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Additional Information

1 **Phenological phases of flowering in hop (*Humulus lupulus* L.) and their**
2 **correspondence with microsporogenesis and microgametogenesis**

3

4 **Running head:** Microsporogenesis and microgametogenesis in hop

5

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16

17

18 **Abstract**

19 Hop (*Humulus lupulus* L.) suffered, as many other crops, a shrinkage of its intraspecific
20 agrobiodiversity. Biotechnological methods of breeding would offer new opportunities
21 to produce improved varieties with interesting phytochemical profiles and adaptable to
22 the challenging conditions of climate change. Doubled haploid (DH) technology could
23 be a useful tool to increase hop agrobiodiversity but, unfortunately, there is a complete
24 lack of information about hop flower biology. For this reason, the main aim of this work
25 is the study of the different phenological phases of flowering in hop and the
26 corresponding developmental stages of microspores/pollen grains contained therein.
27 The results obtained allowed the identification of morphological markers (anther and
28 flower bud length), easy and fast to measure, that would speed up the selection of
29 flower buds containing the highest percentage of vacuolated microspores and young
30 pollen, the stages considered in most species as the most responsive to androgenesis. A
31 further result, derived from the flower bud and anther microscopical observation,
32 evidenced the increase of lupulin glands on bud and anther surface as the bud proceeds
33 in development from microsporogenesis to microgametogenesis.

34

35 **Keywords:** anther length; bud length; lupulin glands; microspore; pollen; flower
36 development.

37

38 **Abbreviations**

39 DIC: Differential Interference Contrast

40 DH: Doubled haploid

41

42 **Introduction**

43

44 Hop (*Humulus lupulus* L.) is a dioecious, anemophilus species belonging to the
45 Cannabaceae family. In recent times, increasing demand of craft beers with innovative
46 flavors and the widening of beer consumption (Barth-Hass, 2016) has resulted in a
47 greater general attention for hop culture, and in particular, in the research of hop
48 characterized by peculiar phytochemical profiles. This adds to the need for adaptation of
49 this crop to the challenging conditions of climate change, as it happens for other beer
50 ingredients such as barley (Xie *et al.*, 2018). Unfortunately, during its domestication,
51 hop suffered from a shrinkage of intraspecific agrobiodiversity (Patzak *et al.*, 2010a;
52 Patzak *et al.*, 2010b), which makes these goals even more challenging. In this context,
53 recent studies revealed the occurrence of different types of aneuploidy and chromosome
54 rearrangements that contribute to segregation distortion, a phenomenon that seriously
55 makes hop breeding difficult (Easterling *et al.*, 2018). To overcome these limitations,
56 we are still far from having the biotechnological toolbox already available for other
57 crops. Although the interest of brewing industry for hop resides in the female flower
58 cones, rich in lupulin glands with bitter compounds, males are essential for breeding
59 new hop varieties, as well as for developing advanced biotechnology-based breeding
60 tools.

61

62 One of these tools is DH technology. In general, high yields in intensive horticulture are
63 based on the use of hybrids between homozygous (pure) lines. Pure lines are
64 traditionally obtained through classical techniques of self-fertilization and selection,
65 which involves many years of work and important economic investments. As a much
66 faster and cheaper alternative, pure lines can also be generated by DH technology. DHs

67 are derived from haploid microspores reprogrammed towards embryogenesis. This
68 reduces the process to a single generation, with huge savings of time and economic
69 resources. These advantages make DHs a very interesting tool for breeding companies,
70 which already use them in those crops where the technology is available. Therefore, the
71 development of a reliable protocol for DH production in hop would be a powerful tool
72 to speed up applied hop breeding. However, it is really surprising that, to the best of our
73 knowledge, there is nothing published about DH production in hop. This means that in
74 order to develop such a DH method, we must start from the very beginning, which is the
75 understanding of hop male flower, microspore and pollen development, and its
76 particularities. Unfortunately, there is not much information about microsporogenesis
77 and microgametogenesis. Neither the classical studies of Ehara, (1955, 1956) on hop
78 morphology and development nor the extensive study of Shephard *et al.*, (2000) on hop
79 flower development covered microspore and pollen formation. Only some palynological
80 data are available, which define hop pollen grains as ~20 µm in size, circular to ovate
81 with very thin and scabrate exine, and triporate, with slightly protrusive 2 µm pori that
82 form a subtle annulus (Berger, 2018). Intine is also very thin, although it thickens
83 beneath pores, forming an oncus.

84

85 The most efficient way to produce DHs is the experimental induction of androgenesis *in*
86 *vitro*, either by anther culture or by isolation and culture of microspores in liquid
87 medium. This can only be achieved in a narrow developmental window during
88 microsporogenesis and microgametogenesis. In particular, this window is restricted, in
89 all known species, to the transition from vacuolated microspores to young, bicellular
90 pollen grains (Seguí-Simarro, 2010). Therefore, the first step to develop a DH protocol
91 in hop would be to characterize male flower development, and to find morphological

92 and easily measurable parameters to identify flower buds and anthers with
93 microspores/pollen at the right developmental window. In this work, we present a study
94 of male hop flower development, characterizing buds, anthers and microspores/pollen at
95 all developmental stages from meiocytes to mature pollen, which would correspond to
96 stages 8-10 of hop male flower development according to Shephard et al., (2000). Based
97 on this study, we propose a criterion to identify the buds containing microspores at the
98 inducible stages, in order to maximize the efficiency of further *in vitro* anther or
99 microspore culture. In order to check the influence of genotype in the measured
100 parameters, this study has been carried out in parallel in three different hop Italian
101 genotypes. To the best of our knowledge, this is first study that reports, firstly, the
102 characterization of the microspore/pollen grain developmental stages in hop, but also
103 that exists a clear correlation between hop microspore/pollen grain developmental stage
104 and male flower bud/anther size. Then, the results presented herein would represent the
105 first step towards the establishment of the optimal parameters to initiate androgenesis
106 induction in hop.

107

108 **Materials and methods**

109

110 *Plant material*

111 Male flowers were isolated from three hop accessions (MA1, Prismi 2, Santa Clara).
112 Donor plants were grown in the collection field of Manaro sul Panaro (Modena, Italy)
113 during 2018. Plants bloomed and samples were taken in July 2018.

114

115 *Characterization of flower bud, anther, microspore and pollen development*

116 In order to study the parallel development of microspore/pollen grains and anthers, 20
117 flower buds per genotype were selected. 50 anthers were randomly isolated, measured
118 from the filament insertion to the apical end with a stereomicroscope equipped with a
119 calibrated eyepiece, separated in dimensional classes, squashed in a glass slide with 10
120 μl of 7.5 $\mu\text{g/ml}$ 4', 6-diamidino-2-phenylindole (DAPI), and observed with a Zeiss
121 Axiovert 40 CFL inverted microscope. For each anther, the developmental stage of 200
122 randomly chosen microspores/pollen grains was determined. Data collected were used
123 to calculate percentages of each stage with respect to the total. For each genotype the
124 average anther and flower bud lengths were calculated, correlated and a correlation
125 function was built. Finally, in order to confirm the validity of the correlation function,
126 50 flower buds were measured with the stereomicroscope from the pedicel insertion to
127 the top of the corolla and divided into dimensional classes. For each dimensional class,
128 20 anthers were isolated and the developmental stage of 200 randomly chosen
129 microspores/pollen grains was determined as described above. Data collected were used
130 to calculate percentages, and images were taken for characterization of microspore and
131 pollen developmental stages. In addition, 50 male flower buds per genotype were
132 observed with a stereomicroscope to evaluate the presence of trichome hairs and lupulin
133 glands on their bud and anther surface.

134

135 **Results and Discussion**

136

137 **Characterization of microspore and pollen development**

138 First, we studied the parallel development of microspores/pollen grains (Figures 1A-G,
139 A'-G'), anthers (Figures 1A''-G'') and flower buds (Figures 1A'''-G'''), covering from
140 tetrads to mature pollen grains. Tetrads contained four independent microspores still

141 enclosed within the post-meiotic cell walls (Figures 1A-A'). At this stage, anthers were
142 small (around 0.5 mm length) and green-yellowish (Figure 1A''), buds were also small
143 (around 1 mm), green and fusiform (Figure 1A'''). Young microspores, upon release
144 from the tetrad, were slightly oval and presented a still thin pollen coat and a centrally
145 located nucleus (Figures 1B, B'). Anthers enlarged dramatically, almost doubling its
146 length with respect to the previous stage (Figure 1B''). The increase in size of anthers,
147 however, was not reflected in a similar size increase in buds, which presented a similar,
148 or slightly larger size (Figure 1B'''). Mid microspores (Figures 1C, C') were similar to
149 young microspores in terms of shape and size, the only remarkable difference being the
150 displacement of the nucleus to the cell periphery, as a consequence of the formation of
151 the central vacuole, typical of this stage. Consequently, anthers (Figure 1C'') and buds
152 (Figure 1C''') underwent minimal changes in size, shape and color. At the vacuolated
153 (mature) microspore stage, remarkable changes were observed. Microspores increased
154 in size and adopted a round morphology (Figure 1D). In addition, a thicker microspore
155 coat was evidenced in DIC images. In fluorescence images (Figure 1D'), an increase in
156 autofluorescence of this coat suggested a compositional change as well. DAPI images
157 also evidenced a nucleus closely apposed to the plasma membrane, indicating the
158 imminence of the first pollen mitosis. In parallel, anthers became larger. Buds enlarged
159 too, adopting an oval shape.

160

161 The transition of vacuolated microspores to young bicellular pollen grains (Figures 1E,
162 E') involved the formation of a vegetative and a generative cell, defined by different
163 levels of chromatin condensation in their nuclei, as revealed by the different intensity of
164 DAPI staining. Typically, the vegetative nucleus, transcriptionally active during pollen
165 development, presents lower DNA condensation, whereas the generative nucleus,

166 precursor of the sperm cells and transcriptionally inactive, presents highly condensed
167 DNA. This transition implied no apparent changes in pollen size or shape, but the
168 formation of a thicker and denser pollen coat, thickened at the apertures. It also implied
169 a notable enlargement of anthers, which adopted a pale yellow color (Figure 1E''), and
170 of flower buds (Figure 1E'''). The mid bicellular pollen stage was defined by a
171 thickening of the coat at the level of apertures, now visible at DIC (Figure 1F) and
172 fluorescence images (Figure 1F'), a movement of the generative nucleus from the cell
173 periphery to a central position, a transition of anther color from pale yellow to yellow as
174 pollen matures (Figure 1F''), and a progressive growth of both anthers and flower buds
175 (Figure 1F'''). At the mature pollen stage, enlarged and densely filled grains were found
176 (Figure 1G). DAPI staining revealed the presence of three nuclei (Figure 1G'),
177 indicative of the occurrence of the second pollen mitosis. Anthers at this stage (Figure
178 1G'') were nearly 2 mm long and yellow, indicative of pollen maturity. In turn, flower
179 buds were wider, and the separation between sepals became more evident (Figure
180 1G'''), which was indicative of imminent anthesis. Further stages consisted on anthesis
181 and anther dehiscence, with no changes in pollen grains other than desiccation (data not
182 shown).

183

184 **Development of lupulin glands in anthers and male flower buds**

185 During all the studied stages of flower bud development, buds remained closed,
186 changing from a fusiform (at early stages) to an oval shape, typical of late stages, in
187 agreement with previous studies that described that hop male flowers open only after
188 pollen maturity has been achieved (Shephard *et al.*, 2000). During all these stages,
189 trichome hairs were abundantly observed on their surface, but no changes in abundance
190 or bulk number were noticed. We also observed the presence of lupulin glands on the

191 bud surface at all stages. However, their presence was scarce at the first stages and
192 increased notably at the transition from vacuolated microspores to pollen grains (arrows
193 in Figures 1A''-G''), coinciding with the increase in bud size and the change in shape.
194 We also found lupulin glands on the surface of anthers at all stages. Again, their number
195 and size increased remarkably in the transition from microspores to pollen and onwards.
196 These newly formed lupulin glands appeared only at the interthecal groove region
197 (arrows in Figures 1A''-G''), as previously suggested (Shephard et al., 2000). Lupulin
198 glands produce lupulin, composed by essential oils, bitter acids and polyphenols, that
199 contribute to beer bitterness and flavor. Our observations on lupulin glands confirm the
200 results of Nagel *et al.*, (2008), who measured a significant presence of polyphenols, and
201 specifically, of xanthohumol in hop male flowers. According to our observations, the
202 presence of xanthohumol would be due to the increase in lupulin glands observed on the
203 bud surface, but principally, on the interthecal grooves of anthers.

204

205 **Morphological markers to identify anthers and buds enriched in vacuolated** 206 **microspores and young pollen grains**

207 As explained above, male flowers do not open until the end of microgametogenesis. In
208 addition, we did not observe any macroscopic change during the entire process studied,
209 other than size and a slight widening of the flower bud. Therefore, we focused on these
210 changes in order to establish criteria to easily identify buds at the right developmental
211 window to induce androgenesis. In the three accessions studied, young anthers (1.5-1.8
212 mm) were characterized by a very homogeneous population of meiocytes/tetrads,
213 comprising 100% of the population in two out of three genotypes. However, as soon as
214 microspores were released from tetrads, anther locules presented a coexisting
215 heterogeneous population of microspores at two or three different stages. Heterogeneity,

216 as is usual for all plant species studied, increased upon gametogenesis, with up to four
217 different stages in the same anther. To identify the intervals containing the
218 microspore/pollen stages most responsive to androgenesis induction (around the first
219 pollen mitosis), we selected those containing mostly vacuolated microspores and young
220 bicellular pollen (bolded rows in Tables 1, 2). In cases where two intervals contained a
221 clear majority of these stages, we selected the range with a majority of vacuolated
222 microspores with respect to young pollen, since they are at a stage immediately prior to
223 mitosis, and would enter it soon, while young pollen would be exiting this stage. MA 1
224 anthers contained these stages at the 1.6-1.8 mm interval, whereas Prismi 2 contained
225 them at the 1.7-1.9 mm interval and Santa Clara at the 1.8-2.0 mm interval. The slight
226 genotype-dependent discrepancy in bud and anther size stresses the need for this type of
227 studies in each particular genotype, as for other species (Parra-Vega *et al.*, 2013; Salas
228 *et al.*, 2012; Seguí-Simarro and Nuez, 2005).

229 As seen, anther length increased in parallel to bud length for the three genotypes.
230 Indeed, we plotted the paired bud and anther lengths (Figure 2) and they matched in all
231 cases to a linear model with remarkably high R^2 coefficients (0,9358 for MA 1, 0,9319
232 for Prismi 2, 0,9009 for Santa Clara). Dioecy implies that male buds contain only
233 anthers. This, together with the fact that buds remain closed up to the mature pollen
234 stage, likely contributes to this high correlation. Since all three genotypes showed the
235 same linear model, it was possible to develop the following correlation function, $y =$
236 $0.9643x - 0.4722$, that will be very useful to infer the anther length (y), knowing the
237 flower bud length (x). Finally, by correlating the percentage of microspores at the
238 different developmental stages with flower bud length, the validity of this function was
239 confirmed. Specifically, the flower bud dimensional class containing the highest
240 percentage of vacuolate microspores (2.1-2.3 mm for MA1 and Prismi2; 2.5-2.7 for

241 Santa Clara; Table 2) corresponded, using the formula mentioned above, to the most
242 suitable anther length (1.6-1.8 mm interval for MA1, 1.7-1.9 mm interval for Prismi2
243 and 1.8-2 mm interval for Santa Clara). This is positive in order to be able to use both
244 anther and bud length indistinctly as a reliable criterion, since in other species, buds
245 open or stop grow at intermediate stages of microspore/pollen development (Parra-Vega
246 et al., 2013; Salas et al., 2012; Seguí-Simarro and Nuez, 2005), which precludes such
247 use. However, the strong correlation between buds and anther length observed for the
248 three hop genotypes, makes us propose to use exclusively bud length as the criterion to
249 identify the appropriate stages. This would constitute a fast and easily measurable
250 marker for suitable stages. In case of doubt, or as a second confirmation, anther length
251 or the abundant presence of lupulin glands on the anther groove could also be used.

252

253 **Conclusion**

254 This work is, to the best of our knowledge, the first detailed characterization of the
255 different microspore/pollen stages during hop male flower development. It represents a
256 first step towards the development of DH technology in hop. First of all, a detailed
257 description of male flowers has been provided, with a particular focus on development
258 of microspores and pollen grains and their features. Furthermore, a correlation between
259 microspore/pollen developmental stages and flower bud/anther size was established. We
260 also showed that in the three genotypes studied, vacuolated microspores and young
261 bicellular pollen are contained in anthers with slightly different lengths. By means of
262 microscopical analysis, it was possible to evidence that lupulin glands on buds and
263 anthers surface, increase in parallel to bud and anther development. Thanks to these
264 results, it will be easier and faster to select flower buds containing microspores at the

265 most suitable stage of development to induce androgenesis. This, in turn, may allow for
266 the development of innovative techniques such as DH technology for hop breeding.

267

268 **Author contribution**

269 CML and ACS performed all the experimental work required for this study. MR
270 contributed to sample harvesting and preparation, BC helped in sample preparation,
271 analysis of results and writing of the manuscript. JMSS designed the experiments,
272 analyzed the results and wrote the manuscript.

273

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277

278 **Declarations of interest:** none

279

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320

321

322 **Tables**

323

324 **Table 1.** Distribution of the stages of microspore/pollen development at different
 325 lengths, during anther development in MA 1, Prismi 2 and Santa Clara. The number of
 326 microspores/pollen grain units counted at each stage is expressed as the mean \pm s.d. of
 327 the percentages of total counted microspores/pollen grains. M+T: meiocytes + tetrads;
 328 YM: young microspores; MM: mid microspores; VM: vacuolated microspores; YP:
 329 young pollen grains; MP: mid pollen grains; LP: late (mature) pollen grains. The bolded
 330 row represents the anther length where a majority of vacuolated microspores can be
 331 found.

MA 1							
Anther length (mm)	M+T	YM	MM	VM	YP	MP	LP
1.0-1.2	90.5 \pm 7.4	9.5 \pm 7.4					
1.3-1.5		49.5 \pm 14.47	33.2 \pm 8.3	17.4 \pm 7.2			
1.6-1.8			6.4\pm3.7	73.2\pm8.4	20.4\pm12.0		
1.9-2.1			3.0 \pm 0.5	12.8 \pm 0.5	84.2 \pm 0.0		
\geq 2.2				12.4 \pm 1.1	64.6 \pm 0.7	19.0 \pm 0.8	4.0 \pm 1.3

Prismi 2							
Anther length (mm)	M+T	YM	MM	VM	YP	MP	LP
1.1-1.3	100 \pm 0						
1.4-1.6	61.9 \pm 15.6	32.4 \pm 12.3	5.7 \pm 3.3				
1.7-1.9			18.3\pm7.5	60.8\pm13.3	20.9\pm12.3		
\geq 2			0.8 \pm 0.5	7.0 \pm 3.1	70.9 \pm 4.5	19.9 \pm 5.2	1.5 \pm 0.9

Santa Clara							
Anther length (mm)	M+T	YM	MM	VM	YP	MP	LP
1.1-1.3	100 \pm 0						
1.5-1.7		39.1 \pm 16.9	32.1 \pm 10.2	28.8 \pm 13.2			
1.8-2.0			1.3\pm0.3	85.0\pm11.3	13.7\pm11.6		
2.1-2.3			0.8 \pm 0.0	34.1 \pm 1.1	65.1 \pm 1.0		
>2.4				12.3 \pm 0.1	58.0 \pm 0.5	27.7 \pm 0.4	2 \pm 0.2

332

333

334 **Table 2.** Distribution of the stages of microspore/pollen development at different
 335 lengths, during bud development in MA 1, Prismi2 and Santa Clara. The number of
 336 microspores/pollen grain units counted at each stage is expressed as the mean \pm s.d. of
 337 the percentages of total counted microspores/pollen grains. M+T: meiocytes + tetrads;
 338 YM: young microspores; MM: mid microspores; VM: vacuolated microspores; YP:
 339 young pollen grains; MP: mid pollen grains; LP: late (mature) pollen grains. The bolded
 340 row represents the bud length where a majority of vacuolated microspores can be found.
 341

MA 1							
Bud length (mm)	M+T	YM	MM	VM	YP	MP	LP
1.5-1.7	82.5 \pm 20.3	17.5 \pm 10.1					
1.8-2.0		52.1 \pm 19.2	20.9 \pm 9.0	27 \pm 14.3			
2.1-2.3				80.0\pm1.2	20.0\pm1.2		
2.4-2.6				34.5 \pm 18.7	65.5 \pm 18.7		
\geq 2.6				12.4 \pm 0.7	65.1 \pm 0.7	18.6 \pm 0.8	430 \pm 0.8

Prismi 2							
Bud length (mm)	M+T	YM	MM	VM	YP	MP	LP
1.5-1.7	100 \pm 0						
1.8-2.0	34.1 \pm 23.6	51.9 \pm 18.3	11.2 \pm 3.9	2.8 \pm 1.6			
2.1-2.3			8.4\pm1.5	78.3\pm5.6	13.3\pm7.1		
\geq 2.4			9.1 \pm 6.6	16.3 \pm 7.6	59.5 \pm 10.1	13.9 \pm 6	1.3 \pm 0.8

Santa Clara							
Bud length (mm)	M+T	YM	MM	VM	YP	MP	LP
1.6-1.8	100 \pm 0						
1.9-2.1	47.8 \pm 27.7	48.0 \pm 25.3	4.2 \pm 2.8				
2.2-2.4		9.8 \pm 5	37.9 \pm 12.8	52.3 \pm 17.0			
2.5-2.7			1.3\pm0.3	85.0\pm11.3	13.7\pm11.6		
$>$ 2.8			0.4 \pm 0.2	23.2 \pm 6.3	61.6 \pm 2.1	13.9 \pm 8	1 \pm 0.6

342

343 **Figure legends**

344

345 **Figure 1.** Changes during microspore/pollen (A-G: DIC images; A'-G': DAPI
346 staining), anther (A''-G''), and bud development (A'''-G''') in hop accession MA 1. A-
347 A''' : meiocytes and tetrads. B-B''' : Young microspores. C-C''' : Mid microspores. D-
348 D''' : Vacuolated microspores. E-E''' : Young bicellular pollen. F-F''' : Mid pollen. G-
349 G''' : Mature pollen. ap: aperture; ex: exine microspore/pollen coat; gn: generative
350 nucleus; n: nucleus; s: sperm cell; vn: vegetative nucleus. Arrows point to lupulin
351 glands on the surface of anthers and flower buds. Bars in A-G and A'-G': 10 μ m; A''-
352 G'' and A'''-G''' : 1 mm.

353

354 **Figure 2.** Correlation between anther and flower bud length in hop male buds of MA 1
355 (A), Prismi 2 (B) and Santa Clara (C). A regression line and the corresponding
356 R^2 coefficient are shown.

357



