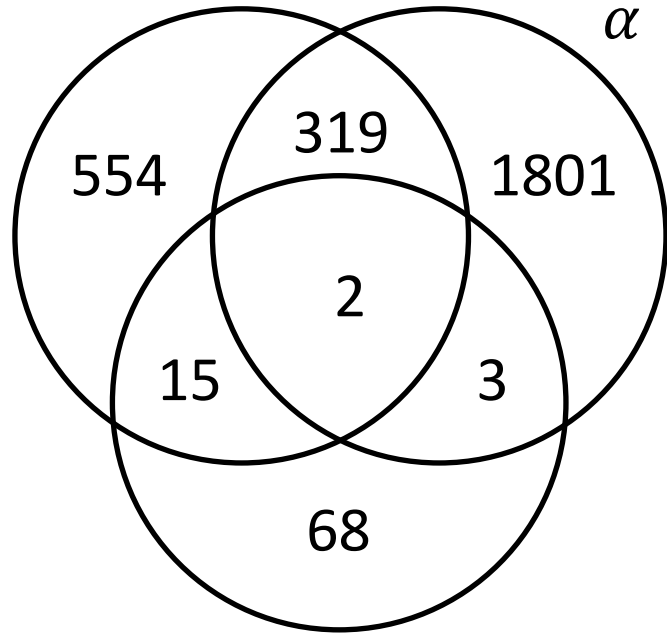
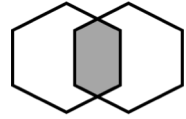


*Ithomia salapia*

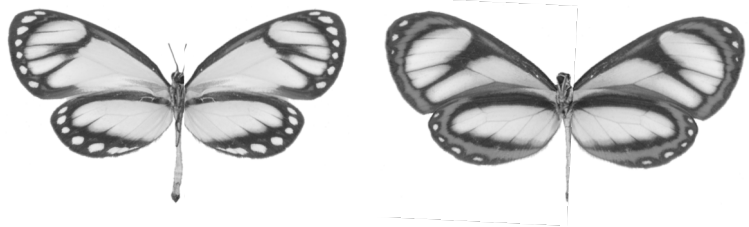
Differentiation  
genome-scan



Introgression  
pattern

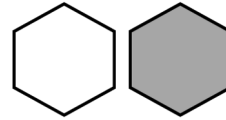


Admixture mapping

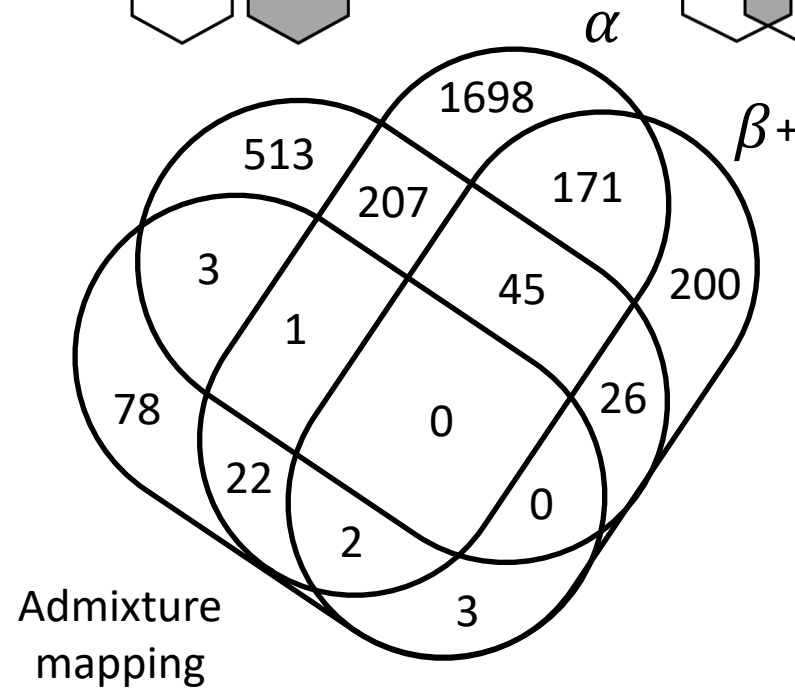
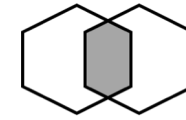


*Oleria onega*

Differentiation  
genome-scan



Introgression  
pattern



# **Contrasting genomic and phenotypic outcomes of hybridization between pairs of mimetic butterfly taxa across a suture zone**

## **SUPPLEMENTARY MATERIAL**

**Supplementary Figure 1.** Mimicry ring example for each studied species and lineages, in black frameworks, including various other butterfly species.

**Supplementary Figure 2.** Barplots with error bars of the Phenotypic Variation Explained (PVE) by genetic for each variable (PC) explaining more than 1% of the wing pattern variation.

**Supplementary Table 1.** Sampling information including species, population, sex, location, region, GPS positions, sampling date. For each sample, the number of reads sequenced and SNPs called has been given.

**Supplementary Table 2.** BLAST results of locus with outlier SNPs identified as potentially involved in local adaptation, adaptive introgression and reproductive isolation, i.e. differential genomic cline center ( $\alpha$ ), high differentiation level ( $F_{ST}$ ) and differential positive genomic cline rate ( $\beta$ ).

**Supplementary Table 3.** BLAST results of loci with SNPs significantly associated with wing pattern variation.

| Sample          | Sample description |                |           | Sampling information |            |                 |  |            |         |                 |                  |              |                | Sequencing statistics |         | SNP calling statistics |  |
|-----------------|--------------------|----------------|-----------|----------------------|------------|-----------------|--|------------|---------|-----------------|------------------|--------------|----------------|-----------------------|---------|------------------------|--|
|                 | Genus              | Species        | Phenotype | Sex                  | Population | Population Code | Location                               | Region     | Country | Latitude        | Longitude        | Altitude (m) | ID by          | Date                  | # reads | # SNP                  |  |
| Ilsa_Az_02_992  | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Amazon     | 1               | Km-26, Yurimaguas-Tarapoto (now Km-24) | San Martín | Peru    | 5° 58' 489" S   | 76° 13' 856" W   | 1066         | Alaine Whinnet | 9/3/2002              | 454952  | 116822                 |  |
| Ilsa_Az_02_991  | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | M                    | Amazon     | 1               | Km-26, Yurimaguas-Tarapoto (now Km-24) | San Martín | Peru    | 5° 58' 489" S   | 76° 13' 856" W   | 1066         | Alaine Whinnet | 9/3/2002              | 230236  | 116707                 |  |
| Ilsa_Az_02_015  | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Amazon     | 1               | Km-26, Yurimaguas-Tarapoto (now Km-24) | San Martín | Peru    | 5° 58' 489" S   | 76° 13' 856" W   | 1066         | Alaine Whinnet | 10/1/2002             | 274811  | 99365                  |  |
| Ilsa_Az_02_014  | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Amazon     | 1               | Km-26, Yurimaguas-Tarapoto (now Km-24) | San Martín | Peru    | 5° 58' 489" S   | 76° 13' 856" W   | 1066         | Alaine Whinnet | 10/1/2002             | 181385  | 77018                  |  |
| Ilsa_Az_05_1605 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | M                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/2/2006              | 381230  | 146396                 |  |
| Ilsa_Az_05_1551 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/1/2006              | 377803  | 145858                 |  |
| Ilsa_Az_05_1560 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | M                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/1/2006              | 336857  | 138789                 |  |
| Ilsa_Az_05_1557 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/1/2006              | 284147  | 131087                 |  |
| Ilsa_Az_05_1545 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 1066         | Lisa de Silva  | 3/1/2006              | 563602  | 118981                 |  |
| Ilsa_Az_05_1604 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | M                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/2/2006              | 412881  | 111760                 |  |
| Ilsa_Az_05_1558 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/1/2006              | 381997  | 110760                 |  |
| Ilsa_Az_05_1603 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/2/2006              | 351247  | 106268                 |  |
| Ilsa_Az_05_1549 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 1066         | Lisa de Silva  | 3/1/2006              | 306833  | 105299                 |  |
| Ilsa_Az_05_1554 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/1/2006              | 337562  | 103432                 |  |
| Ilsa_Az_05_1553 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/1/2006              | 259997  | 94223                  |  |
| Ilsa_Az_05_1547 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | M                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 1066         | Lisa de Silva  | 3/1/2006              | 272700  | 93411                  |  |
| Ilsa_Az_05_1546 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 1066         | Lisa de Silva  | 3/1/2006              | 248524  | 94166                  |  |
| Ilsa_Az_05_1555 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/1/2006              | 234330  | 90613                  |  |
| Ilsa_Az_05_1550 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | M                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 1066         | Lisa de Silva  | 3/1/2006              | 241126  | 89967                  |  |
| Ilsa_Az_05_1548 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 1066         | Lisa de Silva  | 3/1/2006              | 138224  | 87483                  |  |
| Ilsa_Az_05_1563 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/1/2006              | 208816  | 84834                  |  |
| Ilsa_Az_05_1601 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | M                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/2/2006              | 141893  | 60244                  |  |
| Ilsa_Az_05_1552 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | M                    | Middle1    | 2               | San Miguel de Achinamiza               | San Martín | Peru    | 6° 18' 540" S   | 76° 09' 843" W   | 197          | Lisa de Silva  | 3/1/2006              | 99268   | 51065                  |  |
| Ilsa_Mi_02_1371 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle2    | 3.1             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 172          | Alaine Whinnet | 9/9/2002              | 348506  | 128985                 |  |
| Ilsa_Mi_02_1372 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | M                    | Middle2    | 3.1             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 172          | Alaine Whinnet | 9/9/2002              | 591079  | 122518                 |  |
| Ilsa_Mi_02_1373 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle2    | 3.1             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 197          | Alaine Whinnet | 9/9/2002              | 558863  | 117084                 |  |
| Ilsa_Mi_02_1370 | <i>Ithomia</i>     | <i>salapia</i> | aquinia   | F                    | Middle2    | 3.1             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 346          | Alaine Whinnet | 9/9/2002              | 114518  | 55353                  |  |
| Ilsa_Mi_02_1381 | <i>Ithomia</i>     | <i>salapia</i> | derasa    | F                    | Middle2    | 3.2             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 1066         | Alaine Whinnet | 9/9/2002              | 370237  | 140489                 |  |
| Ilsa_Mi_02_1376 | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Middle2    | 3.2             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 197          | Alaine Whinnet | 9/9/2002              | 211612  | 112016                 |  |
| Ilsa_Mi_02_1380 | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Middle2    | 3.2             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 197          | Alaine Whinnet | 9/9/2002              | 187985  | 107720                 |  |
| Ilsa_Mi_02_1374 | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Middle2    | 3.2             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 197          | Alaine Whinnet | 9/9/2002              | 209060  | 82902                  |  |
| Ilsa_Mi_02_1375 | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Middle2    | 3.2             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 197          | Alaine Whinnet | 9/9/2002              | 183092  | 75095                  |  |
| Ilsa_Mi_02_1970 | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Middle2    | 3.2             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 1066         | Alaine Whinnet | 10/1/2002             | 193070  | 73885                  |  |
| Ilsa_Mi_02_1378 | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Middle2    | 3.2             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 197          | Alaine Whinnet | 9/9/2002              | 156393  | 72524                  |  |
| Ilsa_Mi_02_1379 | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Middle2    | 3.2             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 197          | Alaine Whinnet | 9/9/2002              | 170783  | 72014                  |  |
| Ilsa_Mi_02_1971 | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Middle2    | 3.2             | Km-42, Tarapoto-Yurimaguas             | San Martín | Peru    | 6° 25' 29.4" S  | 76° 15' 1.6" W   | 1066         | Alaine Whinnet | 10/1/2002             | 225970  | 70000                  |  |
| Ilsa_Mi_06_952  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/16/2006            | 490526  | 144122                 |  |
| Ilsa_Mi_06_931  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/14/2006            | 507490  | 141484                 |  |
| Ilsa_Mi_06_925  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | F                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/14/2006            | 367821  | 129525                 |  |
| Ilsa_Mi_06_930  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | F                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/14/2006            | 368515  | 125334                 |  |
| Ilsa_Mi_06_960  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/16/2006            | 331577  | 124740                 |  |
| Ilsa_Mi_06_961  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | F                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/16/2006            | 330313  | 123957                 |  |
| Ilsa_Mi_06_953  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/16/2006            | 657199  | 121184                 |  |
| Ilsa_Mi_06_954  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | F                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/16/2006            | 507080  | 111595                 |  |
| Ilsa_Mi_06_932  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/14/2006            | 568199  | 111517                 |  |
| Ilsa_Mi_06_959  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/16/2006            | 503967  | 110317                 |  |
| Ilsa_Mi_06_962  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | F                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/16/2006            | 501325  | 110309                 |  |
| Ilsa_Mi_06_958  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/16/2006            | 455718  | 108748                 |  |
| Ilsa_Mi_06_928  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/14/2006            | 448953  | 104193                 |  |
| Ilsa_Mi_06_924  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | F                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/14/2006            | 403484  | 101895                 |  |
| Ilsa_Mi_06_956  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/16/2006            | 356353  | 94711                  |  |
| Ilsa_Mi_06_926  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/14/2006            | 354030  | 93484                  |  |
| Ilsa_Mi_06_927  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/14/2006            | 156253  | 81048                  |  |
| Ilsa_Mi_06_929  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/14/2006            | 190255  | 72132                  |  |
| Ilsa_Mi_06_955  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes_F    | 4               | La Florida                             | San Martín | Peru    | 5° 56' 57.33" S | 77° 20' 20.19" W | 1014         | Fraser Simpson | 12/16/2006            | 135224  | 56150                  |  |
| Ilsa_An_06_852  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes      | 5               | Agua Clara                             | San Martín | Peru    | 5° 41' 50.9" S  | 77° 36' 30.7" W  | 1201         | Fraser Simpson | 12/12/2006            | 606382  | 150944                 |  |
| Ilsa_An_06_853  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | F                    | Andes      | 5               | Agua Clara                             | San Martín | Peru    | 5° 41' 50.9" S  | 77° 36' 30.7" W  | 1201         | Fraser Simpson | 12/12/2006            | 569526  | 110756                 |  |
| Ilsa_An_06_855  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | F                    | Andes      | 5               | Agua Clara                             | San Martín | Peru    | 5° 41' 50.9" S  | 77° 36' 30.7" W  | 1201         | Fraser Simpson | 12/12/2006            | 597492  | 110614                 |  |
| Ilsa_An_06_854  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes      | 5               | Agua Clara                             | San Martín | Peru    | 5° 41' 50.9" S  | 77° 36' 30.7" W  | 1201         | Fraser Simpson | 12/12/2006            | 465998  | 105811                 |  |
| Ilsa_An_06_849  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | F                    | Andes      | 5               | Agua Clara                             | San Martín | Peru    | 5° 41' 50.9" S  | 77° 36' 30.7" W  | 1201         | Fraser Simpson | 12/12/2006            | 418672  | 103556                 |  |
| Ilsa_An_06_848  | <i>Ithomia</i>     | <i>salapia</i> | derasa    | M                    | Andes      | 5               | Agua Clara                             | San Martín | Peru    | 5° 41' 50.9" S  | 77° 36' 30.7" W  | 1201         | Fraser Simpson | 12/12/2006            | 211662  | 101375                 |  |

|                |                 |           |   |         |   |  |            |      |                |                 |      |                |            |        |        |
|----------------|-----------------|-----------|---|---------|---|--|------------|------|----------------|-----------------|------|----------------|------------|--------|--------|
| Lsd_An_06_851  | Ithomia salapia | derasa    | F | Andes   | 5 | Aguas Claras                           | San Martín | Peru | 5° 41' 50.9" S | 77° 36' 30.7" W | 1201 | Fraser Simpson | 12/12/2006 | 214917 | 98884  |
| Lsd_An_06_850  | Ithomia salapia | derasa    | F | Andes   | 5 | Aguas Claras                           | San Martín | Peru | 5° 41' 50.9" S | 77° 36' 30.7" W | 1201 | Fraser Simpson | 12/12/2006 | 266876 | 81990  |
| Lsd_An_06_836  | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Aguas Verdes                    | San Martín | Peru | 5° 41' 3.3" S  | 77° 39' 30.5" W | 1201 | Fraser Simpson | 12/11/2006 | 704542 | 162179 |
| Lsd_An_05_1052 | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Aguas Verdes                    | San Martín | Peru | 5° 41' 77" S   | 77° 39' 487" W  | 976  | Mathieu Joron  | 11/24/2005 | 342677 | 132559 |
| Lsd_An_05_1098 | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes                    | San Martín | Peru | 5° 41' 77" S   | 77° 39' 487" W  | 976  | Mathieu Joron  | 11/24/2005 | 347770 | 129502 |
| Lsd_An_05_1101 | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes                    | San Martín | Peru | 5° 41' 77" S   | 77° 39' 487" W  | 1201 | Mathieu Joron  | 11/24/2005 | 650088 | 119736 |
| Lsd_An_05_1100 | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes                    | San Martín | Peru | 5° 41' 77" S   | 77° 39' 487" W  | 976  | Mathieu Joron  | 11/24/2005 | 567976 | 118704 |
| Lsd_An_05_1094 | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes                    | San Martín | Peru | 5° 41' 77" S   | 77° 39' 487" W  | 976  | Mathieu Joron  | 11/24/2005 | 441325 | 107140 |
| Lsd_An_06_840  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes                    | San Martín | Peru | 5° 41' 3.3" S  | 77° 39' 30.5" W | 1201 | Fraser Simpson | 12/11/2006 | 379681 | 99587  |
| Lsd_An_02_901  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1066 | Alaine Whinnet | 8/29/2002  | 565740 | 160319 |
| Lsd_An_02_896  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1066 | Alaine Whinnet | 8/29/2002  | 470065 | 151613 |
| Lsd_An_02_1721 | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1090 | Alaine Whinnet | 9/19/2002  | 459893 | 151363 |
| Lsd_An_02_898  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1201 | Alaine Whinnet | 8/29/2002  | 413394 | 142849 |
| Lsd_An_02_899  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1201 | Alaine Whinnet | 8/29/2002  | 690905 | 124531 |
| Lsd_An_02_1722 | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1090 | Alaine Whinnet | 9/19/2002  | 271322 | 122205 |
| Lsd_An_02_902  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1066 | Alaine Whinnet | 8/29/2002  | 257394 | 121014 |
| Lsd_An_02_906  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1066 | Alaine Whinnet | 8/29/2002  | 400639 | 108240 |
| Lsd_An_02_897  | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1201 | Alaine Whinnet | 8/29/2002  | 422771 | 105606 |
| Lsd_An_02_908  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1100 | Alaine Whinnet | 8/29/2002  | 371034 | 103783 |
| Lsd_An_02_905  | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1066 | Alaine Whinnet | 8/29/2002  | 180808 | 101321 |
| Lsd_An_02_1724 | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 976  | Alaine Whinnet | 9/19/2002  | 364472 | 100935 |
| Lsd_An_02_1729 | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 976  | Alaine Whinnet | 9/19/2002  | 257248 | 87472  |
| Lsd_An_02_1723 | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1090 | Alaine Whinnet | 9/19/2002  | 231591 | 79106  |
| Lsd_An_02_900  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1201 | Alaine Whinnet | 8/29/2002  | 577042 | 77838  |
| Lsd_An_02_904  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1066 | Alaine Whinnet | 8/29/2002  | 307487 | 77225  |
| Lsd_An_02_907  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 1100 | Alaine Whinnet | 8/29/2002  | 313912 | 74194  |
| Lsd_An_02_1726 | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Aguas Verdes trail              | San Martín | Peru | 5° 39' 50" S   | 77° 38' 58" W   | 976  | Alaine Whinnet | 9/19/2002  | 220199 | 51733  |
| Lsd_An_02_735  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1201 | Alaine Whinnet | 8/28/2002  | 524492 | 158048 |
| Lsd_An_02_1711 | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 9/19/2002  | 403720 | 143738 |
| Lsd_An_02_1713 | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 9/19/2002  | 659923 | 122440 |
| Lsd_An_02_949  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 8/30/2002  | 481296 | 115849 |
| Lsd_An_02_739  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 8/28/2002  | 192516 | 112003 |
| Lsd_An_02_948  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 8/30/2002  | 255224 | 110614 |
| Lsd_An_02_741  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 8/28/2002  | 211526 | 110333 |
| Lsd_An_02_1620 | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 9/17/2002  | 463807 | 109222 |
| Lsd_An_02_945  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 8/30/2002  | 215777 | 109173 |
| Lsd_An_02_1712 | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 9/19/2002  | 370949 | 103796 |
| Lsd_An_02_736  | Ithomia salapia | derasa    | M | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 8/28/2002  | 265938 | 96506  |
| Lsd_An_02_946  | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 8/30/2002  | 251901 | 89526  |
| Lsd_An_02_947  | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 8/30/2002  | 257666 | 87816  |
| Lsd_An_02_743  | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 8/28/2002  | 213690 | 82570  |
| Lsd_An_02_740  | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 8/28/2002  | 193002 | 77998  |
| Lsd_An_02_737  | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 8/28/2002  | 191013 | 77741  |
| Lsd_An_02_742  | Ithomia salapia | derasa    | F | Andes   | 5 | Puente Serranoyacu                     | San Martín | Peru | 5° 40' 31.6" S | 77° 40' 28.7" W | 1100 | Alaine Whinnet | 8/28/2002  | 147837 | 67703  |
| Ooj_Az_02_2021 | Oleria onega    | janarilla | M | Amazon  | 1 | Km-26, Yurimaguas-Tarapoto (now Km-24) | San Martín | Peru | 5° 58' 489" S  | 76° 13' 856" W  |      | Keith Willmott | 10/1/2002  | 199801 | 170257 |
| Ooj_Az_02_2092 | Oleria onega    | janarilla | F | Amazon  | 1 | Km-26, Yurimaguas-Tarapoto (now Km-24) | San Martín | Peru | 5° 58' 489" S  | 76° 13' 856" W  |      | Keith Willmott | 10/1/2002  | 313305 | 175701 |
| Ooj_Az_05_1505 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 241071 | 150741 |
| Ooj_Az_05_1506 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 172694 | 127069 |
| Ooj_Az_05_1507 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 133191 | 101790 |
| Ooj_Az_05_1508 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 195976 | 139490 |
| Ooj_Az_05_1510 | Oleria onega    | janarilla | M | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 210931 | 143424 |
| Ooj_Az_05_1511 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 190543 | 130808 |
| Ooj_Az_05_1512 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 179412 | 155490 |
| Ooj_Az_05_1513 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 317877 | 180661 |
| Ooj_Az_05_1514 | Oleria onega    | janarilla | M | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 382887 | 191352 |
| Ooj_Az_05_1515 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 154363 | 142230 |
| Ooj_Az_05_1516 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 274775 | 165335 |
| Ooj_Az_05_1517 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 458906 | 206777 |
| Ooj_Az_05_1518 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 153756 | 116095 |
| Ooj_Az_05_1519 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 154909 | 112635 |
| Ooj_Az_05_1520 | Oleria onega    | janarilla | M | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 303033 | 171790 |
| Ooj_Az_05_1521 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 171865 | 120698 |
| Ooj_Az_05_1522 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 292691 | 171716 |
| Ooj_Az_05_1523 | Oleria onega    | janarilla | F | Middle1 | 2 | San Miguel de Achinamiza               | San Martín | Peru | 6° 18' 540" S  | 76° 09' 843" W  | 197  | Lisa de Silva  | 3/1/2006   | 201178 | 133155 |



|                |              |                    |   |         |   |  |                                |            |                 |                  |                  |      |                |            |        |        |
|----------------|--------------|--------------------|---|---------|---|--|--------------------------------|------------|-----------------|------------------|------------------|------|----------------|------------|--------|--------|
| Ooj_Az_05_1524 | Oleria onega | janarilla          | F | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/1/2006   | 295560 | 206342 |
| Ooj_Az_05_1527 | Oleria onega | janarilla          | F | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/1/2006   | 192823 | 164123 |
| Ooj_Az_05_1528 | Oleria onega | janarilla          | F | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/1/2006   | 169102 | 122461 |
| Ooj_Az_05_1529 | Oleria onega | janarilla          | F | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/1/2006   | 289337 | 165440 |
| Ooj_Az_05_1530 | Oleria onega | janarilla          | F | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/1/2006   | 232265 | 153226 |
| Ooj_Az_05_1531 | Oleria onega | janarilla          | F | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/1/2006   | 388445 | 186992 |
| Ooj_Az_05_1532 | Oleria onega | janarilla          | F | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/1/2006   | 121406 | 96990  |
| Ooj_Az_05_1533 | Oleria onega | janarilla          | F | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/1/2006   | 321705 | 172391 |
| Ooj_Az_05_1534 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/1/2006   | 193003 | 135341 |
| Ooj_Az_05_1535 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/1/2006   | 277285 | 162771 |
| Ooj_Az_05_1536 | Oleria onega | janarilla          | F | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/1/2006   | 232091 | 184205 |
| Ooj_Az_05_1564 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 147037 | 112252 |
| Ooj_Az_05_1565 | Oleria onega | janarilla          | F | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 392422 | 137005 |
| Ooj_Az_05_1566 | Oleria onega | janarilla          | F | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 141350 | 107904 |
| Ooj_Az_05_1567 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 381558 | 186296 |
| Ooj_Az_05_1568 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 462862 | 247693 |
| Ooj_Az_05_1569 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 216592 | 146638 |
| Ooj_Az_05_1570 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 200001 | 135074 |
| Ooj_Az_05_1571 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 173924 | 122910 |
| Ooj_Az_05_1572 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 369526 | 192198 |
| Ooj_Az_05_1573 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 237176 | 149081 |
| Ooj_Az_05_1574 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 123924 | 99098  |
| Ooj_Az_05_1575 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 203682 | 138558 |
| Ooj_Az_05_1576 | Oleria onega | janarilla          | M | Middle1 | 2 |  | San Miguel de Achinamiza       | San Martin | Peru            | 6° 18' 540" S    | 76° 09' 843" W   | 197  | Lisa de Silva  | 3/2/2006   | 340248 | 181641 |
| Oos_Mi_02_1482 | Oleria onega | janarilla - hybrid | M | Middle3 | 3 |  | Chumia, Km-14, Shapaja-Chazuta | San Martin | Peru            | 6° 36' 57" S     | 76° 11' 10" W    | 262  | Alaine Whinnet | 9/9/2002   | 378329 | 191328 |
| Ooj_Mi_02_1479 | Oleria onega | janarilla - hybrid | M | Middle3 | 3 |  | Chumia, Km-14, Shapaja-Chazuta | San Martin | Peru            | 6° 36' 57" S     | 76° 11' 10" W    | 262  | Keith Willmott | 9/9/2002   | 268063 | 167629 |
| Ooj_Mi_02_1480 | Oleria onega | janarilla - hybrid | M | Middle3 | 3 |  | Chumia, Km-14, Shapaja-Chazuta | San Martin | Peru            | 6° 36' 57" S     | 76° 11' 10" W    | 262  | Keith Willmott | 9/9/2002   | 273438 | 158741 |
| Oos_Mi_02_1481 | Oleria onega | janarilla - hybrid | M | Middle3 | 3 |  | Chumia, Km-14, Shapaja-Chazuta | San Martin | Peru            | 6° 36' 57" S     | 76° 11' 10" W    | 262  | Keith Willmott | 9/9/2002   | 225757 | 148679 |
| Oos_Mi_06_330  | Oleria onega | ssp. nov. 2        | M | Middle3 | 3 |  | Km-11, Shapaja-Chazuta         | San Martin | Peru            | 6° 36' 979" S    | 76° 12' 136" W   | 180  | Lisa de Silva  | 10/19/2006 | 187840 | 136185 |
| Oos_Mi_06_332  | Oleria onega | ssp. nov. 2        | F | Middle3 | 3 |  | Km-11, Shapaja-Chazuta         | San Martin | Peru            | 6° 36' 979" S    | 76° 12' 136" W   | 180  | Lisa de Silva  | 10/19/2006 | 72091  | 63426  |
| Oos_Mi_06_333  | Oleria onega | ssp. nov. 2        | M | Middle3 | 3 |  | Km-11, Shapaja-Chazuta         | San Martin | Peru            | 6° 36' 979" S    | 76° 12' 136" W   | 180  | Lisa de Silva  | 10/19/2006 | 336381 | 184874 |
| Ooj_Mi_06_347  | Oleria onega | janarilla          | M | Middle3 | 3 |  | Km-19, Shapaja-Chazuta         | San Martin | Peru            | 6° 36' 554" S    | 76° 09' 612" W   | 195  | Lisa de Silva  | 11/17/2006 | 181897 | 132834 |
| Oos_Mi_06_345  | Oleria onega | ssp. nov. 2        | M | Middle3 | 3 |  | Km-19, Shapaja-Chazuta         | San Martin | Peru            | 6° 36' 554" S    | 76° 09' 612" W   | 195  | Lisa de Silva  | 11/17/2006 | 183887 | 132973 |
| Oos_Mi_06_346  | Oleria onega | ssp. nov. 2        | M | Middle3 | 3 |  | Km-19, Shapaja-Chazuta         | San Martin | Peru            | 6° 36' 554" S    | 76° 09' 612" W   | 195  | Lisa de Silva  | 11/17/2006 | 130376 | 99334  |
| Ooj_Mi_02_1166 | Oleria onega | janarilla          | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 9/4/2002   | 346096 | 228682 |
| Ooj_Mi_02_1172 | Oleria onega | janarilla          | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 9/4/2002   | 230260 | 148931 |
| Ooj_Mi_02_1175 | Oleria onega | janarilla          | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 9/4/2002   | 196596 | 134495 |
| Ooj_Mi_02_1176 | Oleria onega | janarilla          | F | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 9/4/2002   | 151164 | 106813 |
| Ooj_Mi_02_1583 | Oleria onega | janarilla          | F | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 9/14/2002  | 510317 | 207543 |
| Ooj_Mi_02_1584 | Oleria onega | janarilla          | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 9/14/2002  | 390247 | 239099 |
| Ooj_Mi_02_1587 | Oleria onega | janarilla          | F | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 9/14/2002  | 362310 | 190647 |
| Ooj_Mi_02_1588 | Oleria onega | janarilla          | F | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 9/14/2002  | 225911 | 140931 |
| Ooj_Mi_02_1959 | Oleria onega | janarilla          | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 10/7/2002  | 297137 | 169368 |
| Ooj_Mi_02_1961 | Oleria onega | janarilla          | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 10/7/2002  | 375111 | 188144 |
| Ooj_Mi_02_1962 | Oleria onega | janarilla          | F | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 10/7/2002  | 183451 | 126185 |
| Ooj_Mi_07_151  | Oleria onega | hybrid             | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 424" S    | 76° 13' 394" W   | 1201 |                | 7/31/2007  | 398209 | 232534 |
| Ooj_Mi_07_153  | Oleria onega | hybrid             | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 424" S    | 76° 13' 394" W   | 1201 |                | 7/31/2007  | 261216 | 127959 |
| Ooj_Mi_07_155  | Oleria onega | hybrid             | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 424" S    | 76° 13' 394" W   | 1201 |                | 7/31/2007  | 367726 | 186259 |
| Ooj_Mi_07_158  | Oleria onega | hybrid             | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 424" S    | 76° 13' 394" W   | 1201 |                | 7/31/2007  | 456383 | 197003 |
| Ooj_Mi_07_159  | Oleria onega | hybrid             | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 424" S    | 76° 13' 394" W   | 1201 |                | 7/31/2007  | 239122 | 182966 |
| Ooj_Mi_07_160  | Oleria onega | ssp. nov. 2        | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 424" S    | 76° 13' 394" W   | 1201 |                | 7/31/2007  | 339588 | 192395 |
| Oos_Mi_02_1585 | Oleria onega | ssp. nov. 2        | F | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 9/14/2002  | 148046 | 121259 |
| Oos_Mi_02_1589 | Oleria onega | ssp. nov. 2        | F | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  | Keith Willmott | 9/14/2002  | 201653 | 145045 |
| Oos_Mi_02_1958 | Oleria onega | janarilla          | F | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 56.33" S  | 76° 13' 10.86" W | 390  |                | 10/7/2002  | 318151 | 178419 |
| Oos_Mi_07_157  | Oleria onega | ssp. nov. 2        | M | Middle3 | 3 |  | Km5 Shapaja-Chazuta            | San Martin | Peru            | 6° 35' 424" S    | 76° 13' 394" W   | 1201 |                | 7/31/2007  | 300656 | 174133 |
| Ooj_Mi_05_829  | Oleria onega | janarilla - hybrid | M | Middle4 | 4 | Camp 2 on trail from Quebrada Yanayacu to Laguna del Mundo Perdido , PNCAZ | San Martin                     | Peru       | 6° 46' 42.06" S | 75° 53' 49.44" W | 517              |      | 9/10/2005      | 406986     | 188518 |        |
| Ooj_Mi_05_830  | Oleria onega | janarilla - hybrid | M | Middle4 | 4 | Camp 2 on trail from Quebrada Yanayacu to Laguna del Mundo Perdido , PNCAZ | San Martin                     | Peru       | 6° 46' 42.06" S | 75° 53' 49.44" W | 517              |      | 9/10/2005      | 389112     | 229671 |        |
| Ooj_Mi_05_831  | Oleria onega | janarilla - hybrid | F | Middle4 | 4 | Camp 2 on trail from Quebrada Yanayacu to Laguna del Mundo Perdido , PNCAZ | San Martin                     | Peru       | 6° 46' 42.06" S | 75° 53' 49.44" W | 517              |      | 9/10/2005      | 169286     | 120139 |        |
| Ooj_Mi_05_832  | Oleria onega | janarilla          | M | Middle4 | 4 | Camp 2 on trail from Quebrada Yanayacu to Laguna del Mundo Perdido , PNCAZ | San Martin                     | Peru       | 6° 46' 42.06" S | 75° 53' 49.44" W | 517              |      | 9/10/2005      | 406041     | 184406 |        |
| Ooj_Mi_05_833  | Oleria onega | janarilla - hybrid | F | Middle4 | 4 | Camp 2 on trail from Quebrada Yanayacu to Laguna del Mundo Perdido , PNCAZ | San Martin                     | Peru       | 6° 46' 42.06" S | 75° 53' 49.44" W | 517              |      | 9/10/2005      | 286051     | 89215  |        |
| Ooj_Mi_05_834  | Oleria onega | janarilla - hybrid | M | Middle4 | 4 | Camp 2 on trail from Quebrada Yanayacu to Laguna del Mundo Perdido , PNCAZ | San Martin                     | Peru       | 6° 46' 42.06" S | 75° 53' 49.44" W | 517              |      | 9/10/2005      | 390592     | 174811 |        |
| Ooj_Mi_05_835  | Oleria onega | janarilla          | M | Middle4 | 4 | Camp 2 on trail from Quebrada Yanayacu to Laguna del Mundo Perdido , PNCAZ | San Martin                     | Peru       | 6° 46' 42.06" S | 75° 53' 49.44" W | 517              |      | 9/10/2005      | 303849     | 171845 |        |
| Ooj_Mi_05_836  | Oleria onega | janarilla          | F | Middle4 | 4 | Camp 2 on trail from Quebrada Yanayacu to Laguna del Mundo Perdido , PNCAZ | San Martin                     | Peru       | 6° 46' 42.06" S | 75° 53' 49.44" W | 517              |      | 9/10/2005      | 385890     | 224777 |        |
| Ooj_Mi_05_837  | Oleria onega | janarilla          | F | Middle4 | 4 | Camp 2 on trail from Quebrada Yanayacu to Laguna del Mundo Perdido , PNCAZ | San Martin                     | Peru       | 6° 46' 42.06" S | 75° 53' 49.44" W | 517              |      | 9/10/2005      | 275970     | 157117 |        |
| Ooj_Mi_05_863  | Oleria onega | janarilla - hybrid | F | Middle4 | 4 | Laguna del Mundo Perdido, PNCAZ  | San Martin                     | Peru       | 6° 45' 4.54" S  | 75° 52' 8.29" W  | 498              |      | 9/11/2005      | 402310     | 184638 |        |

|                |        |       |                    |   |         |   |  |            |      |                 |                  |      |                |           |        |        |
|----------------|--------|-------|--------------------|---|---------|---|--|------------|------|-----------------|------------------|------|----------------|-----------|--------|--------|
| Ooj_Mi_05_864  | Oleria | onega | janarilla - hybrid | M | Middle4 | 4 | Laguna del Mundo Perdido, PNCAZ  | San Martin | Peru | 6° 45' 4.54" S  | 75° 52' 8.29" W  | 498  |                | 9/11/2005 | 357668 | 224635 |
| Ooj_Mi_05_865  | Oleria | onega | janarilla - hybrid | F | Middle4 | 4 | Laguna del Mundo Perdido, PNCAZ  | San Martin | Peru | 6° 45' 4.54" S  | 75° 52' 8.29" W  | 498  |                | 9/11/2005 | 412047 | 189457 |
| Ooj_Mi_05_866  | Oleria | onega | janarilla - hybrid | M | Middle4 | 4 | Laguna del Mundo Perdido, PNCAZ  | San Martin | Peru | 6° 45' 4.54" S  | 75° 52' 8.29" W  | 498  |                | 9/11/2005 | 347567 | 174853 |
| Ooj_Mi_05_810  | Oleria | onega | janarilla - hybrid | M | Middle4 | 4 | Quebrada Yanayacu (Camp 1) to Camp 2 on trail to Laguna del Mundo Perdido, PNCAZ | San Martin | Peru | 6° 44' 55.55" S | 75° 56' 23.44" W | 640  |                | 9/10/2005 | 386582 | 231181 |
| Ooj_Mi_05_811  | Oleria | onega | janarilla - hybrid | M | Middle4 | 4 | Quebrada Yanayacu (Camp 1) to Camp 2 on trail to Laguna del Mundo Perdido, PNCAZ | San Martin | Peru | 6° 44' 55.55" S | 75° 56' 23.44" W | 640  |                | 9/10/2005 | 425980 | 200121 |
| Ooj_Mi_05_812  | Oleria | onega | janarilla - hybrid | F | Middle4 | 4 | Quebrada Yanayacu (Camp 1) to Camp 2 on trail to Laguna del Mundo Perdido, PNCAZ | San Martin | Peru | 6° 44' 55.55" S | 75° 56' 23.44" W | 640  |                | 9/10/2005 | 330543 | 165178 |
| Ooj_Mi_05_813  | Oleria | onega | janarilla - hybrid | M | Middle4 | 4 | Quebrada Yanayacu (Camp 1) to Camp 2 on trail to Laguna del Mundo Perdido, PNCAZ | San Martin | Peru | 6° 44' 55.55" S | 75° 56' 23.44" W | 640  |                | 9/10/2005 | 192508 | 160657 |
| Ooj_Mi_05_815  | Oleria | onega | janarilla          | F | Middle4 | 4 | Quebrada Yanayacu (Camp 1) to Camp 2 on trail to Laguna del Mundo Perdido, PNCAZ | San Martin | Peru | 6° 44' 55.55" S | 75° 56' 23.44" W | 640  |                | 9/10/2005 | 307948 | 168829 |
| Ooj_Mi_05_816  | Oleria | onega | janarilla - hybrid | M | Middle4 | 4 | Quebrada Yanayacu (Camp 1) to Camp 2 on trail to Laguna del Mundo Perdido, PNCAZ | San Martin | Peru | 6° 44' 55.55" S | 75° 56' 23.44" W | 640  |                | 9/10/2005 | 304297 | 130274 |
| Ooj_Mi_05_730  | Oleria | onega | janarilla - hybrid | M | Middle4 | 4 | Robashca to Quebrada Yanayacu, Camp 1, PNCAZ                                     | San Martin | Peru | 6° 44' 26.62" S | 75° 58' 54.31" W | 616  |                | 9/9/2005  | 301524 | 166249 |
| Oos_An_02_1718 | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Aguas Verdes trail  | San Martin | Peru | 5° 39' 50" S    | 77° 38' 58" W    | 1066 | Keith Willmott | 9/19/2002 | 286321 | 169554 |
| Oos_An_02_1719 | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Aguas Verdes trail  | San Martin | Peru | 5° 39' 50" S    | 77° 38' 58" W    | 1066 | Keith Willmott | 9/19/2002 | 462742 | 190396 |
| Oos_An_02_918  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Aguas Verdes trail  | San Martin | Peru | 5° 39' 50" S    | 77° 38' 58" W    | 1066 | Keith Willmott | 8/29/2002 | 392028 | 184165 |
| Oos_An_02_919  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Aguas Verdes trail  | San Martin | Peru | 5° 39' 50" S    | 77° 38' 58" W    | 1066 | Keith Willmott | 8/29/2002 | 342214 | 170008 |
| Oos_An_02_920  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Aguas Verdes trail  | San Martin | Peru | 5° 39' 50" S    | 77° 38' 58" W    | 1066 | Keith Willmott | 8/29/2002 | 349081 | 225905 |
| Oos_An_02_921  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Aguas Verdes trail  | San Martin | Peru | 5° 39' 50" S    | 77° 38' 58" W    | 1066 | Keith Willmott | 8/29/2002 | 350903 | 179186 |
| Oos_An_02_922  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Aguas Verdes trail  | San Martin | Peru | 5° 39' 50" S    | 77° 38' 58" W    | 1066 | Keith Willmott | 8/29/2002 | 348830 | 182579 |
| Oos_An_02_923  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Aguas Verdes trail  | San Martin | Peru | 5° 39' 50" S    | 77° 38' 58" W    | 1066 | Keith Willmott | 8/29/2002 | 254360 | 151347 |
| Oos_An_02_924  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Aguas Verdes trail  | San Martin | Peru | 5° 39' 50" S    | 77° 38' 58" W    | 1066 | Keith Willmott | 8/29/2002 | 142643 | 140786 |
| Oos_An_02_1672 | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/17/2002 | 344175 | 181222 |
| Oos_An_02_1673 | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/17/2002 | 215651 | 187862 |
| Oos_An_02_1675 | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/17/2002 | 215663 | 147556 |
| Oos_An_02_1676 | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/17/2002 | 326070 | 219112 |
| Oos_An_02_1677 | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/17/2002 | 333937 | 175629 |
| Oos_An_02_1678 | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/17/2002 | 199812 | 140256 |
| Oos_An_02_1679 | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/17/2002 | 263049 | 202843 |
| Oos_An_02_1680 | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/17/2002 | 205875 | 141804 |
| Oos_An_02_1682 | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/17/2002 | 222098 | 142853 |
| Oos_An_02_1683 | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/17/2002 | 371159 | 229211 |
| Oos_An_02_1684 | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/17/2002 | 319998 | 173505 |
| Oos_An_02_1685 | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/17/2002 | 280730 | 161994 |
| Oos_An_02_1708 | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/19/2002 | 113182 | 93455  |
| Oos_An_02_1710 | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 9/19/2002 | 347791 | 225594 |
| Oos_An_02_825  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 300325 | 167718 |
| Oos_An_02_826  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 296678 | 172544 |
| Oos_An_02_827  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 210928 | 185109 |
| Oos_An_02_828  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 279793 | 167466 |
| Oos_An_02_830  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 432194 | 238041 |
| Oos_An_02_831  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 366723 | 179649 |
| Oos_An_02_832  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 329948 | 178568 |
| Oos_An_02_833  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 273206 | 158486 |
| Oos_An_02_834  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 252864 | 202717 |
| Oos_An_02_835  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 321874 | 178120 |
| Oos_An_02_836  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 451875 | 187767 |
| Oos_An_02_837  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 310434 | 218288 |
| Oos_An_02_838  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 205329 | 140802 |
| Oos_An_02_839  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 300789 | 212359 |
| Oos_An_02_840  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 212864 | 146524 |
| Oos_An_02_841  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 382792 | 184449 |
| Oos_An_02_842  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 358039 | 226681 |
| Oos_An_02_844  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 192903 | 118397 |
| Oos_An_02_845  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 297813 | 165335 |
| Oos_An_02_847  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 329074 | 179614 |
| Oos_An_02_848  | Oleria | onega | ssp. nov. 2        | F | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 219898 | 137874 |
| Oos_An_02_849  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 351661 | 224683 |
| Oos_An_02_850  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 328030 | 175067 |
| Oos_An_02_851  | Oleria | onega | ssp. nov. 2        | M | Andes   | 5 | Puente Serranoyacu   | San Martin | Peru | 5° 40' 31.6" S  | 77° 40' 28.7" W  | 1201 | Keith Willmott | 8/28/2002 | 238640 | 197139 |

| Locus_ID  | BLASTn Best-Hit           |         |         |       |                  |          |       |                | Danaus plexippus cds                            | Protein homology |
|---|---------------------------|---------|---------|-------|------------------|----------|-------|----------------|---|------------------|
|   | Danaus plexippus scaffold | start   | stop    | %_id  | alignment length | e-value  | Score |                |   |                  |
| <i>Ithomia salapia</i>  |                           |         |         |       |                  |          |       |                |   |                  |
| Adaptive introgression loci (diverging genomic cline center ( $\alpha$ ) + high differentiation level (F <sub>ST</sub> )) |                           |         |         |       |                  |          |       |                |   |                  |
| locus_20794   | DPSCF300001               | 2255382 | 2255463 | 85.37 | 82               | 4,00E-19 | 95.1  | DPOGS207061-TA |   |                  |
| locus_49453   | DPSCF300003               | 1757941 | 1758023 | 80.72 | 83               | 3,00E-14 | 78.8  | DPOGS203415-TA |   |                  |
| locus_19916   | DPSCF300006               | 780102  | 780018  | 83.53 | 85               | 4,00E-18 | 91.5  |                |   |                  |
| locus_20816   | DPSCF300008               | 93324   | 93266   | 87.30 | 63               | 9,00E-14 | 77.0  |                |   |                  |
| locus_14403   | DPSCF300008               | 1238880 | 1238796 | 96.47 | 85               | 1,00E-32 | 140   |                |   |                  |
| locus_28434   | DPSCF300009               | 1937088 | 1937006 | 79.52 | 83               | 1,00E-12 | 73.4  | DPOGS208993-TA |   |                  |
| locus_28611   | DPSCF300010               | 1978358 | 1978428 | 81.69 | 71               | 1,00E-11 | 69.8  |                |   |                  |
| locus_32677   | DPSCF300012               | 1198547 | 1198467 | 81.71 | 82               | 1,00E-11 | 69.8  |                |   |                  |
| locus_91  | DPSCF300014               | 846573  | 846515  | 89.83 | 59               | 8,00E-15 | 80.6  |                |   |                  |
| locus_17576   | DPSCF300015               | 681524  | 681610  | 86.36 | 88               | 3,00E-20 | 98.7  |                |   |                  |
| locus_24148   | DPSCF300017               | 331577  | 331503  | 85.33 | 75               | 2,00E-16 | 86.0  |                |   |                  |
| locus_1838  | DPSCF300017               | 764025  | 763943  | 89.16 | 83               | 2,00E-23 | 109   |                |   |                  |
| locus_13643   | DPSCF300028               | 1192556 | 1192640 | 77.65 | 85               | 5,00E-11 | 68.0  | DPOGS206136-TA |   |                  |
| locus_7322  | DPSCF300064               | 159016  | 158934  | 83.13 | 83               | 5,00E-17 | 87.8  | DPOGS208522-TA |   |                  |
| locus_22050   | DPSCF300073               | 640050  | 639972  | 86.08 | 79               | 1,00E-18 | 93.3  |                |   |                  |
| locus_15377   | DPSCF300081               | 548500  | 548415  | 84.88 | 86               | 1,00E-19 | 96.9  | DPOGS205859-TA | Down syndrome critical region protein 3 homolog |                  |
| locus_18829   | DPSCF300091               | 307474  | 307391  | 85.71 | 84               | 3,00E-20 | 98.7  |                |   |                  |
| locus_16344   | DPSCF300114               | 46930   | 46851   | 81.25 | 80               | 1,00E-13 | 77.0  | DPOGS213191-TA |   |                  |
| locus_15693   | DPSCF300121               | 264102  | 264039  | 84.38 | 64               | 4,00E-12 | 71.6  |                |   |                  |
| locus_12790   | DPSCF300127               | 454398  | 454316  | 83.13 | 83               | 5,00E-17 | 87.8  | DPOGS209486-TA |   |                  |
| locus_11228   | DPSCF300127               | 454413  | 454480  | 83.82 | 68               | 1,00E-12 | 73.4  | DPOGS209486-TA |   |                  |
| locus_11261   | DPSCF300131               | 603666  | 603750  | 80.00 | 85               | 1,00E-13 | 77.0  | DPOGS202495-TA |   |                  |
| locus_15366   | DPSCF300153               | 187359  | 187435  | 81.82 | 77               | 1,00E-13 | 77.0  | DPOGS214916-TA |   |                  |
| locus_14723   | DPSCF300154               | 292667  | 292598  | 85.71 | 70               | 3,00E-14 | 78.8  |                |   |                  |
| locus_874   | DPSCF300176               | 896628  | 896547  | 84.15 | 82               | 2,00E-17 | 89.7  |                |   |                  |
| locus_11740   | DPSCF300177               | 83862   | 83792   | 85.92 | 71               | 6,00E-16 | 84.2  | DPOGS207516-TA |   |                  |
| locus_21620   | DPSCF300200               | 112178  | 112250  | 82.19 | 73               | 1,00E-12 | 73.4  | DPOGS204071-TA | Lactase-phlorizin hydrolase                     |                  |
| locus_5119  | DPSCF300211               | 597     | 508     | 76.67 | 90               | 3,00E-13 | 75.2  |                |   |                  |
| locus_11544   | DPSCF300211               | 279599  | 279549  | 90.20 | 51               | 1,00E-11 | 69.8  |                |   |                  |
| locus_21834   | DPSCF300219               | 461394  | 461479  | 88.37 | 86               | 5,00E-24 | 111   | DPOGS213665-TA |   |                  |
| locus_2581  | DPSCF300232               | 508892  | 508818  | 82.67 | 75               | 1,00E-13 | 77.0  |                |   |                  |
| locus_21052   | DPSCF300268               | 80273   | 80342   | 84.29 | 70               | 1,00E-13 | 77.0  |                |   |                  |
| locus_36372   | DPSCF300307               | 138643  | 138561  | 86.75 | 83               | 3,00E-20 | 98.7  |                |   |                  |
| locus_24886   | DPSCF300324               | 76126   | 76041   | 86.05 | 86               | 2,00E-21 | 102   | DPOGS202701-TA |   |                  |
| locus_63  | DPSCF300338               | 140335  | 140254  | 89.02 | 82               | 6,00E-23 | 107   | DPOGS207656-TA |   |                  |
| locus_29426   | DPSCF300391               | 9101    | 9025    | 87.01 | 77               | 4,00E-19 | 95.1  | DPOGS201653-TA |   |                  |
| locus_47081   | DPSCF300391               | 179887  | 179804  | 80.95 | 84               | 8,00E-15 | 80.6  | DPOGS203107-TA |   |                  |
| <i>Oleria onega</i>   |                           |         |         |       |                  |          |       |                |   |                  |
| Adaptive introgression loci (diverging genomic cline center ( $\alpha$ ) + high differentiation level (F <sub>ST</sub> )) |                           |         |         |       |                  |          |       |                |   |                  |

|             |             |         |         |       |    |          |      |                |  |
|-------------|-------------|---------|---------|-------|----|----------|------|----------------|--|
| locus_39916 | DPSCF300001 | 1760764 | 1760847 | 83.33 | 84 | 2,00E-17 | 89.7 | DPOGS206900-TA |  |
| locus_6600  | DPSCF300001 | 2445655 | 2445571 | 77.65 | 85 | 5,00E-11 | 68.0 | DPOGS207070-TA | Bleomycin hydrolase                                  |
| locus_18737 | DPSCF300001 | 2898435 | 2898352 | 84.52 | 84 | 1,00E-18 | 93.3 | DPOGS206854-TA |  |
| locus_291   | DPSCF300001 | 4348908 | 4348825 | 79.07 | 86 | 1,00E-11 | 69.8 |                |  |
| locus_24405 | DPSCF300004 | 1289625 | 1289544 | 84.15 | 82 | 2,00E-17 | 89.7 | DPOGS211019-TA |  |
| locus_18889 | DPSCF300004 | 1527412 | 1527329 | 88.10 | 84 | 6,00E-23 | 107  |                |  |
| locus_11213 | DPSCF300006 | 94744   | 94826   | 81.93 | 83 | 2,00E-15 | 82.4 | DPOGS201471-TA |  |
| locus_30280 | DPSCF300006 | 804531  | 804587  | 87.72 | 57 | 4,00E-12 | 71.6 | DPOGS201447-TA |  |
| locus_6020  | DPSCF300009 | 179886  | 179969  | 90.48 | 84 | 1,00E-25 | 116  | DPOGS208940-TA | Contactin  |
| locus_63224 | DPSCF300009 | 765102  | 765185  | 89.29 | 84 | 5,00E-24 | 111  | DPOGS208957-TA |  |
| locus_41437 | DPSCF300009 | 1494818 | 1494900 | 95.18 | 83 | 1,00E-30 | 132  |                |  |
| locus_5544  | DPSCF300014 | 973146  | 973230  | 87.06 | 85 | 7,00E-22 | 104  |                |  |
| locus_53694 | DPSCF300019 | 1083985 | 1084069 | 78.82 | 85 | 1,00E-12 | 73.4 | DPOGS212316-TA |  |
| locus_6837  | DPSCF300024 | 24576   | 24661   | 83.72 | 86 | 4,00E-18 | 91.5 |                |  |
| locus_939   | DPSCF300027 | 157690  | 157608  | 89.16 | 83 | 2,00E-23 | 109  |                |  |
| locus_36129 | DPSCF300038 | 1105994 | 1106051 | 91.38 | 58 | 2,00E-15 | 82.4 |                |  |
| locus_28726 | DPSCF300041 | 1563919 | 1563853 | 92.54 | 67 | 3,00E-20 | 98.7 |                |  |
| locus_7639  | DPSCF300042 | 1148866 | 1148782 | 85.88 | 85 | 8,00E-21 | 100  | DPOGS207841-TA |  |
| locus_20657 | DPSCF300048 | 132467  | 132383  | 96.47 | 85 | 1,00E-31 | 136  |                |  |
| locus_5259  | DPSCF300049 | 818458  | 818521  | 87.50 | 64 | 3,00E-14 | 78.8 |                |  |
| locus_39337 | DPSCF300050 | 197880  | 197799  | 87.80 | 82 | 7,00E-22 | 104  | DPOGS214621-TA |  |
| locus_5676  | DPSCF300051 | 459989  | 460071  | 85.54 | 83 | 1,00E-19 | 96.9 | DPOGS207483-TA |  |
| locus_40167 | DPSCF300051 | 482393  | 482477  | 88.24 | 85 | 2,00E-23 | 109  | DPOGS207445-TA |  |
| locus_51320 | DPSCF300052 | 511744  | 511813  | 90.00 | 70 | 4,00E-18 | 91.5 |                |  |
| locus_9796  | DPSCF300053 | 1109584 | 1109645 | 83.87 | 62 | 5,00E-11 | 68.0 |                |  |
| locus_30776 | DPSCF300056 | 274712  | 274639  | 81.08 | 74 | 4,00E-12 | 71.6 | DPOGS205507-TA |  |
| locus_4041  | DPSCF300057 | 52461   | 52377   | 77.65 | 85 | 5,00E-11 | 68.0 |                |  |
| locus_11635 | DPSCF300058 | 44474   | 44542   | 86.96 | 69 | 5,00E-16 | 84.2 | DPOGS208156-TA |  |
| locus_16883 | DPSCF300064 | 259762  | 259678  | 84.71 | 85 | 4,00E-19 | 95.1 | DPOGS208524-TA |  |
| locus_14881 | DPSCF300064 | 1707322 | 1707239 | 89.29 | 84 | 5,00E-24 | 111  | DPOGS208460-TA | Cadherin-related tumor suppressor                    |
| locus_40108 | DPSCF300066 | 454834  | 454751  | 84.52 | 84 | 4,00E-18 | 91.5 |                |  |
| locus_14418 | DPSCF300073 | 565519  | 565435  | 92.94 | 85 | 6,00E-29 | 127  |                |  |
| locus_16119 | DPSCF300082 | 1222334 | 1222416 | 86.75 | 83 | 8,00E-21 | 100  | DPOGS206300-TA |  |
| locus_36677 | DPSCF300089 | 376974  | 376890  | 84.71 | 85 | 4,00E-19 | 95.1 | DPOGS205916-TA | Serine/threonine-protein kinase N3                   |
| locus_35425 | DPSCF300094 | 144496  | 144424  | 82.89 | 76 | 1,00E-13 | 77.0 |                |  |
| locus_25295 | DPSCF300095 | 151289  | 151371  | 91.76 | 85 | 9,00E-27 | 120  |                |  |
| locus_17924 | DPSCF300095 | 220263  | 220183  | 81.48 | 81 | 3,00E-14 | 78.8 |                |  |
| locus_19646 | DPSCF300098 | 588403  | 588320  | 94.05 | 84 | 2,00E-29 | 129  |                |  |
| locus_31990 | DPSCF300122 | 617164  | 617245  | 82.93 | 82 | 2,00E-16 | 86.0 | DPOGS214469-TA | Potassium voltage-gated channel subfamily D member 2 |
| locus_30027 | DPSCF300125 | 447801  | 447882  | 84.34 | 83 | 5,00E-17 | 87.8 |                |  |
| locus_23486 | DPSCF300128 | 685283  | 685351  | 82.61 | 69 | 4,00E-12 | 71.6 | DPOGS200181-TA | Chromodomain-helicase-DNA-binding protein 4          |
| locus_8696  | DPSCF300131 | 292633  | 292709  | 79.22 | 77 | 5,00E-11 | 68.0 | DPOGS202524-TA | Dynein heavy chain, cytoplasmic                      |
| locus_17973 | DPSCF300133 | 205697  | 205773  | 80.52 | 77 | 4,00E-12 | 71.6 |                |  |
| locus_9927  | DPSCF300145 | 423602  | 423519  | 90.48 | 84 | 1,00E-25 | 116  | DPOGS206960-TA |  |
| locus_17455 | DPSCF300154 | 359812  | 359895  | 78.57 | 84 | 4,00E-12 | 71.6 | DPOGS208109-TA |  |
| locus_38972 | DPSCF300162 | 224765  | 224849  | 84.71 | 85 | 4,00E-19 | 95.1 | DPOGS202151-TA |  |
| locus_40071 | DPSCF300168 | 21644   | 21726   | 81.93 | 83 | 2,00E-15 | 82.4 | DPOGS210608-TA |  |
| locus_3709  | DPSCF300168 | 103826  | 103878  | 88.68 | 53 | 1,00E-11 | 69.8 |                |  |
| locus_21454 | DPSCF300170 | 429546  | 429467  | 86.25 | 80 | 4,00E-19 | 95.1 |                |  |

|             |             |        |        |       |    |          |      |                |                                    |
|-------------|-------------|--------|--------|-------|----|----------|------|----------------|------------------------------------|
| locus_14350 | DPSCF300171 | 455112 | 455200 | 88.76 | 89 | 4,00E-25 | 114  |                |                                    |
| locus_38803 | DPSCF300182 | 11272  | 11350  | 87.34 | 79 | 3,00E-20 | 98.7 | DPOGS216113-TA |                                    |
| locus_13278 | DPSCF300184 | 311089 | 310999 | 81.32 | 91 | 2,00E-17 | 89.7 | DPOGS204141-TA |                                    |
| locus_21125 | DPSCF300188 | 254025 | 253943 | 80.72 | 83 | 3,00E-14 | 78.8 | DPOGS207347-TA |                                    |
| locus_27398 | DPSCF300206 | 88373  | 88457  | 88.24 | 85 | 2,00E-23 | 109  |                |                                    |
| locus_14969 | DPSCF300210 | 32672  | 32755  | 83.33 | 84 | 2,00E-17 | 89.7 | DPOGS203241-TA | E3 ubiquitin-protein ligase Smurf1 |
| locus_12981 | DPSCF300212 | 876257 | 876175 | 84.34 | 83 | 4,00E-18 | 91.5 | DPOGS213742-TA |                                    |
| locus_38548 | DPSCF300219 | 579537 | 579452 | 84.88 | 86 | 1,00E-19 | 96.9 | DPOGS213705-TA |                                    |
| locus_23097 | DPSCF300231 | 390393 | 390313 | 92.59 | 81 | 9,00E-27 | 120  | DPOGS204749-TA |                                    |
| locus_38495 | DPSCF300242 | 161615 | 161690 | 82.89 | 76 | 3,00E-14 | 78.8 | DPOGS203439-TA |                                    |
| locus_16210 | DPSCF300258 | 210889 | 210825 | 83.08 | 65 | 5,00E-11 | 68.0 |                |                                    |
| locus_20793 | DPSCF300270 | 226701 | 226777 | 81.82 | 77 | 1,00E-13 | 77.0 | DPOGS208007-TA |                                    |
| locus_6434  | DPSCF300271 | 119860 | 119810 | 94.12 | 51 | 3,00E-14 | 78.8 |                |                                    |
| locus_42203 | DPSCF300296 | 235411 | 235349 | 87.30 | 63 | 3,00E-13 | 75.2 |                |                                    |
| locus_3798  | DPSCF300325 | 4824   | 4749   | 84.21 | 76 | 6,00E-16 | 84.2 | DPOGS211639-TA |                                    |
| locus_52767 | DPSCF300382 | 158605 | 158685 | 90.12 | 81 | 5,00E-24 | 111  | DPOGS206254-TA |                                    |
| locus_21333 | DPSCF300547 | 1509   | 1588   | 92.50 | 80 | 4,00E-25 | 114  |                |                                    |

*Oleria onega*

Reproductive isolation loci (high diverging positive genomic cline rate ( $\beta$ ))

|             |             |         |         |        |    |          |      |                |  |
|-------------|-------------|---------|---------|--------|----|----------|------|----------------|--|
| locus_56496 | DPSCF300002 | 448758  | 448841  | 83.33  | 84 | 2,00E-17 | 89.7 | DPOGS204463-TA |  |
| locus_23233 | DPSCF300002 | 1313553 | 1313619 | 85.07  | 67 | 1,00E-13 | 77.0 |                |  |
| locus_14217 | DPSCF300009 | 1484490 | 1484408 | 97.59  | 83 | 3,00E-32 | 138  |                |  |
| locus_41437 | DPSCF300009 | 1494818 | 1494900 | 95.18  | 83 | 1,00E-30 | 132  |                |  |
| locus_6715  | DPSCF300010 | 503894  | 503822  | 83.56  | 73 | 3,00E-14 | 78.8 |                |  |
| locus_13325 | DPSCF300010 | 1174123 | 1174177 | 96.36  | 55 | 3,00E-18 | 91.5 |                |  |
| locus_7285  | DPSCF300010 | 2856044 | 2856110 | 97.01  | 67 | 1,00E-24 | 113  |                |  |
| locus_16456 | DPSCF300011 | 910922  | 910840  | 81.93  | 83 | 2,00E-15 | 82.4 | DPOGS211875-TA |  |
| locus_2045  | DPSCF300012 | 17595   | 17663   | 88.57  | 70 | 6,00E-16 | 84.2 |                |  |
| locus_5796  | DPSCF300013 | 724317  | 724236  | 85.37  | 82 | 4,00E-19 | 95.1 | DPOGS210690-TA |  |
| locus_5544  | DPSCF300014 | 973146  | 973230  | 88.24  | 85 | 2,00E-23 | 109  |                |  |
| locus_13402 | DPSCF300014 | 2159403 | 2159488 | 95.35  | 86 | 3,00E-32 | 138  |                |  |
| locus_5347  | DPSCF300018 | 791599  | 791676  | 83.33  | 78 | 2,00E-15 | 82.4 | DPOGS202792-TA |  |
| locus_635   | DPSCF300019 | 386290  | 386224  | 91.04  | 67 | 4,00E-19 | 95.1 |                |  |
| locus_6133  | DPSCF300021 | 679108  | 679192  | 94.12  | 85 | 5,00E-30 | 131  |                |  |
| locus_17850 | DPSCF300021 | 1255675 | 1255754 | 82.50  | 80 | 2,00E-15 | 82.4 |                |  |
| locus_3400  | DPSCF300022 | 1406128 | 1406086 | 100.00 | 43 | 3,00E-14 | 78.8 |                |  |
| locus_2334  | DPSCF300025 | 217171  | 217087  | 89.41  | 85 | 1,00E-24 | 113  | DPOGS210344-TA | Low-density lipoprotein receptor-related protein 2 |
| locus_53    | DPSCF300028 | 1715782 | 1715719 | 87.50  | 64 | 8,00E-15 | 80.6 |                |  |
| locus_7065  | DPSCF300030 | 1210754 | 1210819 | 89.39  | 66 | 4,00E-16 | 84.2 |                |  |
| locus_56182 | DPSCF300032 | 800216  | 800170  | 95.83  | 48 | 3,00E-13 | 75.2 |                |  |
| locus_9208  | DPSCF300033 | 37338   | 37255   | 83.33  | 84 | 1,00E-17 | 89.7 | DPOGS213564-TA | Protein disulfide-isomerase                        |
| locus_39358 | DPSCF300034 | 225066  | 225150  | 85.88  | 85 | 8,00E-21 | 100  | DPOGS204184-TA |  |
| locus_36129 | DPSCF300038 | 1105994 | 1106051 | 91.38  | 58 | 2,00E-15 | 82.4 |                |  |
| locus_9061  | DPSCF300041 | 1435324 | 1435406 | 87.95  | 83 | 2,00E-22 | 105  | DPOGS215762-TA |  |
| locus_18124 | DPSCF300041 | 1632655 | 1632739 | 84.71  | 85 | 4,00E-19 | 95.1 | DPOGS215771-TA | Uncharacterized helicase C17H9.02                  |
| locus_7639  | DPSCF300042 | 1148866 | 1148782 | 85.88  | 85 | 8,00E-21 | 100  | DPOGS207841-TA |  |
| locus_15855 | DPSCF300044 | 922991  | 923073  | 83.53  | 85 | 2,00E-15 | 82.4 |                |  |

|             |             |        |        |       |    |          |      |                |  |
|-------------|-------------|--------|--------|-------|----|----------|------|----------------|--|
| locus_9976  | DPSCF300047 | 27674  | 27596  | 83.54 | 79 | 7,00E-16 | 84.2 | DPOGS215265-TA |  |
| locus_13421 | DPSCF300048 | 729948 | 730032 | 87.06 | 85 | 7,00E-22 | 104  | DPOGS206628-TA |  |
| locus_16663 | DPSCF300048 | 860848 | 860929 | 92.68 | 82 | 3,00E-27 | 122  |                |  |
| locus_11355 | DPSCF300052 | 339442 | 339358 | 80.00 | 85 | 1,00E-13 | 77.0 | DPOGS208609-TA |  |
| locus_51320 | DPSCF300052 | 511744 | 511813 | 90.00 | 70 | 4,00E-18 | 91.5 |                |  |
| locus_16883 | DPSCF300064 | 259762 | 259678 | 84.71 | 85 | 4,00E-19 | 95.1 | DPOGS208524-TA |  |
| locus_1104  | DPSCF300066 | 72184  | 72264  | 82.72 | 81 | 8,00E-15 | 80.6 |                |  |
| locus_14418 | DPSCF300073 | 565519 | 565435 | 92.94 | 85 | 6,00E-29 | 127  |                |  |
| locus_26323 | DPSCF300074 | 116559 | 116475 | 84.71 | 85 | 4,00E-19 | 95.1 | DPOGS205078-TA |  |
| locus_3251  | DPSCF300082 | 579057 | 579142 | 83.72 | 86 | 1,00E-18 | 93.3 | DPOGS206318-TA | DNA-directed RNA polymerase I subunit rpa1                 |
| locus_6613  | DPSCF300092 | 467872 | 467788 | 89.41 | 85 | 2,00E-23 | 109  |                |  |
| locus_17924 | DPSCF300095 | 220263 | 220183 | 81.48 | 81 | 3,00E-14 | 78.8 |                |  |
| locus_17571 | DPSCF300099 | 149029 | 149094 | 93.94 | 66 | 2,00E-21 | 102  |                |  |
| locus_6969  | DPSCF300112 | 257821 | 257733 | 87.64 | 89 | 1,00E-24 | 113  |                |  |
| locus_42925 | DPSCF300117 | 317371 | 317306 | 83.58 | 67 | 5,00E-11 | 68.0 |                |  |
| locus_80    | DPSCF300119 | 307017 | 306933 | 98.82 | 85 | 2,00E-35 | 149  |                |  |
| locus_8829  | DPSCF300128 | 685276 | 685191 | 77.91 | 86 | 1,00E-11 | 69.8 | DPOGS200181-TA | Chromodomain-helicase-DNA-binding protein 4                |
| locus_23486 | DPSCF300128 | 685283 | 685351 | 82.61 | 69 | 4,00E-12 | 71.6 | DPOGS200181-TA | Chromodomain-helicase-DNA-binding protein 4                |
| locus_10447 | DPSCF300129 | 295733 | 295816 | 91.67 | 84 | 9,00E-27 | 120  | DPOGS215550-TA |  |
| locus_8696  | DPSCF300131 | 292633 | 292709 | 79.22 | 77 | 5,00E-11 | 68.0 | DPOGS202524-TA | Dynein heavy chain, cytoplasmic                            |
| locus_24658 | DPSCF300153 | 302796 | 302868 | 80.82 | 73 | 1,00E-11 | 69.8 | DPOGS214919-TA | Structural maintenance of chromosomes protein 4 (Fragment) |
| locus_50550 | DPSCF300160 | 254056 | 254135 | 81.25 | 80 | 3,00E-14 | 78.8 |                |  |
| locus_4637  | DPSCF300160 | 502195 | 502271 | 89.61 | 77 | 7,00E-22 | 104  |                |  |
| locus_1279  | DPSCF300160 | 533929 | 534011 | 96.39 | 83 | 1,00E-31 | 136  |                |  |
| locus_25495 | DPSCF300170 | 555014 | 554930 | 92.94 | 85 | 6,00E-29 | 127  | DPOGS204700-TA | Inhibitor of growth protein 4                              |
| locus_760   | DPSCF300171 | 509326 | 509246 | 91.36 | 81 | 4,00E-25 | 114  |                |  |
| locus_15055 | DPSCF300172 | 330603 | 330522 | 81.71 | 82 | 8,00E-15 | 80.6 | DPOGS205104-TA | ATP-binding cassette sub-family G member 4                 |
| locus_44871 | DPSCF300176 | 877906 | 877987 | 81.71 | 82 | 8,00E-15 | 80.6 | DPOGS201276-TA |  |
| locus_13278 | DPSCF300184 | 311089 | 310999 | 81.32 | 91 | 2,00E-17 | 89.7 | DPOGS204141-TA |  |
| locus_10628 | DPSCF300189 | 257    | 334    | 82.05 | 78 | 3,00E-14 | 78.8 | DPOGS212552-TA |  |
| locus_45809 | DPSCF300192 | 328851 | 328931 | 90.12 | 81 | 5,00E-24 | 111  |                |  |
| locus_50    | DPSCF300196 | 630167 | 630237 | 92.96 | 71 | 2,00E-22 | 105  | DPOGS207656-TA |  |
| locus_36202 | DPSCF300224 | 20899  | 20974  | 89.47 | 76 | 2,00E-21 | 102  |                |  |
| locus_3993  | DPSCF300235 | 508167 | 508086 | 84.34 | 83 | 5,00E-17 | 87.8 |                |  |
| locus_4021  | DPSCF300250 | 293523 | 293607 | 95.29 | 85 | 1,00E-31 | 136  |                |  |
| locus_19317 | DPSCF300258 | 53527  | 53451  | 80.52 | 77 | 4,00E-12 | 71.6 | DPOGS212418-TA |  |
| locus_16210 | DPSCF300258 | 210889 | 210825 | 83.08 | 65 | 5,00E-11 | 68.0 |                |  |
| locus_11201 | DPSCF300283 | 220103 | 220179 | 84.42 | 77 | 2,00E-16 | 86.0 | DPOGS210186-TA |  |
| locus_21486 | DPSCF300298 | 103299 | 103230 | 82.19 | 73 | 4,00E-12 | 71.6 | DPOGS215444-TA |  |
| locus_13053 | DPSCF300300 | 50254  | 50175  | 91.25 | 80 | 1,00E-24 | 113  |                |  |
| locus_14218 | DPSCF300304 | 184614 | 184531 | 79.76 | 84 | 3,00E-13 | 75.2 | DPOGS210561-TA | Cyclin-dependent kinase 2                                  |
| locus_9530  | DPSCF300407 | 236218 | 236141 | 84.62 | 78 | 6,00E-16 | 84.2 | DPOGS205394-TA | Fructose-1,6-bisphosphatase isozyme 2                      |
| locus_878   | DPSCF300424 | 30626  | 30707  | 89.02 | 82 | 6,00E-23 | 107  |                |  |
| locus_8293  | DPSCF300446 | 77824  | 77901  | 92.31 | 78 | 5,00E-24 | 111  |                |  |
| locus_17    | DPSCF300575 | 2185   | 2124   | 90.32 | 62 | 2,00E-16 | 86.0 |                |  |

| Locus_ID               | BLASTn Best-Hit           |         |         |       |                  |          |       | Danaus plexippus cds | Protein homology                                |
|------------------------|---------------------------|---------|---------|-------|------------------|----------|-------|----------------------|---|
|                        | Danaus plexippus scaffold | start   | stop    | %_id  | alignment length | e-value  | Score |                      |   |
| <i>Ithomia salapia</i> |                           |         |         |       |                  |          |       |                      |   |
| locus_575              | DPSCF300006               | 929124  | 929055  | 85.71 | 70               | 2E-15    | 82.4  |                      |   |
| locus_10434            | DPSCF300037               | 729941  | 730017  | 81.82 | 77               | 1E-12    | 73.4  |                      |   |
| locus_6641             | DPSCF300038               | 1144841 | 1144764 | 86.42 | 81               | 4E-19    | 95.1  | DPOGS212179-TA       | Serine/threonine kinase                         |
| locus_5230             | DPSCF300046               | 93689   | 93772   | 96.43 | 84               | 3E-32    | 138   |                      |   |
| locus_11053            | DPSCF300054               | 645838  | 645902  | 89.23 | 65               | 3E-14    | 78.8  |                      |   |
| locus_3841             | DPSCF300071               | 431640  | 431701  | 88.71 | 62               | 8E-15    | 80.6  |                      |   |
| locus_15377            | DPSCF300081               | 548500  | 548415  | 84.88 | 86               | 1E-19    | 96.9  | DPOGS205859-TA       | Down syndrome critical region protein 3 homolog |
| locus_10724            | DPSCF300164               | 45882   | 45969   | 85.23 | 88               | 3E-20    | 98.7  |                      |   |
| locus_16002            | DPSCF300171               | 38821   | 38903   | 80.72 | 83               | 3E-14    | 78.8  | DPOGS214065-TA       | Carnitine O-palmitoyltransferase 2              |
| locus_2581             | DPSCF300232               | 508892  | 508818  | 82.67 | 75               | 1E-13    | 77.0  |                      |   |
| locus_9663             | DPSCF300395               | 68400   | 68317   | 89.29 | 84               | 5E-24    | 111   |                      |   |
| locus_4352             | DPSCF300598               | 15776   | 15694   | 80.72 | 83               | 3E-14    | 78.8  | DPOGS200524-TA       |   |
| <i>Oleria onega</i>    |                           |         |         |       |                  |          |       |                      |   |
| locus_6600             | DPSCF300001               | 2445655 | 2445571 | 80.00 | 85               | 1,00E-13 | 77.0  | DPOGS207070-TA       | Bleomycin hydrolase                             |
| locus_54320            | DPSCF300001               | 2487997 | 2488051 | 89.09 | 55               | 1,00E-12 | 73.4  | DPOGS207073-TA       |   |
| locus_2138             | DPSCF300001               | 5999940 | 5999893 | 91.67 | 48               | 1,00E-11 | 69.8  |                      |   |
| locus_5821             | DPSCF300002               | 991352  | 991435  | 78.57 | 84               | 4,00E-12 | 71.6  | DPOGS204406-TA       |   |
| locus_18347            | DPSCF300012               | 275034  | 274963  | 86.11 | 72               | 2,00E-16 | 86.0  |                      |   |
| locus_50               | DPSCF300013               | 1476318 | 1476235 | 90.48 | 84               | 1,00E-25 | 116   | DPOGS207656-TA       |   |
| locus_2696             | DPSCF300016               | 1060706 | 1060623 | 83.33 | 84               | 2,00E-17 | 89.7  | DPOGS213145-TA       | Thioredoxin-like protein 1                      |
| locus_291              | DPSCF300046               | 701709  | 701774  | 92.42 | 66               | 1,00E-19 | 96.9  | DPOGS204311-TA       |   |
| locus_4636             | DPSCF300051               | 713048  | 712964  | 87.06 | 85               | 7,00E-22 | 104   | DPOGS207490-TA       | Teneurin-a                                      |
| locus_302              | DPSCF300063               | 548496  | 548419  | 81.18 | 85               | 3,00E-14 | 78.8  |                      |   |
| locus_14881            | DPSCF300064               | 1707322 | 1707239 | 91.67 | 84               | 9,00E-27 | 120   | DPOGS208460-TA       | Cadherin-related tumor suppressor               |
| locus_2602             | DPSCF300073               | 701149  | 701226  | 88.46 | 78               | 1,00E-19 | 96.9  |                      |   |
| locus_8241             | DPSCF300086               | 693323  | 693404  | 86.59 | 82               | 3,00E-20 | 98.7  |                      |   |
| locus_24045            | DPSCF300115               | 366338  | 366397  | 95.00 | 60               | 3,00E-19 | 95.1  |                      |   |
| locus_6523             | DPSCF300120               | 68784   | 68700   | 83.53 | 85               | 4,00E-18 | 91.5  | DPOGS215317-TA       | Innexin inx1                                    |
| locus_12311            | DPSCF300162               | 175614  | 175527  | 81.82 | 88               | 2,00E-16 | 86.0  |                      |   |
| locus_6481             | DPSCF300196               | 262147  | 262068  | 82.50 | 80               | 2,00E-15 | 82.4  |                      |   |
| locus_1830             | DPSCF300209               | 256021  | 255940  | 86.59 | 82               | 3,00E-19 | 95.1  |                      |   |
| locus_47502            | DPSCF300221               | 281710  | 281775  | 82.86 | 70               | 5,00E-11 | 68.0  |                      |   |
| locus_878              | DPSCF300424               | 30618   | 30696   | 92.50 | 80               | 5,00E-24 | 111   |                      |   |
| locus_14178            | DPSCF300431               | 40916   | 41000   | 77.65 | 85               | 5,00E-11 | 68.0  |                      |   |



*Aeria eurimedia  
negricola*



*Ithomia salapia  
derasa*  
(Andes)



*Napeogenes pharo  
lamia*



*Scada reckia  
junina*



*Scada reckia  
quotidiana*



*Napeogenes pharo  
ssp nov*



*Scada reckia  
ethica*



*Scada zibia  
batesi*



*Episcada sulphurea  
ssp nov*



*Ithomia salapia  
aquinia*  
(Amazon)



*Hypoleria xenophis*



*Pteronymia primula  
primula*



*Mcclungia cymo  
subtilis*



*Napeogenes inachia  
patentia*



*Napeogenes pharo  
pharo*



*Napeogenes inachia  
pozziana*



*Napeogenes juanjuiensis  
juanjuiensis*



*Pseudoleria aelia  
pachiteae*



*Oleria onega  
ssp nov 2*  
(Andes)



*Hypoleria virginia  
oriana*



*Hyoscada zarepha  
flexibilis*



*Napeogenes sylphis  
rindgei*



*Hypoleria virginia  
orianula*



*Hyoscada illinissa  
ssp nov 4*



*Oleria onega  
janarilla*  
(Amazon)



*Oleria onega  
lerida*



*Oleria agarista  
agarista*



*Oleria astrea  
tigilla*



*Oleria gunilla  
lotta*



*Oleria gunilla  
serdolis*



