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1 **A new gall midge (Diptera, Cecidomyiidae) as a potential candidate for biological**
2 **control of the invasive plant *Cortaderia selloana* (Poaceae)**

3

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11

12 **Abstract**

13 A gall midge (Diptera, Cecidomyiidae) is reported here for the first time from spikelets
14 of *Cortaderia selloana*, a prominent invasive grass in southern Europe. The insect is
15 described as a new genus and species, *Spanolepis selloanae* Gagné. Based on
16 morphological and molecular analyses, the new genus and species are tentatively placed
17 within the supertribe Lasiopteridi and tribe Dasineurini. Its effects on seed production
18 were studied in order to ascertain its effectiveness in limiting sexual reproduction of the
19 invasive plant species. The larvae of *S. selloanae* feed on the ovaries with a mean seed
20 depletion of 74% in the population studied in northwest Spain. The new species is a
21 potential candidate for a biological control agent against *C. selloana*.

22

23 **Key words:** Lasiopteridi, Dasineurini, biological control, invasive alien species, DNA
24 barcoding

25

26 **Introduction**

27 The Enemy Release Hypothesis (ERH) states that the lack of natural enemies provides
28 invasive alien species with a competitive advantage, partially explaining the success of
29 invasive species in the new environments (Keane and Crawley 2002). Classical
30 Biological Control consists on the intentional release of natural enemies of non-native
31 species, either predators, herbivores, parasites or pathogens, to counteract their expansion
32 in invaded ecosystems (Van Driesche et al. 2010, Schwarzländer et al. 2010). The use of
33 biological control agents in invasive species management has proved to be an effective
34 method when they affect sensitive stages of the life cycle. However, the release of natural
35 enemies obtained in the native areas of an invader has raised concerns among researchers
36 because they may become harmful to native species or disrupt ecosystem networks
37 (Messing 2000, Simberloff and Stiling 1996). Despite these concerns, biological control
38 is now widely recognized as the most reliable tool for long-term control of invasive
39 species (Sheppard et al. 2006).

40 In invasive plants, insects are some of the most effective biological control agents
41 (Blossey 1995). Insects that reduce seed production are especially effective in plants in
42 which sexual reproduction is the main form of plant regeneration (Paynter et al. 1996,
43 Sheppard et al. 2006). Gall midges (Diptera, Cecidomyiidae) are some of the most
44 important plant-feeding species worldwide (Gagné 1989, 2017). Most species appear to
45 be host-specific, what makes them potentially suitable for biological control with a low
46 risk to the native flora. *Dasineura dielsi* Rübsaamen and *Dasineura rubiformis* Kolesik
47 are two examples of Australian seed-feeding species currently used as biological control
48 agents on two invasive species of *Acacia* (Mimosiidae) in South Africa (Impson et al.
49 2013, Post et al. 2010). Both species show a life cycle synchronized with the phenology
50 of the host plant, whereby females lay their eggs in the flowers before or immediately

51 following anthesis. The high host specificity of these species has been demonstrated,
52 including tests in other *Acacia* species (Adair 2005).

53 *Cortaderia selloana* (Schult. & Schult.f.) Asch. & Graebn. (Poaceae) is an aggressive
54 invader in the Mediterranean and Atlantic oceanic areas of western Europe (Tarabon et
55 al. 2018). It is a perennial grass with large vegetative tussocks of long leaves serrated at
56 their margins. In late summer, adult plants of over 2-3 years develop tall stalks with
57 terminal flowering heads that may reach 4 metres in height (Harradine 1991, Herrera and
58 Campos 2006). The species is described as gynodioecious, with hermaphrodites bearing
59 well developed anthers, and female plants with viable ovaries (Knowles and Ecroyd
60 1985). Hermaphrodite plants act mainly as pollen donors, and produce only limited
61 numbers of viable seeds (Connor 1973). The dispersal unit is the complete floret. The
62 female florets have long hairs on the glume that aid in long distance dispersal, as they are
63 dispersed by the wind (Herrera and Campos 2006, Saura-Mas and Lloret 2005). A single
64 plant can produce up to 800,000 viable seeds per season (Saura-Mas and Lloret 2005).
65 The species invasive behaviour relies on its extremely effective sexual reproduction,
66 suggesting that control methods should focus on preventing seed production and early
67 establishment of seedlings (Fagúndez and Lema 2019).

68 *Cortaderia selloana* is native to Argentina, Uruguay and Brazil (Connor 1973, Lambrinos
69 2001, Harradine 1991, Herrera and Campos 2006). It was introduced into European
70 gardens in the nineteenth century, and from there to other places like California and New
71 Zealand (Lambrinos 2001, Harradine 1991, Okada et al. 2007). Due to the abundance of
72 seeds produced and ability to colonize disturbed environments, the plant has become one
73 of the most successful invaders in South-West Europe (Nentwig et al. 2018), and the
74 Spanish government has promoted a national strategy to tackle its invasion (MTE 2018).
75 Negative effects of *C. selloana* include the formation of impenetrable monospecific

76 stands, increasing the risk of wildfires, and the colonization of natural wetland areas
77 threatening native species and natural habitats (Fagúndez and Barrada 2007, Herrera and
78 Campos 2006, Saura-Mas and Lloret 2005).

79 During a risk assessment analysis of *Cortaderia selloana*, we searched the plant for
80 possible biological control agents. The gall midge newly described in this paper was
81 discovered in a large population of *C. selloana* in the outskirts of the city of A Coruña in
82 Galicia, NW Iberian Peninsula, one of the areas most heavily invaded in Galicia (Pardo-
83 Primoy and Fagúndez 2019). Larvae feed on the developing ovaries and replace the seeds
84 at the time of dispersal. This potential control agent is, to our knowledge, the first to be
85 proposed for *C. selloana* (Herrera and Campos 2006, MTE 2018). The new gall midge is
86 distinctive for characters that separate it from other species known from other grasses,
87 and the genus is unique among the large, heterogeneous tribe Dasineurini (*sensu* Dorchin
88 et al. 2019). Within this clade, recent studies have acknowledged the paraphyly of the
89 large genus *Dasineura* and the need for a comprehensive revision of the tribe (Dorchin et
90 al. 2019, Gagné 2017, 2018, Sevcik et al. 2016, Sikora et al. 2019). Our description
91 includes the “barcode” mitochondrial DNA sequence as a trait of the new taxon. The
92 recognition of the new gall midge as a monotypic genus is preliminary supported by a
93 phylogenetic analysis including all genera within Dasineurini with available homologous
94 sequences on public databases. Lastly, we investigated the effects of the gall midge on the
95 life cycle of the plant and the gall midge, in order to gather essential information on their
96 phenology and reproductive performance.

97

98 **Materials and methods**

99 *Cortaderia selloana* and insect sampling

100 The Zapateira area is located in the outskirts of the city of A Coruña, on the Atlantic coast
101 of Galicia, NW Iberian Peninsula (Fig. 1). The area is densely occupied by commercial
102 facilities, the University of A Coruña campus, a hospital, schools and housing. It is
103 heavily invaded by *C. selloana*, which occurs along roadsides, train lines and worklots,
104 and in nearby fields and *Eucalyptus*-forested areas (Pardo-Primoy and Fagúndez 2019).
105 In 2016, larvae and adults of the gall midge were discovered by the first author while
106 searching for potential natural enemies of the invasive plant, and gathering seeds for a
107 germination experiment (Fagúndez and Lema 2019). In October 2017, a population with
108 over one hundred adult plants of *C. selloana* located on the side of a secondary road was
109 surveyed. Twenty-seven plants were randomly selected and labelled for monitoring. We
110 recorded the sex of each plant after observations in the laboratory, and established the sex
111 ratio for the population. In female plants, gall midge larvae were found within each floret,
112 replacing the caryopsis. The prevalence of the larvae was calculated by the ratio of larvae
113 to fruit (L:V) from a subset of random florets examined in each plant. We counted only
114 apparently viable, well developed seeds. Empty florets with undeveloped ovaries were
115 not considered. A mixture of twenty apparently viable seeds were set for germination in
116 a sealed petri dish with soaked filter paper under indoor temperatures and natural light
117 conditions.

118

119 To assess the phenology of the gall midge and the host plant, ten plants of the same
120 population were selected and labelled again in 2018. Samples of each plant were collected
121 at five different times between August and November 2018. In female plants, each floret
122 was classified as i) flower (viable stigmas developed); ii) fruit (caryopses within the
123 florets) and; iii) dispersion (free florets with a fully developed caryopsis). The percentage
124 of each phenophase was estimated, considering all spikelets, therefore the accumulated

125 percentage was below 100% when some of the florets were found empty. In the male
126 plants, florets were classified as pollinating (visible pollen in the developed anthers) and
127 degenerate (brown empty anthers). The presence of *S. selloanae* was classified as adults,
128 pupae or larvae.

129 From samples gathered in October 2017, larvae were collected and stored in paper bags.
130 From 2018 samples, we collected adults, pupae and larvae directly from the plants by
131 removing large portions of the inflorescences after covering with a paper bag. Individuals
132 for identification were preserved in 70% ethanol.

133

134 *Molecular methods*

135 Genomic DNA was extracted from eight larvae and nine adults using a commercial kit
136 (High Pure PCR Template Preparation Kit, Roche) following the manufacturer's
137 instructions. We sequenced up to 699 bp of the 5' end (barcoding region) of the
138 mitochondrial cytochrome c oxidase subunit I (COI) gene, corresponding to positions
139 [1176-1874] of the mitochondrial genome of *Mayetiola destructor* (Diptera:
140 Cecidomyiidae) (accession number GQ387648.1). Amplifications were carried out in 30
141 μ L volumes containing 1X PCR Buffer (5PRIME), 3 mM MgCl₂, 1U TaqDNA
142 Polymerase (5PRIME), 0.2 mM of each dNTP, 0.3 μ M of each primer (CeciLCOF (5'-
143 TTC TAC TAA TCA TAA AGA TAT TGG-3' modified from LCO-1490 by Folmer et
144 al. 1994) and CeciNancyr (5'-CCW GGT AAA ATT AAA ATA TAA ACT TC-3',
145 modified from C1-N-2191 by Simon et al. 1994)), and approximately 40 ng of DNA.
146 Reaction conditions consisted of 2 min 95 °C followed by 35 cycles of 45 sec 94 °C; 45
147 sec 50 °C; 45 sec 68 °C and, lastly, a final extension of 7 min at 68 °C. Amplified
148 fragments were purified and then bidirectionally sequenced in a 3130xl genetic analyzer

149 (Applied Biosystems). Inspection of electropherograms and alignment of overlapping
150 sequences were performed in CODONCODES 3.7.1.1 (CodonCode, USA).

151 The haplotypes obtained were compared with records available in the NCBI Nucleotide
152 database using BLASTN 2.9.0+ (Zhang et al. 2000) optimised for highly similar
153 sequences (megablast). We accessed the database on 29 April 2020.

154 We investigated the phylogenetic relationships of haplotype 1 of *Spanolepis selloanae*
155 within the tribe Dasineurini using Maximum parsimony (MP), Maximum Likelihood
156 (ML), and Bayesian Inference (BI). We included 38 out of the 42 COI records analysed
157 by Dorchin et al. (2019), the aforementioned records of *Macrolabis fagicola* (JQ684878)
158 and *Janetiella glechomae* (KR740388), a record from *Mayetiola destructor*
159 (GQ387648.1:1145-2680), and haplotype 1 of *Spanolepis selloanae*. The resulting trees
160 were rooted with homologous sequences from two members of the supertribe
161 Lasiopteridi: *Asteromyia carbonifera* (Alycaulini) and *Lasioptera arundinis*
162 (Lasiopterini) (Accession Nos. MN191258 and MN191311, respectively) (see Dorchin et
163 al. 2019). Purging the data produced a final alignment of 44 sequences of 612 bp.

164 We conducted heuristic searches for MP analyses (TBR branch swapping and partial
165 deletion of missing data). The robustness of the topologies was examined after 1000
166 bootstrap replicates. MP calculations were performed using MEGA v10.0.5 (Kumar et al.,
167 2018). The best-fit model of nucleotide substitution was identified using jMODELTEST
168 2 (Darriba et al. 2012) following the Bayesian Information (BIC). Accordingly, we
169 calculated the ML phylogeny using the TPM2uf + I + G model as implemented in the
170 RAxML-NG BlackBox v0.9.0 (Kozlov et al., 2019). Node supports were assessed using
171 the automatic bootstrapping option, which resulted in 200 replicates. High support was
172 interpreted with >70% bootstrap values, whereas low/moderate support corresponded to
173 50-70%.

174 We conducted BI analyses using MrBayes v3.2.7 (Ronquist et al., 2012). In this case, the
175 substitution model applied was GTR + I + G (the third best model according to
176 jMODELTEST). *Asteromyia carbonifera* was selected as outgroup. We ran two
177 independent analyses, each with four simultaneous Monte Carlo Markov chains (MCMC)
178 for 17 million generations. The chain was sampled every 1000th generation. Convergence
179 was indicated by the average standard deviation of splits (< 0.01). Stationarity was
180 confirmed after summarising the sampled parameters values (discarding 25% of the
181 samples) by a “white noise” plot of loglikelihood scores, PSRF values of 1.000 for all
182 parameters as well as verification of suitable effective sample size ($ESS > 400$) for all
183 parameters in TRACER v1.7.1 (Rambaut et al., 2018). We obtained the consensus tree
184 with branch length and clade credibility (Bayesian Posterior Probability, BPP) after
185 removing the first 10% samples. High support was interpreted when $BPP > 0.95$, whereas
186 moderate/low support corresponded to 0.90-0.95 values. Readers are referred to Online
187 Resource 1 for further details on the phylogenetic analyses.

188

189 *Morphological methods*

190 Adults and immature stages were preserved in 70% ethanol and subsequently mounted
191 by RJG in Canada balsam using the technique outlined in Gagné (1989). Terminology for
192 adult morphology follows Gagné (2018), and that for larval and pupal morphology
193 follows Gagné (1989). Line drawings of Fig. 5 were made by RJG with the use of a
194 camera lucida attached to a Wild phase contrast microscope. Most setae become lost in
195 the mounting process, but the illustrations show their sockets in their actual placement
196 and number, and any setae are drawn to their approximate actual length and thickness.

197

198 **Results**

199 *Phenology of Cortaderia selloana*

200 Data from the two years of this study were combined to provide basic data on plants from
201 the population studied. The 27 plants studied in 2017 were 15 males and 12 females (sex
202 ratio 1.25 for males). The development of flowering heads started in mid-August. Each
203 plant had a mean of 8.6 panicles per plant (rank 2 – 21; N=27). No statistical differences
204 were observed for the number of panicles for male and female flowers ($t_{20}=0.176$,
205 $p=0.86$). Flowering started in early September and the peak lasted for c. 15 days (Fig. 2).
206 Fruiting and dispersal lasted for nearly a month. After mid-November, the flowering
207 heads remain in the plant but the number of fertile florets is very low (Fig. 2).

208

209 *Phenology of Spanolepis selloanae*

210 The mean prevalence of the larvae per plant was 74% (rank 58.6 – 87.5; N = 12), meaning
211 the larvae-fruit ratio (L:F) was approximately 3:1. Germination of the intact seeds was
212 100%. T50, the time for the germination of 50% of the seeds, was only eight days but
213 some seeds took as long as 69 days to germinate.

214 Adults of the gall midge were found during a very short period of time. Nearly all were
215 recorded in one visit on September 19th, immediately after the flowering peak of the host
216 plant (Fig. 2). Pupae were also recorded in that visit, but their exuviae persisted longer.

217 Larvae were first detected on September 19th in low numbers, and afterwards followed
218 the same pattern as mature seeds (Fig. 2). All larvae collected were third (last) instars; the
219 two earlier instars were no evident. We also found a wasp of the genus *Aprostocetus*
220 Westwood (Hymenoptera: Eulophidae), most probably a parasitoid of *S. selloanae*.

221

222 *Molecular analyses*

223 Two new haplotypes of the gall midge were found and submitted to Genbank. Haplotype
224 1 (699 bp, accession number MT511669) was observed in all larvae and six adults.
225 Haplotype 2 (667 bp, MT511670) was found only in three adults. It is therefore proved
226 that the larvae and adults we studied belong to the same species. Both haplotypes differed
227 in a single non-synonymous substitution at position 357 of the COI gene (reference:
228 accession number GQ387648.1:1145-2680). The BLAST search produced no identical
229 match for any of the two haplotypes. The most similar sequences to both haplotypes were
230 *Macrolabis fagicola* (Barnes) (JQ684878) with regard to total score (915). With regard
231 to percentage of identity, *Rhopalomyia protrahenda* (De Stefani) (MN191340) was the
232 best match to haplotype 1 (90.6), whereas three records of *Janetiella glechomae* (Kieffer)
233 (KR740388, KR743364, KR956680) were the best matches to haplotype 2 (90.69).
234 The phylogenetic results placed *Spanolepis selloanae* in a single branch within a large
235 polytomy when using the BI (Fig. 3) and MP algorithms (Online resource 1, Fig. 6). The
236 ML method grouped *S. selloanae* with *Dasineura oleae*, but this node received no support
237 (Online resource 1, Fig. 7).

238

239 *Taxonomy*

240 *Spanolepis* Gagné, new genus (Figs. 4-5)

241 Diagnosis. The genus is distinct among all other known Dasineurini by the lack of scales
242 on the adult thoracic sclerites and abdominal terga and sterna, by the very short setae on the
243 female cerci except for the four thickened apical setae (Fig. 5I), and on the larva, the loss
244 of a spatula, one of the two triplets of lateral papillae (Fig. 5L), and four of the eight terminal
245 papillae Fig. 5M).

246 Description. *Adult*. Female head (Fig. 4A): Eye facets circular, nearly contiguous on ventral
247 two-thirds of eye, 1/2 to whole eye facet apart on dorsal third, eye bridge 3 facets long,

248 facets at bridge 1 to 2 facets diameter apart. Antenna: male flagellomeres 12 (n=10), all but
249 last with long necks (Fig. 5A); female flagellomeres, 10-11 (n=10), without necks (Fig.
250 5B). Labella hemispherical, with several stout setae. Palpus 4-segmented with scattered
251 setae and no scales.

252 Thorax: Wing (Fig. 4B): C broken beyond junction with R₅; R₅ reaching C before wing
253 apex; Rs evanescent; wing fold barely evident; M₄ and CuA forming a fork; scales on
254 membrane sparse. Scutum with 4 discrete longitudinal rows of setae without scales
255 intermixed; median rows mostly single, not reaching scutellum posteriorly, lateral rows
256 sparse with 10-12 setae, mostly placed near midlength of scutum. Scutellum with about 10
257 dorsal setae. Anepimeron with 6-8 setae, remaining pleural sclerites bare. Acropod (Fig.
258 5C): claws strongly curved beyond midlength, with basal tooth; empodia as long as claws;
259 pulvilli diminutive.

260 Male abdomen (Fig. 5D-H): First through sixth tergites rectangular, each with anterior pair
261 of trichoid sensilla, a single, sparse, medially interrupted row of setae along posterior
262 margin, 2-3 lateral setae, and no scales; seventh tergite unsclerotized posteriorly, with only
263 anterior pair of trichoid sensilla, 2-3 lateral setae and no scales; eighth tergite pigmented
264 only anteriorly, with pair of anterior trichoid sensilla the only vestiture. Second through
265 seventh sternites rectangular, with mostly single horizontal row of posterior setae, single to
266 double horizontal row of setae at midlength, pair of closely adjacent trichoid sensilla
267 anteriorly and no scales; eighth sternite with anterior trichoid sensilla missing, midlength
268 and posterior setal rows commingling. Terminalia (Fig. 5E-G): cerci nearly triangular with
269 a few setae apically; hypoproct about as wide as a cercus, divided apically into 2 narrow
270 lobes, each with a pair of setae; aedeagus with convex apex, reaching end of hypoproct;
271 gonocoxite cylindrical laterally, its mediobasal lobe broad, subdivided, the dorsal part of
272 the lobe short, hemispherical, elongate-microtrichose, the ventral part longer, closely

273 sheathing much of one side of the aedeagus, mostly microtrichose, terminating in apical,
274 short-cylindrical, glabrous appendix tipped with two short setae; gonostylus tapering from
275 base, glabrous and carinate dorsally, microtrichose nearly to apex ventrally, glabrous and
276 carinate beyond.

277 Female abdomen (Fig. 5I-J): First through seventh tergites rectangular, all with anterior pair
278 of trichoid sensilla, single row of posterior setae interrupted medially except on sixth, with
279 no lateral setae and no scales; seventh tergite square, much narrower than sixth, with sparse
280 row of setae along posterior margin and pair of trichoid sensilla; eighth tergite divided into
281 two narrow, elongate sclerites about twice as long as seventh tergite, each with trichoid
282 sensillum near anterior end and 1-2 setae near posterior end. Second to seventh sternites as
283 for male; eighth sternite not apparent. Ovipositor elongate, protrusible, evenly
284 microtrichose and sparsely short-setose to cerci, protrusible part approximately 5 times
285 length of sixth tergite, with narrow, faintly pigmented dorsolateral sclerite along length;
286 cerci fused, evenly cylindrical to rounded apex, with 4 thick setae with large sockets near
287 apex, elsewhere with scattered short setae no longer than width of their sockets and barely
288 longer than covering microtrichia; hypoproct narrow, nearly twice as long as wide, with 2
289 distal setae.

290 *Pupal exuviae* (Fig. 5K). Head and thorax brown, abdomen hyaline. Antennal bases
291 rounded, not differentially sclerotized or modified into anteriorly pointed projections;
292 with single papilla with seta, situated mediobasally. Vertex on each side with long seta
293 situated on conspicuously raised base. Face smooth, without lobes, with single papilla
294 with setae and 1-2 papillae without setae anterior to clypeus and triplet of papillae on each
295 side near palpal bases, 1 with seta. Prothoracic spiracle elongate. Abdominal terga, pleura
296 and sterna evenly covered with short spicules.

297 *Larva*. Third instar (Figs. 3C, 4L-M). Head capsule hemispherical, cephalic apodemes
298 about half length of head capsule, antennae about twice as long as wide. Integument white
299 except posterior segment darkened, entirely covered with pebbled verrucae except along
300 narrow spiculose band surrounding the 4 ventral papillae on abdominal first through
301 seventh segments. Spatula absent. Papillar pattern basic for Lasiopteridi except only one
302 triplet of papillae present on each side of thoracic segments (Fig. 5L) and 4 terminal
303 papillae (Fig. 5M).

304 Type species, *Spanolepis selloanae* Gagné.

305 Etymology. The name *Spanolepis* combines the Greek words for sparse and scales with
306 reference to the lack of scales on the head and thoracic and abdominal sclerites and their
307 paucity elsewhere on the adult body. The gender is feminine.

308 Remarks. *Spanolepis* belongs to the reconstructed tribe Dasineurini (Dorchin et al. 2019).
309 According to the key for Nearctic species in Gagné (2018), *Spanolepis* resembles
310 *Dasineura* Rondani in the following ways: antennae have a variable number of
311 flagellomeres within a species; male flagellomeres, except for the apicalmost, have a
312 single basal node and distinct apical neck, while those of the female have almost no neck
313 beyond the node; the costal wing vein is broken just posteriad of its juncture with the R₅
314 vein, which terminates anterior to the wing apex; claws are robust, curved beyond
315 midlength, and have a basal tooth; empodia are usually approximately as long as the claws
316 and pulvilli are about 1/3 the length of the claws; the gonocoxite has a tapered mediobasal
317 lobe that is closely juxtaposed to the side of the aedeagus; the female eighth tergite is
318 usually completely divided longitudinally into two separate sclerites; the ovipositor is
319 elongate-protrusible and its cerci are fused to form a single lobe (Gagné 2018). The new
320 genus is distinct from *Dasineura* as well as all other Dasineurini for the following derived
321 attributes: thoracic and abdominal sclerites lack scales, although narrow scales are present

322 but sparse on legs, wings and abdominal pleura; the male gonocoxal mediobasal lobe
323 terminates in a single, large, glabrous, lobe; the female fused cerci have four short,
324 thickened setae that are especially prominent because the remaining scattered setae are
325 barely longer than the width of their sockets; the larva lacks a spatula and has but one
326 triplet of lateral setae instead of two on each side of the thoracic segments and only four
327 instead of eight papillae on the terminal segment.

328

329 ***Spanolepis selloanae* Gagné, new species** (Figs.4-5)

330 Description. *Adult*. Female head as in Fig. 4A. Antenna: scape with 3-4 setae ventrally;
331 pedicel circled with 7-9 setae shorter than those of scape; male flagellomeres 12 (n=10), all
332 but last with long necks (Fig. 5A); female flagellomeres, 10-11 (n=10), without necks.
333 Frons with 10-12 setae. Wing (Fig. 5B): length in males, 1.4-1.5 mm (n=10); in females,
334 1.5 mm (n=10). Male abdomen as in Figs. 4D-H. Female abdomen as in Figs. 4I-J.

335 *Pupal exuviae* as in Fig. 5K.

336 *Larva*. Third instar (Fig. 4C): Length 1.3-1.5 mm (n=10). Sternal, lateral and ventral
337 papillae of first thoracic segment as in Fig. 5L. Dorsum of eighth and terminal segments
338 as in Fig. 5M.

339 **Material examined.** Holotype, male, from *Cortaderia selloana*, Zapateira, A Coruña,
340 Spain, IX-19-2018, J. Fagúndez, deposited in USNM. Paratypes, 6 males, 8 females, 4
341 pupal exuviae, and 20 larvae, same data as holotype, deposited as follows: 1 male,
342 1 female, 5 larvae in Museo Nacional de Ciencias Naturales, Madrid, Spain; 1 male, 1
343 female, 5 larvae in The Natural History Museum, London, United Kingdom; remainder
344 in USNM.

345 **Etymology.** *Spanolepis selloanae* is named after the specific epithet of the host plant. That
346 name originally honored Friedrich Sellow (1789-1831), a Prussian botanist and zoologist

347 who made extensive collections of flora and fauna in Brazil, Uruguay and Argentina from
348 1814 to 1831 (Rego et al. 2013).

349 **Remarks.** To initially identify the gall midge on pampas grass we needed to ascertain that
350 it did not belong to any other of the seven Lasiopteridi previously recorded from flower
351 heads of grasses. All are from Europe and/or North America and currently in *Dasineura*,
352 but none of them is well known. We list them here with the specific differences that
353 distinguish them from *S. selloanae*.

354 *Dasineura airae* (Kieffer) (1897: 300) was described from spikelets of *Deschampsia*
355 *flexuosa* (L.) Trin. (originally given as *Aira flexuosa*) in France. It has not been found again
356 since its original collection (Skuhrová et al. 2005). The original description includes no
357 illustrations but does mention that the abdomen has transverse bands of scales, which *S.*
358 *selloanae* lacks.

359 *Dasineura alopecuri* (Reuter) (1895: 3) (synonym, *Dasineura agropyronis* Barnes (1927:
360 214)) comes from *Alopecurus pratensis* L. and possibly *Elymus repens* (L.) Gould. It is
361 widespread in northern Europe from where it immigrated into Canada (Ontario and New
362 Brunswick) and New Zealand. Larvae of this species feed in seeds. The most striking
363 distinguishing character of *D. alopecuri* is the pointed fused cerci that Reuter (1895)
364 illustrated, as did later Sylvén and Tastás-Duque (1993). Barnes (1930) reported that
365 Reuter's specimens had banded scales on the abdomen and he later (Barnes 1946) stated
366 that the larva had a spatula. All three attributes separate this species from *S. selloana*.
367 Barnes's *D. agropyronis* was based on females found swarming in large numbers on *E.*
368 *repens* (as *Agropyron repens*). Barnes (1930) sank *D. agropyronis* under *D. alopecuri*,
369 writing only that "it is undoubtedly *D. alopecuri*." Nevertheless, the species should
370 eventually be reexamined if only because it was found associated with a different host.

371 *Dasineura dactylidis* Metcalfe (1933: 329) is widespread in Europe on *Dactylis glomerata*
372 L. In England adults were found mating at the end of May. Larvae fed on seeds and were
373 full-grown by end of June. One generation occurred per year. Metcalfe (1933) noted that
374 the adult abdomen had "dorsal bands of dark fuscous scales" and that the "harpes (the
375 gonocoxal mediobasal lobes) [were] irregularly digitiform." Both characters differentiate
376 this species from *S. selloanae*.

377 *Dasineura festucae* Barnes (1939: 172) is widespread in Europe on *Festuca rubra* L. Adults
378 were reared in June from seed kept over the winter. Duncan Sivell (in litt.) kindly sent a
379 photo of the abdomen of one of the syntypes that shows rows of wide scales on the terga,
380 which the new species lacks.

381 *Dasineura graminis* Felt (1908: 342) was originally collected in New York (USA) from
382 *Agrostis capillaris* L. (originally as *Agrostis vulgaris*). It is based on two females caught in
383 early June while laying eggs on flower heads. Their abdominal terga are well covered with
384 wide scales. It is possible that *D. graminis* is an introduced species. A *Dasineura* identified
385 by Barnes (1931) as this species was reared from seeds of the same host in England. Larvae
386 of that record fed on the developing seeds and the species reportedly has at least two
387 generations per year (Barnes 1946).

388 *Dasineura poae* Mühle (1957: 547) is from northern Europe on *Poa pratensis* L. Larvae
389 develop in the inflorescence. The female of this species was described with pointed fused
390 cerci and the larva with a spatula and six terminal papillae. All three attributes distinguish
391 this species from *S. selloanae*.

392 *Dasineura trisetae* Barnes (1939: 174) is known from Austria from *Trisetum flavescens*
393 (L). P. Beauv. Barnes separated the male of this species from *D. festucae* by its male
394 "ventral lamella" (hypoproct) "that ... had a shallow but wide emargination, each lobe
395 approaching equilateral triangle in shape, roundly pointed," as opposed to that of *D.*

396 *festucae* “with a deep V-shaped emargination, each lobe narrow, roundly pointed.” In a
397 companion paper on *D. trisetae*, Watzl (1939) treated the biology and all stages and
398 included some fine illustrations. Larvae of this species feed in the seed, have a spatula, and
399 form a cocoon after they drop to the soil. In contrast, larvae of *S. selloanae* lack a spatula
400 and remain in the plant to pupate.

401

402 **Discussion**

403 The new species of gall midge is placed in a new genus because of its distinctiveness
404 compared to all other known Dasineurini. We suspect that the new species is native to South
405 America and was probably introduced into Europe with its host plant. This is supported by
406 several exclusive morphological traits not found in European Dasineurini. No Dasineurini
407 or Lasiopteridi has been described from Poaceae in South America (Gagné 1994). Further
408 field work and collections are needed to establish the origin of *S. selloanae*.

409 From the DNA results, we confirmed that the larvae and adults found in *C. selloana* belong
410 to the same species. Other studies have successfully applied DNA genotyping to the
411 identification of larval specimens of Diptera (Failla et al. 2016). It is interesting that none
412 of the 449 COI sequences available in Genbank for genus *Dasineura* are a close match to
413 any of the two haplotypes of *S. selloanae*. Closer matches were observed for *J. glechomae*
414 and *Macrolabis fagicola* but these feed on Lamiaceae and Fagaceae, respectively. The two
415 species belong to genera that are closely allied to *Dasineura* and differ in the same ways as
416 *Dasineura* to *Spanolepis* (Gagné 2018). Our phylogenetic results rule out a close
417 relationship with any of the other genera included in the study. Disentangling the
418 evolutionary history of the tribe Dasineurini, and therefore a proper placing of the genus
419 *Spanolepis*, requires a much denser taxon and gene sampling which is beyond the scope of
420 the present work.

421

422 *Spanolepis selloanae* effects on the host plant

423 In our study area, we found *S. selloanae* only on female plants, none in hermaphrodite
424 plants at any stage. We did not find any viable seeds in hermaphrodites in the studied
425 population, where we recorded a sex ratio of 1:1.25 in favour of hermaphrodite plants.
426 According to the literature, female plants develop exclusively unisexual flowers, but
427 hermaphrodite plants produce fertile anthers and viable seeds, albeit at lower fertility rates
428 than female plants (Connor 1973, 1981, Astegiano 1995, Lambrinos 2001). Connor
429 (1973, 1981) found that female plants produce larger seeds than hermaphrodites, probably
430 related to a higher seed viability and seedling vigour. Seed viability was 99% in female
431 plants, and 47% in hermaphrodite plants on populations from New Zealand (Knowles and
432 Ecroyd 1985). In addition, sex ratio is commonly described as 1:1 (Connor 1973). Our
433 findings, which show different results for hermaphroditism and sex ratio, has clear
434 implications on the impact of the midge and its effects on the population.

435 The new gall midge was observed to reduce seed production to nearly one fourth,
436 considering the ratio of larvae and intact seeds in the population. This can be considered
437 a high prevalence compared to other similar species. For example, Ahee et al. (2013)
438 found a mean prevalence of 9.5% of *Stenodiplosis phragmicola* Sinclair and Ahee, a gall
439 midge of the supertribe Cecidomyiidi that feeds on seeds of *Phragmites australis*. In our
440 population, viability of the remaining intact seeds was not affected.

441

442 **Conclusions and applications**

443 *Spanolepis selloanae* is, to the best of our knowledge, the only described natural enemy
444 of *C. selloana*, a harmful invader of the coasts of southern Europe. The larvae strongly
445 affect seed production, the main source of propagation of *C. selloana*. The insect is

446 therefore a good candidate for biological control of the invasive plant. The description of
447 the new species and its effects on the host plant is a first step towards the development of
448 a new control agent for the weed, which should follow the standard procedures of
449 assessing its life cycle, native range, potential impacts on non-target species, and
450 feasibility of translocation to other populations of *C. selloana* in the Iberian Peninsula
451 and elsewhere.

452

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630 **Figure Legends**

631

632 **Fig. 1.** A. Location of the study site (yellow star) in A Coruña council (pink borders)
633 located in NW Galicia (B), in NW Spain (C). Urban areas are in red, rural areas in green,
634 and semi-urban areas in orange. D shows sampling in the studied population, E is a detail
635 of the inflorescence of one female plant.

636

637 **Fig. 2.** Reproductive phenology of female plants of *C. selloana* (A) and phenology of *S.*
638 *selloanae* (B).

639

640 **Fig. 3.** Bayesian phylogram obtained for 42 members of the tribe Dasineurini using
641 *Asteromyia carbonifera* and *Lasioptera arundinis* as outgroups. The position of
642 *Spanolepis selloanae* is highlighted. Support values (Bayesian posterior probabilities /
643 ML > 50% bootstrap / MP > 50% bootstrap) are shown next to nodes, above branches.

644

645 **Fig. 4.** *Spanolepis selloanae*. A, Female head. B, Wing. C, Larva. Scale line = 0.1 mm.

646

647 **Fig. 5.** *Spanolepis selloanae*. A, Male third flagellomere (ventral) B, Female third
648 flagellomere (ventral). C, Acromere. D, Male sixth through eighth tergites (dorsolateral).
649 E, Gonopod, cerci and hypoproct (dorsal). F, Gonostylus (ventral). G, Gonocoxal
650 mediobasal lobes and aedeagus (dorsal). H, Male sixth through eighth sternites (ventral).
651 I, Female fused cerci and hypoproct (dorsolateral). J, Female sixth tergite through fused
652 cerci (dorsal). K, Anterior structures of pupal exuviae. L, Larva, ventral setation of
653 prothorax: from center, sternal papilla, triplet of lateral papillae and ventral papilla. M,
654 Eighth and terminal segments (dorsal).

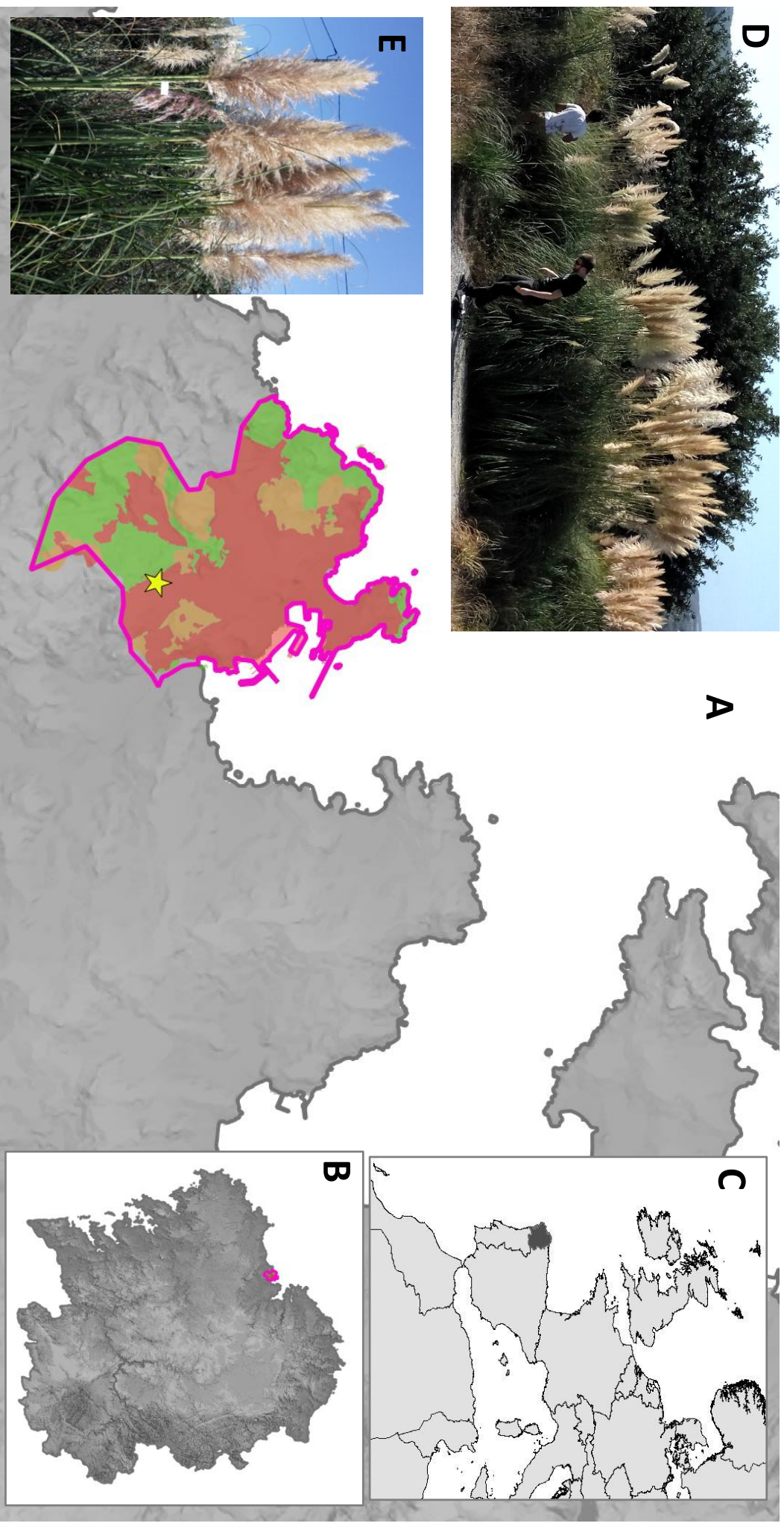
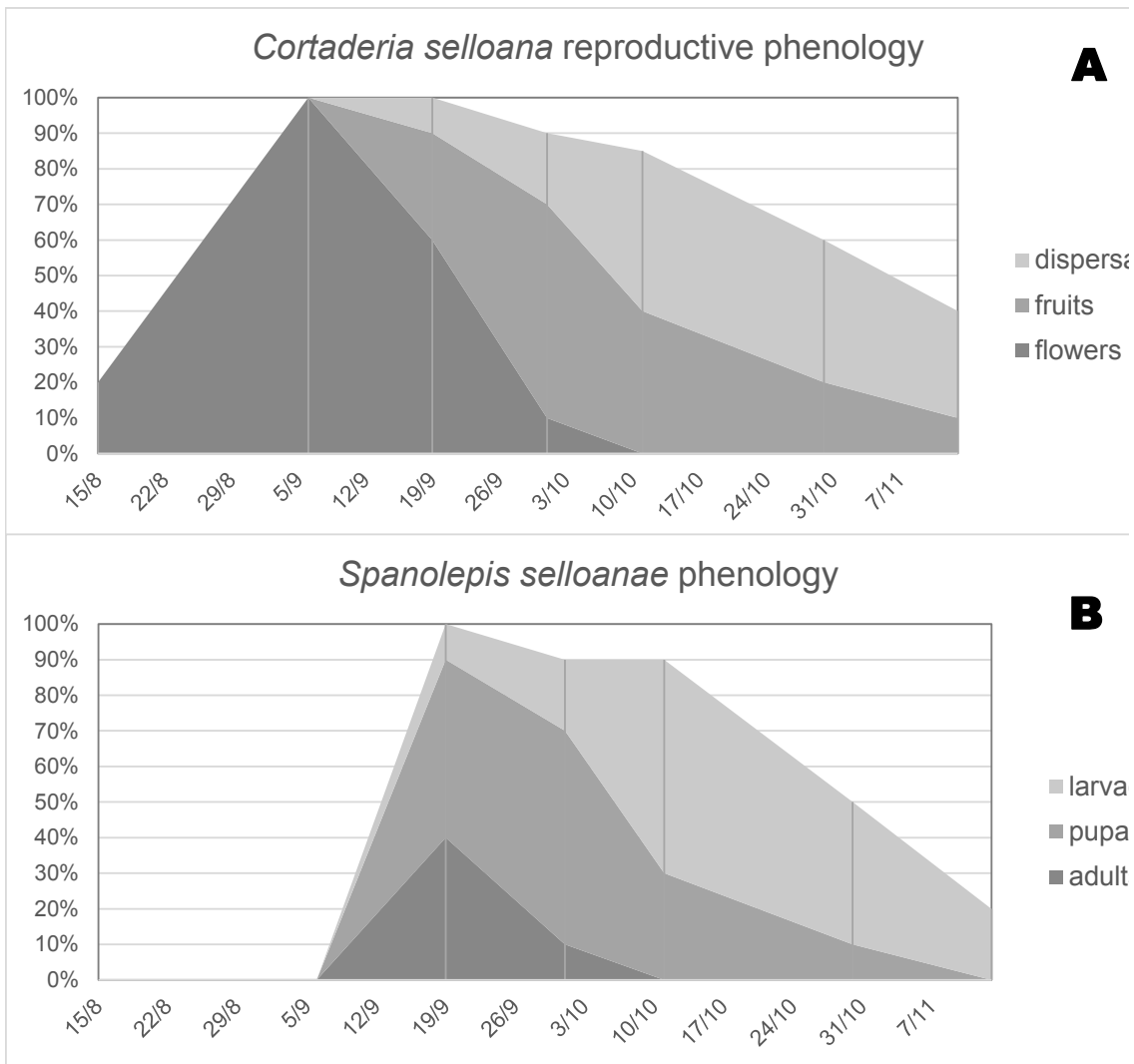


Figure 2

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	15-Aug	6-Sep	19-Sep	1-Oct	11-Oct	30-Oct
flowers	0.2	1	0.6	0.1	0	0
fruits	0	0	0.3	0.6	0.4	0.2
dispersal	0	0	0.1	0.2	0.45	0.4

	15-Aug	6-Sep	19-Sep	1-Oct	11-Oct	30-Oct
adults	0	0	0.4	0.1	0	0
pupae	0	0	0.5	0.6	0.3	0.1
larvae	0	0	0.1	0.2	0.6	0.4

13-Nov

0

0.1

0.3

13-Nov

0

0

0.2

Figure 3

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