Title: Reproductive modes of polyploid *Ludwigia grandiflora subsp. hexapetala* in western Europe: the effects of a late-acting self-incompatibility system and its absence on genetic diversity within populations

Short running title: Mixed reproductive modes in *Ludwigia*

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Abstract

Reproductive mode, *i.e.,* the proportion of individuals in populations produced by clonality, selfing and outcrossing in populations, determines how hereditary material is transmitted through generations. It shapes genetic diversity and its structure over time and space.

Ludwigia grandiflora subsp. *hexapetala* (*Lgh*) is a partially clonal, polyploid, hermaphroditic, and heteromorphic plant that recently colonized multiple countries worldwide. In western Europe, individuals in this species are either self-incompatible caused by a late-acting self-incompatibility (LSI) system developing long-styled flowers, or self-compatible (SC) developing short-styled flowers. We do not yet know if the LSI system is effective in driving genetic diversity within populations, as previously showed for gametophytic and sporophytic SI systems. In addition, determining the reproductive mode of newly established *Lgh* populations in Europe will contribute to understand their ecological and evolutionary roles at the margins of species distribution. However, we still lack of a full approach including the essential step to unfold population genetic indices to estimates rates of clonality, selfing and outcrossing in autopolyploids.

In this study, we proposed such an approach to measure genetic diversity to assess reproductive modes on 53 LSI and SC populations on newly colonizing France and northern Spain, using SNPs amplifying on a distinct autotetraploid part of the *Lgh* genome. SNPs are easily reproducible, adapted for intraspecific genetic studies and allowed confident allele dosage to genotype autopolyploid individuals. Such genotyping data in turn made it possible to use recent methodological developments to compute and interpret genetic diversity to assess reproductive mode in each population.

We found that populations reproduced mainly clonally but with a high diversity of genotypes and with substantial estimated rates of sexual events, up to 40%. We also found evidence for

local admixture between LSI and SC populations in a background of genetic structure between pairs of LSI and SC populations that was twice the ones found among pairs of LSI populations or pairs of SC populations, arguing that SC and LSI populations may follow distinct expansion dynamics. These evidences of sexual events in nearly all populations and of high diversity in clonal lineages changes the way we think about managing *Lgh* worldwide invasive populations.

We also took advantage of the spatial segregation of LSI and SC populations invading France to characterize the population genetic consequences of an LSI system. LSI and SC populations showed similar rates of clonality but significantly different rates of selfing, as expected considering their breeding system, and despite the small rates of failure of LSI system. Within the 53 studied populations, the 13 SC-only populations distinguished with fewer effective alleles, lower observed heterozygosity, and higher inbreeding coefficients, linkage disequilibrium and estimates of selfing than found in LSI populations. These results suggested that genetic differences significantly found between LSI and SC populations mainly came from the increased selfing rates in SC populations rather than due to the genome-wide consequences of outcrossing in LSI populations or due to different rates of clonality. The overall maintenance of higher genetic diversity, with the possibility of resorting to clonality, selfing and outcrossing altogether, may explain why LSI populations seem to be more prevalent in all newly expanding populations worldwide.

Beyond *Lgh*, our methodological approach may inspire future studies to assess reproductive mode of other autopolyploid eukaryote populations, and our results emphasize the necessity to consider the variations of reproductive modes when managing invasive plant species.

Keywords: Partial clonality, Mating system, Late-acting self-incompatibility system, Selfing, Outcrossing, Autopolyploidy, Water primrose

70 # Introduction

71 Plants can reproduce using different mechanisms (i.e., breeding system), including clonality
72 and different types of sexuality (i.e., mating system, including allogamy and selfing;
73 Holsinger 2000). Reproductive mode corresponds to the actual balance between sexual and
74 clonal reproduction, measured by the rate of clonality (De Meeus et al. 2007; Stoeckel et al.
75 2021a), and, within the proportion of offspring produced by sexuality, the balance between
76 autogamy and geitonogamy (hereafter *selfing*) and allogamy (*outcrossing*) measured by the
77 rate of selfing (Bürkli et al. 2017). Reproductive mode is one of the main drivers of genetic
78 diversity in populations and species (Duminil et al. 2007, Ellegren & Galtier 2016, Glémin et al.
79 2019). It determines the way hereditary material is transmitted over generations, and thus
80 constrains the range of genetic diversity that can evolve within populations and species (De
81 Meeus et al. 2007, Fehrer 2010, Stoeckel & Masson 2014, Rouger et al. 2016). Its genetic
82 consequences are deep enough to be discernible even in the presence of other affecting
83 factors (Charlesworth 2003). Considering its influence on genetic diversity and its structure in
84 populations, reproductive mode is one of the major biological traits to decipher before
85 interpreting other biological and ecological forces using molecular data (Duminil et al. 2007,
86 Reichel et al. 2016, Bürkli et al. 2017, Orive & Krueger-Hadfield 2021). Given an adequate
87 theoretical framework, population geneticists can use genotypic data to infer reproductive
88 modes in populations (Halkett et al. 2005, Arnaud-Haond et al. 2007, Hardy 2016, Bürkli et al.
89 2017, Stoeckel et al. 2021a).

90 Approximately 80% of plant species are partially clonal (Barrett 2010, Vallejo-Marin et al.
91 2010). Clonality consists of a parent producing a new descendant that is a genetic copy of itself
92 with the exception of rare somatic mutations and mitotic recombinations (De Meeus et al.

93 2007). Clonality generates repeated genotypes in populations when parents can breed
94 multiple descendants (Arnaud-Haond et al. 2007). This yields an average excess of
95 heterozygotes compared to Hardy-Weinberg expectations (*i.e.,* negative F_{IS}), large variance of
96 F_{IS} among polymorphic markers along the genome and a small excess of linkage
97 disequilibrium, increasing with decreasing population size (Navascues et al. 2010, Stoeckel &
98 Masson 2014, Stoeckel et al. 2021a). These effects vary with the rates of clonality and, in turn,
99 can be used to infer the rates of clonality themselves within populations (De Meeus et al.
100 2006, Becheler et al. 2020, Arnaud-Haond et al. 2020).
101 Approximately 70% of angiosperm species are hermaphroditic (Dellaporta & Calderon-
102 Urrea 1993) and have thus the possibility to sexually reproduce with themselves (selfing).
103 Selfing decreases effective population sizes and thus fastens the effect of genetic drift, leading
104 gene diversity to decrease in populations and even to allele fixing (Wright et al. 2008, Roze
105 2016, Glémin et al. 2019). Selfing also prohibits genetic mixing between different ancestral
106 lineages, resulting in decreased heterozygosity within individuals (David et al. 2007,
107 Hardy 2016) and increased linkage disequilibrium between genes along genomes (Golding &
108 Strobeck 1980, Norborg 2000, Lucek & Willi 2021).
109 Around half of hermaphrodite plants restrict self-fertilization using a variety of molecular
110 mechanisms grouped under the term "self-incompatibility (SI) systems" which favour
111 outcrossing within populations (De Nettancourt 2001, Castric & Vekemans 2004, Gibbs 2014,
112 Steinecke et al. 2022). Outcrossing is overall expected to increase genetic diversity, to limit
113 allele fixation and to reduce linkage disequilibrium when compared to selfing. However, such
114 expectations depend on the genetic linkage between the considered loci and the genomic
115 region carrying the genes involved in self-recognition (Glémin et al. 2001, Stoeckel et al. 2006,
116 Navascues et al. 2010). Within the different identified SI systems (Charlesworth et al. 2005,

117 Franklin-Tong 2008), the late-acting SI system (hereafter LSI) is still poorly studied despite
118 being identified in multiple taxonomic groups in angiosperms (De Nettancourt 1997,
119 Gibbs 2014). In LSI systems, self-pollen tubes grow and are only blocked shortly before
120 penetrating the ovule, or at the micropyle, or, in some species, the ovules are penetrated but
121 their syngamy fails. Such species may present reduced female fertility due to self-pollen
122 disabling ovules, favouring the clonal regeneration of populations (Vaughton et al. 2010). LSI
123 systems are also characterized by low but recurrent failures of the self-recognition system due
124 to its late mechanism, leading to the production of a low amount of selfed seeds in populations
125 (Seavey & Bawa 1986; Chen et al. 2012, Gibbs 2014). Gametophytic and sporophytic self-
126 recognition mechanism occurring very early in the pistil drastically limit self-pollination thus
127 selfed seeds (Lawrence 1985, Gibbs 2014) and need specific chemical or physical treatments
128 to be overcome (Cabin et al. 1996, Ahmad et al. 2022). We however don't know yet if these
129 rare selfed seeds may contribute to the dynamics of genetic diversity of LSI populations and
130 species, especially in peripatric conditions or in any situation when compatible partners may
131 lack. Due to these selfed seeds, LSI system may even be less effective in driving genetic
132 diversity within populations, as already described previously for gametophytic and
133 sporophytic SI systems (Brennan et al. 2002, Stoeckel et al. 2006, Koelling et al. 2011, Busch &
134 Urban 2011). In such situation, the LSI systems could become a new evolutionary puzzle
135 among the reproductive systems.
136 Autopolyploidy is pervasive in plants whether it derives from whole genome duplication or
137 from multiple hybridization events (Baduel et al. 2018). Clonality and selfing tend to occur
138 more frequently in polyploids than in their diploid counterparts (Husband et al. 2008, Herben
139 et al. 2017, Van Drunen & Husband 2018). Autopolyploid species bring two more main
140 challenges when tackling population genetics (Dufresne et al. 2014): The first issue is achieving

141 confident allele dosage to obtain a robust genotype for each individual at each locus. For
142 instance, disentangling between AAAC, ACCC and AACC genotypes in an autotetraploid
143 requires a reproducible and robust quantitative approach to genotyping. Second, computing
144 values of genetic diversity, identities and heterozygosity within autopolyploid populations
145 requires adapted methods (Hardy 2016, Meirmans et al. 2018). For instance, in
146 autopolyploids, heterozygosity, i.e., the probability that two random alleles are not identical-
147 in-state, can take more different values than in the case of diploids (Haldane 1930, Hardy
148 2016). Autopolyploids require dedicated computations of population genetic indices to not
149 result in artefactual population genetic values. These dedicated methods can now be
150 commonly computed using dedicated software such as Spagedi (Hardy & Vekemans 2002) and
151 GenAPoPop (Stoeckel et al. 2024).
152 Water primrose*, Ludwigia grandiflora* subsp. *hexapetala* (Hook. & Arn.) Nesom and Kartesz
153 (2000), hereafter *Lgh*, is one of the most invasive aquatic plants in the world (Thouvenot et al.
154 2013). *Lgh* is an alloautodecaploid species (2n=10x=80 chromosomes), resulting from
155 hybridization of different ancestral diploid species, some of which are represented more than
156 once in the total genome of *Lgh*, which belongs to the genus *Ludwigia* L. section Jussiaea (Hoch
157 et al. 2015, Barloy et al, 2024). Interestingly, *Lgh* includes an autotetraploid set of
158 chromosomes, shared with *L. peploides* subsp. *montevidensis* (2n=2x=16), hereafter *Lpm*, that
159 is clearly distinct from the other ancestral part of *Lgh* genome (Barloy et al. 2024). *Lpm* is a
160 self-compatible-only diploid species with only one common floral morphology (Estes & Thorp
161 1974, Grewel et al. 2016). On its side, *Lgh* presents heteromorphic flowers corresponding to
162 two floral morphs: L-morph individuals develop long-styled flowers and S-morph individuals
163 develop short-styled flowers (Portillo-Lemus et al. 2021). L-morph flowers express an active
164 LSI in western European populations (Portillo-Lemus et al. 2022). During the core flowering

165 season (summer), in experimental greenhouse conditions, L-morph individuals show a stable
166 seemingly insignificant rate of autogamy (around 0.2‰ of the available ovules) that increases
167 at the end of the flowering season, during autumn, to 1‰, which is common in LSI systems
168 (Gibbs 2014. Due to the massive blossoming of this species, growing in very dense populations,
169 these selfed seeds would add up yearly in field populations to thousands of seeds per metre
170 square (Portillo-Lemus et al. 2021). This pattern of low rates of autogamy, that increase at the
171 end of the flowering season, may provide the advantage of reproductive assurance
172 (Goodwillie & Weber 2018). In contrast, S-morph individuals are self-compatible (SC) in
173 western European populations but pollen tubes of the L-morph grow significantly faster and
174 are thus advantaged to fertilize ovules when in competition with self-pollen (Portillo-Lemus
175 et al. 2022). In addition, peripatric *Lgh* populations, including European populations, were
176 previously reported as exclusively clonal with few clonal lines (Dandelot 2004, Okada et al.
177 2009). Recently established populations in France and northern Spain mostly present only one
178 of the two compatibility modes locally, sometimes with a population of the other type a few
179 to tens kilometers away, which may result in effective allogamy (Portillo-Lemus et al. 2021,
180 2022). All these different breeding systems make possible very different reproductive modes
181 in populations, comprising all possible quantitative combinations of mainly clonal,
182 autogamous and allogamous modes. Genotyping with confident allele dosage an
183 autotetraploid inherited genome, analyzing the genotyping to obtain population genetic
184 measures to estimate the respective and quantitative contributions of these different
185 reproductive modes still constitute challenging tasks in autopolyploid species as pointed out
186 by Dufresne et al. (2014)'s review and synthesis. If using genetic diversity within population to
187 estimate rates of clonality versus sexuality, and of selfing versus allogamy is now commonly
188 achieved for diploids and haplodiplontics (David et al. 2007, Arnaud-Haond et al. 2020,

189 Krueger-Hadfield et al. 2021, Stoeckel et al. 2021a,b), we still lack of such a framework to
190 estimate the reproductive modes in autopolyploid populations with their specificities, with an
191 applied case study which would demonstrate its effectiveness.
192
193 In this study, we proposed a complete framework, from genotyping autotetraploid part of *Lgh*
194 genome with allele dosage to the estimation of reproductive modes per population using
195 genetic data, compiling recent molecular and software developments (Besnard et al. 2023,
196 Hardy 2016, Stoeckel et al. 2024) to fill the gaps identified by Dufresne et al. (2014) for
197 confidently genotyping autopolyploid individuals. First, we developed a codominant and
198 reproducible set of single-nucleotide polymorphism (SNP) markers for this species that are
199 more adapted for intraspecific genetic studies, being able to distinguish between siblings and
200 different clonal lineages, and that allowed to perform reproducible and confident allele
201 dosage. Indeed, allele dosage at each marker within each individual is mandatory to compute
202 confident population genetic measures within populations that have no reason to follow
203 genotype frequencies expected under Hardy-Weinberg proportions, being partially clonal,
204 outcrossed and selfed. To be sure of the ploidy level of the studied markers and that the
205 genotyped markers did not interact with genomes of the other ancestral species of *Lgh*
206 genome, we genotyped SNPs only the autotetraploid part of *Lgh* genome shared with the
207 diploid species *Lpm*. The *Lpm* genome is sufficiently genetically distinct from the other
208 ancestral genomes of *Lgh* to avoid misgenotyping (Barloy et al. 2024).
209 We then used this approach to identify and study the variability of the reproductive modes of
210 *Lgh* populations within the invaded region of Western Europe considering their LSI and SC
211 status. To assess the reproductive modes of each sampled population and estimate their rates
212 of clonality and selfing, we measured gene diversity, heterozygosity, linkage disequilibrium

213 and genotypic diversities within 53 populations sampled in western Europe. Being able to
214 assess reproductive modes in each population, we will discuss the potential advantage of
215 uniparental reproduction including clonality and selfing, of recombination (selfing and
216 allogamy) and of heterozygosity in such peripatric invasive populations.
217 Second, due to the fact that recent local populations in France and northern Spain present
218 only one of the two compatibility modes, we took advantage of this contrasted situation
219 within the same species and in comparable ecological situations to compare genetic diversity
220 among LSI and SC populations, to assess the influence of LSI on genetic diversity as similarly
221 tackled in sporophytic self-incompatible and SC Brassicaceae species (Koelling et al. 2011).
222 Indeed, genetic diversity underlies the evolvability of species and their survival and adaptation
223 to environmental change and ecosystem resilience (Booy et al. 2008, Hoban et al. 2021). The
224 small proportions of selfed seeds allowed by the LSI mechanism may mitigate the difference
225 in genetic diversity between LSI and SC populations compared to sporophytic and
226 gamethophytic self-incompatible systems. Considering the complex case of *Lgh* in western
227 European populations, we hypothesized that LSI populations should present typical genetic
228 footprints of dominant outcrossing, and perhaps higher rates of clonality due to the local lack
229 of compatible partners and self-pollen interferences, while SC populations should present
230 higher rates of sexuality prevailed by selfing. To understand the genetic impacts of
231 reproductive modes, we also quantified the covariations of genetic indices and their
232 importance to define the genetic diversity within the 53 genotyped populations, and
233 compared these observations to the theoretical expectations obtained from a Wright-Fisher-
234 like model extended to autotetraploids (Stoeckel et al. 2024). Finally, we interpreted the
235 genetic differences found within and between LSI and SC populations to understand how
236 reproductive mode(s) contributed to the genetic diversity in these peripatric *Lgh* populations.

237 # Materials and methods

238 **Sampling strategy and floral morphology of populations**

239 We collected 795 stems of *Lgh* from 53 locations (52 locations in France and one in Catalonia,
240 Spain), corresponding to an area that spans 880 kilometres east-to-west and 1,100 kilometres
241 north-to-south (Figure SI1). At each location, we collected 15 stems (hereafter individual)
242 along a linear transect measuring 40 meters length. Along each transect, we randomly
243 collected 3 stems at coordinates X_1 = 0m; X_2 = 10m; X_3 = 20m; X_4 = 30m and X_5 = 40m within a
244 1 meter-square quadrat. The young leaves of each sampled individual were stored after
245 lyophilization until DNA extraction. We visually identified floral morphologies of flowers found
246 along each transect within the sampled *Lgh* populations.

247

248 **Definition of the SNP marker set**

249 As no molecular markers suitable for clonal discrimination were yet available for *Lgh* and *Lpm*,
250 we generated an original set of SNP markers using RAD-Seq strategy (Baird et al., 2008) from
251 five and three *Lgh* and *Lpm* western European populations, respectively using a pool of 15
252 individuals sampled for each population. RAD DNA library, RAD-sequencing and pipeline to
253 identify *Lgh* SNP markers were carried out as described in Delord et al. (2018). To summary,
254 DNA of *Lgh* and *Lpm* were digested by *Sbfl* restriction enzyme and used to prepare DNA
255 libraries then sequenced using a illumine HiSeq3000 (150bp paired-end reads). After different
256 steps of filtering, a total of 14,233 and 34,287 RAD-Seq was found in *Lgh* and *Lpm* respectively.
257 At the end, 340 and 326 SNPs were obtained for *Lpm* and *Lgh*, respectively. Design of primers
258 compatible with Hi-Plex multiplexing was carried out at the Melbourne Bioinformatics lab.
259 Finally, sixty and fifty SNP markers were obtained for *Lpm* and *Lgh*, respectively. In our study,

260 we only considered polymorphic SNPs that were shared between *Lgh* and *Lpm* to be sure they
261 belong to the tetraploid part of *Lgh* genome derived from *Lpm* (Barloy et al. 2024). We finally
262 kept a set of 36 polymorphic and stable SNP markers to genotype *Lgh* samples and analyze
263 genetic diversity in each sampled population (primer sequences are openly listed in Stoeckel
264 et al. 2023).
265
266 **DNA extraction, SNP marker production and genotyping**

267 To genotype the 795 individually-tagged samples with these 36 SNPs, we extracted DNA from
268 25 to 30 mg of dried young leaf tissues. The DNA extractions were performed using the
269 NucleoSpin Plant II from MACHEREY-NAGEL kit, following the manufacturer's
270 recommendations. We used L1 buffer as lysis buffer. All individuals were genotyped from a
271 solution of 20ng/µl of *Lgh* DNA, using a modified version of the Hi-Plex protocol (Hammet et
272 al. 2019; Besnard et al. 2023). Hi-Plex is an amplicon sequencing technique (*sensu* Meek &
273 Larson 2019) in which all SNPs are co-amplified in a multiplex reaction before Illumina or Ion-
274 Torrent sequencing. Here, we used Illumina. Intermediate steps include dual indexing of
275 individual samples used for demultiplexing. Reads were then assigned to loci by aligning them
276 to reference sequences with BWA-MEM 0.7.15-r1140 (Li & Durbin 2010) and alleles were
277 counted with Samtools 1.9 (Danecek et al. 2021).
278
279 **Allele dosage**

280 The posterior probabilities of each single SNP genotype within each individual (hereafter
281 *single SNP genotype*) were computed using the likelihood of all possible genotypes considering
282 a multinomial distribution of the number of times each nucleobase was genotyped at one SNP

283 locus within one individual. In order to obtain the most confident dataset possible, we only
284 assigned a genotype when its posterior probability of allele dosage exceeded 70%. When one
285 SNP within one individual presented a posterior probability of allele dosage equal or lower
286 than 70%, we labelled and analysed it afterward as a missing genotype.

287

288 **Genotypic and genetic descriptors**

289 We expected that populations reproducing clonally may yield repeated multi-locus genotypes
290 (MLGs, i.e., the same genotype at all the 36 SNPs found in multiple individuals). By possibly
291 producing these repeated genotypes and by varying the relative distribution of the number of
292 samples of each of these distinct genotypes, rates of clonality impact genotypic richness and
293 evenness in populations (Halkett et al. 2005; Arnaud-Haond et al. 2007).
294 We measured genotypic richness using the R index (Dorken & Eckert 2001, Arnaud-Haond et
295 al. 2005), which is defined as:

296 $$R = \frac{G-1}{N_g-1}$$

297 where G is the number of distinct genotypes (genets) and N_g is the number of genotyped
298 individuals. We also measured genotypic evenness as the parameter β of the Pareto
299 distribution, which describes the slope of the power-law inverse cumulative distribution of the
300 size of MLGs (Arnaud-Haond et al. 2007):

301 $$N \geq X = aX - \beta$$

302 where N≥X is the number of sampled ramets belonging to genets containing X or more ramets
303 in the sample of the population studied, and the parameters *a* and *β* are fitted by regression
304 analysis. Low β-values indicate the dominance of one or few clonal lineages. Pareto β is less
305 biased by the sampling effort than clonal richness R (Stoeckel et al. 2021a). In our sample of

306 15 individuals, we expected a population with only one repeated MLG to present a Pareto β
307 value of 0.03 and a value of 3 in samples with no repeated genotypes. $\beta < 2$ indicates a
308 population reproducing with high rates of clonality (greater than 0.8 to 0.9). For a sample size
309 of 15 individuals, $2 < \beta < 3$ indicates intermediate to low rates of clonality (0.6 to 0.8). A β at
310 3, its maximum value, is indicative of a mainly sexual population, with rates of clonality ranging
311 from zero to 0.6, depending on the other genetic indices.
312 Rates of clonality and selfing confer different effects on the range of within-population genetic
313 polymorphism as well as on probabilities of genetic identities within individuals. We thus also
314 estimated expected and observed heterozygosity H_E and H_O, allelic richness A_E, inbreeding
315 coefficient F_{IS}, and linkage disequilibrium within each sampled population.
316 The Wright (1931, 1949) inbreeding coefficient F_{IS} accounts for intraindividual genetic
317 variation at one locus as a departure from Hardy-Weinberg assumptions of the genotyped
318 populations. We computed one F_{IS} value per locus per population. We then reported the mean
319 values of F_{IS} (MF_{IS}) and the inter-locus variance of F_{IS} ($VarF_{IS}$) for each population. Both MF_{IS}
320 and $VarF_{IS}$ are very informative about the underlying reproductive systems (Stoeckel et al.
321 2006, David et al. 2007). Clonality makes the MF_{IS} values tend toward -1 along with high
322 interlocus variance (Stoeckel & Masson 2014, Stoeckel et al. 2021a). A moderate amount of
323 sexual reproduction results in MF_{IS} values around 0 (Balloux et al. 2003). $VarF_{IS}$ varies with
324 rates of clonality, from very limited variance expected in sexual populations to high variance
325 in very clonal populations (Stoeckel & Masson 2014, Stoeckel et al. 2021a). Positive MF_{IS}
326 values are expected in populations reproducing using consanguinity and selfing (Castric et al.
327 2002, David et al. 2007). All sexual reproductive modes, allogamous and autogamous, result
328 in low $VarF_{IS}$ within a population as massive recombination tends to homogenize intra-
329 individual genetic identities along the genomes (Stoeckel et al. 2021a).

330 We measured linkage disequilibrium over all markers using the unbiased multilocus linkage
331 disequilibrium index, $\bar{r}_d$ (Agapow & Burt 2001). This mean correlation coefficient (*r*) of genetic
332 distances (*d*) between unordered alleles at *n* loci ranges from 0 to 1. This metric has the
333 advantage of limiting the dependency of the correlation coefficient on the number of alleles
334 and loci, and it is well suited to measure linkage disequilibrium in partially clonal populations
335 (De Meeus & Balloux 2004, De Meeus et al. 2006). In general, LD is only slightly affected by
336 clonality, except when clonality is high (c > 0.9) and/or when genetic drift dominates over
337 mutation rate (*e.g.,* when population sizes are small N<50 compared to u=0.001; Navascues
338 et al. 2010, Stoeckel et al. 2021a). In contrast, inbreeding and selfing are efficient processes
339 for quickly generating strong LD, after only few generations. Finally, we measured genetic
340 differentiation between populations of LSI, between populations of SC and between LSI and
341 SC populations using ρ_{ST}, an index adapted to study autopolyploid populations (Ronfort et al.
342 1998). All these indices were computed using GENAPOPOP (Stoeckel et al. 2024), a software
343 dedicated to analysing genetic diversity and differentiation in autopolyploid populations
344 genotyped with confident allele dosage and reproducing through all possible rates of clonality
345 and selfing.
346 We also used SPAGEDI (V1.5, Hardy & Vekemans 2002) to estimate rates of selfing within
347 autopolyploid populations genotyped with confident allele dosage. This approach infers rate
348 of selfing (Sg) from identity disequilibrium coefficients (g_{2z} estimator), assuming that
349 populations reproduce by self-fertilization and random mating and are at inbreeding
350 equilibrium (David et al. 2007 for diploids, Hardy 2016 for autopolyploids). Identity
351 disequilibrium coefficients are measured as the correlation in heterozygosity of distinct loci
352 within the genome, and present the advantage of being more robust to null alleles and
353 genotyping errors than raw F_{IS} (David et al., 2007). The effect of partial clonality on g_{2z}

354 estimator is not yet defined. We thus considered for this study that clonality would only
355 marginally impact identity disequilibrium coefficients, the possibility to be at the inbreeding
356 equilibrium and the corresponding estimates of selfing. A synthesis of all these hypotheses
357 based on previous knowledge is provided in Table SI1.
358

359 **Ranking populations by clonality and selfing**

360 We proposed and computed a synthesis index ($\Sigma\mathrm{clon}$) calculated from Pareto β and $\mathrm{VarF_{IS}}$ to
361 rank the studied populations from the less to the more clonal. These two population genetic
362 indices are known to vary with rates of clonality being unbiased in samples (Stoeckel et al.
363 2021a). To avoid issues of scaling as the range of values of these descriptors are different by
364 several orders of magnitude, $\Sigma\mathrm{clon}$ is computed in each population i as the sum of Pareto $\beta(i)$
365 and $\mathrm{VarFIS}(i)$ values that were previously normalized over the whole dataset, respectively
366 $z_\beta(i)$ and $z_{\mathrm{VarFIS}}(i)$.

367 $$z_\beta(i) = 1 - \frac{\beta(i) - min(\mathrm{B})}{max(\mathrm{B}) - min(\mathrm{B})}$$

368 $$z_{\mathrm{VarFIS}}(i) = \frac{\mathrm{VarFIS}(i) - min(\mathrm{VF})}{max(\mathrm{VF}) - min(\mathrm{VF})}$$

369 $$\Sigma\mathrm{clon}(i) = {}^{1}/_{2}\left[z_\beta(i) + z_{\mathrm{VarFIS}}(i)\right]$$

370 where $\beta(i)$ and $\mathrm{VarFIS}(i)$ are the measured Pareto β and variance of $\mathrm{F_{IS}}$ over loci in the
371 population i, and where $\mathrm{B} = \{\beta(1), \beta(2), \dots, \beta(55)\}$ and $VF =$
372 $\{\mathrm{VarFIS}(1), \mathrm{VarFIS}(2), \dots, \mathrm{VarFIS}(55)\}$ are the respective sets of Pareto β and $\mathrm{VarF_{IS}}$ over loci
373 in the 53 populations used to obtain their minimum (min) and maximum (max) values.
374 Using the same approach as for $\Sigma\mathrm{clon}$, we computed a synthesis index ($\Sigma\mathrm{self}$) calculated from
375 $\bar{r}_d$, $\mathrm{MF_{IS}}$ and Sg to rank the studied populations from the less to the more selfed.

376 $$\Sigma\mathrm{self}(i) = {}^{1}/_{3}\left[z_{\bar{r}_d}(i) + z_{\mathrm{MFIS}}(i) + z_{\mathrm{Sg}}(i)\right]$$

Statistical data analysis

First, to better understand the correlation between population genetic indices and estimates of reproductive modes from a large field dataset and to compare with the theoretical correlations obtained from simulations (Stoeckel et al. 2024), we computed a Principal Component Analysis (PCA) to comprehend the covariations of genetic indices, the correlations and the redundancies between the 17 genetic diversity indices (described above: G, R, D, Pareto β, $\bar{r}_d$, Ae, varAe, He, varHe, Ho, varHo, MF_{IS}, $varF_{IS}$, PIDsib, PIDu, Sg, SE.Sg) measured among the 53 sampled populations, and their link with reproductive modes including self-compatibility. We reported the amount of variation retained by the first two principal components and the correlation circle on which we plotted predictions of $\Sigma\mathrm{clon}$ and $\Sigma\mathrm{self}$ as supplementary variables. We also reported the score plot to visualize how LSI and SC populations distribute along the principal components of population genetic diversity. To avoid scaling issues, all descriptors were normalized before analysis.

We analyzed the relationship between genetic diversity indices and their relationships with $\Sigma\mathrm{clon}$ and $\Sigma\mathrm{self}$ measured in the 53 sampled populations using Kendal partial rank-order correlation tests. We reported the corresponding matrices of correlation.

To detect differences in distribution of population genetic indices, $\Sigma\mathrm{clon}$ and $\Sigma\mathrm{self}$, among floral morphs, we computed non-parametric Kruskal-Wallis tests that do not make any assumptions about the type of distribution and about homogeneity of variances between the tested distributions. When needed, we used post-hoc pairwise tests for multiple comparisons of mean rank sums (Nemenyi's test).

All statistical tests were computed using PYTHON 3.11, SCIPY.STATS 1.9.3 (Virtanen et al. 2020) and SCIKIT-POSTHOCS (Terpilowski 2019), except the PCA that was performed using R V4.2.2 and the library FACTOMINER (Lê et al. 2008).

402 # Results

403 Among the 53 populations, we found 40 populations with only L-morph individuals and 13
404 populations with only S-morph individuals (Table SI2, Figure SI1). The 36 SNP markers we
405 developed for *Lgh* using RAD-Seq and used to genotype the 795 sampled individuals via Hi-
406 Plex allowed confident allele dosage and sufficient statistical power to identify repeated
407 genotypes due to clonal reproduction and to assess the respective proportions of clonality,
408 selfing and allogamy in each population.

409

410 **Allele dosage and missing genotypes**

411 Within the 795 individuals genotyped at 36 SNPs (resulting in a total of 28,620 single-SNP
412 genotypes), 99.97% (28,612) were genotyped with posterior probability of allele dosage
413 superior to 70% (Table SI3). 785 individuals were thus genotyped with a full set of 36 SNPs
414 with posterior probabilities of allele dosage higher than 70%. Ten individuals distributed in
415 nine populations showed one of their SNP markers with posterior probabilities of allele dosage
416 equal or lower than 70%, that we assigned therefore as missing genotypes.

417

418 **Statistical power of the developed SNP marker set**

419 Over the 36 polymorphic SNPs, we found an effective number of alleles (A_E) of 1.36 per SNP
420 over all populations (Table SI2). Among populations, mean A_E values over the 36 SNPs were
421 homogenous, ranging from 1.22 to 1.55 (median=1.34). We, however, found large standard
422 deviation of A_E between SNPs within populations, ranging from 1.6 to 2.3 (median=2.1). Some
423 SNPs were apparently fixed in some populations while polymorphic at the scale of the whole
424 dataset. When not fixed, gene diversity H_E in polymorphic SNPs ranged from 0.14 to 0.33

425 (median=0.2).

426 These 36 SNPs in the autotetraploid part of *Lgh* would theoretically allow $4^{36}=4.7\times10^{21}$
427 different possible MLGs considering the four possible nucleobases and $2^{36}=6.9\times10^{10}$ different
428 possible MLGs assuming two possible nucleobases per locus. Considering allele frequencies in
429 the sampled populations, the probabilities of identities under panmixia ranged from $8.5\times10^{-}$
430 ^{12} to 5.2×10^{-5} (median=2.1×10^{-7}) and the unbiased probabilities of identity between sibs $P_{ID\text{-}SIB}$
431 ranged from 4.2×10^{-6} to 8.3×10^{-3} (median=5.6×10^{-4}; Table SI2). We then considered that the
432 SNP set we used showed sufficient statistical power to distinguish between true MLGs, and
433 that individuals with identical MLGs were true repeated genotypes (ramets) of a clonal lineage
434 (a genet).

435

436 **Genetic and genotypic diversity**

437 Across populations, we identified a total of 462 distinct MLGs (genets) within the 795 sampled
438 individuals genotyped. Among them, we found 404 genets (88%) with a single ramet and only
439 58 genets (12%) with more than two ramets (Table SI4). Forty-eight genets had two to seven
440 ramets distributed over one to six populations (median=2), seven genets with 10 to 33 ramets
441 distributed over two to 17 populations (median=9), and one large genet of 99 individuals
442 distributed over 24 populations (Figure 1).

443 Within populations, we found from three to 15 different genets (median=12) per population
444 among the 15 sampled individuals (Table SI4), implying the clear occurrence of repeated
445 genotypes but also a wide diversity of genets within most populations (Figure 1). Accordingly,
446 genotypic richness (R) ranged from 0.14 to 1 (median=0.79). The genotypic evenness, Pareto
447 β, ranged from 0.056 to 3 (median=1.478, Table SI2).

448 Observed heterozygosity H_O was also high in most populations, slightly above expected
449 heterozygosity, ranging from 0.13 to 0.38 (median=0.26). The mean standard inbreeding
450 coefficients (MF_{IS}) averaged over all genotyped loci within populations were negative in all 53
451 populations and ranged from -0.33 to -0.126 with a very negative median of -0.274 (Table SI2).
452 Variances of F_{IS} between loci within population were very high, ranging from 1.75 to 36.60
453 (median=27.57). All these measures argued for reproductive modes implying high rates of
454 clonality.
455 Estimates of selfing (S_g) were overall low with a handful of high values, ranging from 0 to 0.61
456 (median=0.06). Fifteen populations (28%) were estimated with no selfing. Nineteen
457 populations (36%) showed non-zero estimates under 0.1, 13 populations (25%) between 0.1
458 and 0.29, and six populations (11%) with estimates between 0.42 and 0.61.
459 Finally, linkage disequilibria within populations between genotyped SNPs were overall low,
460 with r_d values ranging from 0 to 0.51 with a median value of 0.12. Forty-two populations (79%)
461 were under 0.25, and only eight populations (21%) showed linkage disequilibrium between
462 0.25 and 0.51.
463
464 **Analyses of covariations between population genetic indices**
465 The first two components of the principal component analysis on the values of genetic
466 diversity found in the 53 genotyped populations accounted for 78.4% of the total variance
467 between populations (Figure SI2). Non-parametric Kendall partial rank-order correlations
468 between genetic indices (Table SI5) and correlations on the first two principal components
469 from the 17 population genetic indices measured showed three non-collinear groups of
470 associated genetic indices (Figure SI1.A) that are very similar to the theoretical groups of
471 population genetic indices expected to covary with different rates of clonality, selfing and

472 outcrossing in autopolyploids (Stoeckel et al. 2024). A first cluster regrouped G, D*, R, Pareto
473 β and $VarF_{IS}$, indices that are known to be sensitive to clonality (Stoeckel et al. 2021a) but also
474 VarHe, VarHo, and VarAe. This cluster largely explains the first dimension (50.2% of the total
475 variance) of the PCA and was collinear to Σ_{CLON} (also see Figure SI1.B). As expected under
476 partial clonality, $VarF_{IS}$ was negatively correlated to genotypic diversity indices (R and β; Figure
477 SI3). The second cluster regrouped $P_{ID\text{-}SIB}$, $P_{ID\text{-}u}$, H_E, A_E and H_O, indices that are linked to the
478 general genetic diversity of populations (Figure SI1). The third cluster regrouped S_g, SE.Sg, MF_{IS}
479 and r_D, indices that are usually used to identify, rank and estimate rates of selfing versus
480 outcrossing in sexual populations (Castric et al. 2002, Bürkly et al. 2017). The second
481 dimension of the PCA (23.4% of the total variance) was mostly correlated to Ho, Sg, He and r_D
482 which was collinear to Σ_{SELF} (Figure SI1.C). The clusters of genetic indices were corroborated
483 by the correlation between Σ_{CLON} and genetic indices (Figure SI2) and Σ_{SELF} and genetic indices
484 (Figure SI4).
485 The correlation across populations between Σ_{CLON} and Σ_{SELF} was negative and highly significant
486 (r_s = -0.66; $p < 0.001$; Figure 2). This correlation within LSI populations was negative and highly
487 significant (r_s = -0.65; $p < 0.001$) while it was nonsignificant in SC populations (r_s = -0.32; p
488 =0.289).
489

490 **Differences in genetic diversity and structure between L- and S-morph populations**

491 The number of ramets per genet was similar in LSI and SC populations (H=1.85, p=0.173,
492 Figure 1 & SI5), as well as were their genotypic richness (R, H=1.23, p=0.267) and evenness
493 (Pareto's β, H=1.60, p=0.206; Table SI2). The distributions of other population genetic indices

494 related to clonality were also not significantly different between LSI and SC populations
495 ($VarF_{IS}$: H=2.94, p=0.086; P_{ID-SIB}: H=1.98, p=0.160 and Σ_{CLON} H=2.28, p=0.131; Figure 3).
496 Mean observed heterozygosity (Ho, H=5.27, p=0.022) and their variances (VarHo, H=13.85,
497 p<0.001), mean effective number of alleles per locus (Ae, H=5.13, p=0.024) and its variance
498 over locus (VarAe, H=9.49, p=0.002), MF_{IS} (H=11.85, p<0.001), linkage disequilibrium (r_D,
499 H=5.55, p=0.018), estimate of selfing rates (Sg, H=12.39, p<0.001) and its standard error over
500 loci (SESg, H=9.58, p=0.002) significantly differed between LSI and SC populations. SC
501 populations, compared to LSI, showed lower mean observed heterozygosity (medians, LSI:
502 0.262, SC: 0.210) and less variance between loci (medians, LSI: 2.400, SC: 1.859), lower
503 effective number of alleles (medians, LSI: 1.341, SC: 1.283) and less variance between loci
504 (medians, LSI: 4.419, SC: 3.580), higher linkage disequilibrium (medians, LSI: 0.113, SC: 0.152),
505 higher estimates of selfing rate (medians, LSI: 0.045, SC: 0.175) even if with higher standard
506 error between loci (medians, LSI: 0.058, SC: 0.156) and higher Σ_{SELF} (medians, LSI: 0.222, SC:
507 0.495).
508 Genetic differentiation (ρ_{ST}) among pairs of SC populations (median value of ρ_{ST}=0.27) was
509 comparable to the genetic differentiation found among pairs of LSI populations (median value
510 of ρ_{ST}=0.26; H=319.37, post-hoc p=0.322; Figure 4). The median of ρ_{ST} between pairs of LSI and
511 SC populations reached 0.65. The distribution of inter-morph ρ_{ST} values differed both from the
512 distribution of pairs of intra-LSI ρ_{ST} values (post-hoc p<0.001) and from the distribution of pairs
513 of intra-SC ρ_{ST} values (post-hoc p<0.001). The minimum spanning tree of LSI and SC individuals
514 computed with *GenAPoPop* showed quite clustered distributions of LSI and SC individuals but
515 also with clear evidence of admixtures between LSI and SC lineages (Figure 5).
516

517 # Discussion

518 We used population genetics on autotetraploid SNPs with allele dosage to assess the rate of
519 clonality, of selfing and of outcrossing (i.e., reproductive mode) of 53 populations of *Ludwigia*
520 *hexapetala* subsp. *grandiflora* (*Lgh*) recently colonizing western European watersheds. To
521 achieve such goal, we developed reproducible codominant molecular markers (SNPs) enabling
522 allele dosage to genotype sampled individuals and used tailored computational analyses that
523 answer the remaining challenges to perform confident population genetic analyses in
524 autopolyploids (Dufresne et al. 2014), This framework can be applied to any autopolyploid
525 species.

526 *Lgh* develops two floral morphs respectively associated with an active Late-acting self-
527 incompatible system (L-morph) and a self-compatible system (S-morph, Portillo-Lemus et al.
528 2021, 2022). Interestingly, the sampled populations in western Europe showed either L or S-
529 morph resulting in two groups of sampled populations: one group of 40 LSI (L-morph)
530 populations and one group of 13 SC (S-morph) populations. They live in close ecological
531 conditions (Portillo-Lemus et al. 2021) which thereby provides a rare opportunity to
532 characterize the genetic consequences of an LSI system compared to a group of SC populations
533 in the same species and ecological context.

534

535 **Nearly three quarters of the genetic variance explained by different rates of clonality and**
536 **selfing among *Lgh* populations**

537 The correlation of variations of population genetics indices on the 53 genotyped *Lgh*
538 populations were congruent with theoretical predictions on the variations of genetic indices
539 with different rates of clonality and selfing for autopolyploid populations (Stoeckel et al.

540 2024). Similarly, such correlations were already predicted from Wright-Fisher-like models
541 adapted for diploid (Stoeckel et al. 2021a) and haplodiplontic life-cycles (Stoeckel et al.
542 2021b), and validated respectively using multiple field populations of marine phanerogams
543 for diploids (Arnaud-Haond et al. 2020) and of brown, green and red algae and mosses for
544 haplodiplontics (Krueger-Hadfield et al. 2021). These predictions and observations for
545 diploids, haplodiplontics and now autopolyploids argue again for the primary importance of
546 reproductive mode, especially of high clonality, to drive variation of genetic diversity among
547 populations (Duminil et al. 2007). They support the methodological importance to preliminary
548 estimate confident rates of clonality and of selfing before starting to interpret genetic diversity
549 with any other factor.
550
551 **Underestimated clonal diversity in the western European populations of *Lgh***
552 In our study, we chose to develop and use SNPs rather than AFLP markers which variation in
553 the precision of sizing of fragments leads to suboptimal reproducibility, particularly across
554 different platforms (Fry et al. 2009). These 36 SNPs are easily reproducible, accurate enough
555 to distinguish between offspring of sibling mating as evidence by the probabilities of identity
556 we obtained, and less expensive in time and money. With these SNPs, we found typical genetic
557 signatures of high clonality, including clear occurrence of replicated genotypes and mean
558 negative F_{IS} values with high interlocus variances in all the 53 western European populations.
559 Previous field and lab observations of peripatric *Lgh* populations reported massive production
560 of dispersal propagules, rapid expansions of patches and an important capacity for
561 spontaneous cutting-planting (Dandelot et al. 2005, Thouvenot et al. 2013, Grewell et al. 2016,
562 Skaer-Thomason et al. 2018a, b). Okada et al. (2009) genotyped around 800 individuals
563 sampled in 27 *Lgh* populations in Californian wetlands using a set of eight AFLP markers and

564 reported an extremely reduced clonal diversity: 95% of the samples had the same genotype
565 and 18 populations over 27 (67%) supported a single AFLP-genotype. All over UK, only two
566 haplotypes on 14 sampled stems were found using chloroplasts sequences (Armitage et al.
567 2013). These haplotypes were even shared with some *Lgh* samples invading California. All
568 these studies concluded that invasive populations of *Lgh* in Europe and in USA reproduce by
569 exclusive clonality, with a very narrow base of ancestral clones or being monoclonal (Dandelot
570 et al. 2005, Okada et al. 2009, Thouvenot et al. 2013, Grewell et al. 2016).
571 However, we found 462 distinct MLGs (genets) out of 795 individuals within these populations
572 and the large majority of these MLGs (404, thus 88%) were only sampled once in the 53
573 populations. Our results report a previously-underestimated genotype diversity in the invasive
574 populations in western Europe, yet congruent with Dandelot (2004) unpublished measures
575 obtained in three Mediterranean populations using inter-simple sequence repeats (ISSRs).
576 Dandelot (2004) reported three and seven genotypes over 11 sampling units within two *Lgh*
577 populations and two genotypes over nine sampling units in a third population, all sampled in
578 the south-east of France. These results could reveal contrasted situations between *Lgh*
579 populations introduced in the USA and continental Europe.
580 Among the 58 MLGs with replicates, seven MLGs were found in a single population and 51
581 MLGs were found in multiple sites. Clonal propagules of *Lgh* are known to disperse carried by
582 river current and by birds (zoochory: seedlings have the ability to stick to feathers; Grewel et
583 al. 2016). Even rare, MLGs found in multiple sites are likely to blur the genetic structure among
584 *Lgh* populations if ignored as clonal dispersal. Preliminary detection of these MLGs distributed
585 among geographical locations will help to understand and interpret the invasive dynamics in
586 a subsequent study.
587

588 **Between 10 to 40% of sexual reproduction in *Lgh* populations in western Europe**

589 The large genotype diversity observed in western European populations may either result
590 from an initial or continuous introduction of a large clonal diversity that could have
591 propagated clonally in European watershed or be due to local sexual events mixing introduced
592 lineages into new local genotypes. Beyond the qualitative indication of clonality, we thus
593 aimed at estimating the quantitative rates of clonality versus sexuality using genetic indices in
594 this autotetraploid dataset.

595 Thirty-two populations showed Pareto β values of their distributions of clonal sizes under 2,
596 which are only found in theoretical populations with rates of clonality higher than 0.8 in
597 diploids, haplodiplontics and autopolyploids (Stoeckel et al. 2021a,b, 2024). All 53 populations
598 showed mean negative F_{IS} with high interlocus variance as expected in highly clonal
599 populations (Balloux et al. 2003, Stoeckel & Masson 2014, Reichel et al. 2016). These values
600 can be observed in theoretical populations with rates of clonality higher than 0.6 (Stoeckel et
601 al. 2021a, b, 2024). All 53 populations also showed small to medium values of linkage
602 disequilibrium between SNPs as expected in highly clonal populations with large population
603 sizes (Navascues et al. 2010, Stoeckel et al. 2021a). Globally, gene diversities measured in
604 these invasive *Lgh* populations were in the higher range of values commonly found for SNPs
605 (Fischer et al. 2017, Schmidt et al. 2021). Such levels of gene diversity are in line with strong
606 rates of clonality that buffer the loss of alleles due to genetic drift (Reichel et al. 2016, Becheler
607 et al. 2020, Stoeckel et al. 2021b). All these values of population genetic indices were
608 consistent with the interpretation that *Lgh* populations in western Europe must reproduce
609 with effective rates of clonality between 60% and 90% (De Meeus et al. 2006, Arnaud-Haond
610 et al. 2020, Stoeckel et al. 2021a, b), even if rates of clonality were variable within this range
611 among populations. Clonal reproduction by rhizomes at the local scale and, in a lesser

612 proportion, by the dispersal of clonal propagules at larger (*i.e.*, inter-locations) scales would
613 thus be the main source of population growth and invasive spread of *Lgh* out of its native
614 range.
615 Despite being predominant, clonality is, however, not the exclusive reproductive mode. Our
616 population genetic measures didn't match with exclusive clonality, even being recent.
617 Despites estimation of rate of sexuality using temporal genotyping would be more resolutive
618 (Becheler et al. 2017), the values of population genetic indices rather fit between 10% to 40%
619 of sexuality (DeMeeus et al 2006, Stoeckel et al. 2021a,b, Stoeckel et al. 2024). We also found
620 local evidence of recombination between clonal lineages, and even rare crosses between LSI
621 and SC lineages as advocated by the genetic distances between individuals (Figure 5). The
622 diversity of genotypes detected in western Europe would thus rather match rare but
623 significant sexual events than the introduction of a large clonal diversity that would have
624 maintain and propagate by exclusive clonality. Our results newly advocate that sexual
625 reproduction should not, therefore, be overlooked in these invasive populations, especially in
626 management plans.
627
628 **Genetic consequences of LSI compared to self-compatible populations**
629 The late-acting SI system is still one of the less studied breeding systems among the
630 mechanisms favouring outcrossing in plants (Gibbs 2014). Its efficiency to favour outcrossing
631 and its consequences on genetic diversity within populations, especially considering its low
632 but common failures, were not yet deciphered and not yet compared to SC populations in the
633 same ecological conditions, as already previously explored for gametophytic and sporophyte
634 SI systems (Busch 2005, Koelling et al. 2011).

635 The maintenance of SI systems is one of the most intriguing evolutionary puzzles (Porcher &
636 Lande 2005). Indeed, SI systems are fated to breakdown because SC individuals present the
637 advantage of reproductive assurance when compatible partners are limited, especially in
638 peripatric conditions (Eckert et al. 2006). This advantage is even absolute when no compatible
639 partners are available within pollination range, as we commonly found in *Lgh* populations in
640 western Europe (see Figure SI1). Conversely, outcrossing imposed by SI systems decreases the
641 probability of expressing deleterious mutations in descendants as compared to selfing with
642 the same genetic background (Rice 2004, Navascues et al. 2010).
643 We found that the 40 *Lgh* populations with L-morph individuals (LSI) showed relatively more
644 effective alleles, higher gene diversity, higher observed heterozygosity and less linkage
645 disequilibrium than found in the 13 populations with S-morph individuals (SC). However, these
646 genetic differences may either be due to the consequences of outcrossing in LSI populations,
647 or due to different rates of clonality, with potentially higher rates of clonality in LSI populations
648 due to the local lack of compatible partners and reduced female fertility due to self-pollen
649 disabling the available ovules, or due to the consequences of autogamy in SC populations. We
650 develop and disentangle between these three hypotheses thereafter.
651
652 **Origin of the higher genetic diversity in LSI populations as compared to SC**
653 A first hypothesis to explain the genetic differences found between LSI and SC populations
654 may be due to the outcrossing consequences on LSI populations. Indeed, similar genetic
655 differences between SC and SI were recurrently reported in populations mating with
656 sporophytic and gametophytic SI systems (Igic et al. 2008, Mable 2008). For example,
657 *Leavenworthia alabamica* and *L. crassa* are two sister-species mating with a sporophytic SI
658 within a small genus of eight annual species in which self-fertilization has evolved at least four

659 times (Beck et al. 2006). In these species, comparisons between SI and SC populations also
660 showed higher mean genetic diversity in SI populations as compared to the SC, in an overall
661 background of high genetic diversity (Busch 2005, Koelling et al. 2011). High Ho, negative Fis
662 and high effective number of alleles per marker are also found in species mating with
663 gametophytic SI systems, such as in the *Prunus* genius (Stoeckel et al. 2006, Stoeckel et al.
664 2008, Abdallah et al. 2019). However, theoretical predictions argue that this kind of higher
665 genetic diversity favored and maintained in SI populations as compared to panmictic and SC
666 populations must only be found on polymorphic markers highly physically linked to the
667 genomic regions involved in the SI mechanisms that evolve under balancing selection, and
668 also, at a lesser magnitude, on physically unlinked markers but only in small population, with
669 less than 100 individuals including clones (Glémin et al. 2001, Navascues et al. 2010). The 36
670 SNPs we developed must randomly distribute over the 16 chromosomes inherited twice from
671 a common ancestor with *Lpm*, i.e., 32 chromosomes out of 80 total chromosomes of *Lgh*
672 (Barloy et al. 2024), with no reason that all aggregate around the genes involved in the LSI self-
673 recognition. In addition, *Lpm* is an SC-only species (Estes& Thorp 1974, Grewel et al. 2016). By
674 parsimony, there is less chance that genes involved in LSI reaction would be stored on these
675 chromosomes than on some of the 48 other chromosomes; And therefore, very unlikely that
676 our SNPs would be physically linked to genes under balanced selection due to LSI. *Lgh*
677 populations in western Europe include far more than one thousand stems per local population
678 (Portillo-Lemus et al. 2021). It is thus unlikely that differences in genetic diversity observed
679 between LSI and SC populations would directly result from the consequences of the LSI system
680 hitchhiked to the whole genome (Navascues et al. 2010).
681 The second hypothesis is that high genetic diversity in LSI populations may arise and be
682 maintained due to higher rates of clonality (Stoeckel & Masson 2014, Reichel et al. 2016,

683 Stoeckel et al. 2021a) as compared to SC populations. In LSI, self-pollen tubes physiologically
684 blocked at the micropyle may prevent outcrossed-pollen tubes to reach the available ovules,
685 decreasing female fertility and increasing the importance of clonal regeneration in
686 populations (Vaughton et al. 2010). In addition, clonality is another uniparental reproductive
687 mode that allows the local maintenance of populations in the absence of sexually compatible
688 partners, which is more probable in peripatric conditions (Pannel et al. 2015). Dominant clonal
689 reproduction and propagation are commonly found in peripatric populations extending their
690 living range into new areas (Pyšek 1998, Wang et al. 2017). Furthermore, there is an
691 established intriguing co-occurrence of clonality in SI populations of flowering plants (Vallejo-
692 Marin et al. 2010). We know that dominant clonal reproduction theoretically favours the
693 accumulation of deleterious mutations and that these deleterious mutations contribute to the
694 advantage of outcrossing, which decreases the probability of inbreeding depression in
695 offsprings, as compared to SC reproducers (Navascues et al. 2010). The observed genetic
696 differences between LSI and SC populations may thus result from higher clonality in LSI
697 populations lacking of compatible partners. But we found here no difference in estimates of
698 clonality between LSI and SC populations, in Σ_{CLON} and in all indices sensible to clonality (R,
699 Pareto Beta and VarFis; Figure 3).
700 We rather found significant difference in estimates of selfing between LSI and SC populations,
701 in Sg (Hardy 2016), in Σ_{SELF} and in all indices sensible to selfing (Ae, linkage disequilibrium, Ho,
702 mean Fis) revealing typical signatures of higher selfing rates in SC populations. Using Hardy's
703 method (2016) extended from David et al. (2007) for autopolyploids, SC populations were
704 estimated to reproduce using a mean selfing rate of 0.18 while LSI populations with only a
705 mean selfing rate of 0.05, both estimated with similar rates of sexuality. Congruent with higher
706 estimates of selfing rates and Σ_{SELF} in SC populations, we found higher linkage disequilibrium,

707 lower observed heterozygosity and less effective number of alleles in SC populations (Figure
708 3). The observed differences in genetic diversity between LSI and SC populations must thus be
709 rather caused by the genetic consequences of higher selfing in SC populations, decreasing
710 their genetic diversity, than due to a direct outcrossing effect of the LSI hitchhiked over all the
711 *Lgh* genome within these large populations of *Lgh* (see Navascues et al. 2010). Interestingly,
712 the outcrossing breeding system allowed by LSI, with a small rate of selfing allowed especially
713 at the end of the flowering season, was measurable at the population level in genotyping (5%
714 of selfing in LSI versus 18% in SC) and thus may be efficient at an eco-evolutionary scale.
715 The recent arriving of *Lgh* in western Europe may also have contributed to shape these genetic
716 differences. Recent founding events in SC populations are indeed expected to decrease the
717 overall genetic diversity all along the genomes, including fewer effective alleles, lower gene
718 diversity, and potentially more linkage disequilibrium as compared to outcrossing populations
719 (Flanagan et al. 2021). Despite the ρ_{ST} values we observed between pairs of SI and SC
720 populations being approximately double those measured within pairs of SC populations and
721 within pairs of LSI populations, we also found clues of admixture in the genetic distances
722 between LSI and SC individuals in western Europe (Figure 5). This result would thus tend to
723 minimize the contribution of the foundation in the differences in genetic diversity we
724 observed between LSI and SC populations, and stress again the importance of selfing to shape
725 the genetic differences we found between SC and LSI populations.
726
727 **Advantages of partially clonal LSI populations over SC populations in *Lgh***
728 Interestingly, we found no correlation between estimates of rates of clonality and of selfing in
729 SC populations. Selfing rates rather decreased when outcrossing increased, while rates of
730 clonality remained similar in all populations.

731 In SC populations of *Lgh* (S-morph), pollen tubes of the L-morph (LSI type) grow significantly
732 faster in SC individuals (Portillo-Lemus et al. 2022). It seems a sufficient and efficient
733 mechanism to favour outcrossing when compatible pollens are available in western European
734 *Lgh* SC populations. The micro-physiological mechanism(s) impacting self-pollen tube growing
735 rather than blocking them in simultaneous (as opposed to dichogamy) monoecious or
736 hermaphrodite species seems to be currently overlooked in literature (e.g. Glover 2007,
737 Nasrallah 2017). Our result obtained on SC *Lgh* calls for a better appraisal of such mechanism
738 in species in which outcrossed offspring seems to be favoured without the occurrence of a
739 clear macro SI system.
740 Considering we found no differences in the estimated rates of clonality between LSI and SC
741 populations, our results thus argue for an overall stable background rate of clonal
742 propagation, common to the whole species in western Europe, and for an adjustment of the
743 mating system to the local availability of the compatible partners, shifting from selfing
744 allowing reproductive insurance, to outcrossing when possible. In such system, selfing
745 advantage, if any, would result from a transient reproductive insurance, decreasing the cost
746 of developing sexual organs when no outcrossed partners would be available at pollination
747 range, rather than as an efficient uniparental reproductive mode to expand into new areas
748 with no compatible partners, as compared to clonality. Heterozygosity rather than
749 recombination in *Lgh* would thus present some ecological and/or evolutive advantage. This
750 reproductive mode, dominant clonality with some allogamy, is commonly observed in
751 multiple plants (Vallejo-Marin et al. 2010). In such system, we should find higher vigour and
752 fertility of the outcrossed and most heterozygous individuals (heterosis) as compared to the
753 selfed and more homozygous individuals (Darwin 1876, Lippman & Zamir 2007, Birchleret al.
754 2010).

755 Reduced allele diversity, heterozygosity and increased linkage disequilibrium between
756 markers in SC populations due to the higher selfing rates as compared to LSI populations may
757 explain why only 24% of the western European populations were SC against 76% of LSI.
758 (Portillo et al. 2021). Based on an analysis of photo collected on the web, Portillo et al (2021)
759 reported that LSI populations of *Lgh* were more frequent in peripatric populations than in
760 natives in which SC populations seem in majority. Some successful invasive populations
761 develop with low genetic diversity (He et al. 2024), questioning on the biological and
762 environmental factors that may explain their successes in such peripatric conditions (called
763 the genetic paradox of invasions, Allendorf & Lundquist 2003). This seems to not be the case
764 of *Lgh* in western Europe: reproductive modes avoiding the effects of inbreeding depression
765 in *Lgh* populations may on the opposite facilitate their peripatric spreading, as commonly
766 observed in multiple other invasive plants (Roman & Darling 2007, Forsman 2014), mostly
767 when developing in harsh and stressful conditions (Fox & Reed, 2011) or when the costs of
768 inbreeding depression expressed by selfing are superior to the benefits of reproductive
769 insurance (Layman et al. 2017). Peripatric populations of *Lgh* in western Europe by mixing
770 clonality with preferential allogamy would thereby solve the problem of maintaining
771 populations locally without the presence of compatible or less related sexual partner while
772 reducing the probability to express inbreeding depression (uniparental clonal reproduction,
773 Baker's conjecture: Barrett et al. 2008, Pannel et al. 2015), and would maximize the probability
774 of developing offspring with hybrid vigour thanks to LSI and faster growth of crossed-pollen
775 tubes. In such peripatric conditions, selfing in SC populations would only have limited or
776 transient advantage to provide behedging reproductive insurance. To disentangle between
777 the genetic advantages of outcrossing versus reproductive insurance and better state if *Lgh*
778 populations belong to the genetic paradox of invasions genetic, our results call for measuring

779 the true proportion of LSI and SC in invasive versus native worldwide *Lgh* populations with
780 estimation of the rates of clonality and of selfing.
781
782 **Unusual selfing syndrome in *Lgh* populations**
783 Surprisingly, in *Lgh*, SC populations reproducing with higher selfing rates develop S-morph
784 flowers that are significantly larger than L-morph flowers that are allogamous controlled by
785 an LSI system (Portillo-Lemus et al. 2021). Yet, highly selfed populations of plant species tend
786 to share similar morphology and function resulting in a set of traits called the 'selfing
787 syndrome', including reduced flower size (Darwin 1876, Tsuchimatsu & Fujii 2022). In *Lgh*,
788 such high selfing rates may only have occurred recently and endemically in these isolated and
789 founding European invasive populations, explaining such anomaly trait. Indeed, pioneering
790 *Lgh* populations in western Europe only appeared during the last century (Dandelot 2004). But
791 selfing syndrome, including reduced flower size, seems to evolve rapidly, as observed for
792 example in five generations in *Mimulus guttatus* (Bodbyl-Roels & Kelly 2011), in four
793 generations in *Silene latifolia* (Delph et al. 2004), in three generations in *Phlox drummondii*
794 (Lendvai & Levin 2003) and after only two generations in *Eichhornia paniculata* (Worley &
795 Barrett 2000). However, in *Lgh*, SC populations with higher selfing rates also reproduce using
796 intermediate to high rates of clonality, which may delay or even impact the emergence of the
797 first steps of a selfing syndrome. Our results in *Lgh* thus call for further studies on the
798 emergence of selfing syndrome in partially clonal and selfed populations.
799
800 **Conclusion**
801 Using reproducible molecular markers enabling allele dosage to genotype sampled individuals
802 and tailored computational analyses that answer the remaining challenges to perform

803 population genetic analyses in autopolyploids (Dufresne et al. 2014), we found that peripatric
804 populations of *Lgh* in western Europe reproduced using dominant clonality with subtle but
805 significant sexuality, in nearly all populations, within a large clonal diversity.
806 *Lgh* is one of the most invasive aquatic plants in the world, and considerable effort are made
807 to limit its deleterious effects on the newly colonized ecosystems and on their native species
808 (Thouvenot et al. 2013, Grewell et al. 2016, Portillo-Lemus et al. 2021). The rare sexual events,
809 allogamous when possible, occurring in invasive peripatric populations of *Lgh* may favour the
810 emergence of new genotypes, more adapted to local conditions. Managers should thus chiefly
811 concentrate their actions on the most sexual populations. We also found variations of the
812 rates of clonality and of selfing between *Lgh* populations. Considering the importance of
813 reproductive modes on the dynamics and evolution of populations (Duminil et al. 2007,
814 Ellegren & Galtier 2016, Glémin et al. 2019), our results advocate that management actions to
815 control *Lgh* should be built considering their effective reproductive modes, population by
816 population.
817 Finally, knowing the reproductive modes of populations, the distribution of clones and the
818 self-compatibility across western European populations will help to decipher and interpret
819 their current population structure in a next future, with the aim to identify the origin and the
820 routes of this recent invasion and to predict its possible short-term dynamics.
821

822 **Data Accessibility Statement**

823 The data that support the findings of this study are openly available on Zenodo
824 (https://doi.org/10.5281/zenodo.10246264).

825

826 **Benefits Generated**

827 Benefits from this research accrue from the sharing of our data and results on public databases
828 as described above.

829

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844

845 **Conflict of interest**

The authors declare that they have no financial conflicts of interest based on the content of this article.

Author contributions

DB and SS laid the foundation of this work, conceived the study and were responsible for funding applications. LPL, MH and DB collected samples and performed field observations. EP and DB conceived and supervised RAD4SNP and Hi-Plex methodology, BJP and DJP contributed to define the SNP set. LPL, MH and ALB performed RAD4SNP approach to develop the SNPs. LPL and MH extracted DNA and genotyped the samples, SMC and RCV sequenced the data. GL performed the bioinformatic analyses and SS computed the Bayesian allele dosage. DB, LPL and SS performed early data explorations at the end of LPL PhD thesis that was supervised by DB and SS. RB and SS performed computations and analyses, tracked and managed the bibliography, produced tables, figures and interpretation. DB, RB and SS wrote the manuscript. All authors read and approved the final manuscript.

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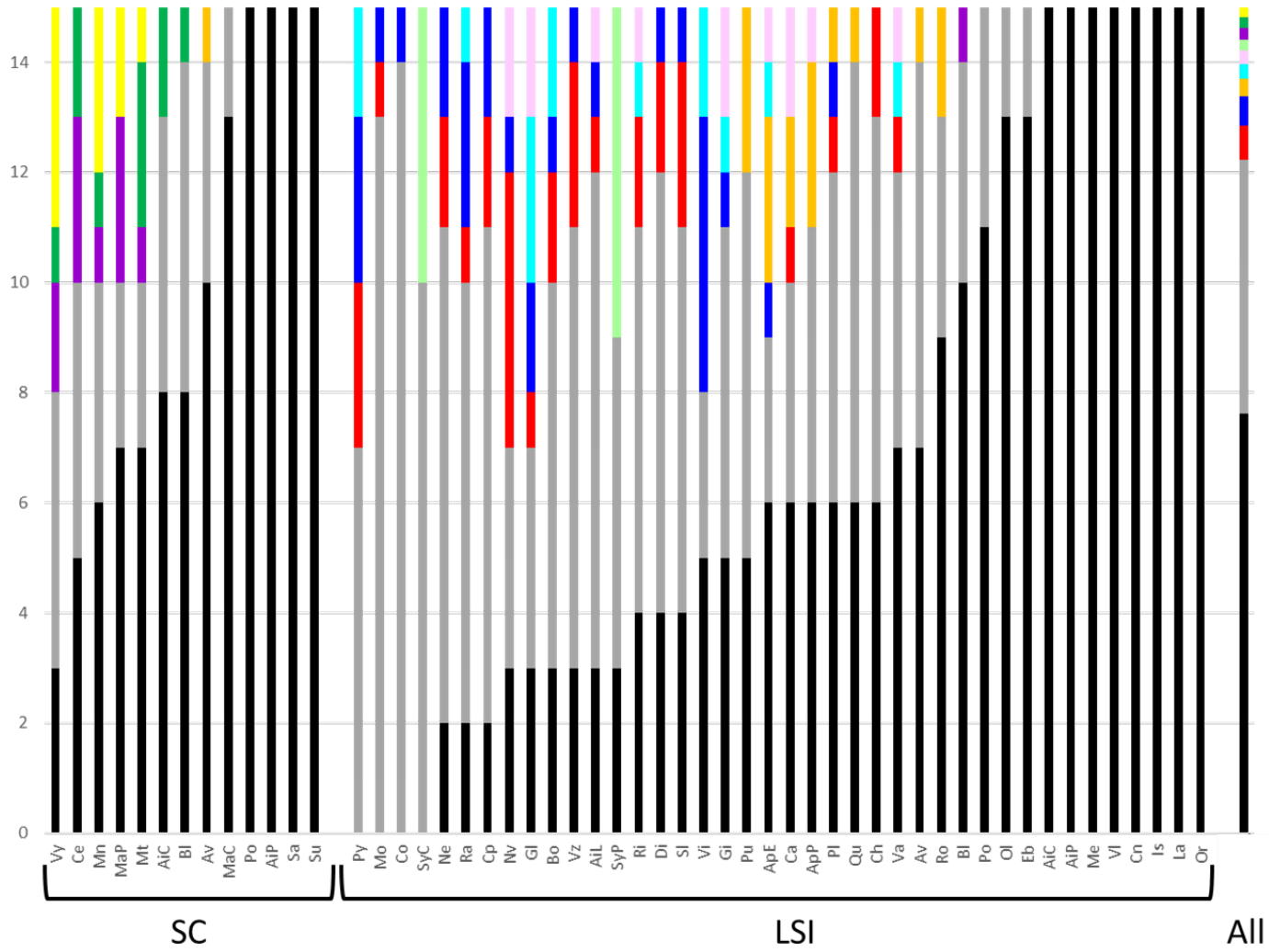

Figure 1: Distributions of Multi-Locus Genotypes (MLGs) among LSI and SC *Lgh* populations in western Europe. In black, the number of unique MLGs; In grey, the number of MLGs with less than 7 ramets; In color, MLGs with more than 10 ramets found in multiple populations. Proportions of each MLGs over all the populations are plotted in the last right bar (All). More than half the samples are unique genotypes.

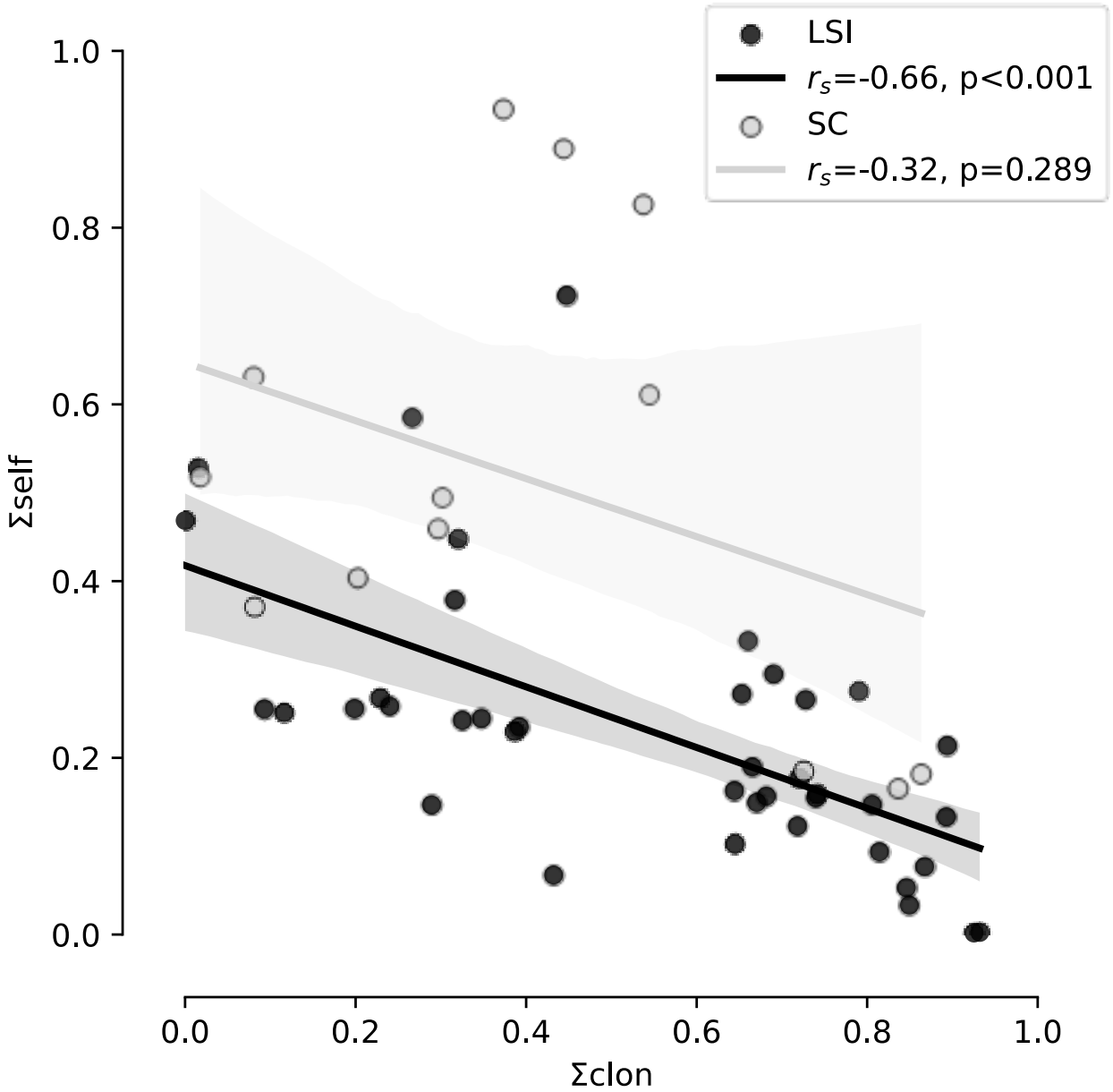

Figure 2: Correlations between Σ_{CLON} and Σ_{SELF} found in 13 SC populations (light grey points and regression line) and 40 LSI populations (black points and regression line). 95% confidence intervals are given for LSI and SC populations in dark grey and light grey, respectively. Spearman rank-order correlation coefficients (r_s) and probabilities that Σ_{CLON} and Σ_{SELF} would not be correlated (p) are reported for LSI and SC populations.

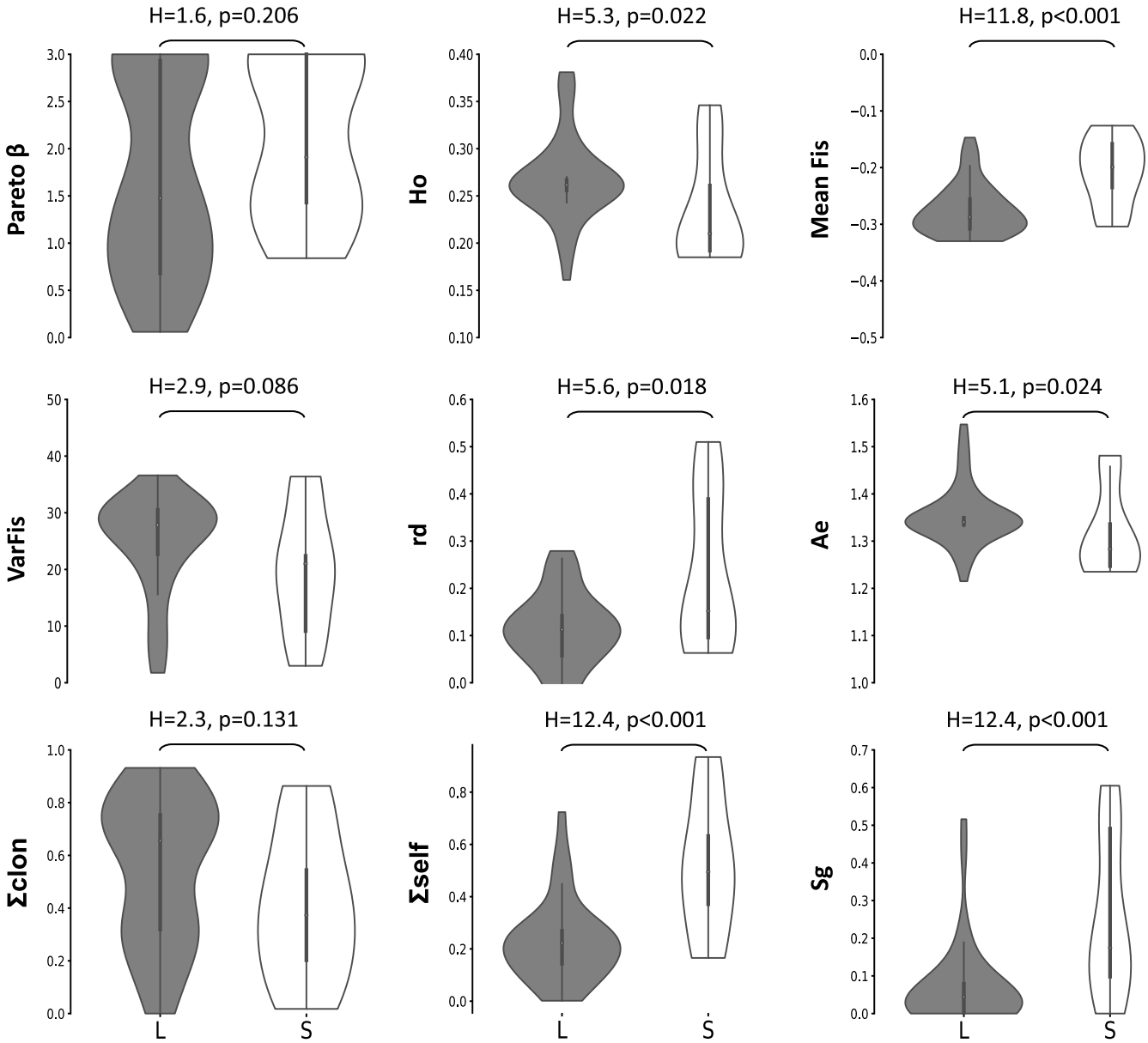

Figure 3: Violin plots comparing distributions of genetic indices in LSI (L, grey) versus SC (S, white) populations. Violin plots are cut for their minimum and maximum values. Kruskall-Wallis tests are reported as H-statistics as well as the probability that LSI and SC population would present the same distribution of genetic indices.

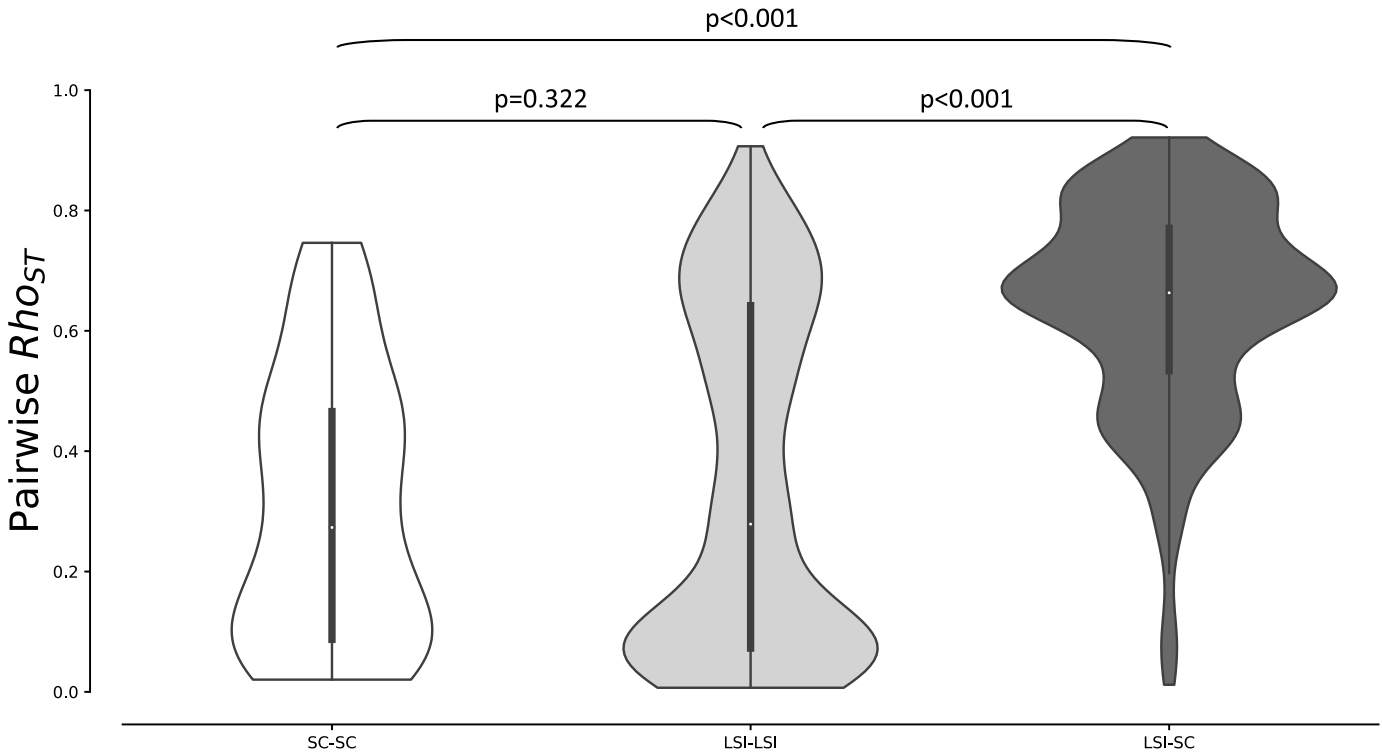

Figure 4: Distributions of pairwise rho_{st} within pairs of SC populations (white violin plot), pairs of LSI populations (light grey violin plot) and between pairs of LSI and SC populations (dark grey violin plot). Probabilities that pair of non-parametric distributions are equal are reported.

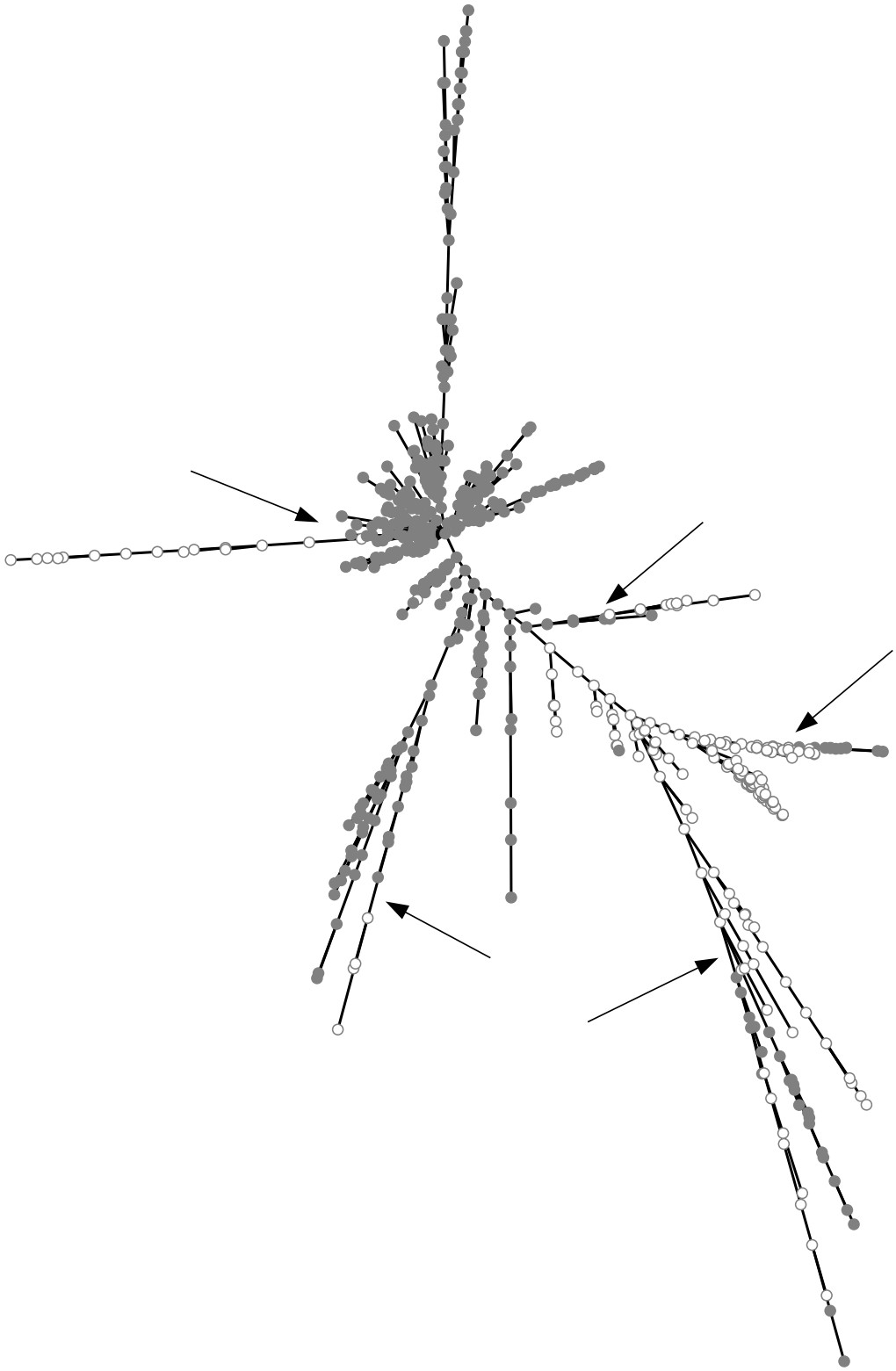

Figure 5: Minimum spanning tree of the genetic distances (number of different alleles) between LSI (grey points) and SC (white points) individuals. Arrows indicate some of the evidences of admixture between LSI and SC lineages.

1299 # Supplementary Information (SI)

1300

Situation of *Lgh* in USA and Mediterranean populations in previous studies (Dandelot 2004, Okada et al. 2009, Armitage et al. 2013):
- nearly monoclonal populations arguing for the ecological advantage of clonality (fragmentation and rhizome propagation) in these invasive populations.
But
- using weakly polymorphic markers,
- before the demonstration of the heterostyly and of the Late-acting self-incompatibility system in *Lgh*

Situation of *Lgh* in western Europe, studied here:
- Spatial context: The other compatible type populations are away from hundreds of meters to several kilometers (Portillo-Lemus et al. 2021)
- Clonality through fragmentation and rhizomes, as in other populations (Portillo-Lemus 2021).
- Massive blossoming with a lot of pollinators harvesting flowers (Portillo-Lemus 2021).
- Faster pollen tube elongation of pollen from the other compatible type (Portillo-Lemus et al. 2022)

Our working hypotheses about the main, realized reproductive modes in population:

- **LSI populations:** A very limited production of seeds (Portillo-Lemus et al. 2021)

  Hypothesis 1: **preferential clonality** due to lack of compatible partners to produce seeds → Baker's conjecture on reproductive modes (Pannell et al. 2015).

  Hypothesis 2: The rare seeds really contribute to the populations → biological feature of seeds or recombination would have advantage over clones. If so, are they mainly:

  Selfed seeds → reproductive insurance and advantage of recombination over clonality in a uniparental context?

  Outcrossed seeds → advantage of outcrossed seeds due to heterosis and/or recombination despite the lack of locally-available compatible partners → selection of long pollination ranges

- **SC populations:** Production of a lot of seeds in natural populations

  Hypothesis 1: despite a huge production of seeds, **preferential clonality** due to the physiological and/or ecological advantage of clones over seed germination process?

  Hypothesis 2: the mass of seeds does contribute to the populations or some evolutionary advantage of recombination in offspring compared to clonal fragmentation and rhizome propagation to adapt local conditions? If so, are these seeds mainly:

  Selfed seeds → within uniparental reproduction, biological feature of seeds or genetic recombination would provide advantage over clones?

Outcrossed seeds → Faster pollen tube elongation of pollen from the other type gives real advantage or advantage to allogamy to adapt new local conditions?

1301

1302 **Supplementary information1:** Synthesis of the questionings of our study to estimate reproductive
1303 mode of 53 populations of invasive Lgh using genetic diversity on the autotetraploid part of its
1304 genome.

1305

Genotypic or genetic index	Range of values	Main driver	Behavior	references
β*	ϵ [0; +∞]	Rate of clonality	↘ when c ↗ $\beta \rightarrow 0$ when $c \rightarrow 1$	Halkett et al. 2005, Arnaud-Haond et al. 2007, 2020, Stoeckel et al. 2021
$varF_{IS}$	ϵ [0; +∞]	Rate of clonality	↗ when c ↗ $VarF_{IS} \rightarrow 0$ when $c \rightarrow 0$	Stoeckel & Masson 2014, Stoeckel et al. 2021
r_d	ϵ [0; 1]	Rate of selfing	slightly ↗ when c ↗ ↗ when s ↗ $r_d \rightarrow 1$ when $s \rightarrow 1$	Weir and Cockerham 1973, Navascues et al. 2010, Halkett et al. 2005
H_O	ϵ [0; 1]	Rate of selfing	↘ when s ↗ $H_O \rightarrow 0$ when $s \rightarrow 1$	David et al. 2007, Halkett et al. 2005
F_{IS}	ϵ [-1; 1]	Both rates	↘ when c ↗ $FIS \rightarrow -1$ when $c \rightarrow 1$ $FIS \rightarrow +1$ when $s \rightarrow 1$	Stoeckel & Masson 2014, Balloux et al. 2003, Stoeckel et al. 2021
H_E	ϵ [0; 1]	Rate of selfing	↘ when s ↗ $H_E \rightarrow 0$ when $s \rightarrow 1$	Glémin et al. 2001, Ritland & Ganders 1987
$P_{ID\text{-}SIB}$	ϵ [0; +∞]	Both rates	↘ when c ↗ ↘ when s ↗	Waits et al. 2001
S_g**	ϵ [0; 1]	Rate of selfing	↗ when s ↗	David et al. 2007, Hardy et al. 2016

* similar behavior of the clonal richness R
** inferred values of s, according to the method of Hardy (2016)

Table SI1: Hypotheses about the influence of clonality and selfing on the expected variations of genetic indices.

see the attached xls file

Table SI2: All genetic and genotypic indices computed on the 53 sampled populations. Each index was obtained from 15 individuals sampled in each population. (See spreadsheet supplementary material).

Population with missing genotype	nb_missing_genotypes	nb_individuals_concerned
Bléré_Ls	1	1
Chambéon_écopôle_du_Forez	2	2
Le_Port_Ls	1	1
Plougonver_Léguer	1	1
Quevillon	1	1
Rennes_apigné_prairie	1	1
Roost-Warendin	1	1
Saint_Aignan_Couflons_Ls	1	1
Vichy	1	1

Over single SNP genotypes	N	%age
single SNP genotype P(cad)>70%	28610	0.99965
single SNP genotype P(cad)≤70%	10	0.00035
total	28620	1

Over individuals	N	%age
nb_individuals_with_full_genotype	785	0.98742
nb_individuals_with_one_missing_genotype	10	0.01258
total	795	1

Table SI3: Summary of the allele dosage. First subtable lists populations with individual genotyped with at least one individual with missing genotype at one locus. Second subtable reports the frequency of single SNP genotypes with posterior probability of allele dosage strictly superior to 70%. Third subtable reports the frequency of individuals with their 36 SNP genotypes assigned with posterior probability superior to 70%.

Table SI4: Distribution of the different repeated Multi-Locus Genotypes (MLGs) found with 36 SNPs among populations considering their mating system (LSI or SC). Figure 1 presents a summarized plot of this table. (See spreadsheet supplementary material).

	G	H_O	H_E	A_E	R	β	F_{IS}	$VarF_{IS}$	r_d	PID_{SIB}	S_g	Σ_{clon}	Σ_{self}
G	-	0.438	**0.013**	**0.009**	***	***	***	***	0.057	**0.008**	**0.008**	***	***
H_O	0.076	-	***	***	0.397	0.462	0.122	**0.025**	0.653	***	**0.032**	0.065	0.142
H_E	**0.244**	**0.742**	-	***	**0.01**	**0.014**	0.212	***	**0.026**	***	0.844	***	0.372
A_E	**0.255**	**0.722**	**0.82**	-	**0.008**	**0.013**	0.353	***	0.094	***	0.347	***	0.845
R	**0.991**	0.083	**0.251**	**0.258**	-	***	***	***	0.052	**0.007**	**0.005**	***	***
β	**0.91**	0.071	**0.238**	**0.24**	**0.919**	-	***	***	0.126	**0.009**	**0.004**	***	***
F_{IS}	**0.602**	-0.144	0.116	0.086	**0.603**	**0.557**	-	***	***	0.163	***	***	***
$VarF_{IS}$	**-0.579**	**-0.209**	**-0.435**	**-0.346**	**-0.589**	**-0.551**	**-0.626**	-	***	***	***	***	***
r_d	0.187	0.042	**0.207**	0.156	0.19	0.148	**0.432**	**-0.365**	-	**0.021**	***	**0.006**	***
PID_{SIB}	**0.259**	**0.729**	**0.981**	**0.833**	**0.265**	**0.251**	0.13	**-0.443**	**0.214**	-	0.936	***	0.286
S_g	**0.264**	**-0.202**	-0.019	-0.089	**0.277**	**0.28**	**0.542**	**-0.379**	**0.353**	-0.008	-	***	***
Σ_{clon}	**-0.79**	**-0.171**	**-0.376**	**-0.347**	**-0.799**	**-0.809**	**-0.604**	**0.756**	**-0.254**	**-0.387**	**-0.34**	-	***
Σ_{self}	**0.388**	**-0.136**	0.083	0.018	**0.399**	**0.361**	**0.723**	**-0.524**	**0.631**	0.099	**0.69**	**-0.451**	-

Table SI5: Correlations between genetic indices using non-parametric Kendall partial rank-order correlation. Below the diagonal, the values of the coefficient of correlation τ are consigned. Above, the related p-values are provided. Values inferior to the threshold 0.05, and the related coefficient τ were bold. The parameters Σ_{CLON} and Σ_{SELF} correspond to the sum of normalized indices sensitive to clonality and selfing, respectively.

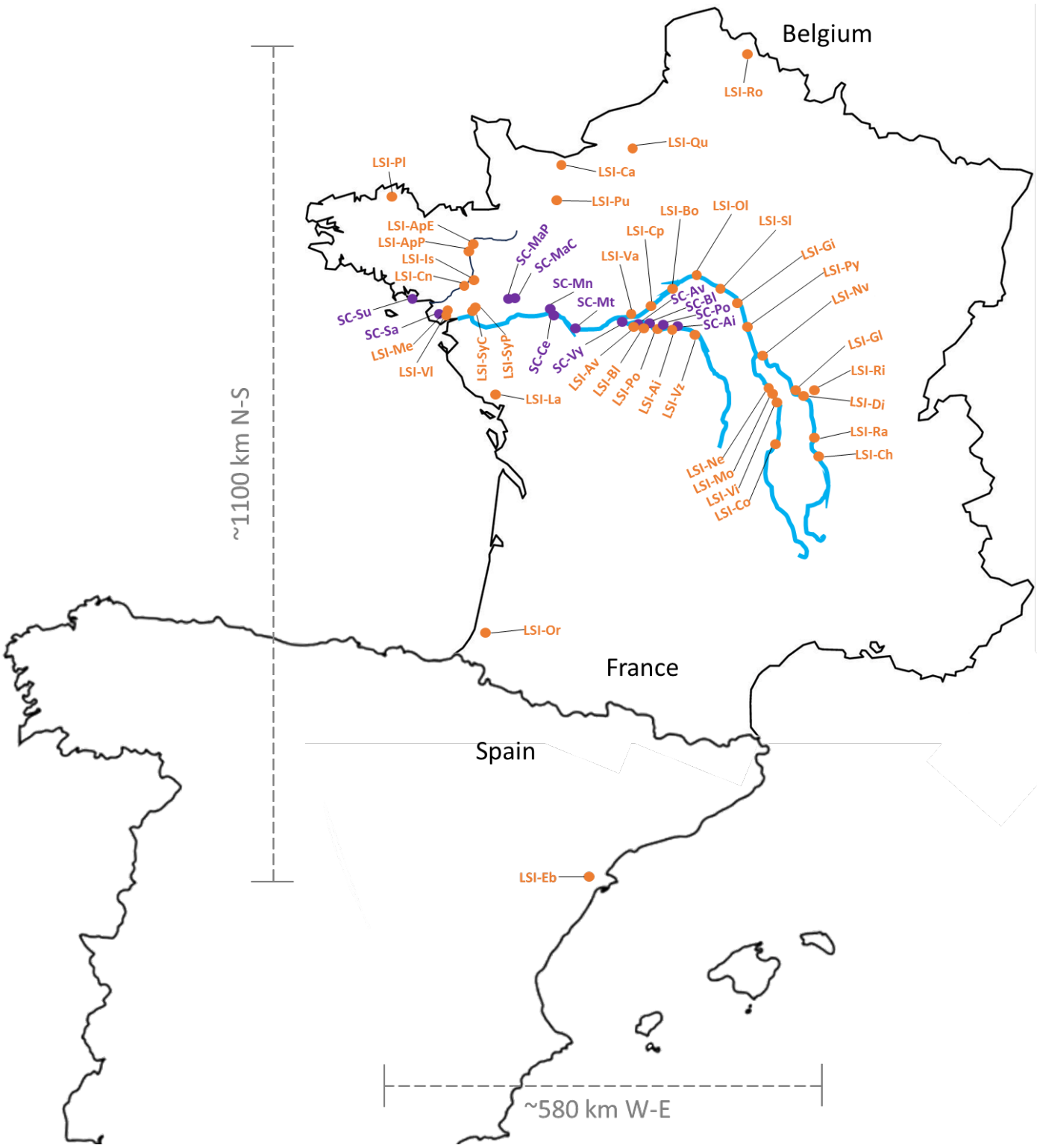

Figure SI1: Map of the locations of the 53 sampled populations across France and Spain. In orange, the late-acting self-incompatible (LSI) populations; In purple, the self-compatible (SC) populations. In light blue, the Loire river system. In grey, the North-to-South (N-S) and West-to-East (W-E) scale distances of the sampled populations.

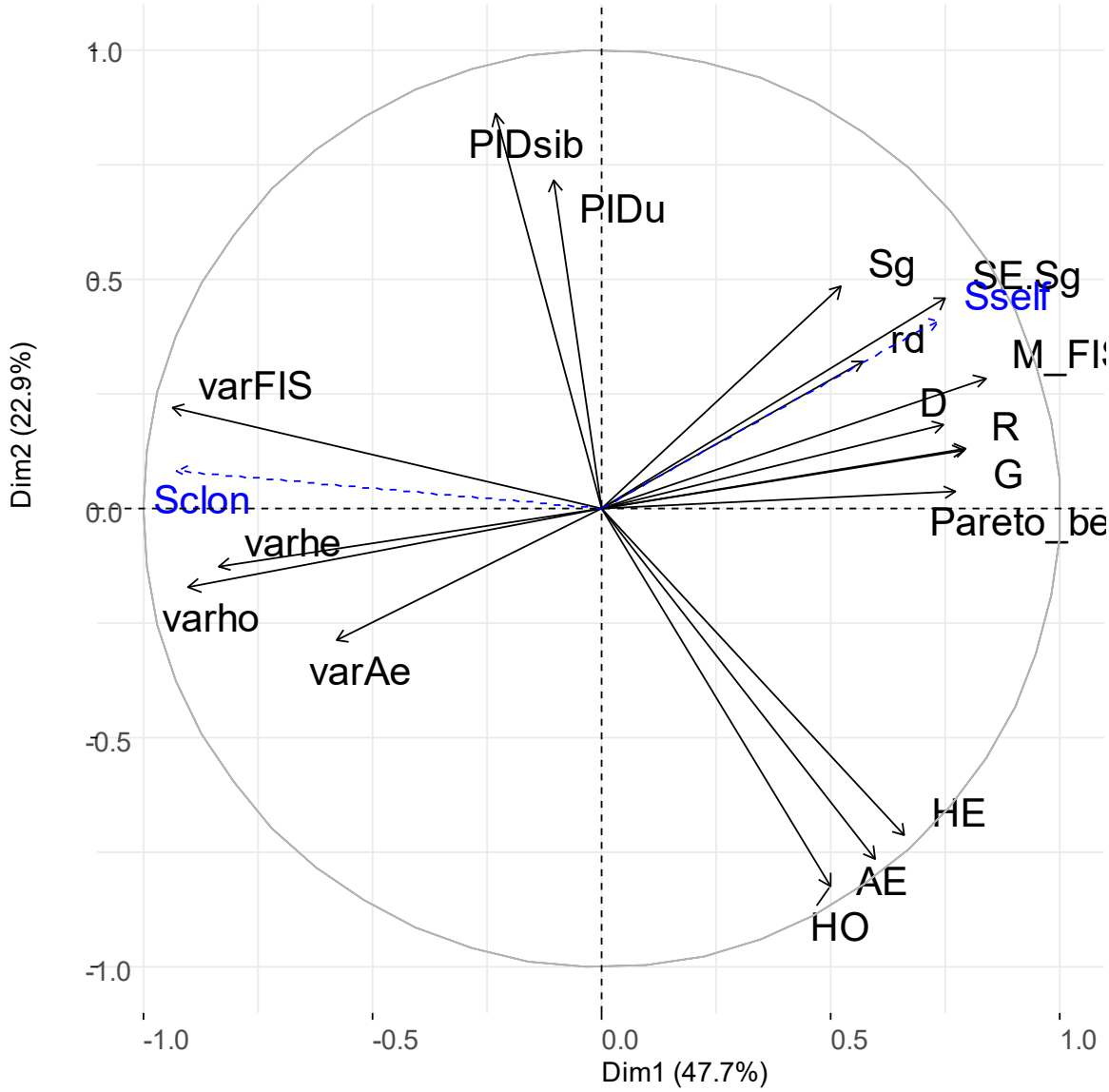

Figure SI2.A: Correlation circles of the principal component analysis on the 17 centered and scaled genetic indices measured in 53 *Lgh* populations in western Europe. The first horizontal dimension accounting for 50.24% of the variance regroups indices related to clonality (number of genotypes *G*, genotypic diversity *R*, clonal heterogeneity *D*, clonal evenness *Beta_Pareto*, variance of Fis *varFis*, variance of expected heterozygosity *varHe*, variance of observed heterozygosity *varHo* and variance of effective number of alleles varAe between loci). The second vertical dimension accounting for 23.39% of the variance with a main contribution of estimate of selfing Sg. Other indices, *i.e.*, mean observed heterozygosity *Ho*, mean expected heterozygosity *He*, effective number of alleles *Ae*, inbreeding coefficient *Mfis*, linkage disequilibrium *rd*, standard error of estimate of selfing *SE.Sg*, unbiased probability of identity under panmixia *PIDu* and between sibs *PIDsib*. In blue and dashed lines, the predictions of Σclon (*Sclon*) and Σself (*Sself*) provided as supplementary variables.

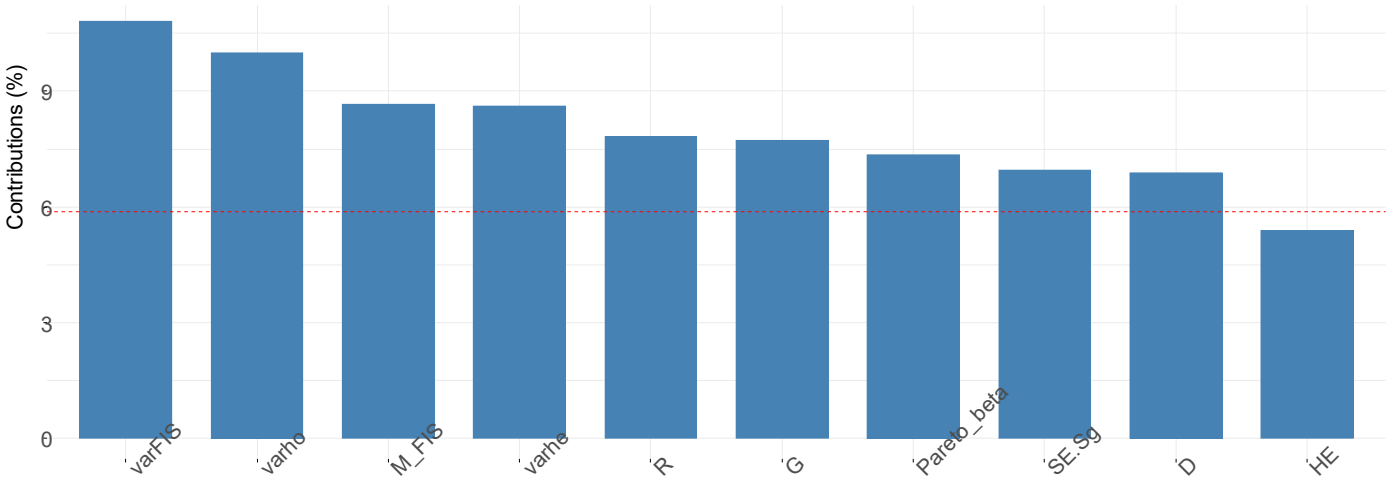

Figure SI2.B: Bar plot of the genetic index contributions to the first principal component. The expected average contribution *1/(number of genetic indices)* is plotted as the red dashed line. VarFis and indices of genotypic diversity (Pareto , R, G & D) are the main contributors to the first component.

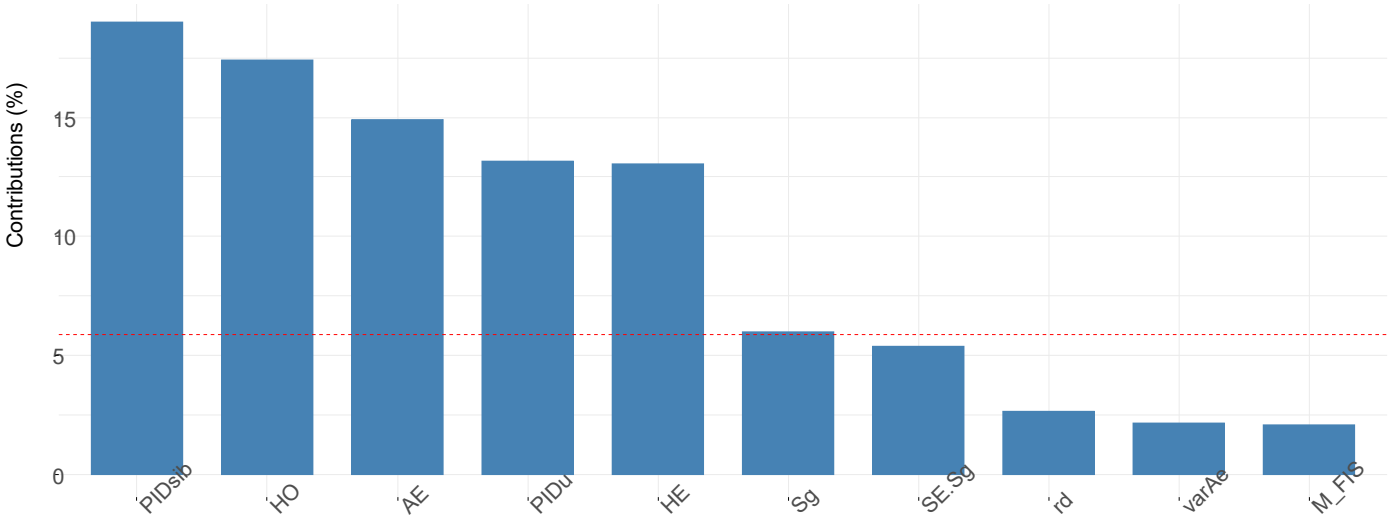

Figure SI2.C: Bar plot of the genetic index contributions to the second principal component. The expected average contribution *1/(number of genetic indices)* is plotted as the red dashed line. Estimates of selfing (Sg), mean observed heterozygosity (H_O), mean effective number of alleles (A_E) and probabilities of identities (pid_u and pid_{sib}) are the main contributors to the second component.

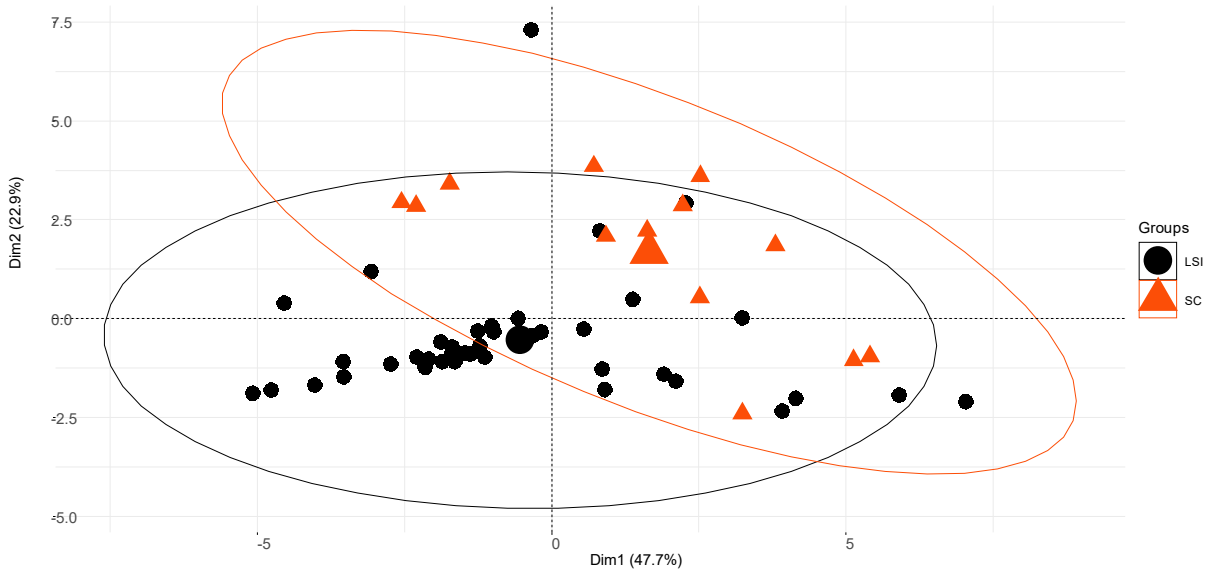

Figure SI2.D: Plot of the projection of each population onto the two first principal components. SC populations are plotted as red triangles and LSI populations as black diamonds. Concentration ellipses around LSI and SC populations are plotted in black and red, respectively. Barycenters of the two groups are represented as bigger black diamond and red triangle, respectively.

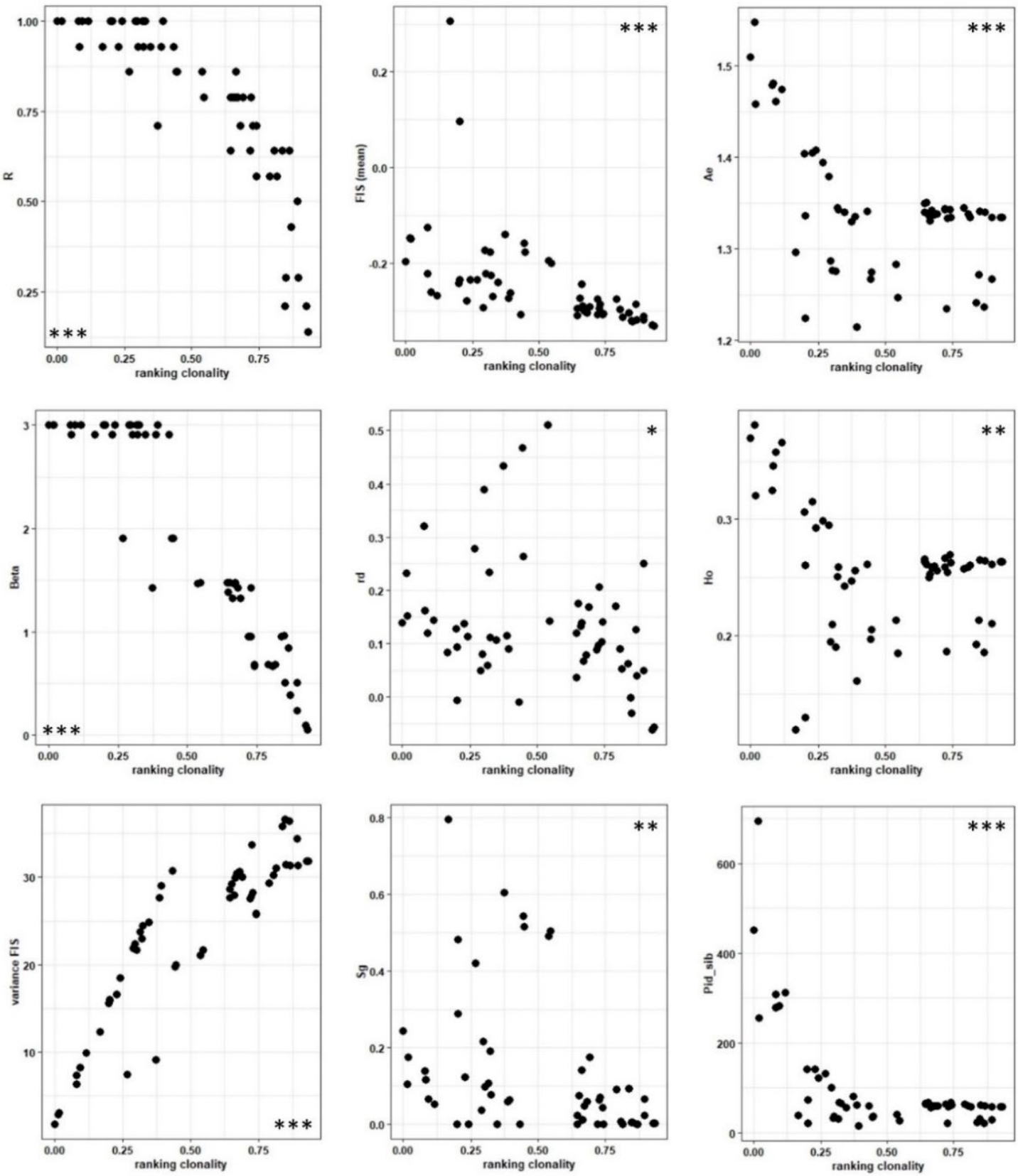

Figure SI3: Relationship and correlation between Σ_{CLON} and genetic indices (R, Pareto β, MFis, VarFis, Ho, Ae, Sg, pidsib and $\bar{r}_d$). Per graph, all the 53 populations were plotted as black dots. *: p<0.05, **: p<0.01, ***: p<0.001.

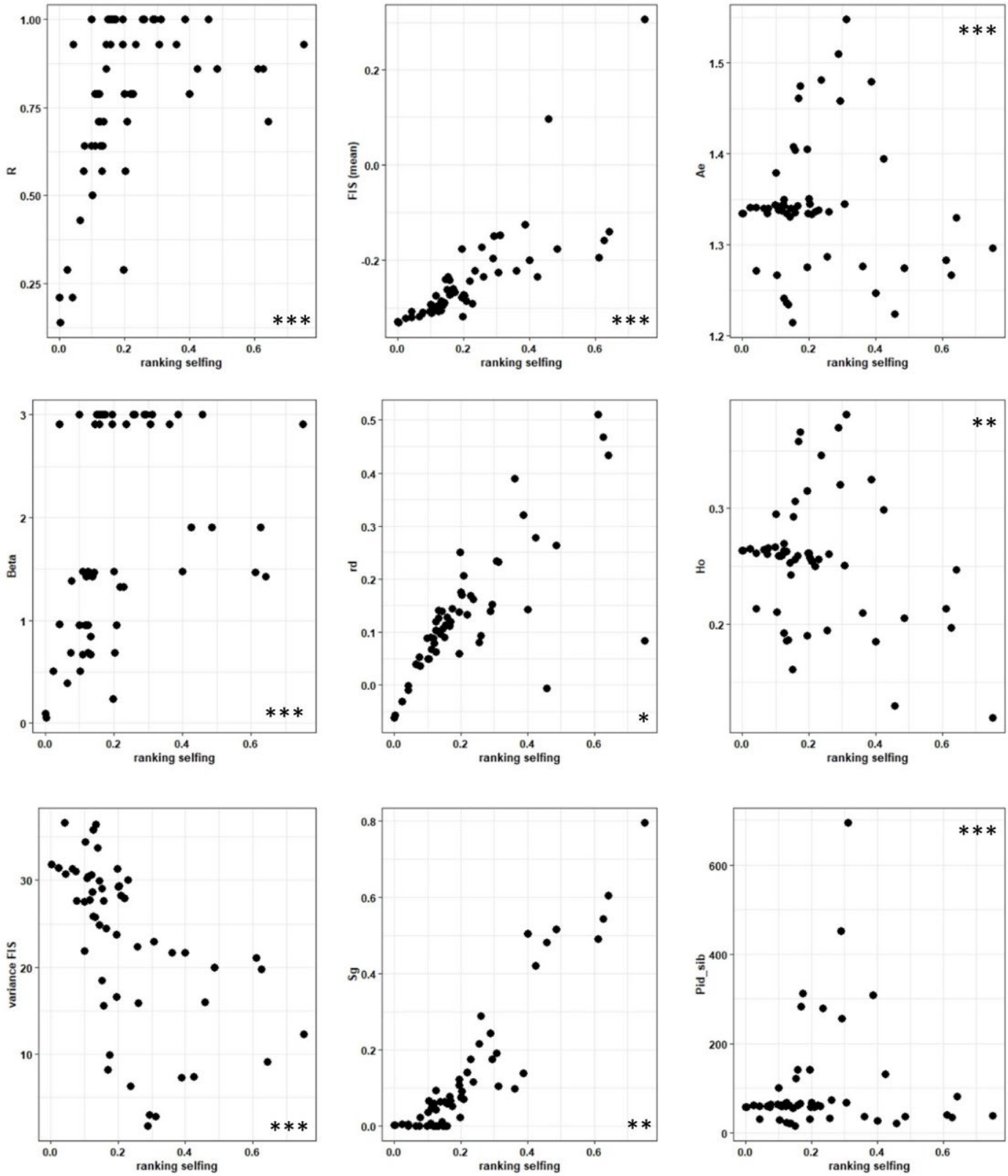

Figure SI4: Relationship and correlation between Σ_{SELF} and genetic indices (R, Pareto β, MFis, VarFis, Ho, Ae, Sg, pidsib and $\bar{r}_d$). Per graph, all the 53 populations were plotted as black dots. *: p<0.05, **: p<0.01, ***: p<0.001.

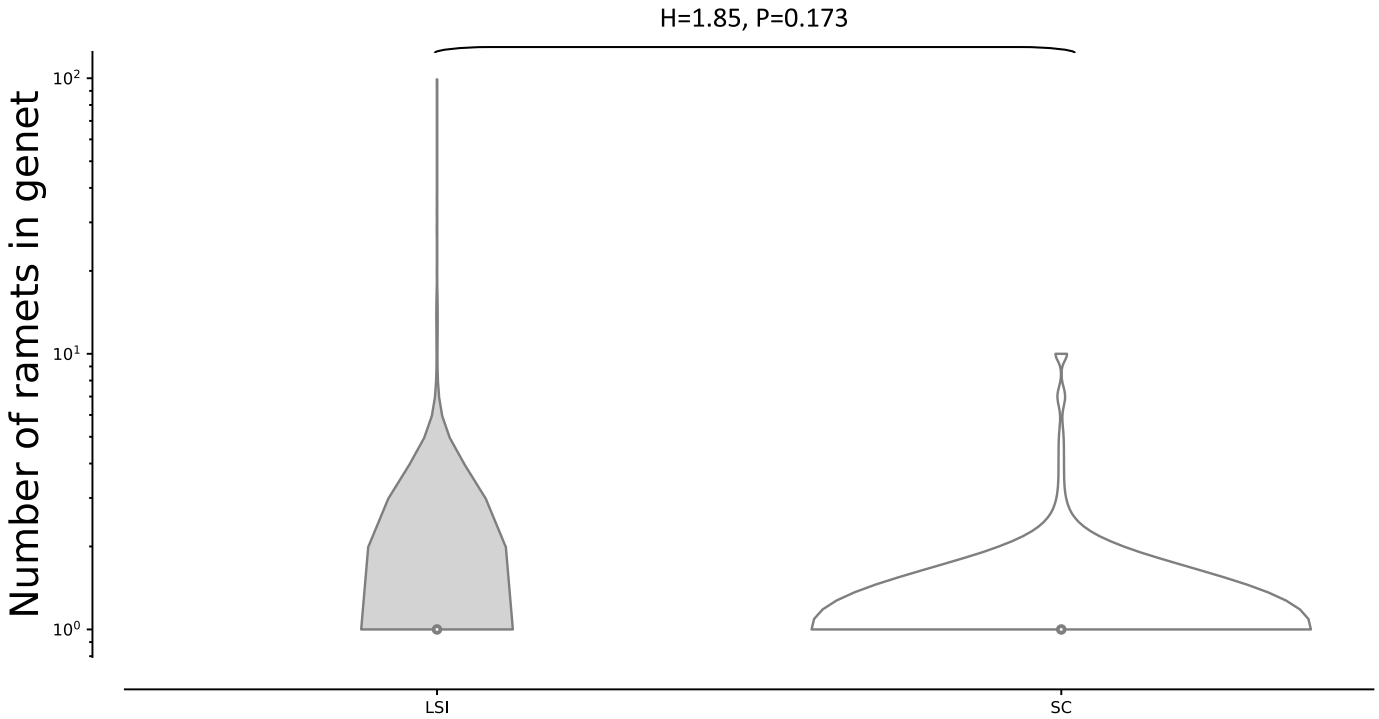

Figure SI4: Distributions of the logarithms of the number of ramets per genet in LSI (grey) and SC (white) populations. We report the Kruskal-Wallis probability that the two distributions are identical.