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Additional Information

1 **First successful backcrossing towards eggplant (*Solanum melongena*) of a New**
2 **World species, the silverleaf nightshade (*S. elaeagnifolium*), and characterization**
3 **of interspecific hybrids and backcrosses**

4
5 Edgar García-Fortea¹, Pietro Gramazio¹, Santiago Vilanova¹, Ana Fita¹, Giulio
6 Mangino¹, Gloria Villanueva¹, Andrea Arrones¹, Sandra Knapp², Jaime Prohens¹,
7 Mariola Plazas^{1,*}

8
9 ¹Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat
10 Politècnica de València, Camino de Vera 14, 46022 Valencia, Spain

11 ²Department of Life Sciences, Natural History Museum, Cromwell Road, London SW7
12 5BD, United Kingdom

13
14 *Corresponding author.

15 *E-mail address:* maplaav@btc.upv.es (M. Plazas)

16
17 **ABSTRACT**

18 Silverleaf nightshade (*Solanum elaeagnifolium* Cav.) is a drought tolerant invasive
19 weed native to the New World. Despite its interest for common eggplant (*S. melongena*
20 L.) breeding, up to now no success has been obtained in introgression breeding of
21 eggplant with American *Solanum* species. Using an interspecific hybrid between
22 common eggplant and *S. elaeagnifolium* as maternal parent we were able to obtain
23 several fruits with viable seed after pollination with *S. melongena* pollen. Twenty
24 individuals of the first backcross (BC1) generation were crossed again to the *S.*
25 *melongena* parent and second backcross (BC2) seed was obtained for 17 of them,
26 suggesting that most of the genome of *S. elaeagnifolium* is likely to be represented in
27 the set of BC2 families. Five plants of each of the two parents, interspecific hybrid and
28 BC1 generation were characterized with morphological descriptors and for pollen
29 viability. The interspecific hybrid was intermediate among parents, although in overall
30 morphological characteristics more similar to the *S. elaeagnifolium* parent. However,
31 pollen viability of the hybrid was very low (2.6%). The BC1 generation was
32 intermediate in characteristics between the hybrid and the *S. melongena* parent, with
33 pollen viability increasing to an average of 19.4%. The root system of the interspecific
34 hybrid indicated that it is able to explore larger areas of the soil than the *S. melongena*

35 parent. The phenolics profile of the fruit of the two parents and hybrid revealed a higher
36 diversity in phenolic constituents in *S. elaeagnifolium* compared to *S. melongena*, where
37 the major phenolic compound was chlorogenic acid, while the interspecific hybrid was
38 intermediate. By using flow cytometry it was found that *S. elaeagnifolium*, *S.*
39 *melongena*, and their interspecific hybrid were diploid, although the genome size of *S.*
40 *elaegnifolium* was slightly smaller than that of *S. melongena*. Our results represent the
41 first report of successful development of backcross generations of common eggplant
42 with a New World *Solanum* species. This makes available a relatively unexplored,
43 phylogenetically distant genepool for eggplant breeding. The backcross materials
44 obtained can make a relevant contribution to developing new eggplant cultivars with
45 new nutritional and environmental properties.

46

47 **Keywords:**

48 Backcrosses

49 Introgression breeding

50 Flow cytometry

51 Phenolics profile

52 *Solanum elaeagnifolium*

53 *Solanum melongena*

54

55

56 **1. Introduction**

57

58 Crop wild relatives can contribute to widening the genetic background of crops
59 and adapting them to new challenges, such as climate change (Dempewolf et al., 2014).
60 The economic impact of the utilization of crop wild relatives in crop breeding has been
61 estimated at the global level in $164.5 \cdot 10^9$ US\$ annually, while the current value of crop
62 wild relatives for breeding in the most important crops could triple in a climate change
63 scenario (Tyack and Dempewolf, 2015). This clearly shows how research in crop wild
64 relatives and its utilization in breeding may have an important economic impact by
65 developing new cultivars with improve characteristics. In this way, a new approach
66 known as “introgressiomics” calling for the systematic development of plant materials

67 containing introgressions from wild species has recently been proposed (Prohens et al.,
68 2017).

69 One of the vegetable crops in which significant efforts are being done in the last
70 years for introgression breeding from related species for adaptation to climate change is
71 the common eggplant (*Solanum melongena* L.) (Toppino et al., 2008; Liu et al., 2015;
72 Kouassi et al., 2016; Plazas et al., 2016). The common or brinjal eggplant is an Old-
73 World crop domesticated in Southeast Asia (Meyer et al., 2012), and is related to wild
74 species of spiny solanums (Leptostemonum clade) occurring in Asia and Africa (Knapp
75 et al., 2013; Vorontsova et al., 2013; Aubriot et al., 2016; Vorontsova and Knapp,
76 2016).

77 Interspecific hybrids and backcrosses of eggplant have been obtained with many
78 related Old World species, and this has included the development of introgression
79 materials with different species and one set of introgression lines with *S. incanum*
80 (Rotino et al., 2014; Kouassi et al., 2016; Plazas et al., 2016; Gramazio et al., 2017;
81 Gramazio et al., 2018). In addition, sexual and somatic hybridization have also been
82 used to develop interspecific hybrids between eggplant and several New World species.
83 In this way, *Solanum aculeatissimum* Jacq. (Zhou et al., 2018), *S. elaeagnifolium* Cav.
84 (Kouassi et al., 2016), *S. sisymbriifolium* Lam. (Gleddie et al., 1986), *S. torvum* Sw.
85 (Jarl et al., 1999; Collonnier et al., 2003), and *S. viarum* Dunal (Prabhu et al., 2009) are
86 of great interest for breeding for its resistance or tolerance to biotic and abiotic stresses
87 (Kashyap et al., 2003; Rotino et al., 2014; Kouassi et al., 2016; Zhou et al., 2018). In
88 fact, some of these New World species, like *S. torvum*, are regularly used as eggplant
89 rootstocks due to their resistance to multiple soil diseases and nematodes (Arao et al.,
90 2008; King et al., 2010; Gisbert et al., 2012; Sabatino et al., 2018). However,
91 interspecific hybrids between brinjal eggplant and New World *Solanum* species have to
92 date been highly sterile (Lester and Kang, 1998; Prohens et al., 2012; Rotino et al.,
93 2014; Liu et al., 2015; Çürük and Dayan, 2017; Afful et al., 2018). Ploidy modification
94 techniques, like the development of tetraploids containing the full chromosome
95 complements of both parental species allowed fertility restoration in hybrids of common
96 eggplant with the Old World relative *S. aethiopicum* L. (Isshiki and Taura, 2003) but
97 not in hybrids with New World *S. torvum* (Sihachakr et al., 1989). Thus, to our
98 knowledge no backcrosses have been obtained for the introgression of genes or genomic
99 fragments of interest from New World *Solanum* species into the genetic background of
100 eggplant.

101 One of the New World species of greatest interest in the improvement of
102 eggplant is the silverleaf nightshade (*S. elaeagnifolium*). This distant wild relative of
103 eggplant is native to deserts and dry forests of North and South America and belongs to
104 the sister group of all Old World spiny solanums, the *Elaeagnifolium* clade (Knapp et
105 al., 2017). It is highly tolerant to drought (Christodoulakis et al., 2009) and has spread
106 as an invasive noxious weed in arid and semi-arid regions of the world, where it causes
107 considerable economic damage (Mekki, 2007). In addition, *S. elaeagnifolium* has been
108 barely explored for other traits that may be of interest for eggplant breeding such as the
109 content of nutritionally important bioactive phenolics (Kaushik et al., 2015). Despite its
110 evident interest for eggplant breeding, obtaining interspecific hybrids between common
111 eggplant and *S. elaeagnifolium* has not been described until recently (Kouassi et al.,
112 2016). After multiple crosses between six different accessions of *S. melongena* and one
113 of *S. elaeagnifolium* a few fruit set when using one *S. melongena* accession (MEL3) as
114 female parent, and nine hybrid plants could be obtained after embryo rescue of
115 immature fruits by Kouassi et al. (2016).

116 Within the Leptostemonum Clade, New World *Solanum* species of the
117 *Elaeagnifolium* clade are those phylogenetically closest to the Old World species
118 (Vorontsova and Knapp, 2016; Knapp et al., 2017). This led us to hypothesize that,
119 compared to other New World species, using interspecific hybrids with *S.*
120 *elaegnifolium* would result in higher success in achieving introgression breeding in
121 eggplant. In this way, a New World genepool could be accessible for breeding and for
122 widening the genetic background of eggplant.

123 In this paper, using the hybrids obtained by Kouassi et al. (2016) we describe the
124 characteristics of interspecific hybrids between *S. melongena* and *S. elaeagnifolium*, and
125 we make a first report of the development and characteristics of backcross generations
126 between eggplant and this New World species. We consider that these results open a
127 way to the use of the characteristics of interest of *S. elaeagnifolium* and its closest
128 relatives for eggplant improvement. Given the high tolerance to drought of *S.*
129 *elaegnifolium* (Christodoulakis et al., 2009) these materials may be of great interest for
130 developing a new generation of eggplant varieties adapted to climate change.

131

132 **2. Material and methods**

133

134 *2.1. Plant material and hybridizations*

135

136 Parental materials consisted of one accession of *S. melongena* (MEL3) and one
137 accession of *S. elaeagnifolium* (ELE2). *Solanum melongena* MEL3 is an accession from
138 Ivory Coast used in an introgression breeding programme (Kouassi et al., 2016; Plazas
139 et al., 2016) having semi-long fruits. *Solanum elaeagnifolium* ELE2 was collected as a
140 weed in Greece and has small round fruits (Kouassi et al., 2016). Both parents have
141 green fruits with dark green stripes (Figure 1) that ripen to yellow or orange-brown.
142 Also, materials used included clonal replicates of a plant of the interspecific hybrid *S.*
143 *melongena* MEL3 × *S. elaeagnifolium* ELE2 obtained after embryo rescue (Kouassi et
144 al., 2016).

145 In order to obtain backcross generations towards the *S. melongena* parent, the *S.*
146 *melongena* MEL3 × *S. elaeagnifolium* ELE2 interspecific hybrid, due to its low pollen
147 viability, was always used as female parent in crosses for obtaining the first backcross
148 (BC1) generation. Also, the plants obtained of the BC1 generation were used as female
149 parents for developing the second backcross (BC2) generation. All plants used for
150 hybridizations were grown in an insect-free greenhouse in 15 l pots filled with coconut
151 fiber. Plants were watered and fertilized using a drip irrigation system. Hybridizations
152 were performed early in the morning. Basically, flower buds one or two days before
153 anthesis were opened and emasculated with a forceps and pollen from the male parent
154 was gently deposited on the stigma of the female parent using a glass slide. Flowers
155 were tagged and fruits were harvested when physiologically ripe, with the exception of
156 a first fruit of the backcross between the interspecific hybrid *S. melongena* MEL3 × *S.*
157 *elaeagnifolium* ELE2 and *S. melongena* MEL3, which was harvested physiologically
158 unripe for embryo rescue using the protocol indicated in Plazas et al. (2016). For fruits
159 left to ripen, seeds were extracted from each individual fruits and left on filter paper for
160 drying at room temperature. Subsequently they were placed in paper bags and stored at
161 4°C in hermetic glass jars which contained silica gel for maintaining seed moisture low.
162 Seed germination was performed using the protocol described in Ranil et al. (2015).

163 Plants used for characterization were transplanted in June 2017 to soil in a
164 screenhouse. Plants were watered and fertilized by drip irrigation and trellised using
165 vertical strings. Weeds were removed manually and phytosanitary treatments against
166 spider mites and whiteflies were performed when necessary. Five plants of each of the
167 parentals, their interspecific hybrid, and of the first backcross (BC1) of the interspecific
168 hybrid towards the *S. melongena* parent were used for the morphological

169 characterization of above-ground parts. Three additional plants of *S. melongena* and of
170 the interspecific hybrid were used for the evaluation of the root system.

171

172 2.2. *Characterization*

173

174 Traits used for the characterization of the aerial part included 18 qualitative
175 (Table 1) and 16 quantitative (Table 2) descriptors mostly based on EGGNET and
176 IBPGR descriptors (IBPGR, 1990; van der Weerden and Barendse, 2007; Kaushik et
177 al., 2016). Descriptors used included traits of the habit, leaf, inflorescence, flower, and
178 fruit. Except for plant height and stem diameter, for which only one measurement was
179 taken per plant, at least five measurements were taken from each individual plant in
180 order to obtain individual plant averages for the conventional morphological descriptors
181 (i.e., five measurements per replicate). Pollen viability was evaluated according to Aref
182 (1992) with some modifications. From a cell suspension with a concentration of
183 500,000 cells/ml, 1 ml of dilution was distributed in a 6 mm diameter Petri dish and
184 stained with 0.001% FDA solution (fluorescein diacetate, 1 µl per ml of suspension) and
185 allowed to incubate for 5 minutes. Fluorescence in FDA was determined by scoring the
186 percentage of fluorescing pollen grains under an ultraviolet (UV) source provided by a
187 mercury lamp. The principle is based on the uptake of non-fluorescing FDA by the
188 vegetative cells of a viable pollen grain and subsequent hydrolysis by esterase to release
189 fluorescein, which fluoresces under UV (excitation filter = 485 nm and barrier filter =
190 520 nm). In contrast, nonviable cells are incapable of hydrolyzing FDA and, therefore,
191 do not fluoresce (Heslop-Harrison et al., 1984). Each determination of pollen fertility
192 consisted was performed by counting 300 to 500 pollen grains by examining 10
193 locations in a series of random areas across the Petri dish that contained the sample
194 under test.

195 For the characterization of the root traits, four traits were measured. Firstly, the
196 plants were carefully removed from the ground, with the help of a hoe, to reduce root
197 damage; once extracted they were cleaned with water to eliminate the earth or the
198 accumulated mud. Finally, the characters indicated in Table 3 were evaluated manually
199 with the help of a phenotyping scoreboard.

200

201 2.3. *Phenolics content*

202

203 Chlorogenic acid (CGA), the main phenolic compound in the eggplant flesh
204 (Stommel and Whitaker, 2003; Whitaker and Stommel, 2003; Prohens et al., 2013), and
205 other hydroxycinnamic acid conjugates were extracted and analyzed using the
206 methodology indicated in Plazas et al. (2014) in order to assess overall phenolic content
207 of the fruit. Extractions were performed with 0.1 g of lyophilized sample homogenized
208 in 1.8 ml of methanol:water (80:20, v/v) plus 0.1% (w/v) of 2,3-tert-butyl-4-
209 hydroxyanisole (BHT). After that the extract was vortexed vigorously, sonicated for 1 h
210 and centrifuged at 2000 rpm for 3 min and the supernatant filtered through 0.2- μ m
211 polytetrafluoroethylene (PTFE) membrane filters.

212 Extracts were analyzed on a HPLC 1220 Infinity LC System (Agilent
213 Technologies, Santa Clara, CA, USA) operated by the OpenLAB CDS ChemStation
214 Edition software package (Agilent Technologies). Aliquots of 10 μ L were injected into
215 a ZORBAX Eclipse Plus C18 (3.5 μ m; 4.6 mm \times 12.5 mm; Agilent Technologies)
216 column protected by a ZORBAX Eclipse Plus C18 guard column (5 μ m; 4.6 mm \times 12.5
217 mm; Agilent Technologies). A binary gradient consisting of 0.1% formic acid (Solvent
218 A) and methanol (Solvent B) was used. The mobile phase gradient described in Plazas
219 et al. (2014) was used and absorbance was measured at 325 nm for quantification. CGA
220 concentration in the extracted samples was calculated using calibration curves. The
221 CGA peak area and the total peak area (TPA) of other phenolic acids were determined.

222

223 *2.4. Determination of ploidy level*

224

225 Cell nuclei from leaf tissues were isolated mechanically according to Dpooležel
226 et al. (1989) with some modifications. Approximately 0.5 cm² of fresh young leaf tissue
227 was chopped with a razor blade in a glass Petri dish containing 0.5 ml lysis buffer LB01
228 (pH 7.5) containing 15 mM Tris (hydroxymethyl) aminomethane, 2 mM Na₂EDTA and
229 0.5 mM spermine, and was left to incubate for 5 min. Subsequently, the suspensions
230 containing nuclei and cell fragments were passed through a 30 μ m CellTrics filter
231 (Sysmex). The nuclei in the filtrate were stained by CyStain UV Ploidy (Sysmex) by
232 incubation for 5 min. The fluorescence intensity of the homogenate was measured using
233 CyFlow ploidy-analyzer (Partec, Münster, Germany), measuring at least 4000 nuclei for
234 each sample.

235

236 3. Results

237

238 3.1 Backcrossing results

239

240 Twenty-two fruits developed after performing over 800 crosses between the
241 interspecific hybrid *S. melongena* MEL3 × *S. elaeagnifolium* ELE2 as a female parent
242 and the recurrent *S. melongena* MEL3 as male parent. The first fruit to set was collected
243 before physiological maturity and it was found to contain developing seeds, from which
244 10 embryos were rescued (in heart and torpedo stages), which developed well and gave
245 phenotypically normal BC1 plants. Because opening of this first fruit revealed an
246 apparently normal development of the seeds, several subsequent fruits were allowed to
247 develop to physiological maturity; these yielded seeds with a germination rate higher
248 than 50%. We subsequently, therefore, abandoned embryo rescue, and the fruits
249 containing seeds with the BC1 zygotes were allowed to ripen on the plant for extraction
250 of mature seeds. Except for a single fruit that was parthenocarpic, all of the other 21
251 fruits of the interspecific hybrid after pollination with the recurrent parent *S. melongena*
252 MEL3, presented seeds with a range between 4 and 40 seeds (mean ± SD = 12.32 ± 8.13
253 seeds/fruit). No fruits were obtained from non-pollinated flowers, although some
254 seedless pseudofruits occasionally formed from non-pollinated flowers.

255 We put all 40 seeds from the fruit containing the largest seed number to
256 germinate; this resulted in 50% germination, giving us 20 BC1 plants. These BC1 plants
257 were grown for a next cycle of backcrossing for obtaining the BC2 generation. Multiple
258 crosses (over 3,000) were performed using the BC1 plants as female parent, resulting in
259 at least one fruit obtained in 17 out of the 20 BC1 plants. A total of 92 fruits (between 1
260 and 9 per individual plant) were obtained and all of them had seeds, with a range
261 between 1 and 150 seeds/fruit (mean ± SD = 62.86 ± 35.99 seeds/fruit). Several BC2
262 seeds from each BC1 plant were germinated to obtain between 5 and 12 plants per
263 individual BC2 family.

264

265 3.2 Characterization of parents, hybrid, and BC1 generations

266

267 Important differences were observed between the *S. melongena* MEL3 and *S.*
268 *elaegnifolium* ELE2 parents in the morphology of the vegetative part of the plant,

269 leaves, inflorescences and flowers, and fruits. In fact, for 21 out of the 37 characters
270 evaluated, there was no overlap in the ranges of variation (Tables 1 and 2).

271 Regarding plant habit, *S. melongena* has an upright growth habit and is much
272 taller (more than two-fold) and has a thicker stem than *S. elaeagnifolium* (Table 1 and
273 2). The hybrids have an upright growth habit and are intermediate for plant height and
274 stem diameter, although the values are closer to those of *S. elaeagnifolium* (Tables 1
275 and 2; Figures 1A-C). For the BC1 generation, the five plants characterized had an
276 upright growth habit, but a great segregation was observed for plant height and stem
277 diameter, with ranges of variation wider than those of the parents for these characters
278 (Tables 1 and 2; Figure 1D). Amazingly, interspecific hybrids displayed prickles
279 between nodes, while none of the parents did. Some BC1 plants had prickles between
280 nodes, but their degree of prickliness was much lower than that of the F1 (Table 2).

281 Leaf morphology also displayed great differences between the parents (Tables 1
282 and 2; Figures 1E-F). None of the two parents had prickly leaves; however, *S.*
283 *melongena* leaves had stronger lobing, were more erect, and much larger than those of
284 *S. elaeagnifolium*. The leaves of the hybrid were intermediate for all the observed
285 characters, and again quite variable in the individuals of the BC1, which displayed
286 segregation for the leaf lobing (Tables 1). As occurred with the prickles between nodes,
287 some prickles appeared in the leaves of the hybrids. However, all BC1 plants had non-
288 prickly leaves.

289 Many differences were observed among parents in inflorescence and flower
290 traits. *Solanum melongena* had flowers with light violet corolla, connivent anther cone,
291 and straight style, while those of *S. elaeagnifolium* had a darker bluish violet corolla,
292 spreading anther cone, and curved style (Table 1; Figures 1G, 2A and 2C). Flowers of *S.*
293 *melongena* were considerably larger than those of *S. elaeagnifolium*, while pollen
294 viability was very high in *S. melongena* (>90%) and moderate (around 50%) in *S.*
295 *elaeagnifolium* (Table 2). On the other hand, the number of flowers per inflorescence
296 was similar among both parents and none of the parents displayed anthocyanins in the
297 pistil. Flowers of *S. melongena* were fasciated and displayed higher numbers of petals,
298 sepals and anthers than those of *S. elaeagnifolium*, which were strictly pentamerous
299 (Tables 1 and 2; Figures 1G). Hybrids had light violet corolla and a connivent cone of
300 anthers (like *S. melongena*) and curved style (like *S. elaeagnifolium*) and segregated for
301 the presence of anthocyanins in the pistil (Table 1; Figure 2B). Flower number per
302 inflorescence was transgressive to both parents (Table 2). Flowers of hybrids were

303 pentamerous like those of *S. elaeagnifolium* although smaller than either parent any of
304 them (Table 2; Figure 1G), and pollen viability of the hybrid was very low (<3%). A
305 wide range of diversity was observed for color and size of flowers in the BC1
306 generation, with wide segregation for these traits (Tables 1 and 2; Figure 1G).
307 Segregation was observed for corolla color, presence of anthocyanins in the pistil, and
308 style curvature, with most plants displaying anthocyanin pigmentation and curved
309 styles. The number of flowers per inflorescence was similar to that of the parents, and
310 like *S. elaeagnifolium* and the interspecific hybrid, flowers of BC1 plants were
311 exclusively pentamerous (Table 2). Corolla diameter was very variable, but average
312 corolla diameter was similar to that of the F1 hybrid (Table 2; Figure 1G). Finally,
313 pollen viability also exhibited a wide range of variation, with a considerable increase
314 (average of around 20%) over pollen fertility levels of the F1 (Table 2).

315 Few differences existed among parents in fruit firmness and color, except that
316 the predominant fruit color at physiological ripeness was yellow-orange for *S.*
317 *melongena* and orange for *S. elaeagnifolium*, and the fruit flesh was white and green,
318 respectively (Table 1). However, large differences were observed in fruit size and shape
319 (Table 2). Fruits of *S. melongena* were much larger and more elongated than those of *S.*
320 *elaegnifolium*, with fruit length and width on average 15.7-fold and 6.4-fold larger in
321 *S. melongena* than in *S. elaeagnifolium* (Table 2). Also, fruits of *S. melongena* had a
322 thicker peduncle than those of *S. elaeagnifolium*. Regarding the calyx, its relative length
323 in relation to the berry length was shorter in *S. melongena* than in *S. elaeagnifolium*, and
324 it was non-prickly in *S. melongena* and prickly in *S. elaeagnifolium* (Table 2). The F1
325 fruits were less firm than those of either of the two parents, probably as a consequence
326 of being parthenocarpic, and in color were similar or intermediate (for those traits that
327 display differences among parents) to the two parents. Fruit size and shape was
328 intermediate to those of the parents, although much more similar to the *S.*
329 *elaegnifolium* parent (Table 2). For fruit calyx characteristics, F1 hybrids had a relative
330 calyx length and prickliness similar to the ones observed in *S. elaeagnifolium*. The BC1
331 plants were also similar to the parents and F1 in color characteristics (Table 1).
332 Although variation was observed for fruit size and shape, fruits from BC1 plants were
333 generally intermediate between those of the F1 and the *S. melongena* parent, although
334 much more similar to the former than to the latter (Table 2). For fruit calyx
335 characteristics, the relative fruit calyx length of BC1 individuals was similar to that of *S.*

336 *melongena*, while calyx prickliness was variable, with a range from 0 to 10 prickles and
337 an average value slightly lower than that of the F1 hybrid (Table 2).

338 The root system of developed mature plants of the *S. melongena* parent and of
339 the F1 hybrid *S. melongena* × *S. elaeagnifolium* was characterized and considerable
340 differences were observed (Table 3; Figure 3). Unfortunately the root system of *S.*
341 *elaeagnifolium* could not be scored, as when the plants were uprooted out plants were
342 already senescent and the root system damaged. The main differences observed were
343 that, compared to *S. melongena*, the F1 had a somewhat longer and thinner main root, a
344 reduced whorl diameter, a higher number of roots of diameter >2 and a lower density of
345 lateral roots in the main root (Table 3). It is also evident from Figure 3 that the F1
346 hybrid has a root system that explores the soil to longer distances than *S. melongena*,
347 which has a large part of the root system concentrated to a few centimeters around the
348 stem.

349

350 3.3 Phenolics profile of parents and hybrids

351

352 The analysis of phenolic acids reveals clear differences in the profiles obtained
353 for *S. melongena* and *S. elaeagnifolium* (Figure 4). For *S. melongena*, chlorogenic acid
354 (CGA) was the main compound, representing over 85% of the chromatogram total peak
355 area (TPA) (Figure 4A); also, an unidentified peak very close to the CGA peak and
356 probably representing an isomer or a derivative of CGA (Whitaker and Stommel, 2003)
357 makes a secondary peak. *Solanum elaeagnifolium* also has an important CGA peak, but
358 it represents slightly less than 30% of the TPA, although another peak close to CGA,
359 which probably is also a CGA isomer or derivative, accounts for almost 19% of the
360 TPA. Another important peak corresponding to an unidentified phenolic compound that
361 appears at a retention time of 20.2 minutes in *S. elaeagnifolium*. Also, several other
362 minor peaks appear in the *S. elaeagnifolium* chromatogram that do not appear, or have
363 very low percentage of TPA, in *S. melongena* (Figure 4B). For example, a peak at 15.9
364 min is detected in *S. elaeagnifolium* but not in *S. melongena*, and a small peak in *S.*
365 *melongena* at 19.1 min is much higher in *S. elaeagnifolium*. The individuals of the F1
366 present a chromatogram in which all the major peaks present in the chromatograms of
367 the parents are also present. In this case, the secondary CGA peak disappears, revealing
368 a clear CGA peak representing almost 70% of the TPA (Figure 4C). The unidentified
369 compound from *S. elaeagnifolium* with a peak at 20.2 minutes also appears in the F1

370 hybrid, although it only represents around 10% of the TPA. In the F1 chromatogram
371 most of the minor peaks observed in the chromatograms of both parents also appear
372 (Figure 3C). Here, the peak at 15.9 min is similar in area to the one found in the *S.*
373 *elaeagnifolium* parent (Figures 3B and 3C).

374

375 3.4 Flow cytometry analysis of parents and hybrids

376

377 The analysis with flow cytometry revealed that both parents and the interspecific
378 hybrid were diploid (Figure 5). No large differences were apparent for the genome size
379 among parents and interspecific hybrid, although ELE2 seems to have a slightly smaller
380 genome than *S. melongena*.

381

382 4. Discussion

383

384 The use of crop wild relatives in breeding has demonstrated in many crops that
385 can make a significant economic impact (Tyack and Dempewolf, 2015). For example,
386 in tomato, introgressions in commercial varieties from a wild relative have contributed
387 to the increase of 2.4% in the soluble solids content of the fruit, which has had an
388 economic impact of $250 \cdot 10^6$ US\$ annually only in the US (Hunter and Heywood, 2011).
389 This latter example reveals that although at the global level eggplant has less economic
390 value than tomato (around 6.5-fold less) (FAO, 2018), wild relatives may make an
391 important economic impact in eggplant breeding. However, up to now, to our
392 knowledge, no commercial cultivars of eggplant with introgressions from crop wild
393 relatives are available, and the potential of wild eggplant relatives for the development
394 of commercial cultivars remains untapped. Here we report the successful backcrossing,
395 up to the BC2 generation, of a species native to the New World (*S. elaeagnifolium*) with
396 *S. melongena*, an Old World domesticate (Meyer et al., 2012). According to our
397 knowledge, it is the first time that introgression materials of eggplant with a New World
398 species have been obtained. This has important implications for eggplant breeding, as
399 the introgression materials obtained (up to BC2 generation) indicate that a new distant
400 untapped genepool has become available for eggplant breeding.

401 By using the interspecific hybrid *S. melongena* × *S. elaeagnifolium* as a female
402 parent and *S. melongena* as a male parent, fruits containing viable seeds were obtained,
403 although the degree of success was lower compared to backcrosses made with other

404 interspecific hybrids of eggplant with Old World species (Kouassi et al., 2016). This is
405 probably due to a greater sterility of the hybrid, as indicated by low pollen fertility. The
406 fact that no seeded fruits appeared in the non-pollinated flowers suggests that pollen
407 sterility in *S. melongena* × *S. elaeagnifolium* hybrids is a more limiting factor than that
408 of the ovules, as has been shown in other crops (Dwivedi et al., 2008; Prohens et al.,
409 2017). The extraction of embryos made in the first fruit of the hybrid pollinated with *S.*
410 *melongena* pollen revealed a normal appearance in all immature seeds, suggesting that
411 there are no major problems of embryo degeneration and abortion. In this way, mature
412 seeds containing the BC1 zygotes presented a percentage of germination higher than
413 50%.

414 Of the 20 BC1 plants we used to develop the BC2 generation, seeds and BC2
415 offspring were obtained from 17 of them. Assuming a normal segregation and
416 recombination in the F1 hybrid gametes, it would mean that the percentage of *S.*
417 *elaeagnifolium* genome represented in the BC1 17 plants would be $1-0.5^{17}$ (>0.99999).
418 Even though it is likely that distortions in the segregation and lack of recombination in
419 some areas of the genome may have occurred (Kreike and Stiekema, 1997; Gramazio et
420 al., 2018), a large part of the genome of *S. elaeagnifolium* is likely represented in the
421 BC1 plants and the BC2 offspring. On the other hand, although variations in the ploidy
422 degree are common in *S. elaeagnifolium* (Moscone E., 1992; Acosta et al., 2005; Powell
423 and Weedon, 2005; Scaldaferrero et al., 2012; Knapp et al., 2017) the results of flow
424 cytometry indicate that the accession used of *S. elaeagnifolium* is diploid and presents a
425 genome size similar to that of *S. melongena*, which could have contributed to the
426 success of the backcrosses.

427 The interspecific hybrids were intermediate in most of the parental
428 characteristics, although generally closer to *S. elaeagnifolium*. This is a common
429 phenomenon in interspecific hybrids in eggplant with wild relatives (Prohens et al.,
430 2013; Kaushik et al., 2016). However, unlike many other interspecific hybrids of
431 eggplant (Kaushik et al., 2016), hybrids between common eggplant and *S.*
432 *elaeagnifolium* did not display heterosis for vigor, perhaps due to the great phylogenetic
433 distance between the two species (Vorontsova et al., 2013). The hybrid displayed
434 prickles in the leaf, although none of the parents had prickly leaves. This is a common
435 phenomenon in interspecific eggplant hybrids when crossing with a non-prickly species,
436 probably because the mutations that confer lack of leaf prickles are different in the two

437 species (Lester, 1986; Varoquaux et al., 2000; Kouassi et al., 2016; Plazas et al., 2016;
438 Prohens et al., 2012).

439 In the hybrids the style was curved as in *S. elaeagnifolium*; in addition, some
440 plants of the F1 presented anthocyanins in the style while others did not. Differences
441 among F1 hybrids in style pigmentation could be due to environmental effects or
442 epigenetic modifications (Hahlbrock and Scheel, 1989; Dixon and Harrison, 1990;
443 Shichijo et al., 1993; Noda et al., 2004). Something similar, in addition to segregation,
444 could be taking place in the individuals of the BC1. The fact that the flowers of the
445 hybrid are smaller than those of both parents, but at the same time there are more
446 flowers per inflorescence, has already been observed in hybrids between eggplant and
447 other relatives (Daunay et al., 1993; Kaushik et al., 2016). The fruits of the hybrid have
448 intermediate characteristics between those of both parents, although more similar to
449 those of the wild species, again common in interspecific eggplant hybrids (Prohens et
450 al., 2013; Kaushik et al., 2016).

451 As in other studies (Prohens et al., 2012, 2013), a regression towards the
452 characteristics of the *S. melongena* parent was observed in the BC1 generation, although
453 an important segregation was observed for all the characters in which the parents
454 differed, except for the number of parts of the flower, which was consistently five, as in
455 the wild parent. Amazingly, the fertility of pollen increased considerably, with an
456 average of 19.4% and a minimum value of 7.4% in one of the five plants characterized,
457 which suggests a rapid recovery of fertility already in this first generation of
458 backcrossing, as described in other crops (Wall, 1970; Prohens et al., 2017).

459 Although the aerial part of interspecific hybrids is smaller than that of the *S.*
460 *melongena* parent, the main root of both materials has a similar length. In addition, the
461 fact that the relative density of lateral roots in the main root of the hybrid is smaller than
462 that of *S. melongena* suggests that the hybrid explores other areas of the soil (Chen et
463 al., 2014), whereas the *S. melongena* root system is mostly concentrated in the area
464 where the drip irrigation system supplies water and nutrients. This suggests that an
465 improved eggplant root system can be obtained through introgression from *S.*
466 *elaeagnifolium* which, apart from being drought tolerant (Christodoulakis et al., 2009),
467 has a rhizomatous root system (Knapp et al., 2017)

468 Wild species of eggplant generally present a more diverse phenolic profile that
469 that of *S. melongena*, in which chlorogenic acid is the main component (Stommel and
470 Whitaker, 2003; Whitaker and Stommel, 2003; Prohens et al., 2013). In our case, the

471 profile of phenolic compounds shows that *S. elaeagnifolium* and *S. melongena* are also
472 considerably different. In addition, *S. elaeagnifolium* presents a greater total peak area
473 in the chromatogram, while the hybrid presents an intermediate profile, although more
474 similar to that of *S. elaeagnifolium*. This suggests that *S. elaeagnifolium* can contribute
475 to improving the content of phenolic bioactive compounds of eggplant (Kaushik et al.,
476 2015) without lowering the chlorogenic acid content. In this way, the use of another
477 New World species (*S. viarum*) has been suggested as a potential source of variation to
478 improve the caffeoylquinic acid content and its derivatives in eggplant (Wu et al.,
479 2012).

480 In conclusion in this study we present for the first time, to our knowledge, the
481 development of backcross generations of a hybrid between eggplant and a wild relative
482 from the New World belonging to its tertiary germplasm pool (Kouassi et al., 2016).
483 Our results suggest that these introgression materials will be of great interest for the
484 genetic improvement of eggplant; they may have an tremendous potential to increase
485 tolerance to abiotic stresses, such as to drought by improving the eggplant root system,
486 as well as by enhancing its bioactive properties by increasing the contents in bioactive
487 phenolics and modifying its profile (Kaushik et al., 2015). In addition, the introgression
488 materials may also contribute to other traits that remain unexplored in *S.*
489 *elaegnifolium*, such as tolerance to pests and diseases. Also, because *S. elaeagnifolium*
490 is not phylogenetically closely related to *S. melongena* (Vorontsova et al., 2013) the
491 introgression materials obtained may represent an appropriate model to study epigenetic
492 modifications occurring in the genome following distant hybridization and introgression
493 breeding (Wang et al., 2005; Dong et al., 2006). Finally, we hope that this seminal study
494 opens the way for the incorporation of the *Elaeagnifolium* clade New World genepool
495 (Knapp et al., 2017) for eggplant breeding, ultimately contributing to the development
496 of a new generation of plants adapted to climate change and with improved nutritional
497 and diseases and pest resistance properties.

498

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500

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521

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720

721 **Table 1**

722 Descriptor states for the qualitative traits evaluated in *S. melongena* MEL3 (P1), *S. elaeagnifolium* ELE2 (P2), the interspecific hybrid *S.*
 723 *melongena* MEL3 × *S. elaeagnifolium* ELE2 (F1), and first backcross (BC1) towards *S. melongena* (BC1) generations. For each generation, five
 724 plants (n=5) were evaluated. Where segregation was observed within generation the numbers of plant of each class are indicated.

Trait	P1	P2	F1	BC1
Vegetative part				
Plant growth habit	Upright	Intermediate	Upright	Upright
Prickle color	-	-	Green	Green
Leaf				
Leaf blade lobing	Strong	Weak	Intermediate	1 Intermediate : 3 Strong : 1 Weak
Leaf surface	Flat	Flat	Flat	Flat
Inflorescence and flower				
Corolla color	Light violet	Bluish violet	Light violet	2 Pale violet : 3 Light violet
Style curvature	Straight	Curved	Curved	4 Curved : 1 Straight
Presence of anthocyanins in pistil	No	No	3 Yes : 2 No	4 Yes : 1 No
Fruit				
Fruit apex shape	Rounded	Rounded	Rounded	Rounded
Firmness in the wide part	Very firm	Very firm	Firm	Very firm
Size of the stylar scar	Small	Small	Small	Small

Fruit predominant color (at commercial ripeness)	Green	Green	Green	Green
Fruit predominant color (at physiological ripeness)	Yellow-Orange	Orange	Orange	Yellow-Orange
Fruit predominant color intensity (at commercial ripeness)	Clear	Clear	Dark	Clear
Fruit additional color (at commercial ripeness)	Dark green	Dark green	Dark green	Dark green
Fruit additional color distribution	Striped	Striped	Striped	Striped
Fruit flesh color (cut fruit at commercial ripeness)	White	Green	Intermediate	Intermediate
Fruit calyx color	Green	Green	Green	Green
Fruit color intensity under calyx	Medium	Medium	Medium	Medium

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727 **Table 2**

728 Mean value, standard error and range of the morphological quantitative traits evaluated in *S. melongena* MEL3 (P1), *S. elaeagnifolium* ELE2
 729 (P2), the interspecific hybrid *S. melongena* MEL3 × *S. elaeagnifolium* ELE2 (F1), and first backcross (BC1) towards *S. melongena* (BC1)
 730 generations. For each generation, five plants (n=5) were evaluated.

Trait	P1		P2		F1		BC1	
	Mean	Range	Mean	Range	Mean	Range	Mean	Range
Vegetative part								
Plant height (cm)	205 ± 4	190-215	84 ± 10	50-108	109 ± 12	80-140	117 ± 21	87-200
Stem diameter (cm)	4.5 ± 0.3	4.0-5.5	3.3 ± 0.3	3.0-4.0	2.9 ± 0.1	2.5-3.0	2.7 ± 0.4	1.5-4.0
Prickles between nodes (n)	0.0 ± 0.0	0-0	0.0 ± 0.0	0-0	2.8 ± 0.4	2-4	0.3 ± 0.2	0-1
Leaf								
Leaf prickles ^a	0 ± 0	0-0	0 ± 0	0-0	1 ± 0	1-1	0 ± 0	0-0
Length of the largest prickles (cm)	-	-	-	-	0.1 ± 0.0	0.1-0.1	-	-
Leaf pedicel length (cm)	6.4 ± 0.2	6.0-7.0	1.6 ± 0.3	1.0-2.5	3.1 ± 0.2	2.5-3.5	3.2 ± 0.6	2.0-5.5
Leaf apex angle ^b	3 ± 0	3-3	5 ± 0	5-5	3 ± 0	3-3	5 ± 0	5-5
Leaf blade length (cm)	15.8 ± 0.4	15.0-17.0	8.5 ± 0.2	8.0-9.0	11.9 ± 1.2	8.5-15.0	13.2 ± 1.0	11.0-17.0
Leaf blade width (cm)	9.4 ± 0.2	9.0-10.0	2 ± 0	1.8-2.2	6.1 ± 0.4	5.5-7.0	6.9 ± 0.6	6.0-9.0
Inflorescence and flower								
Flowers/inflorescence (cm)	4.4 ± 0.2	4-5	4.8 ± 0.2	4-5	7.6 ± 0.4	6-8	4.8 ± 0.6	3-6
Petals/flower	5.4 ± 0.3	5.2-5.5	5 ± 0	5-5	5 ± 0	5-5	5 ± 0	5-5

Sepals/flower	5.2 ± 0.1	5.0-5.3	5 ± 0	5-5	5 ± 0	5-5	5 ± 0	5-5
Stamens/flower	5.5 ± 0.4	5.2-5.6	5 ± 0	5-5	5 ± 0	5-5	5 ± 0	5-5
Corolla diameter (cm)	4.9 ± 0.1	4.5-5.0	3.7 ± 0.1	3.5-4.0	2.4 ± 0.1	2.0-2.5	2.5 ± 0.5	1.5-4.5
Pollen viability (%)	91.5 ± 2.4	84.2-97.3	50.7 ± 4.3	41.7-61.4	2.6 ± 0.2	2.3-2.8	19.4 ± 8.7	7.4-53.3
Fruit								
Fruit length (cm)	11.8 ± 0.6	11.0-14.0	0.75 ± 0.16	0.5-1.0	1.25 ± 0.13	1.0-1.5	2.75 ± 0.52	1.5-4.0
Fruit width (cm)	5.4 ± 0.5	4.0-7.0	0.85 ± 0.09	0.7-1.0	1.25 ± 0.13	1.0-1.5	2.0 ± 0.0	2.0-2.0
Fruit pedicel length (cm)	6.0 ± 1.0	5.0-7.0	2.3 ± 0.2	2.0-2.5	1.8 ± 0.1	1.5-2.0	2.0 ± 0.0	2.0-2.0
Fruit pedicel thickness (cm)	1.0 ± 0.0	1.0-1.0	0.35 ± 0.03	0.3-0.4	0.3 ± 0.0	0.3-0.3	0.4 ± 0.1	0.3-0.5
Relative fruit calyx length ^c	1 ± 0	1-1	3 ± 0	3-3	3 ± 0	3-3	1 ± 0	1-1
Fruit calyx prickles (n)	0 ± 0	0-0	5 ± 0	5-5	5 ± 0	5-5	3.75 ± 2.14	0-10

731 ^aMeasured in a scale (0=Absent; 1= 1 to 2; 3= 3 to 5; 5= 6 to 10; 7: 11 to 20; 9= More than 20).

732 ^bMeasured in a scale (1= Less than 15°; 3=aprox. 45°; 5= aprox. 75°; 7= aprox. 110°; 9= aprox. 160°).

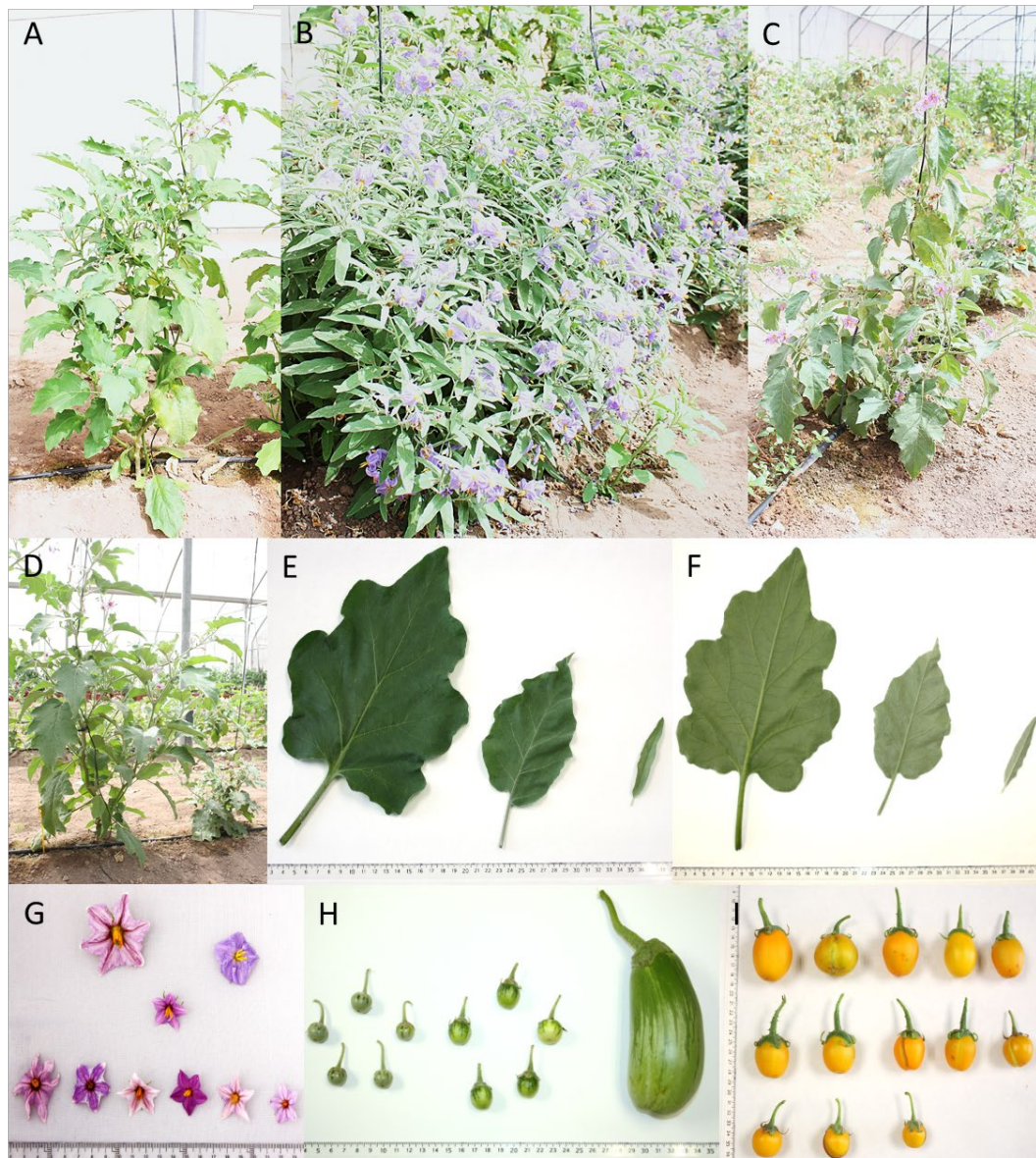
733 ^cMeasured in a scale (0=Less than 10%; 3=aprox. 20%; 5=aprox. 50%; 7=aprox. 70%; 9=More than 75%).

734 **Table 3**735 Mean value, standard error and range of the root morphological traits evaluated in *S.*736 *melongena* MEL3 (P1), and interspecific hybrid *S. melongena* MEL3 × *S.*737 *elaeagnifolium* ELE2 (F1). For each generation, three plants (n=3) were evaluated.

Trait	P1		F1	
	Mean	Range	Mean	Range
Whorl angle (°)	136.0 ± 3.0	130-140	151.3 ± 5.9	140-160
Main root length (cm)	42.7 ± 0.9	28-68	54.0 ± 2.0	33-66
Main root diameter (mm)	8.7 ± 0.2	8-9	5.0 ± 0.0	5-5
Relative density of laterals in the main root	Intermediate		Low	

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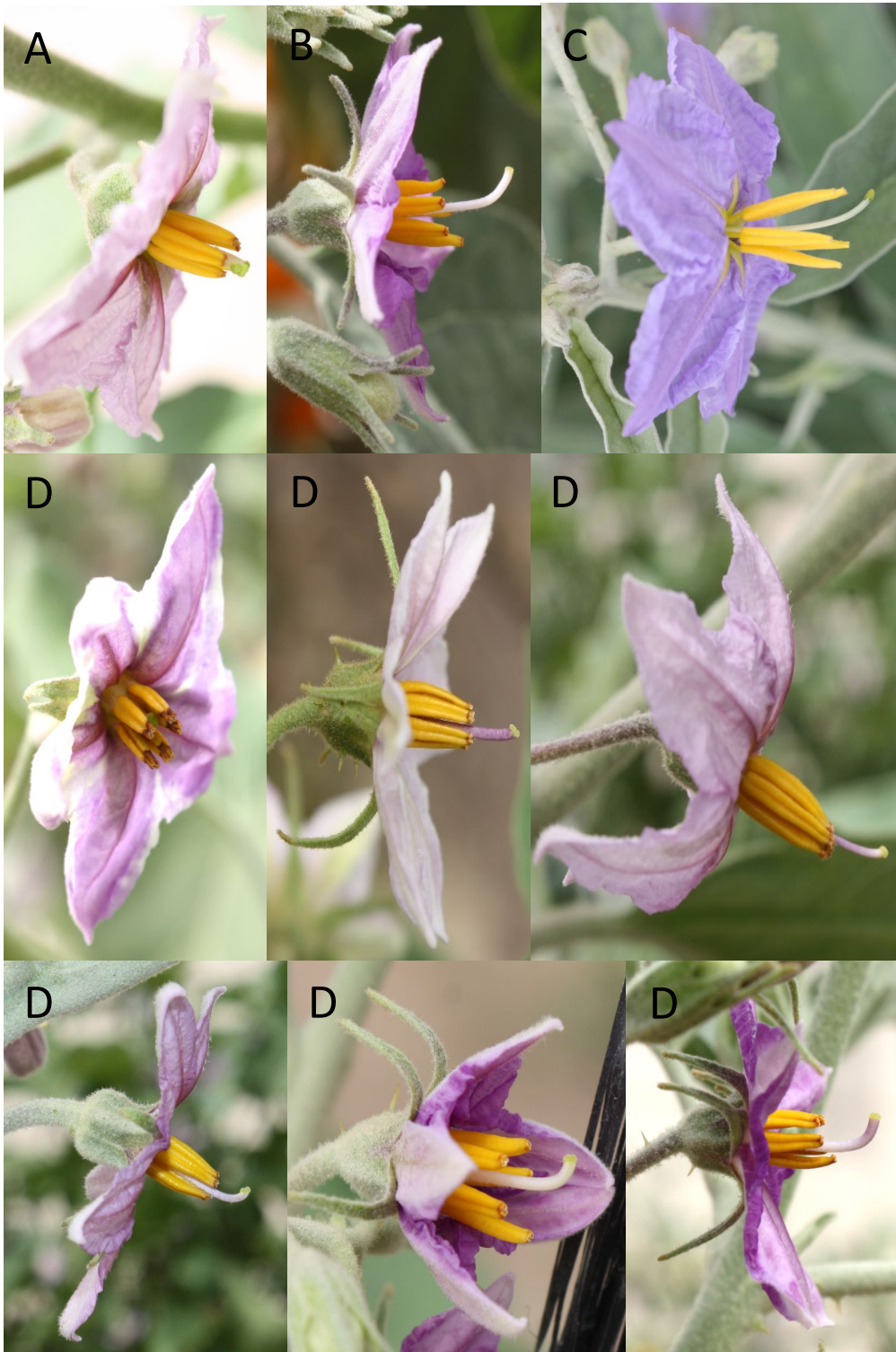


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741 **Figure 1**

742 Morphology of plant materials evaluated: *S. melongena* MEL3 plant (A); *S.*
 743 *elaegnifolium* ELE2 plant (B); *S. melongena* MEL3 × *S. elaeagnifolium* ELE2
 744 interspecific hybrid (F1) plant (C); two plants of the first backcross (BC1) of the F1
 745 interspecific hybrid towards *S. melongena* displaying extreme difference in plant size (D);
 746 adaxial part of the leaf of *S. melongena* (left), F1 interspecific hybrid (center) and *S.*
 747 *elaegnifolium* (right) (E); abaxial part of the leaf of *S. melongena* (left), F1 interspecific
 748 hybrid (center) and *S. elaeagnifolium* (right) (F); Flowers of *S. melongena* (left), F1
 749 interspecific hybrid (center), *S. elaeagnifolium* (right) and BC1 individuals (below) (G);
 750 Fruits of *S. elaeagnifolium* (left), F1 interspecific hybrid (center) and *S. melongena* (right)
 751 (H); Segregation for fruit size and shape in physiologically mature fruits of the first
 752 backcross (BC1) of the F1 interspecific hybrid towards *S. melongena* (I). Scale in cm.

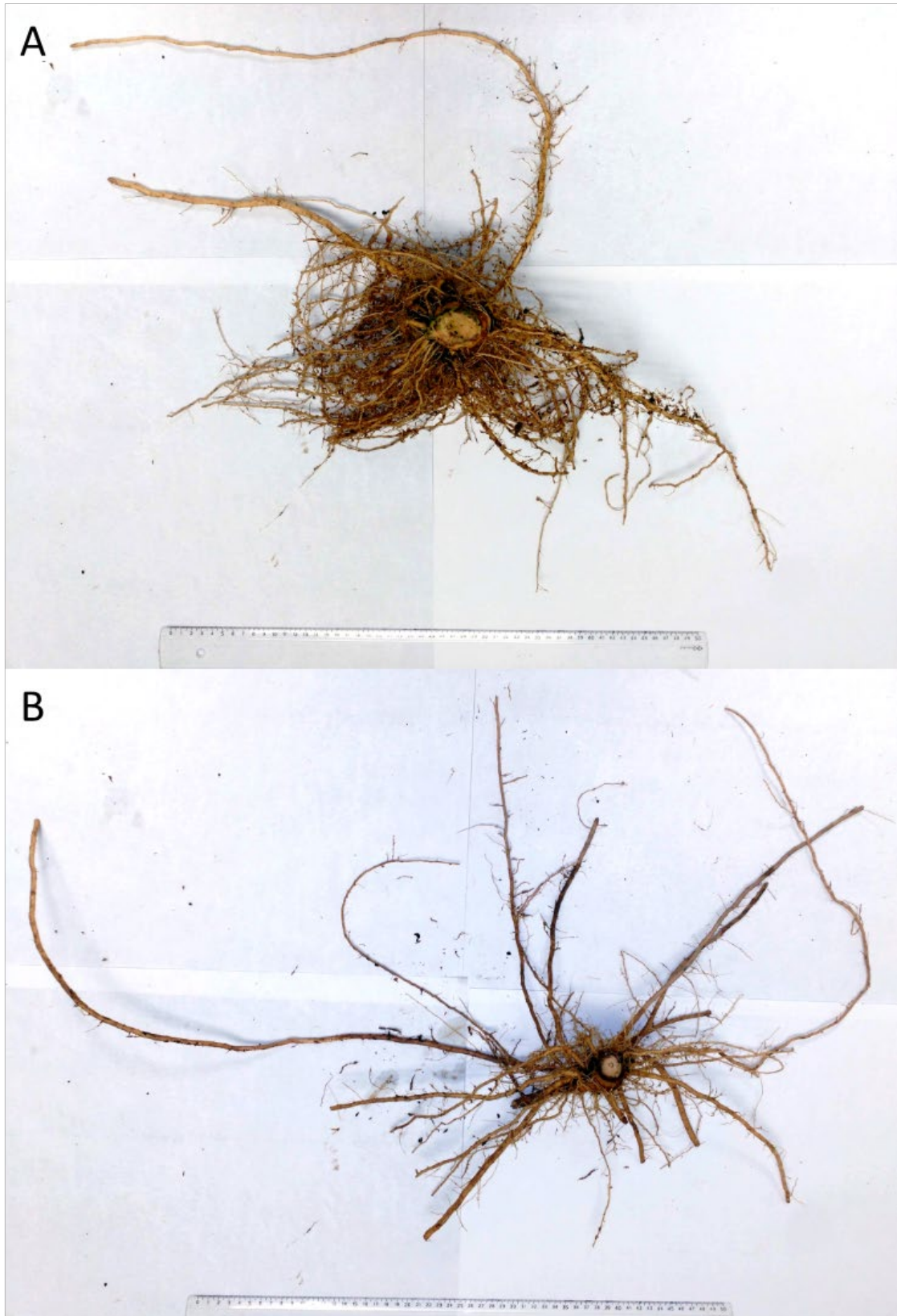
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755 **Figure 2**

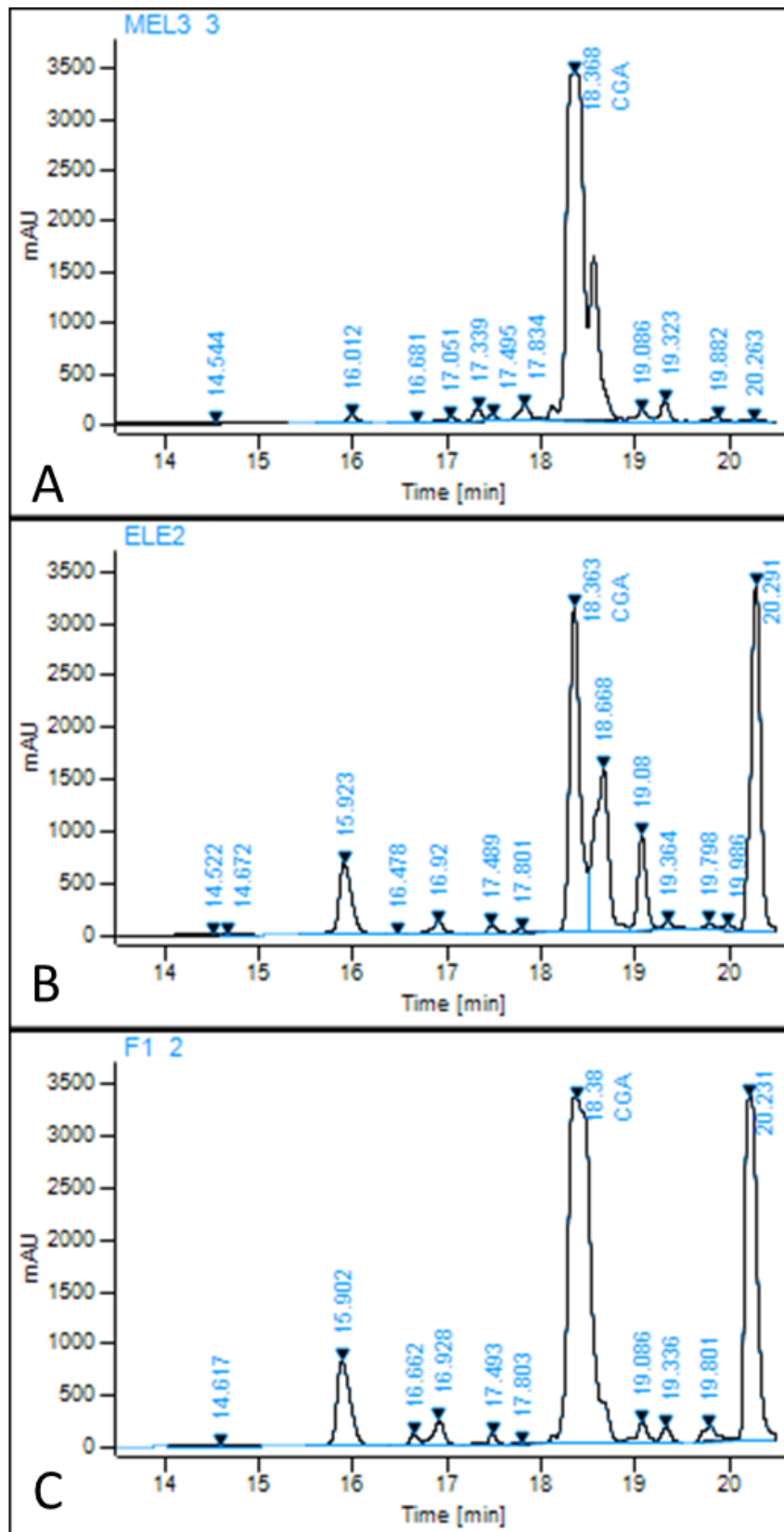
756 Variation for flower morphology in: *S. melongena* MEL3 (A); *S. melongena* MEL3 × *S.*
 757 *elaeagnifolium* ELE2 interspecific hybrid (B); *S. elaeagnifolium* ELE2 (C); Flowers of
 758 different plants of the first backcross (BC1) of the F1 interspecific hybrid towards *S.*
 759 *melongena* (D). Large variation is observed in BC1 plants for flower size, corolla color,
 760 style length, curvature and color, anthers length, and opening of the anthers cone.



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Figure 3

Root morphology in: *S. melongena* MEL3 (A) and F1 interspecific hybrid *S. melongena* MEL3 x *S. elaeagnifolium* ELE2 (B).



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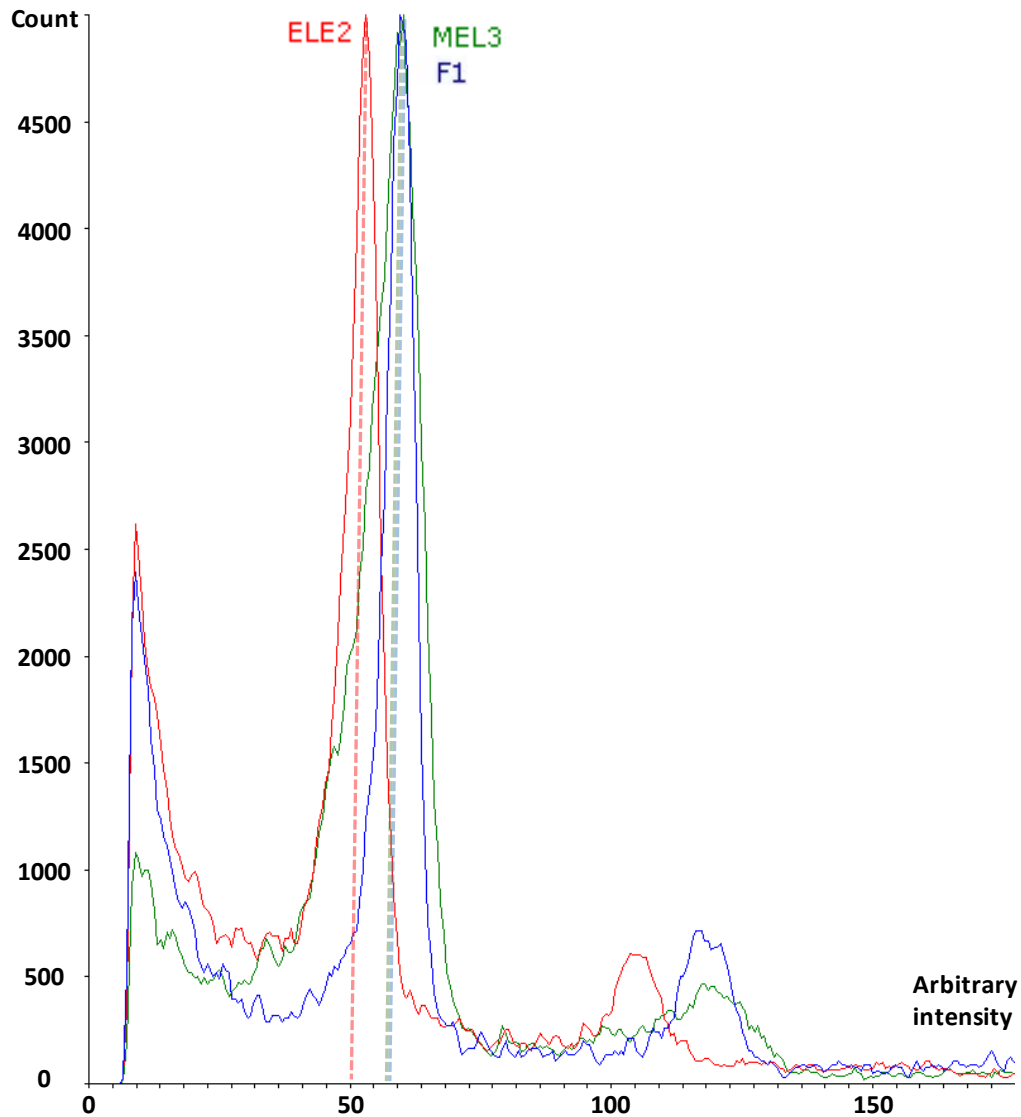
767 **Figure 4**

768 Phenolics profile of fruits of *S. melongena* MEL3 (A), *S. elaeagnifolium* ELE2 (B), and

769 *S. melongena* MEL3 × *S. elaeagnifolium* ELE2 F1 hybrid (C).

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773 **Figure 5**

774 Flow cytometry histogram of the relative nuclear DNA contents of: *S. melongena*

775 MEL3 (green), *S. elaeagnifolium* ELE2 (red) and F1 interspecific hybrid *S. melongena*

776 MEL3 × *S. elaeagnifolium* ELE2 (blue). The x-axis represents the proportional

777 fluorescence intensity level to the nuclear DNA quantity; the position of the main peak

778 reflects the ploidy level. The y-axis indicates the number of nuclei analyzed.