

# 24 **Author contributions**

25 Conceived and designed the experiments: JNF, IMDC. Performed the experiments: IMDC, JNF, 26 PLV. Analyzed the data: IMDC, JM, JNF. Contributed reagents/materials/analysis tools: IMDC, 27 JNF, CMFO, PLV, JM. Wrote the paper: IMDC, JNF, JM.

28

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- 71 **Abstract**
- 72

73 Since most species are collections of genetically variable populations distributed to habitats 74 differing in their abiotic/biotic environmental factors and community composition, the pattern 75 and strength of natural selection imposed by species on each others' traits are also expected to be 76 highly spatially variable. Here, we used genomic and quantitative genetic approaches to 77 understand how spatially variable selection operates on the genetic basis of plant defenses to 78 herbivores. To this end, an F2 progeny was generated by crossing *Datura stramonium* 79 (Solanaceae) parents from two populations differing in their level of chemical defense. This  $F_2$ 80 progeny was reciprocally transplanted into the parental plants' habitats and by measuring the 81 Identity by Descent (IBD) relationship of each F<sub>2</sub> plant to each parent, we were able to elucidate 82 how spatially variable selection imposed by herbivores operated on the genetic background 83 (IBD) of resistance to herbivory, promoting local adaptation. The results highlight that plants 84 possessing the highest total alkaloid concentrations (sum of all alkaloid classes) were not the 85 most well-defended or fit. Instead, specific alkaloids and their linked loci/alleles were favored by 86 selection imposed by different herbivores. This has led to population differentiation in plant 87 defenses and thus, to local adaptation driven by plant-herbivore interactions.

88

89 **Key words.** *Datura stramonium*, identity by descent, local adaptation, plant-herbivore 90 interactions, phenotypic selection, resistance.

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# 95 **Introduction**

96 Coevolution between plants and insects that feed on them is thought to be fueled by reciprocal 97 selection imposed by traits (or trait states) that mediate the interaction, potentially given rise to 98 arms races (Ehrlich and Raven 1964; Dawkins and Krebs 1979; Thompson 2005; Janz 2011). At 99 the microevolutionary scale, spatial environmental variation may result in a selection mosaic that 100 favors different traits (or trait states), hence promoting phenotypic and genetic/genomic 101 divergence among populations, and thereby local adaptation (Gomulkiewicz *et al*. 2002; 102 Thompson and Cunningham 2002; Thompson 2005; Briscoe Runquist *et al*. 2020). For instance, 103 plant populations are likely to encounter different communities of herbivores both in space and 104 time (Stam *et al*. 2014), making it highly improbable that selection pressures on plant defense 105 traits (*e. g*., chemical secondary compounds) would be homogenous across populations 106 (Berenbaum *et al*. 1986; Charlesworth 1998; Züst *et al.* 2012). Thus, it is expected that natural 107 selection on plant-herbivore interactions between environments can lead to population 108 differentiation of plant defense traits and ultimately to local adaptation. However, evidence of 109 how varying herbivore communities impose selection of phenotypic defense variation, and their 110 role in shaping the genomic constitution of populations is still scarce (Briscoe Runquist *et al*. 111 2020).

112 Local adaptation of plant defense against insect herbivores has been primarily studied 113 using traditional quantitative genetic approaches such as common garden and reciprocal 114 transplant experiments (Kawecki and Ebert 2004; de Villemereuil *et al.* 2016). These traditional 115 approaches along with recent advances in genomics and mass spectrometry have made it 116 possible to conduct detailed analyses of the genetic basis of chemical-based plant defense 117 (Savolainen *et al.* 2013). For example, Identity by Descent analyses (IBD), genome-wide

118 association analyses (GWAS), quantitative trait loci mapping (QTL), or *F*ST *vs*. *Q*ST comparisons, 119 provide methodologies to conduct in-depth studies on how plant chemical defense have evolved 120 in response to spatial variation in plant-insect interactions (Browning and Browning 2012; 121 Savolainen *et al.* 2013; Anderson *et al*. 2014; Flood and Hancock 2017). 122 In particular, IBD analysis estimates to what extent two or more individuals inherit a 123 similar nucleotide sequence from a common ancestor (Thompson 2013) and describes the degree 124 of genetic/familial similarity among a group of individuals (*e. g*., parents-offspring; Albrechtsen 125 *et al.* 2010; Thompson 2013). Thus, IBD can be used to evaluate whether the genetic background 126 of a plant is associated with its ability to face its herbivores. Furthermore, it also allows to detect 127 patterns of very recent or ongoing selection in the genome (Albrechtsen *et al.* 2010). For 128 instance, if insect herbivores are reducing the fitness of individual plants, one might suppose that 129 more resistant plants to herbivory will produce more progeny than less resistant plants (Núñez-130 Farfán *et al.* 2007). If so, then ongoing natural selection will increase, across generations, the 131 amount of IBD sharing in a population in the region surrounding the allele(s) that confer(s) 132 resistance to herbivory (Browning and Browning 2012). The reasoning behind this is that as a 133 positively selected allele increases in frequency, the region containing the resistance allele will 134 increase in homozygosity and experience less intra-allelic recombination at the population level 135 (Albrechtsen *et al.* 2010). While IBD analysis has been used to identify how recent or ongoing 136 selection operates on human diseases caused by pathogens (Albrechtsen *et al.* 2009; 2010; 137 Daniels *et al*. 2015; Wong *et al*. 2017; Henden *et al.* 2018), to best of our knowledge, no studies 138 have used this approach to evaluate how the genetic background of plant resistance to herbivory 139 is driven by natural selection.

140 The main aim of this study was to assess the extent to which the evolution of plant 141 defenses to insect herbivores has been driven by natural selection. To this end, we generated an 142 F2 progeny derived from the cross between two populations of the annual herb *Datura*  143 *stramonium* (Asteridae; Solanaceae), known to differ in their level of chemical defense and 144 herbivore community (De-la-Cruz *et al.* 2020). The F2 plants were reciprocally transplanted to 145 the natural environments (populations) of the grandparents. In this way, we were able to 1) 146 determine the level of infestation and damage exerted by different herbivores on plants sowed in 147 each locality, 2) to determine whether the seven most abundant constitutive alkaloids of *D.*  148 *stramonium* are linked to the level of herbivore infestation. 3) by estimating the Identity by 149 Descent (IBD) relationship of each F<sub>2</sub> plant to each grandparent, we were able to evaluate 150 whether genomic similarity to either of the grandparents predicts survival/fitness and resistance 151 to herbivores in each experimental site. Finally, 4) by quantifying the strength of natural 152 selection on plant defense traits in the two experimental sites, we assessed whether natural 153 selection favors an increase in plant resistance against herbivores in each of the two study sites. 154 155 **Materials and Methods**  156 **The study sites**  157 The two study sites, Teotihuacán (State of Mexico, 19°41'6.96"N, 98°52'19.63"W) and Ticumán 158 (State of Morelos, 18°45'39.90"N, 99° 7'13.86"W), were selected for four main reasons. First, 159 the two populations occur in different habitats with distinct climatic characteristics (xerophytic 160 shrub and tropical dry forest, respectively; Valverde *et al*. 2001). Second, species of herbivores 161 that infest upon *D. stramonium* differ between the sites (see also Results); in Ticuman, *D.*  162 *stramonium* is attacked mainly by the specialist flea beetle *Epitrix* sp. (Valverde *et al.* 2001;



173

# 174 **Experimental design**

175 To produce the F2 generation progeny for this study, we randomly collected fruits from 45 and 176 47 different plants from the Teotihuacán and Ticumán sites, respectively. Ten seeds from each of 177 the 92 plants were soaked in water containers and maintained in an environmental chamber at a 178 photoperiod of 12:12 L:D, and at a temperature of 30°C during the day and 25°C at night, at 179 constant humidity of 85%. Seeds were scarified to facilitate germination (Fornoni *et al.* 2000). 180 Germinated seeds were transferred to plastic pots (237 ml) and randomly allocated to positions 181 on benches in the greenhouse. When the first true leaves developed, each plant was transplanted 182 into 10 L plastic pots filled with a 1:1 mix of sand and vermiculite, and again, the pots were 183 placed randomly on the benches. Each plant received the same daily quantity of water (500 ml) 184 during the entire experiment. When the plants reached the flowering stage, flowers were hand 185 pollinated. Plants from Teotihuacán were used as pollen receptors and plants from Ticumán were

186 used as pollen donators. Prior to manual pollination, flowers from Teotihuacán were emasculated 187 before dehiscence and covered with bags to avoid pollen contamination from other plants.

188 Cross-pollination was achieved by rubbing anthers of pollen donors onto the stigma of a 189 flower. Mating pairs were set at random. After pollination, flowers were tagged and bagged. 190 Because a plant can produce several flowers, each flower could be pollinated by different pollen 191 donors. Thus, we produced *ca*. 200 crosses. Fruits of each cross (F1 generation progeny) were 192 tagged and collected in paper bags and stored at room temperature. When plants reached the 193 flowering stage and second bifurcation  $(\sim]30$  days after planting in pots), 6-8 leaves from each 194 plant were harvested to quantify the diversity and concentration of tropane alkaloids. There is 195 evidence that the highest concentration of tropane alkaloids in *D. stramonium* occurs at the 196 flowering stage, which is related to the timing of infestation by the main herbivores of *D.*  197 *stramonium* (Kariñho-Betancourt *et al*. 2015). A total of 21 tropane alkaloids were identified and 198 analyzed for all parental plants using methods described in De-la-Cruz *et al.* (2020). 199 Once the total tropane alkaloid concentration of the parental plants was completed, we 200 selected the individual plant with the lowest (Teotihuacan) and the highest (Ticumán) 201 concentration of tropane alkaloids (grandparents Teotihuacán 1 and Ticumán 23) (S1). These 202 plants differed 58-fold in their total alkaloid concentration (1,013 *vs*. 59,000 ng/g of leaf, 203 respectively) (S1).  $F_1$  seeds derived from the cross between these two parental plants were 204 sowed, following the procedure described above, to produce the  $F_2$  progeny (single family: S1). 205 To this end, we used seeds from three fruits of the same crossing. From the germinated  $F_1$  plants  $206$  (n = 8), we randomly chose one plant whose flowers were bagged to avoid pollen contamination 207 from other plants (although plants were grown in a glasshouse; S1). We allowed this  $F_1$ 208 individual to self-pollinate to produce the  $F_2$  generation progeny (S1).

209

# 210 **Transplant experiment in the two sites**

211 *Experiment*. F2 seeds, taken randomly, were germinated and grown in the greenhouse as 212 described above. When the two true leaves appeared,  $F_2$  seedlings (n = 430) were transplanted to 213 experimental plots in Teotihuacán (n = 230) and Ticumán (n = 200) in order to expose the  $F_2$ 214 plants to the local herbivores and natural environmental conditions of their grandparents (S1). 215 During the first days after transplanting, high seedling mortality occurred at the tropical site 216 (Ticumán), reducing sample size to 103 plants. In each site, seedlings were planted in the 217 experimental plot according to a complete randomized design. Plants were spaced 1 m apart in a 218 regular grid. Experimental plots were regularly weeded to prevent interference and competition 219 by other species.

220 *Damage by herbivores.* Leaf damage to plants by herbivores was measured with the mobile 221 application BioLeaf (Machado *et al.* 2016) on four sampling periods (15, 30, 45, 60 days after 222 planting). On each sampling date, we took photographs of eight randomly chosen full expanded 223 leaves per plant using a mobile phone (Samsung Galaxy S6 edge). The app automatically 224 calculates the injured leaf regions caused by insect herbivory and then estimates the damage (in 225 percentage) relative to the total leaf area (Machado *et al.* 2016). Thus, we were able to quantify 226 the damage inflicted by herbivores to the plants during the experiment. Likewise, the average 227 proportion of leaf damage by herbivores per plant was obtained. However, it is important to 228 highlight that in the Teotihuacán site, most leaf tissue was completely eaten by herbivores in 229 many plants. In these cases, we assigned 100% of the damage to these plants. 230 *Herbivore infestation*. At the Teotihuacán site, three species of herbivores were recorded during

231 three sampling periods (15, 30, 45 days after planting). In each plant, we counted the number of

232 1) adults *Epitrix parvula*, 2) adults *Lema daturaphila,* 3) larvae of *Lema daturaphila*, and 4) 233 adults *Trichobaris soror*. Since larval development and pupation of *E. parvula* occur in the soil, 234 we were unable to record these stages. Therefore, only the number of adults on plants was 235 obtained for this insect species, as well as for *T. soror*. To minimize bias in insect counting, only 236 one person counted the herbivores on each plant in all the sampling periods. In the Ticumán site, 237 we recorded the infestation accounted only by *Epitrix* sp., since *L. daturaphila* is absent and *T.*  238 *soror* is very rare (only 3 individuals registered at this site). At the end of the experiments, we 239 had a measurement of total infestation that each plant experienced by each herbivore in both 240 sites.

241 *Leaf tissue sampling*. In order to determine alkaloid concentration, we collected one leaf (10 cm 242 in length) per plant when plants reached their second bifurcation and were flowering  $\sim$  25 days 243 after sowing). The leaf sampled was packed in aluminum foil, labeled and immediately frozen in 244 liquid nitrogen. All samples were transported and stored in a freezer at -80ºC. In order to obtain 245 DNA from each F2 plant for genetic analyses, one additional leaf was collected, frozen and 246 stored as described above.

247 *Plant survival and reproduction*. In the Teotihuacán site, plant mortality was caused by heavy 248 damage exerted by insects ( $n = 66$ ). We recorded plant survival as a nominal variable 249 (dead/alive). At the Ticumán site, however, there was no record of single plant mortality due to 250 damage exerted by herbivores.

251 At the end of the experiment (two months after sowing), we collected all fruits produced 252 by each plant in each experimental site. Fruits were bagged individually and labelled. In the lab, 253 seed set per fruit was counted and total number of seeds per plant was used as an estimator of

254 maternal plant fitness (*see* statistical analyses section; Motten and Antonovics 1992; Núñez-255 Farfán *et al*. 1996; Mauricio and Rausher 1997).

256

# 257 **Alkaloid extraction of F2 plants**

258 In order to extract tropane alkaloids from each plant, frozen leaf tissue was first transferred to 2 259 mL Eppendorf tubes, grinding it with a plastic pestle while keeping it frozen by adding liquid 260 nitrogen. Second, we weighted the pulverized frozen leaf tissue in Eppendorf tubes. Third, we 261 added two steel balls to each Eppendorf tube along with 1.5 mL of extraction buffer (80% 262 methanol; MeOH and 1% formic acid); the tubes were then shaken for 60 s at 30 Hz in a 263 TissueLyser II (QIAGEN). Finally, the samples were centrifuged for 20 min at 14,000 rpm; 700 264 μL of supernatant was collected and stored in glass vials (1.5 mL) and maintained at -4ºC until 265 quantified in the Liquid Chromatography/Time-of-Flight/Mass Spectra (HPLC-TOF-MS).

266

# 267 **Liquid Chromatography/Time-of-Flight/Mass Spectra**

268 Before analysis, 300 μL of MeOH was added to each sample (stored in a glass vial; *see* above)

269 and then injected into an Agilent 1260 Infinity, coupled to an Accurate-Mass Time-of-Flight

270 (TOF) LC/MS-6230, with an auto-sampler Agilent Technology 1200 Infinity. The

271 chromatographic separations were performed in a HPLC Agilent ZORBAX column. Before

272 samples were injected into the column, it was cleaned with 15 mL of MeOH. For this, a gradient

273 of mobile phase A ( $1\%$  (v/v formic acid in water) and mobile phase B ( $1\%$  (v/v formic acid in

274 methanol) were used. The gradient profile was set to 0.00 min 90% A eluent, 10 min 10% A

275 eluent, 17 min 90% A eluent, 17.10 min 90% A eluent. Conditions of this last step were

276 maintained for 5 min to balance the column. The flow rate was  $0.200 \mu L$  l min<sup>-1</sup> each 5 min, so

277 each sample was analyzed for 23 min, and the column temperature was  $50^{\circ}$ C. The injection 278 volume was 1  $\mu$  for all samples. The electrospray source (ESI) was operated in the positive 279 mode, and the interface conditions were as follows: the fragmentor of 200 V; Skimmer 65 V; oct 280 1 RF Vpp 750 V; gas temperature of  $350^{\circ}$ C; drying gas flow rate of 6 L min<sup>-1</sup>; the nebulizer

281 worked at 50 psig. The ions of the compounds and their retention times are given in S2.

282 To standardize the method and optimize the detection of alkaloids in the HPLC-TOF-MS 283 system, we prepared standard solutions (1:1000; mg/ml) of Atropine and Scopolamine (Sigma-284 Aldrich, St. Louis, MO, USA) of MeOH and injected these at volumes of 2, 4 and 8  $\mu$ l. Since 285 atropine showed a better calibration curve, we used this curve to calculate the concentration for 286 each identified alkaloid per plant.

287

# 288 **Identification and quantification of alkaloids in** *D. stramonium* **leaves**

289 First, we identified the seven most abundant constitutive alkaloids in *D. stramonium*: four

290 tropane alkaloids (atropine, scopolamine, 3-hydroxy-6-tigloyloxytropane and anisodamine; De-

291 la-Cruz *et al*. 2020), one alkaloid derived from the phenylalanine biosynthesis

292 (phenylacetaldehyde), one pyrrolizidine alkaloid (pyrroline), and one triterpenoid of unknown

293 name but of similar structure and molecular weight to azadirone triterpenoid (Álvarez-Caballero

294 and Coy-Barrera 2019) (S2). Each alkaloid was searched and integrated (peak integration)

295 individually in each chromatogram of each plant. The MassHunter Workstation software (v. B.

296 06.00; Agilent Technologies) was used to identify the alkaloids using data of mass spectra,

297 retention time, and molecular formula obtained in the chromatograms (S2). The total

298 concentration for each alkaloid per plant was obtained using the slope and the intersect from the

299 regression equation of the calibration curve (curve from atropine standard):

$$
300 \qquad \qquad \left( \left( \frac{\left( a + bX \right) \times 1000}{d} \right) \times 1000 \right)
$$

301 where *a,* is the intercept obtained from the regression of the calibration curve; *b,* is the slope 302 obtained from the regression of the calibration curve, *X* is the concentration of given alkaloid in 303 each plant and *d* is the dry weight of the sample. Alkaloid concentration was expressed in  $\mu$ g/g 304 units of leaf weight. Total alkaloid concentration was obtained as the sum of the seven alkaloids 305 per plant (Kariñho-Betancourt *et al*. 2015).

306

#### 307 **DNA extraction, library preparation for ddRad- sequencing**

308 Genomic DNA (gDNA) was extracted from 163 individuals planted in Teotihuacán and 51 309 individuals planted in Ticumán. Since we had high mortality of seedlings at the beginning of the 310 experiment in Ticumán, we extracted DNA from more individuals sowed in Teotihuacán. gDNA 311 was isolated from fresh leaves with a modified CTAB mini-prep protocol for ddRad-seq (Doyle 312 and Doyle 1987). The total amount of gDNA was measured using Qubit dsDNA HS Assay Kit 313 (Invitrogen, Thermo Fisher Scientific, Waltham, USA). A total of 200 ng of gDNA was used for 314 library preparation. The qualified DNA samples were digested with EcoRI and Hin1II (NlaIII) 315 restriction enzymes (Takara, Osaka, Japan) and subjected to adapter ligation. The digestion and 316 ligation were performed at  $37^{\circ}$ C for 16 hrs. The ligation products barcoded with unique P1 317 adapter were pooled and purified by size selection using E-Gel SizeSelect 2% agarose (Life 318 Technologies, Carlsbad, CA, USA). Approximately 400-600 bp fragments were retrieved. The 319 selected size and adaptor-ligated DNA was subsequently amplified by PCR. The PCR products 320 were purified using AMpure XP beads (Beckman Coulter, Brea, CA, USA). The purified library 321 was sequenced using Illumina Hiseq X Ten platform (Illumina, San Diego, CA, USA). Library 322 preparation and sequencing were carried out by CD Genomics company (Shirley, NY, USA). For

323 the two grandparents, gDNA was isolated and measured as above. However, whole genome 324 sequencing was carried out for both, rather than ddRad-seq. Libraries were sheared on the 325 Covaris and then prepped for 150PE (paired-end) Illumina HiSeq 4000 sequencing using the 326 Kapa Hyper prep Illumina library prep kits. Final libraries were visualized on the Agilent 327 Fragment Analyzer, then quantified and pooled at equimolar amounts with Kapa qPCR Illumina 328 library quant Universal Kits. The sequencing and library preparations for the grandparents were 329 carried out in the QB3 Functional Genomics and Vincent J. Coates Sequencing Laboratories at 330 the University of California, Berkeley.

331

# 332 **Identity by Descent (IBD)**

333 Two haplotypes are identical by descent (IBD) if they share the same alleles inherited from a 334 common ancestor (Thompson 2013). Thus, closely related individuals have a high proportion of 335 IBD (Thompson 2013). We estimated IBD between each individual F2 plant and each of the two 336 grandparents (214 F2 plants *vs*. grandparent from Teotihuacán/grandparent from Ticumán). This 337 information was used to evaluate whether F2 plants more related to a given grandparent (*i. e.*, 338 grandparent from Ticumán or grandparent from Teotihuacán) were more or less resistant to 339 herbivory or had higher or lower fitness/survival in the experimental sites (*see* below). 340 For IBD estimation, demultiplexing was performed with the Illumina bcl2fastq v2.19 341 software, which returned sequence data in fastq format for each individual. Barcodes and indexes 342 had been removed previously by CD Genomics and QB3 services. Illumina reads were trimmed 343 using a Phred quality score > 20 in TRIMMOMATIC v0.32 (Bolger *et al.* 2014). We visually 344 verified the quality of the grandparents and some individuals  $(\sim 80)$  before and after trimming

345 with FastQC (Andrews 2010). This allowed us to keep only high-quality reads for IBD analyses.



369 experimental site. To assess the severity of damage as a function of the total infestation rate by 370 each species of herbivore in each of the two populations, a Pearson correlation analysis (Zar 371 1999) was performed between the average damage and the total infestation by each herbivore in 372 each population.

373

# 374 **IBD and survival in Teotihuacán**

375 To analyze if genomic similarity among the F2 individuals to their Ticumán and Teotihuacán 376 grandparent was associated with their survival probability (alive/dead), two-tailed *t*-tests were 377 used to compare mean IBD of individuals that survived or died. This analysis was only carried 378 out for plants grown at the Teotihuacan site, because there was not plant mortality due to damage 379 exerted by herbivores at the Ticumán site (*see* above).

380

# 381 **Relationships between resistance, IBD and herbivory**

382 Prior to analyses, all variables were standardized to a mean of zero and a standard deviation of 383 one  $(x = 0, SD = 1)$ . Generalized linear models (GLMs) were employed to evaluate the 384 relationships between resistance and IBD and herbivory. The GLMs described hereafter, were 385 selected based on the statistical significance of the model and on the lowest corrected AIC 386 values, *i. e*., models that best explained the relationship between the variables (Akaike 1974). 387 First, general plant resistance  $(R_i)$  of the plant *i* was defined as  $R_i = 100$ -*def*, where *def* is 388 the average proportion of leaf damage experienced by each plant (Núñez-Farfán and Dirzo 389 1994). To evaluate the relationship between resistance and IBD, two GLMs (link = identity, 390 distribution = normal) were constructed; one using the IBD values between  $F_2$  plants and the 391 Teotihuacán grandparent, and the other using the IBD values between F2 plants and the Ticumán

392 grandparent. In these models, the response variable was resistance, whereas IBD, the 393 experimental site, and their interaction were used as predictors. Adding the interaction between 394 experimental site and the covariate in the models allowed us to assess whether the effect of the 395 IBD to each one of the grandparents (Teotihuacán or Ticumán) differed depending on the site of 396 testing (*cf*. Zar 1999).

397 Since herbivore species differed between the sites, we independently assessed resistance 398 as a function of herbivore species by GLMs (link  $=$  identity, distribution  $=$  normal). In 399 Teotihuacán, we used the abundance of adults and/or larvae of *L. daturaphila*, *T. soror* and *E.*  400 *parvula* as covariates, whereas in Ticumán, only the abundance of *Epitrix* sp. (the only herbivore

401 detected in this site) was used as a predictor*.*

402

#### 403 **Relationship between herbivore infestation and alkaloid concentration**

404 To assess the effect of the alkaloids on herbivore infestation, we also carried out GLMs (link  $=$ 405 identity, distribution = normal) in which the response variables were *E. parvula*, *Epitrix* sp. 406 adults or larvae of *L. daturaphila* or *T. soror* abundances on plants. The predictors in these 407 models were the concentrations of the seven alkaloids. In addition, we performed stepwise 408 GLMs (link = identity, distribution = normal) following a backward selection, which starts with 409 all predictors in the model (seven alkaloids), and iteratively removes the least contributive 410 predictors (Sokal and Rohlf 1994; Zar 1999). This allowed us to detect which alkaloid 411 configuration had a greater positive or negative effect (or both) on the infestation of each 412 herbivore species. The best GLMs were selected based on the statistical significance of the 413 model and on the lowest corrected AIC values (Akaike 1974). An additional GLM (link = 414 identity, distribution = normal) with the total alkaloid concentration as a predictor was carried

415 out to see the impact of total alkaloid concentration on herbivores. Tests for the interaction 416 between experimental site and one particular herbivore were not possible because different 417 species were present in the two sites.

418

# 419 **Natural selection on alkaloids, resistance, herbivore infestation and IBD**

420 To quantify the magnitude and direction of natural selection acting on the seven alkaloids, we 421 used the number of seeds produced by each plant as a fitness proxy to perform phenotypic-422 selection analyses (Lande 1979; Lande and Arnold 1983). For this purpose, standardized 423 individual fitness (relative fitness) was calculated as  $w_i = x_i/x$ , where  $x_i$  is the total number of 424 seeds produced per plant, and  $x$  is the average number of seeds per plant in the population in 425 each site. In all analyses,  $w_i$  was used as a response variable. Thus, one GLM (link = identity, 426 distribution = normal) was constructed using the concentrations of seven alkaloids, the 427 experimental site, and their interactions. An additional two separate GLMs were constructed 428 using resistance and total alkaloid concentration as predictors, as well as experimental site as a 429 factor. Interactions between site and predictors allowed us to test if the effects of predictors on 430 fitness differed between the two sites.

431 Two separate models, one for each experimental site, were carried out to assess selection 432 on the infestation by each herbivore (independent variables). As pointed out earlier, we could not 433 evaluate the effect of the experimental site and its interaction with predictors, since different 434 species of herbivores were present in the two populations.

435 Finally, to evaluate the effects of identity by descent (IBD) on fitness (seed production), 436 two GLMs were constructed (one using the IBD values between F2 plants and the Teotihuacán 437 grandparent, and the other using the IBD values between F<sub>2</sub> plants and the Ticumán

438 grandparent). In these models, the response variable was relative fitness, whereas IBD,

439 experimental site and its interaction were predictors.

440 The generalized linear coefficients (*i. e*., the selection gradients; *βi*, Lande and Arnold 441 1983) obtained from the selection analyses represent the strength and direction of selection 442 acting directly on each alkaloid, resistance, infestation by each herbivore and IBD in comparable 443 units (standard deviations; Wise and Rausher 2013).

- 444
- 

#### 445 **Results**

446 **Damage, herbivore infestation and alkaloid concentrations in the two experimental sites** 

447 Damage by herbivores varied between sampling dates in each site (Teotihuacán: *F*<sub>710</sub> = 110.98,

448  $R^2 = 0.41$ ,  $p = 0.0001$ ; Ticumán:  $F_{262} = 27.16$ ,  $R^2 = 0.27$ ,  $p = 0.0001$ ; S3 a, b, S4). There were

449 clear differences in level of infestation by the different species of herbivores ( $F_{545} = 215.32$ ,  $R^2 =$ 

450 0.61, *p* = 0.0001; S3 c, S4). Correlation analyses indicated that plant damage in Teotihuacán site

451 was mainly imposed by larvae *of L. daturaphila*, whereas that in the Ticumán site mainly by

452 *Epitrix* sp. (S5).

453

# 454 **Effect of the Identity by Descent (IBD) on fitness/survival and on resistance**

455 The GLM between fitness and the IBD to the Ticumán grandparent as measured by genome wide

456 IBD was significant, revealing a positive effect of increasing IBD on fitness  $(L-R \text{ chi-square}_3 =$ 

457 12.91, *AICc* = 273.68, *p* = 0.0048, Table 1, Fig. 1 a, b). The model between fitness and the IBD

458 with the Teotihuacán grandparent was not significant (L-R chi-square<sub>3</sub> = 2.68, AICc = 283.90, *p* 

 $459 = 0.4424$ , Table 1, Fig. 1 c, d). Our results also showed that plants more related to the Ticumán

 $460$  grandparent had higher survival than  $F_2$  plants less related to the Ticumán grandparent in the

461 Teotihuacán site ( $F_{129}$  = 17.52,  $R^2$  = 0.12,  $p = 0.0001$ ; Fig. 1 e). In contrast, plant survival was not  $\delta$  462 significantly associated with IBD to the Teotihuacán grandparent in Teotihuacán (*F*<sub>129</sub> = 1.92, *R*<sup>2</sup>)  $463 = 0.014$ ,  $p = 0.1682$ ; Fig. 1 f). The effect of IBD on plant survival in the Ticumán site was not 464 evaluated because there was not plant mortality due to damage exerted by herbivores in this site 465 (*see* above). The mean F2 full-sibs relatedness (IBD) was 0.47 (range 0.006-0.803, standard error  $466 = 0.0007$ . Identity by descent between the F<sub>2</sub> plants to each grandparent range between 0.006-467 0.5 (Teotihuacán grandparent) and 0.031-0.5 (Ticumán grandparent). Relatedness between the 468 two grandparents was zero (Fig. 1 g). 469 The GLM between resistance and the IBD with the Ticumán grandparent was significant 470  $(L-R \text{ chi-square}_3 = 54.21, \text{ AICc} = 441.47, p = 0.0001)$ . Significant effects included population, 471 and the interaction between population and IBD to the Ticumán grandparent (positive 472 relationship in Teotihuacán site, while an opposite effect was observed in the Ticumán site; 473 Table 2, Fig. 2 a, b). The GLM between resistance and the IBD with the Teotihuacán 474 grandparent was significant  $(L-R \text{ chi-square}_3 = 32.50, \text{ AICc} = 463.18, p = 0.0001)$ . However, 475 only the population effect was significant (Table 2, Fig. 2 c, d). 476 477 **Resistance against herbivore infestation levels in the two experimental sites**  478 Resistance to herbivory was significantly related to herbivore infestation levels in Teotihuacán 479  $(L-R \text{ chi-square}_4 = 111.09, AICc = 426.37, p = 0.0001)$ . Resistance was only positively related to 480 levels of *E. parvula* infestation and negatively related to infestation by larvae of *L. daturaphila* 481 in Teotihuacán (Table 2, Fig. 2 e, f). However, resistance and *Epitrix* sp. infestation levels were 482 negatively related in Ticumán (*L-R* chi-square1 = 14.96, *AIC*c = 223.89, *p* = 0.0001; Table 2, Fig. 483 2 g).



507 *T. soror* infestation was also not significant  $(L-R \text{ chi-square}_1 = 0.11, AICc = 478.92; p = 0.7367;$ 508 S6).



529 significant in either of the populations  $(L-R \text{ chi-square}_3 = 2.86, \text{ AICc} = 418.28; p = 0.41; \text{ Table}$ 530 1).

531 The GLM of relative fitness against level of herbivore infestation (larvae and adults of 532 *Lema, E. parvula* and *T. soror*) was significant in Teotihuacán (L-R chi-square<sub>4</sub> = 17.29, AICc = 533 342.00; *p* = 0.002) (Table 1). Nevertheless, only the negative effect of *L. daturaphila* larvae on 534 fitness was significant (Table 1). Likewise, a significant positive effect of *Epitrix* sp. infestation 535 level on fitness was detected in Ticumán (*L-R* chi-square<sub>1</sub> = 13.06, AICc = 130.18,  $p = 0.001$ ; 536 Table 1).

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#### 538 **Discussion**

539 Our results revealed differentiation in plant-herbivore interactions among the study sites. First, 540 different herbivore species are present in each population, and the infestation levels and the 541 amount of foliar damage exerted by each herbivore on plants differed within and between 542 populations. Second, different chemical compounds were related to infestation by each specific 543 herbivore. Third, variable spatial selection was detected on identity by descent (IBD), resistance, 544 chemical defensive traits and herbivore infestation levels. 545 A number of studies have also documented geographic variation in the level of herbivory 546 and chemical defenses (Castells *et al.* 2005; Muola *et al*. 2010; Agrawal *et al*. 2012; Züst *et al.*

547 2012; Castillo *et al.* 2014; Verçosa *et al.* 2019; Hanh *et al.* 2019). However, there has been no

548 previous attempts to determine how the plants' genetic background (IBD) is driven by ongoing

- 549 natural selection-imposed by herbivores. Furthermore, the results provide strong evidence of
- 550 local adaptation in plant-herbivore interactions in both populations of *D. stramonium*.

551 In the locality of Teotihuacán, F2 plants more related to the local grandparent (selected as 552 a parent due to its low alkaloid concentration) were less resistant and had higher mortality due to 553 herbivory than F2 plants more related to the Ticumán grandparent. Furthermore, we did not 554 detect any relationship between fitness and IBD to the Teotihuacán grandparent in this site. This 555 result was anticipated since it is not expected that natural selection would favor poorly defended 556 plants in a habitat where damage by herbivores can be lethal (*e. g*., plant deaths due to herbivory 557 caused by larvae of *Lema daturaphila*) (Valverde *et al.* 2001; 2003; Fornoni *et al.* 2004). Hence,  $558$  it is plausible that  $F_2$  plants more related to the Teotihuacán grandparent inherited the loci/alleles 559 that do not confer resistance (Albrechtsen *et al.* 2010; Browning and Browning 2012). Likewise, 560 alkaloid concentration in F2 plants more related to the Teotihuacán grandparent remained at low 561 levels after damage by different herbivores in Teotihuacán. This result indicates that the 562 chemical defenses studied here are not induced and have a genetic basis, since a positive 563 significant relationship between plant resistance and IBD to the Teotihuacán grandparent would 564 be expected if plant defenses were induced after herbivore damage (Baldwin 1998; Karban and 565 Baldwin 2007).

566 In marked contrast, we detected strong positive selection on IBD to the Ticumán 567 grandparent in the locality of Teotihuacán. Also, plant resistance to herbivores and IBD to the 568 Ticumán grandparent were positively related in this site. We suggest that  $F_2$  plants more related 569 to the Ticumán grandparent - selected as a parent on the basis of its high alkaloid concentration - 570 had higher survival in Teotihuacán as they inherited the loci/alleles that confer resistance to 571 herbivores; positive selection of these loci/alleles would be associated with different defensive 572 chemical compounds which are produced in high concentration (Albrechtsen *et al.* 2010; Lowry 573 *et al.* 2019). In fact, our findings indicate that the higher resistance of F<sub>2</sub> plants more related to

574 the Ticumán grandparent in the Teotihuacán site was provided by specific alkaloids that are 575 produced in very high concentration to face different herbivore species. Total alkaloid 576 concentration (sum of the concentration of all classes of alkaloids; Moore *et al.* 2014) only seems 577 to affect negatively the infestation levels of *E. parvula*. Since alkaloid concentrations vary in 578 wild Teotihuacán plants (Castillo *et al*. 2014; Miranda-Pérez *et al.* 2016; De-la-Cruz *et al.* 2020), 579 we think that wild plants from Teotihuacán that produce specific alkaloids in very high 580 concentrations (*i. e*., plants more related to the Ticumán grandparent) have strong chemical 581 defense against the herbivores in this site. For instance, we observed strong positive selection to 582 increase the concentration of the triterpenoid compound in Teotihuacán, which seems to affect 583 negatively the infestation levels of the most harmful herbivore of *D. stramonium*, the larvae of *L.*  584 *daturaphila*.

585 The defensive role of specific alkaloids in the Teotihuacán site revealed unexpected 586 results, namely, changing the sign of their relationship with the infestation by different 587 herbivores. For instance, while the triterpenoid compound appears to reduce the infestation of 588 *Lema* larvae (the most dangerous herbivore of *D. stramonium*), it was also positively associated 589 with infestation levels by *E. parvula* and *T. soror*. Triterpenoids are structurally similar to insect 590 hormones known as ecdysones (Oliveira *et al*. 2019) known to control metamorphosis as insects 591 pass from larva to pupa to adult (Yamanaka *et al.* 2013). It has been reported that many 592 triterpenoids function as ecdysone blockers (*e. g*., azadirone; Ujváry 2010; Oliveira *et al*. 2019). 593 Therefore, the most parsimonious explanation for our observations is that this triterpenoid of *D.*  594 *stramonium* is acting mainly on larvae of *Lema* (Miller *et al.* 1989; Ujváry 2010), and since this 595 compound is structurally similar to insect hormones (Ujváry 2010), it may be used by *E. parvula* 596 and *T. soror* adults to trace *D. stramonium* plants (and potential mates on them). Complex

597 interactions where one compound is toxic to insects at one developmental stage (*e. g*., larvae) or 598 to a particular herbivore species, but functioning as an attractant at other stage (adults) or to other 599 herbivore species have been reported, for instance, in *Nicotiana attenuata* (Zhou *et al.* 2017).

600 Local adaptation of plant defenses to herbivores depends on (1) the strength of selection 601 as a result of the interaction, and (2) the level of specificity on the interaction (*e. g*., folivores, 602 seed predators, stem-borers) (Thompson *et al*. 2005; Cogni and Futuyma 2009; Agrawal *et al*. 603 2012). In the Teotihuacán site, our results suggest that the strong selection pressure exerted by 604 one herbivore (the folivore *L. daturaphila*) on *D. stramonium* plants may affect the interaction 605 between plants and other insects, leading to local adaptation of plant defenses to different 606 herbivore species (Wise 2009, 2010).

607 On the other hand, in the Ticumán site, we detected strong positive selection on pyrroline 608 alkaloid. It has been reported that pyrroline is a defensive compound against many insect species 609 and pathogens (bacteria, virus, fungi) (Qamar *et al*. 2015; Martins *et al.* 2015; Tamariz *et al.* 610 2018). Pyrroline has also been related to different physiological processes such as plant growth 611 (Chen *et al.* 2018; Tamariz *et al.* 2018). It is worth mentioning that polyamine oxidase, an 612 enzyme involved in the biosynthesis of the pyrroline, is a growth-regulating enzyme (Chen *et al.*  613 2018). Nevertheless, an unexpected finding is that we observed a positive association between 614 pyrroline concentration and infestation level by *Epitrix* in Ticumán. It has reported that some 615 herbivore insects can tolerate pyrrolizidine alkaloids and use them for defense against their 616 predators or as precursors of insect hormones (Martins *et al.* 2015). Thus, our most parsimonious 617 explanation is that *Epitrix* sp. is surpassing the defensive role of the pyrroline alkaloid in 618 Ticumán. This could explain why the  $F_2$  plants more genetically related to the Ticumán 619 grandparent (with higher concentration of pyrroline) had lower resistance towards *Epitrix* sp.

620 infestation. Furthermore, since pyrroline could be positively related to plant growth (Chen *et al.*  621 2018; Tamariz *et al.* 2018), it is also possible that *Epitrix* sp. searches for more vigorous plants, 622 which have more biomass to feed (Agrawal 2005; Wise and Rausher 2013). On the other hand, 623 we observed that 3-hydroxy-6-tigloyloxytropane negatively affected the infestation levels of 624 *Epitrix* sp. in Ticumán. Then, it seems that the latter alkaloid is providing resistance against this 625 herbivore in this site.

626 Interestingly, pyrroline affected negatively the infestation levels of *E. parvula* in 627 Teotihuacán. However, negative selection on this compound was detected also in Teotihuacán. 628 Thus, while *Epitrix* sp. appears to be adapted to this compound in Ticumán, the production of 629 this compound in high concentrations in Teotihuacán may involve physiological costs, as plants 630 also have to allocate resources for production of other compounds (*e. g.,* triterpenoid) to tackle 631 their most harmful herbivore (*Lema* larvae). Indeed, as we mentioned above, it seems that total 632 alkaloid concentration should be the option to face with *E. parvula* infestation in Teotihuacán. 633 De-la-Cruz *et al*. (2020) found that plants from Ticumán have on average higher alkaloid 634 concentration than those in Teotihuacán. Why we did not observe strong selection to increase the 635 IBD to the Ticumán grandparent (higher alkaloid concentration) in Ticumán? Our most 636 parsimonious explanations are, first, as mentioned above, that *Epitrix* sp. (the main herbivore in 637 this site) seems locally adapted to plant chemical defenses (pyrroline) in Ticumán, and that other 638 alkaloids could now be providing defense against this herbivore. Second, since these compounds 639 are expressed constitutively, it is possible that all these powerful chemical weapons are being 640 used to face other natural enemies (virus, bacteria, nematodes, fungi, oomycete, other herbivore 641 species) that we did not detect or that were not present during our experiment. Third, it is also 642 possible that these compounds have other functions in this habitat (*e. g*., growth, plant-plant

643 communication). For instance, recent genomic evidence from *D. stramonium* indicates that 644 tropane alkaloids such as atropine and scopolamine also act as defenses against pathogens and 645 viruses (De-la-Cruz *et al*. under review).

646 Finally, the lack of association between the IBD to the Teotihuacán grandparent with 647 resistance or fitness in Ticumán suggests that the chemical defenses studied here are not induced 648 (see above; Karban and Baldwin 2007).

649

#### 650 **Conclusions**

651 The methodology used in this study allowed us to get insights on how natural selection imposed 652 by herbivores drives the genetic underpinnings of plant resistance traits. The lack of association 653 between plant fitness and IBD to the Teotihuacán grandparent (low resistance) in both 654 populations, as well as different magnitude and direction of selection on the IBD to the Ticumán 655 grandparent (high resistance) across populations, provides evidence of how ongoing natural 656 selection operates on plant resistance and promotes local adaptation. Likewise, the results of this 657 study shed some new light on how plants defend themselves against the attack from different 658 herbivores. It seems that in populations where plants are suffering frequent or heavy damage by 659 different herbivores, plants are able to produce and "use" different chemical defensive 660 compounds to face each insect species that feed on them (Wittstock and Gershenzon 2002). The 661 same alkaloids were produced by plants in both populations, but plants possessing the highest 662 total alkaloid concentrations were not the most well-defended or fit in either of the populations. 663 Instead, different specific alkaloids appear to be favored by natural selection imposed by 664 herbivores in the two study populations.



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**Table 1.** Analyses of natural selection testing the effects of (a) Identity by Descent to Ticumán grandparent, (b) Identity by Descent to Teotihuacán grandparent, (c) resistance, (d) the seven alkaloids, (e) total alkaloid concentration, (f) herbivores at Teotihuacán and (g) *Epitrix* sp. infestation at Ticumán. N = number of individuals, d.f. = degrees of freedom,  $\beta_i$  = selection gradients (generalized linear coefficients), se = standard error,  $t$  = t-ratio. Significant *p*-values (*p*) are in bold. Pop = effect of the experimental site.

<b>Response variable</b>	$\mathbf N$ <b>Effects</b> d.f. $\beta_i$ se		t	$\boldsymbol{p}$			
$w_i$ fitness (a)	<b>IBD-Ticumán</b> grandparent	135	3	2.19	0.99	2.20	0.0302
	Pop	135	3	$-0.13$	0.10	$-1.22$	0.2262
	$Pop \times IBD$	135	3	1.39	0.99	1.40	0.1646
$w_i$ fitness (b)	IBD-Teotihuacán grandparent	135	3	0.41	0.89	0.46	0.6484
	Pop	135	3	$-0.17$	0.11	$-1.49$	0.1390
	$Pop \times IBD$	135	3	$-0.71$	0.89	$-0.80$	0.4252
$w_i$ fitness (c)	Resistance	177	$\mathbf{1}$	0.11	0.27	0.43	0.6624
	Pop	177	1	$-0.15$	0.31	$-0.50$	0.6143
	$Pop \times Resistance$	177	1	0.64	0.27	2.36	0.0179
$w_i$ fitness (d)	3-hydroxy-6-tigloyloxytropane	136	$\mathbf{1}$	$-0.36$	0.21	$-1.71$	0.0899
	Anisodamine	136	1	$-0.07$	0.28	$-0.25$	0.7961
	Atropine	136	1	$-0.07$	0.12	$-0.56$	0.5719
	Triterpenoid	136	1	0.26	0.18	1.46	0.1459
	Scopolamine	136	1	$-0.24$	0.19	$-1.24$	0.2151
	Phenylacetaldehyde	136	1	$-0.21$	0.21	$-0.98$	0.3254
	Pyrroline	136	1	0.32	0.14	2.19	0.0304
	Pop	136	1	$-0.12$	0.09	$-1.29$	0.1997
	Pop $\times$ 3-hydroxy-6-tigloyloxytropane	136	1	0.13	0.21	0.62	0.5362
	Pop $\times$ Anisodamine	136	1	$-0.06$	0.28	$-0.24$	0.8104
	$Pop \times Atropine$	136	1	0.19	0.12	1.55	0.1224
	Pop × Triterpenoid	136	1	0.38	0.18	2.10	0.0378
	$Pop \times Scopolamine$	136	1	$-0.04$	0.19	$-0.20$	0.8375
	$Pop \times Phenylacetaldehyde$	136	1	$-0.14$	0.21	$-0.67$	0.5015
	$Pop \times Pyrroline$	136	1	$-0.43$	0.14	$-2.93$	0.0040
$w_i$ fitness (e)	Total alkaloid concentration	144	1	$-0.05$	0.08	$-0.58$	0.5657
	Pop	144	1	$-0.12$	0.09	$-1.34$	0.1838
	Pop × Total alkaloid concentration	144	1	0.09	0.08	1.04	0.2988
(f) $w_i$ fitness	Adults of Lema daturaphila	113	$\mathbf{1}$	0.08	0.09	0.90	0.3692
	Adults of <i>Epitrix parvula</i>	113	1	0.09	0.09	0.97	0.3324
	Adults of Trichobaris soror	113	1	0.09	0.08	1.03	0.3070
	Larvae of Lema daturaphila	113	1	$-0.27$	0.08	$-3.22$	0.0017
$w_i$ fitness (g)	Adults of <i>Epitrix</i> sp.	63	1	0.30	0.081	3.75	0.0004

**Table 2.** General linear models testing the effect of (a) Identity by Descent to the Ticumán grandparent, (b) Identity by Descent to the Teotihuacán grandparent, (c) herbivore infestation at Teotihuacán and (d) *Epitrix* sp. infestation at Ticumán, on whole plant resistance.  $N =$  number of individuals, d.f. = degrees of freedom, Estimate = generalized linear coefficients, se = standard error,  $t = t$ -ratio. Significant  $p$ -values  $(p)$  are in bold. Pop = effect of the experimental site.



#### **Figure legends**

Fig. 1. Relationships between plant fitness (log scale) and identity by descent (IBD) relationship to the Ticumán grandparent for (a) plants grown in the Teotihuacán population and (b) plants grown in the Ticumán population. Relationships between plant fitness and IBD relationship to the Teotihuacán grandparent for (c) plants grown in the Teotihuacán population and (d) plants grown in the Ticumán population. (e) Box plot of IBD to the Ticumán grandparent for plants that survived and died. (f) Box plot of IBD to the Teotihuacán grandparent for plants that survived and died. (g) Distribution of the relatedness between all F2 fullsibs, and relatedness of F<sub>2</sub> plants to each grandparent. A relatedness of  $\sim 0.5$  is the mean expected value between all F<sub>2</sub> full-sibs. A relatedness of  $\sim$ 0.5 is the maximum expected value between the  $F_2$  progeny and each one of the grandparents (Falconer and Mackay 1996). *p*-values of full GLMs are shown in each plot (a-f). Each dot depicts observation for an individual. See also Table 1.

**Fig. 2.** Relationships between resistance to herbivory and identity by descent (IBD) relationship to the Ticumán grandparent for (a) plants grown in the Teotihuacán population and (b) plants grown in the Ticumán population. Relationships between resistance to herbivory and IBD relationship to the Teotihuacán grandparent for (c) plants grown in the Teotihuacán population and (d) plants grown in the Ticumán population. Relationship between resistance and (e) adults of *Epitrix parvula* in Teotihuacán, (f) larvae of *Lema daturaphila* in Teotihuacán, (g) adults of *Epitrix* sp. in Ticumán. *p*-values of GLMs are shown in each plot (a-g). Each dot depicts observation for an individual. Pop = population. See also Table 2.





# **Supplementary Information (Figures and Tables) of the manuscript "Genomic and chemical evidence for local adaptation in resistance to different herbivores in** *Datura stramonium***"**

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# **Evolution**

**S1**. Depiction of the experimental design used to produce the  $F_2$  generation progeny used in the study (*see* Methods for details).



**Experiment design to select the parents and to produce the F<sub>2</sub> generation progeny** 

**S2.** Alkaloids identified in leaves of *Datura stramonium*. RT, the retention time of each alkaloid; *m/z* = mass/charge, MS = mass spectrometry reference.



**S3.** Plant damage (in percentage) experienced by each F<sub>2</sub> plant during four sampling dates at (A) Teotihuacán and (B) Ticumán. Plants experienced the most severe damage at 45 days after transplanting in the two localities, and damage levels were higher in Teotihuacán than in Ticumán. (C) Violin plot showing total infestation accounted by different herbivore (log scale). The circle inside each violin depicts the mean value. Overall, *Lema daturaphila* larvae was the most abundant insect herbivore. A quasirandom jittering was used to reduce datapoint overlap. TEO = Teotihuacán, TIC = Ticumán. *p*-values of ANOVAs are showed in each plot. For figures  $(A)$  and  $(B)$ : black line = mean.



**S4.** Mean differentiation in the level of damage (expressed as percentage) between sampling sessions in (a) Teotihuacán and (b) Ticumán. (c) Mean differentiation in the level of herbivore infestation (Log transformed data). N = number of individuals, se = standard error, d.f. = degree of freedoms, SS = Sum of Squares, MS = Mean Square,  $F =$  Fisher-statistic,  $p = p$ -values of ANOVAs.



**S5.** Correlations between infestation by each herbivore and plant leaf average damage. a = Teotihuacán and b = Ticumán. ALd = adults of *Lema daturaphila*, Ep = *Epitrix parvula*, Ts = *Trichobaris soror*, LLd = larvae of *Lema daturaphila*.

Variable	by Variable	<b>Correlation</b>	Lower $95\%$	Upper $95\%$	<i>p</i> -value
		(a)	Teotihuacán		
Damage	LLd	0.615779	0.517482	0.698035	1.079E-20
<b>Ts</b>	Ep	0.241138	0.100361	0.37245	9.446E-04
Ep	A <sub>L</sub>	0.168386	0.024718	0.305239	2.195E-02
<b>Ts</b>	AL d	0.137232	$-0.00718$	0.276036	6.250E-02
LLd	AL d	$-0.03421$	$-0.1776$	0.110605	6.439E-01
Damage	<b>Ts</b>	$-0.123$	$-0.26261$	0.021649	9.531E-02
Damage	A <sub>L</sub>	$-0.13037$	$-0.26956$	0.014169	7.694E-02
L I d	<b>Ts</b>	$-0.15396$	$-0.29175$	$-0.00991$	3.640E-02
LLd	Ep	$-0.31356$	$-0.43802$	$-0.17731$	1.386E-05
Damage	Ep	$-0.32261$	$-0.44611$	$-0.18704$	7.516E-06
		(b)	Ticumán		
Damage	<i>Epitrix</i> sp.	0.387549	0.187536	0.556704	2.949E-04

**S6.** Generalized linear models (GLMs) between herbivore infestation levels and the seven alkaloids and total alkaloid concentration: (a) infestation by adults of *E. pavula*, (b) stepwise GLM between larvae of *Lema* and alkaloids. (c) stepwise GLM between adults of *Lema* and alkaloids, (d) stepwise GLM between adults of *T. soror* and alkaloids. (e) GLM between *Epitrix* sp. and alkaloids in Ticumán. N = number of individuals, d.f. = degree of freedoms, Estimate = generalized linear coefficients, se = standard error, *t* = *t*-ratio, Significant *p*-values are in bold. Notice that for the total alkaloid concentration was performed a different model for each herbivore (*i. e*., the effect of this variable was not included in the GLMs between each herbivore and the seven alkaloids (see methods).



**S7.** Relationships between fitness and resistance in (A)  $F_2$  plants grown in Teotihuacán and (B)  $F_2$  plants grown in Ticumán. Positive selection to resistance was observed in Teotihuacán while a negative trend was detected in Ticumán. Each dot depicts observation for an individual. *p*-value of full model is shown in the plots. See Table 1.





**S8.** Prediction profilers from the GLM between fitness (*w<sub>i</sub>*) and concentrations of the seven alkaloids. Response effects are shown separately for the two experimental sites. Envelops = confidence intervals  $(95\% \text{ CI})$ . See table 1. 4



3-hydr

1c

log3hydro logAniso trop. men Phenylacetaldehyde

Alkaloid concentration Alkaloid concentration

Triterpenoid Atropine Anisodamine

Alkaloid con

2.5 5 7.5 10

loganis ropine noia. ropan nylacetaldehyde

3-hydroxy-6-tigloyloxyt

Triterp Atr Anisodamine

> $2.5$  5.0  $2.5$  7.5 10.0 1.1.5 1.1.  $T$ <br>TEO $\overline{t}$ <br>Alkaloid concentration

2.5 5 7.5 10 12.5

**S9.** Ridgeline plot showing the distribution of the concentration of the seven alkaloids and total alkaloid

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