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**Intra-specific variation in the little-known Mediterranean plant *Ptilostemon casabonae* (L.) Greuter analysed through phytochemical and biomolecular markers**

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(Article begins on next page)

1 **Intra-specific variation in the little-known Mediterranean plant *Ptilostemon***  
2 ***casabonae* (L.) Greuter analysed through phytochemical and biomolecular**  
3 **markers**

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16

17 **Abstract**

18 *Ptilostemon casabonae* (L.) Greuter is a Mediterranean endemism traditionally used for its health-  
19 giving properties. Little is known about this species, therefore this study provides additional  
20 information about the phytochemical and biomolecular patterns of this plant, to have a combined  
21 fingerprint as a taxonomic tool. Several *P. casabonae* specimens were therefore collected from three  
22 different sites, two from Sardinia (Italy) and one from Corsica and the hydroalcoholic extracts of their  
23 aerial parts were investigated through HPLC-PDA-MS/MS analysis to study the phenolic  
24 composition. Quercetin, luteolin, kaempferol, apigenin and diosmetin *O*-glycosides, and  
25 caffeoylquinic acid derivatives were found as main components. Samples from the three sites showed  
26 similar phenolic profiles, although statistical analyses highlighted some quantitative differences for  
27 several compounds.

28 The biomolecular analysis included amplification and sequencing of *ITS*, *5S-rRNA-NTS* and *psbA*  
29 regions. No difference was found in the nucleotides among the *P. casabonae* samples from different  
30 geographical origins; however, a comparison with other *Ptilostemon* species sequences from  
31 Genbank, revealed an inter-species variability of *ITS* and *psbA* regions.

32 The combination of the results of the phytochemical and biomolecular studies provide information  
33 on *P. casabonae* useful to depict this little-known plant, which can also be applied for future

34 investigations and to obtain a fingerprint of it. Moreover, the stability of the phenolic profile within  
35 the species affords to identify a set of specialised metabolites useful for its chemotaxonomic  
36 characterization. At the same time, the stability of the biomolecular profile of *P. casabonae*, and the  
37 identification of sequences specific for this species, enables to identify useful biomolecular markers  
38 to distinguish it unequivocally.

39

40 **Keywords:** *Ptilostemon casabonae* (L.) Greuter, Compositae, HPLC-PDS-MS/MS, PCR,  
41 sequencing, polyphenols, *ITS* sequence, *psbA* sequence, *5S-rRNA-NTS* sequence

42

## 43 1. Introduction

44 *Ptilostemon casabonae* (L.) Greuter. (Compositae) ([www.theplantlist.org](http://www.theplantlist.org)) belongs to the genus  
45 *Ptilostemon* Cass., which is part of the larger informal “*Cynara* group”, included in the *Carduinae*  
46 subtribe (*Cardueae* tribe) (Susanna et al., 2006; Susanna and Garcia-Jacas, 2009; Vilatersana et al.,  
47 2010; Barres et al., 2013). The *Ptilostemon* genus is distributed throughout the Mediterranean area,  
48 from Crimea and Turkey to the Iberian Peninsula and Morocco. The genus includes 15 species, among  
49 them *Ptilostemon casabonae* (L.) Greuter, a central Mediterranean endemism mainly localized in  
50 Sardinia (Italy), Corsica and the Hyères islands (France). The limited geographic distribution of *P.*  
51 *casabonae* is peculiar, since usually “thistles” are widespread colonizing weeds (Médail and  
52 Verlaque, 1997; Vilatersana et al., 2010; Marengo et al., 2015). *P. casabonae* is a monocarpic  
53 perennial spiny herb with sparsely arachnoid-hairy to glabrescent stem and lanceolate to linear-  
54 lanceolate leaves, entire or very slightly sinuate (Tutin et al., 1968; Marengo et al., 2015). It is largely  
55 spread in Sardinia and Corsica, where it grows spontaneously, preferring dry and open habitats, with  
56 riverbed gravel, screes or mining dumps as secondary habitats (Tutin et al., 1968; Ferrauto et al.,  
57 2016). *P. casabonae* is the only species of the *Ptilostemon* genus growing in Sardinia and Corsica  
58 (Pignatti, 1982). The aerial parts of this species are traditionally used in Sardinia as intestinal  
59 antispasmodic. Additionally, the boiled sprouts and immature flower heads are considered edible  
60 (Atzei, 2003).

61

62 To the best of the authors’ knowledge, no phytochemical studies on *P. casabonae* have to date been  
63 reported. The literature gives acetylenes, triterpenes, sesquiterpenes and lignans as the main chemical  
64 constituents of the *Ptilostemon* species, but no information is available concerning the flavonoid and  
65 phenolic acid composition (Bohlmann et al., 1974; Bohlmann and Ziesche, 1980; Bruno et al., 2001;  
66 Janačković et al., 2002; Djordjevic et al., 2008; Di Stefano and Pitonzo, 2012). Conversely, molecular  
67 phylogenetic analyses on the *Cardueae* tribe are available, and provide some DNA barcoding  
68 sequences of species belonging to the *Ptilostemon* genus including *P. casabonae* from Southern  
69 Corsica (Garcia-Jacas et al., 2002; Susanna et al., 2006; Vilatersana et al., 2010; Barres et al., 2013).  
70 The aim of the present study is to contribute to improving knowledge of this little-studied species, by  
71 combining phytochemical and biomolecular approaches in order to obtain a representative fingerprint  
72 of the investigated plant that can be adopted as a taxonomic tool.

73 Samples of the aerial parts of *P. casabonae* from three different sites, two in Sardinia (Gennargentu  
74 and Iglesias) and one in Southern Corsica (Bocca di Tana) were therefore collected and submitted to  
75 phytochemical and biomolecular investigation. The combination of these two different approaches

76 can provide more information on this species and a reliable fingerprint of the plant useful for the  
77 unequivocal identification of *P. casabonae* and its distinction from closely related species.  
78 Similarities and dissimilarities in the chemical and molecular patterns in the samples from the three  
79 harvesting sites were therefore investigated and the variability/stability of the investigated DNA  
80 regions might give useful molecular markers of *P. casabonae*.

81 The hydroalcoholic extracts from this species were analysed by HPLC-PDA-MS/MS to obtain useful  
82 information about the non-yet-investigated polyphenolic fraction, whose composition can be used to  
83 characterize this endemic species and its intraspecific variations with geographical origin.

84 At the same time, three specific DNA regions were amplified, sequenced and compared to obtain  
85 diagnostic molecular markers for *P. casabonae* and to verify the variability/stability of samples from  
86 different geographical origins. The nuclear internal transcribed spacer (*ITS*) and *5S-rRNA-NTS* genes  
87 and the chloroplast photosystem II protein D1 (*psbA-trnH*) genes were analysed. With the exception  
88 of *5S-rRNA-NTS* region, these sequences are DNA barcoding genes, used to discriminate plant  
89 species (Hebert et al., 2003; Galimberti et al., 2013; Dong et al., 2014). Conversely, the *5S-rRNA-*  
90 *NTS* sequence is used for plant DNA fingerprinting, although it is not yet considered a barcoding  
91 gene (Gnavi et al., 2010; Kress, 2017; Marengo et al., 2017b). The *PsbA-trnH* and *5S-rRNA-NTS*  
92 genes of *P. casabonae* are sequenced here for the first time.

93

## 94 **2. Results and discussion**

95

### 96 2.1. Phytochemical analysis

97

#### 98 2.1.1. Chemical composition by HPLC-PDA-MS/MS

99 The phytochemical investigation of the hydroalcoholic extracts of *Ptilostemon casabonae* aerial parts  
100 from Sardinia (Gennargentu and Iglesias) and Corsica (Bocca di Tana) was carried out by HPLC-  
101 PDA-MS/MS and revealed a remarkable abundance of phenolic compounds, and in particular a  
102 complex polyphenolic fraction. Moreover, all the investigated extracts show a similar chemical  
103 composition (Fig. 1 and Fig. S1).

104 In agreement with existing reports on the polyphenols of related species, flavonoids are the most  
105 representative group, in particular *O*-glycosides of quercetin, luteolin, kaempferol, apigenin and  
106 diosmetin, and caffeoylquinic acid derivatives have been reported (Jordon-Thaden and Louda, 2003;  
107 González-Tejero et al., 2008; Li et al., 2014; Ha et al., 2015; Ma et al., 2016; Marengo et al., 2017a).

108 Chromatographic profiles, UV spectra, and mass spectral information, acquired for 10 samples per  
109 site, enabled 25 informative compounds to be detected. The UV spectra obtained for each peak  
110 provided a first indication of the compound class. In addition, the molecular weight of each peak was  
111 obtained from their mass spectral pattern, through the complementary correspondence between the  
112 positive and negative pseudomolecular ions in ESI<sup>+</sup> and ESI<sup>-</sup>. The Product Ion Scan analysis of the  
113 pseudomolecular ions under investigation (in both ESI<sup>+</sup> and ESI<sup>-</sup> modes) provided diagnostic  
114 fragments for each molecule. Lastly, the identity of 15 compounds in the extract was confirmed by  
115 the co-injection of authentic standards, whereas 10 peaks were putatively identified by comparison  
116 with literature data (Table 1).

117 In particular, compounds for which reference standards were not available, were tentatively identified  
118 through their tandem mass spectrometry fragmentation pattern, as reported in Marengo et al., 2017a.  
119 This approach also provides further structural information on unknown compounds. As an example,  
120 all the phenolic acid derivatives (mainly caffeoylquinic acid derivatives), compounds **5**, **8**, **14**, **15**, **18**,  
121 **20**, were tentatively identified by their UV spectral data (UV<sub>max</sub>=330nm) and pseudomolecular  
122 diagnostic fragments at 163 m/z and 191 m/z in ESI<sup>+</sup> and ESI<sup>-</sup> ionization modes (Marengo et al.,  
123 2017a; Martini et al., 2017). *p*-coumaric acid containing chlorogenic and quinic acid derivatives  
124 (compounds **17**, **19**) were putatively identified on the basis of their UV maximum absorption at about  
125 310 nm, and pseudomolecular diagnostic fragments in accordance with those reported by Clifford  
126 and co-workers (Clifford et al., 2006). Finally, peaks **8** and **12** were tentatively attributed to quercetin  
127 *O*-glycosides derivatives, since their UV spectrum and MS/MS fragmentation pattern are similar to  
128 those of quercetin derivatives (Marengo et al., 2017a).

129 The detected compounds have been found in other “thistle” species (Jordon-Thaden and Louda, 2003;  
130 Li et al., 2014; Marengo et al., 2017a, 2018), but, to the best of the authors’ knowledge this is the first  
131 time that these specialised metabolites have been identified in *P. casabonae* and in general in the  
132 *Ptilostemon* genus (Bohlmann et al., 1974; Bohlmann and Ziesche, 1980; Bruno et al., 2001;  
133 Janačković et al., 2002; Djordjevic et al., 2008; Di Stefano and Pitonzo, 2012). The analysis of the  
134 composition of these specialised metabolites can be very useful in the taxonomic characterization of  
135 *P. casabonae*, to discriminate it from other closely related species and to define a representative  
136 chemical pattern for the species. Phenolic compounds, in particular flavonoids, have a wide structural  
137 diversity, diffuse occurrence, chemical stability and have been already isolated in large scale from  
138 Compositae species and used as taxonomic markers at lower hierarchical levels (Emerenciano et al.,  
139 2001; Míka et al., 2005). Moreover, polyphenols have been shown to be diagnostic markers to  
140 characterize species within *Hieracium rohacsense* Kit. ex Kit. group (Švehlíková et al., 2002), *Rosa*

141 L. species belonging to the section *Gallicanae* (Sarangowa et al., 2014), species for the genus *Drosera*  
142 L. (Braunberger et al., 2015), *Salvia* L. species (Navaz Kharazian, 2014), *Rhodiola* L. species (Liu et  
143 al., 2013), *Camellia sinensis* (L.) Kuntze hybrids (Li et al., 2010). Phenolic compounds are not only  
144 of interest for their taxonomical value but also for their biological activity. The literature describes  
145 their anti-inflammatory, antibacterial, antioxidant, and enzyme inhibitory activities (Jordon-Thaden  
146 and Louda, 2003; Jeong et al., 2008; Kuklev et al., 2013; Marrelli et al., 2013; Al-Shammari et al.,  
147 2015; Tacchini et al., 2015; Marengo et al., 2018).

148

#### 149 2.1.2. Statistical analysis

150 Since the *P. casabonae* samples investigated showed very similar polyphenolic profiles, Principal  
151 Component Analysis (PCA), an unsupervised multivariate data analysis method, was applied to  
152 evaluate the potential for discrimination among samples from different sites, using the 25 detected  
153 compounds listed in Table 1 as variables (Marengo et al., 2017a).

154 Figure 2 reports score and loading plots. The first component (PC1), which explained 30.4% of the  
155 variation, individually separated samples from Corsica from those from Sardinia, although samples  
156 from Corsica were not clustered in a homogeneous group (Fig. 2A). Discrimination between samples  
157 from the two Sardinian sites (Gennargentu and Iglesias) was less evident. Figure 2A shows that the  
158 second component (26.5% of the variation) barely separated samples from Gennargentu and Iglesias.  
159 The loading plot illustrates the influence of the variables in sample distribution (Fig. 2B). The PCA  
160 results showed that twelve compounds with higher and lower weights in PC1 and PC2 (highlighted  
161 in fig. 2B with black circles and squares, respectively) could be selected, quantified in each individual,  
162 and submitted to ANOVA analysis, to determine whether there were statistically significant  
163 differences among *P. casabonae* samples from Sardinia and Corsica. The variables for which co-  
164 elution occurred were quantified by SRM (Selected Reaction Monitoring) acquisition, based on  
165 specific transitions in ESI<sup>+</sup> for each compound. The SRM quantification showed that some  
166 compounds were present in trace amounts in the extracts (tr<0.05 w/v); luteolin and diosmetin were  
167 therefore not included in the following ANOVA statistical analysis.

168 Among the variables with lower weights in PC1, compounds **12** (quercetin hexoside), **24**  
169 (kaempferol) and **22** (quercetin) were significantly more abundant in statistical terms in samples from  
170 Corsica than in those from Sardinia, while compound **11** (apigenin 7-O-glucoside) was more  
171 abundant in Sardinian samples (in particular from Gennargentu) (Fig. 3). At the same time,  
172 compounds **14** (succinyl-dicaffeoylquinic acid), **18** (succinyl-dicaffeoylquinic acid), and **19**  
173 (succinyl-*p*-coumaroyl-caffeoylquinic acid/succinyl-caffeoyl-*p*-coumaroylquinic acid), positively  
174 correlated with PC1, were more abundant in samples from Sardinia. Although samples from Iglesias

175 and Gennargentu were not easily discriminated, variables with positive and negative correlations with  
176 PC2 were selected, in order to determine similarities or dissimilarities between the two Sardinian  
177 sites. Among the three compounds positively correlated with PC2, compounds **9** (1,5 dicaffeoylquinic  
178 acid) and **4** (quercetin 3-*O*-glucoside) had significantly higher concentrations in samples from  
179 Gennargentu than in those from Iglesias; the same occurred for compound **5** (dicaffeoylquinic acid),  
180 although the concentration difference was not statistically significant. At the same time, compounds  
181 **15** (succinyl-dicaffeoylquinic acid), **23** (apigenin) and **20** (succinyl-succinyl dicaffeoylquinic acid),  
182 which were negatively correlated to PC2, were significantly more abundant in statistical terms in  
183 samples from Iglesias than in those from Gennargentu. These results indicate that, although *P.*  
184 *casabonae* samples from different sites have similar chemical compositions, there are some  
185 differences in the relative abundance of common compounds, in particular between samples from  
186 Sardinia and Corsica. The quantitative differences in Sardinian samples are slight, and thus not  
187 sufficient to state that samples from the two Sardinian sites can clearly be discriminated. These few  
188 intra-species quantitative differences may depend on the geographical origin and on environmental  
189 factors such as temperature, humidity, etc. (Labra et al., 2004; Rahali et al., 2016). A biomolecular  
190 analysis was then performed, to seek specific DNA regions not influenced by the environment as  
191 markers for this species, to reliably evaluate the stability of *P. casabonae*.

192

## 193 2.2. Sequence analysis of *P. casabonae* deriving from the three sites

194 In this study, two nuclear regions (*ITS*, *5S-rRNA-NTS*) and one mitochondrial gene (*psbA-trnH*) were  
195 amplified and sequenced for each *P. casabonae* site. *ITS* and *PsbA* regions are usually used as  
196 barcoding genes to discriminate and identify plant samples. The *ITS* region includes the partial  
197 sequences of the *18S* and *28S* ribosomal RNA genes, and the complete sequences of the internal  
198 transcribed spacers 1 and 2 and the *5.8S* ribosomal RNA gene, while *psbA-trnH* consists of the  
199 noncoding intergenic spacer of the photosystem II protein D1 (Wu et al., 2011; Liu et al., 2014). The  
200 *5S-rRNA-NTS* region is not considered a barcoding gene, but it has recently been used to evaluate the  
201 phylogenetic relationships of some higher plant species. It refers to the non-transcribed spacer of the  
202 gene linked to the *5S-rRNA*, a ribosome component (Rubiolo et al., 2009; Gnani et al., 2010; Marengo  
203 et al., 2017b).

204 The data obtained in this study may be useful to integrate missing information in the GenBank  
205 database, in order to obtain biomolecular markers able to discriminate the species and to verify the  
206 intra-species stability or variability of these sequences.



207 The nucleotide composition and the alignment of all the resulting sequences is shown in Fig.S2. *ITS*,  
208 *5s-rRNA-NTS* and *PsbA* sequences are 729, 324, 504 bp, respectively. The alignment of the three site  
209 sequences suggests a stability of these biomolecular markers for *P. casabonae* species, since no  
210 nucleotide variation was detected among sequences originating from the sites on the two islands  
211 where the species is considered endemic (Sardinia and Corsica).

212 A *P. casabonae ITS* sequence from Corsica (GU907728.1) is already available in GenBank. It is thus  
213 interesting to evaluate similarities or differences with those from Sardinia and from a different  
214 Corsican locality. The alignment of the *ITS* sequences obtained in this study with those from Southern  
215 Corsica: Solaro (Musaei Parisiensis) (BC) shows 98% of query cover and 100% of identity with the  
216 present data; this confirms the stability of this region for *P. casabonae* (Zhang et al., 2000; Vilatersana  
217 et al., 2010).

218 A comparison with *ITS* sequences belonging to other *Ptilostemon* species, taken from GenBank, was  
219 also made. The *P. casabonae ITS* sequence appears more similar (about 7-8 nucleotide position  
220 variations, 99% of identity) to those of *P. abylenis* (Maire) Greuter, *P. dyricola* (Maire) Greuter, *P.*  
221 *rhypaeus* (Pau & Font Quer) Greuter, and *P. strictus* (Ten.) Greuter. The other *Ptilostemon* available  
222 sequences show lower percentages of identity (Vilatersana et al., 2010).

223 Comparison of the *P. casabonae PsbA* sequence to that of the only *Ptilostemon PsbA* sequence (*P.*  
224 *affer* AF129850.1) available in the database shows two variable sites at positions 296 and 335. A  
225 thymine and an adenine are present in the *P. affer* (Jacq.) Greuter sequence, substituted, at the same  
226 positions, by a guanine and a cytosine in the samples studied here. A gap is also present at the far end  
227 of the sequence.

228 These data confirm that the *ITS* region could be considered a good molecular marker for *P.*  
229 *casabonae*, since it shows inter-species variability and an intra-species stability. *PsbA*, likewise,  
230 presents sequence stability among samples from the same species, and nucleotide variation among  
231 different species; however, few sequences are present in the database, and it would be interesting to  
232 increase the dataset to confirm the potential of *PsbA* as barcoding gene for *Ptilostemon* species.

233 Unfortunately, no other *5S-rRNA-NTS* sequences are available in GenBank, making it impossible to  
234 compare them to the nucleotide composition of this region from other species. This could be of  
235 interest for further investigations on this gene, since this is a documented variable region, used also  
236 to distinguish species varieties (Rubiolo et al., 2009; Gnavi et al., 2010; Sun et al., 2014).

237

### 238 3. Conclusions

239 The study reports the first phytochemical investigation of the hydroalcoholic extract of the aerial parts  
240 of the Mediterranean endemic species *P. casabonae*. Interesting compounds were detected in terms  
241 of polyphenols, chiefly flavonoids and phenolic acid derivatives and their presence may support the  
242 traditional use of this herb. The study also provides useful biomolecular markers for this plant,  
243 enabling *P. casabonae* to be discriminated from other *Ptilostemon* species.

244 Despite some differences in abundance, the compounds present in extracts from the three sites were  
245 qualitatively the same. Nor was any difference found in the nucleotide composition of the investigated  
246 *P. casabonae* DNA regions from Sardinia and Corsica, confirming that the compound abundance  
247 variability is due to environmental factors.

248 The combination of chemical and biomolecular patterns was found to be extremely useful to provide  
249 a reliable *P. casabonae* fingerprint that can be used as a taxonomic tool, thanks to the intra-specific  
250 geographical stability of the species. Moreover, the similar chemical pattern of samples from different  
251 sites may be a positive feature for future applications of this plant in the food and well-being fields,  
252 although further investigations will be necessary.

253

## 254 **4. Experimental section**

### 255 4.1. Chemicals

256 HPLC-grade acetonitrile (LC-MS grade), formic acid (> 98% purity), quercetin, apigenin, kaempferol  
257 and rutin were from Sigma Aldrich (Bellefonte, USA). De-ionized water (18.2 MΩ cm) was obtained  
258 from a Milli-Q purification system (Millipore, Bedford, MA, USA). Luteolin, quercetin 3-*O*-  
259 glucoside, kaempferol 3-*O*-rutinoside and apigenin 7-*O*-glucoside were from Extrasynthese (Genay  
260 Cedex, France). Chlorogenic acid, cynarin, 1,5-dicaffeoylquinic acid, 3,5-dicaffeoylquinic acid, 4,5-  
261 dicaffeoylquinic acid, luteolin 7-*O*-glucoside, luteolin 7-*O*-glucuronide, apigenin 7-*O*-glucuronide  
262 and diosmetin were from Phytolab (Vestenbergsgreuth, Germany).

263

### 264 4.2. Plant material

265 *P. casabonae* (L.) Greuter (Compositae) aerial parts were collected from three natural populations:  
266 two sites in Sardinia (Italy) and one site in Corsica (France). In detail, samples from Sardinia were  
267 collected from Gennargentu (OG, 39°53'54.9"N -9°26'27.9"E) and Iglesias (SU, 39°21'45.8"N -  
268 8°32'24.0"E) in June 2017. *P. casabonae* from Corsica was kindly collected by Prof. Felix Tomi  
269 (Université de Corse Pascal Paoli) from Bocca di Tana (Southern Corsica, 41°45.791'N ;  
270 009°02.300'E) in June 2017. Ten specimens were collected from each site. The fresh plant material  
271 was dried at 40°C to constant weight. The plants were identified at the Department of Life and

272 Environmental Sciences, University of Cagliari, Italy, where a voucher specimen was deposited  
273 (CAG-796).

274

#### 275 4.3. Extraction method

276 Five hundred mg of each dried and ground aerial part were submitted to ultrasonic extraction with 10  
277 mL of methanol/water (70:30, v/v), thrice, for 10 min each. The resulting three extracts were  
278 combined and centrifuged at 4000 rpm for 10 min. The supernatant was brought to a volume of 30  
279 mL and filtered through a 13 mm diameter, 0.22  $\mu\text{m}$  pore diameter, hydrophilic PTFE syringe filter,  
280 prior to HPLC-PDA-MS/MS analysis. Each extract was analysed three times and the repeatability of  
281 extract composition was evaluated on at least three plants per site.

282

#### 283 4.4. HPLC-PDA-MS/MS analysis and quantification

284 The chromatographic analysis was conducted on a Shimadzu Nexera  $\times 2$  system equipped with a SPD-  
285 M20A photodiode detector in series to a triple quadrupole Shimadzu LCMS-8040 system provided  
286 with electrospray ionization (ESI) source (Shimadzu, Dusseldorf Germany) as reported by Marengo  
287 et al., 2017a, without any modification. For the UV quantification, apigenin ( $\lambda=340\text{nm}$ ) and quercetin  
288 3-*O*-glucoside ( $\lambda=350\text{nm}$ ) were used for quantification of the relative compounds. 1,5  
289 dicaffeoylquinic acid ( $\lambda=330\text{nm}$ ) and *p*-coumaric acid ( $\lambda=310\text{nm}$ ) were used for quantification of  
290 dicaffeoylquinic acid derivatives and coumaroyl-caffeoylquinic acid derivatives, respectively. Only  
291 when co-elution was present, quantification by Selected Reaction Monitoring (SRM) acquisition in  
292 ESI+ (collision energy: - 35.0 V for ESI+, dwell time: 20) on specific ion products derived from  
293 precursor ion fragmentation was performed. The transitions, used for the quantification, were based  
294 on the Product Ion Scan (PIS) analysis of each standard (Fig. S3). Apigenin 7-*O*-glucoside  
295 (433 $\rightarrow$ 271), luteolin (287 $\rightarrow$ 153), quercetin (303 $\rightarrow$ 153), kaempferol (287 $\rightarrow$ 153) and diosmetin  
296 (301 $\rightarrow$ 258) were used to quantify the relative compounds, quercetin 3-*O*-glucoside (465 $\rightarrow$ 303) was  
297 used to quantify quercetin hexoside since the two compounds showed a similar fragmentation pattern  
298 (Fig. S3). Each standard solution and the extracts were analysed in three replicates. The calibration  
299 curve of 1,5 dicaffeoylquinic acid was prepared with seven different concentrations in the range of  
300 0.1–200  $\mu\text{g}/\text{mL}$ . Five different concentrations were prepared for all other compounds, in the range of  
301 0.1–25  $\mu\text{g}/\text{mL}$  for all of them with the exception of *p*-coumaric acid/diosmetin and apigenin 7-*O*-  
302 glucoside/luteolin whose concentration range was; 0.1–10  $\mu\text{g}/\text{mL}$  and 0.1-5  $\mu\text{g}/\text{mL}$ , respectively. The  
303 determination coefficients were in the range of 0.996-1. The calibration curve equations were as  
304 follows: apigenin (UV):  $y = 69736x - 1125,9$ ; quercetin 3-*O*-glucoside (UV):  $y = 23785x + 1206,7$ ;

305 1,5 dicaffeoylquinic acid (UV):  $y = 56041x - 137821$ ; *p*-coumaric acid (UV):  $y = 190076x + 113336$ ;  
306 apigenin 7-*O*-glucoside (SRM):  $y = 3E+06x + 762083$ ; quercetin 3-*O*-glucoside (SRM):  $y = 1E+06x$   
307  $+ 163544$ ; luteolin (SRM):  $y = 408509x + 268263$ ; quercetin (SRM):  $y = 202793x - 6021,7$ ;  
308 kaempferol (SRM):  $y = 253441x + 116146$ ; diosmetin (SRM):  $y = 2E+06x + 542654$ .

309

#### 310 4.5. DNA extraction, PCR amplification and sequencing

311 Ten milligrams of leaves from each specimen were ground to a fine powder, with the addition of  
312 approximately 5 mg polyvinylpyrrolidone (PVPP, Sigma Aldrich, Bellefonte, USA). Genomic  
313 DNA was isolated from the ground powder using the Nucleospin Plant II Kit (Macherey Nagel,  
314 Düren, Germany) following the manufacturer's instructions. The quantitative and qualitative analyses  
315 of the isolated genomic DNA were assessed by spectrophotometry using a Nanophotometer (Implen  
316 GmbH, Munich, Germany) and by gel electrophoresis. Approximately 20 ng of genomic DNA were  
317 used as a template for PCR amplification, with forward and reverse primers specific for the  
318 amplification of the *ITS*, *5S-rRNA-NTS* and *PsbA* regions (Table S1). Amplification was performed  
319 in a 25  $\mu$ L reaction mixture containing 2.5  $\mu$ L of 10 $\times$  PCR buffer (Thermo-Scientific, Waltham, MA  
320 USA), 0.2 mM deoxynucleotide triphosphates (dNTPs), 20 pmol of forward and reverse primers, and  
321 0.5 U of *Taq* DNA polymerase (Thermo-Scientific, Waltham, MA USA). PCR reactions were carried  
322 out in a T-Gradient Thermalcycler (Biometra, Jena, Germany). Cycling conditions consisted of an  
323 initial 4 min at 94  $^{\circ}$ C, followed by 30 s denaturing at 94  $^{\circ}$ C, 45 s annealing, respectively at 53 $^{\circ}$ , 52 $^{\circ}$ ,  
324 and 56 $^{\circ}$ C for *ITS*, *5s-rRNA-NTS*, and *PsbA*, and 45 s elongation 72  $^{\circ}$ C, repeated for 35 cycles and  
325 with 10 min final extension at 72  $^{\circ}$ C. PCR products were separated by 1.5% (w/v) agarose gel  
326 electrophoresis and visualized by ethidium bromide staining under UV. PCR products were employed  
327 as a template for sequencing (Eurofins Genomics, Vimodrone (MI), Italy). Both DNA strands were  
328 sequenced.

329

#### 330 4.6. Statistical analysis

331 Peak areas (integrated at  $\lambda=330$ nm and scaled to unit variance) obtained from the chemical analysis  
332 were used for the Principal Component Analysis (PCA), to reduce the multivariate space over which  
333 objects were distributed.

334 Abundance differences of characteristic compounds identified by PCA, among samples, were  
335 determined by analysis of variance (ANOVA). One-way ANOVA and post hoc multiple means  
336 comparison (Tukey's range test) were carried out and statistical significance was accepted at  $p<0.05$ .  
337 Both PCA and ANOVA were evaluated using SPSS 15.0 (IBM Corporation) software.

338 Gene sequences were aligned with CLC sequence viewer software using default parameters to check  
339 the integrity of each sample sequence. Consensus sequences, obtained by aligning the individual  
340 sequences of each site, were then aligned by modifying the Gap Opening and Gap Extension Cost  
341 values to 15 and 1, respectively.

342

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346 2018) of the University of Turin, Turin (Italy).

347

348 **Figure captions**

349

350 **Figure 1.** Representative profiles of *P. casabonae* hydroalcoholic extracts from different sites  
351 ( $\lambda=330\text{nm}$ , intensity range: 0-800000 mAU). For compound identities see Table 1. (A) *P. casabonae*  
352 from Gennargentu (OG); (B) *P. casabonae* from San Benedetto (SU); (C) *P. casabonae* from Bocca  
353 di Tana (Southern Corsica)

354

355 **Figure 2.** Principal Component Analysis (PCA) of 30 samples from different *P. casabonae* sites  
356 based on the 25 informative compounds as variables. (A) Score plot of samples from the three *P.*  
357 *casabonae* sites; (B) loading plot of the variables (compound numbers refer to Table1). Black circle  
358 and squares indicate potential discriminating variables for the three sites. (C) Score plot legend.

359

360 **Figure 3.** Concentration (w/v) of discriminating compounds selected by PCA analysis, in extracts  
361 from each site. Bars indicate standard deviation of at least two technical replicates of 10 individuals  
362 per site. Different letters indicate significant differences at  $p<0.05$  for each compound (Tukey range  
363 test).

364

365

366 **Table1.** List of identified and putatively-identified compounds in *P. casabonae* extracts. For each compound the relative  
 367 retention time, UV spectrum, pseudomolecular ions, fragment ions obtained by Product Ion Scan mode (PIS) and  
 368 identified or tentatively-identified compound names are given. Identification Confidence values and references are also  
 369 included.

N°	RT	$\lambda$ max (nm)	Mol. weight g/mol	MS <sup>2+</sup> m/z	MS <sup>2-</sup> m/z	Compound name	IC <sup>b</sup>	References
1 <sup>a</sup>	8.691	325	354	163	191	5- <i>O</i> -Caffeoylquinic acid (Chlorogenic Acid)	1	(Li et al., 2014; Dimitrova-dyulgerova et al., 2015)
2 <sup>a</sup>	15.068	329	516	163	191	1,3 Dicafeoylquinic acid (Cynarin)	1	(Li et al., 2014; Dimitrova-dyulgerova et al., 2015)
3 <sup>a</sup>	21.207	254 352	610	303	301	Quercetin 3- <i>O</i> -rutinoside (Rutin)	1	(Li et al., 2014; Dimitrova-dyulgerova et al., 2015)
4 <sup>a</sup>	21.726	260 352	464	303	301	Quercetin 3- <i>O</i> -glucoside	1	(Li et al., 2014)
5	23.512	325	516	163	191	Dicafeoylquinic acid	3	(Marengo et al., 2017a)
6	23.707	253 350	550	303 159 127 109	336 301 271 135 121	Quercetin malonylhexoside	2	(Marengo et al., 2017a)
7 <sup>a</sup>	23.932	265 344	594	287	285	Kaempferol 3- <i>O</i> -rutinoside	1	(Marengo et al., 2017a)
8	23.932	330	632	163 145	335 191 133	Phenolic acid derivative	3	(Clifford et al., 2006)
9 <sup>a</sup>	24.318	329	516	163	191	1,5 Dicafeoylquinic acid	1	(Li et al., 2014; Marengo et al., 2018)
10 <sup>a</sup>	24.588	329	516	163	191	3,5 Dicafeoylquinic acid	1	(Li et al., 2014; Marengo et al., 2018)
11 <sup>a</sup>	25.042	337 266	432	271	269	Apigenin 7- <i>O</i> -glucoside	1	(Li et al., 2014)
12	25.042	255 351	464	303	301	Quercetin hexoside	3	(Marengo et al., 2017a)

13 <sup>a</sup>	25.322	335 266	446	271	269	Apigenin 7- <i>O</i> -glucuronide	1	(Li et al., 2014)
14	25.736	330	616	163	191	Succinyl-dicaffeoylquinic acid	2	(Marengo et al., 2018)
15	26.165	330	616	163	191	Succinyl-dicaffeoylquinic acid	2	(Marengo et al., 2018)
16 <sup>a</sup>	26.373	329	516	163	191	4,5 Dicaffeoylquinic acid	1	(Li et al., 2014; Marengo et al., 2018)
17	26.965	313	500	163;1 45;13 5;119	337 191 163	<i>p</i> -coumaroyl- caffeoylquinic acid/caffeoyl- <i>p</i> - coumaroylquinic acid	2	(Clifford et al., 2006; Li et al., 2014)
18	27.807	330	616	163	191	Succinyl-dicaffeoylquinic acid	2	(Marengo et al., 2018)
19	28.331	319	600	163;1 47	337 191 173	Succinyl- <i>p</i> -coumaroyl- caffeoylquinic acid/Succinyl-caffeoyl- <i>p</i> - coumaroylquinic acid	2	(Clifford et al., 2006; Li et al., 2014; Marengo et al., 2018)
20	29.188	325	716	163	191	Succinyl-succinyl Dicaffeoylquinic acid	2	(Marengo et al., 2018)
21 <sup>a</sup>	30.321	349 252 266	286	135;1 37;15 3;161		Luteolin	1	(Li et al., 2014; Dimitrova-dyulgerova et al., 2015)
22 <sup>a</sup>	30.321	369 254	302	127;1 37;15 3;165		Quercetin	1	(Li et al., 2014)
23 <sup>a</sup>	33.178	336 267	270	119;1 53;16 3		Apigenin	1	(Li et al., 2014; Dimitrova-dyulgerova et al., 2015)
24 <sup>a</sup>	33.565	365 265	286	121;1 37;15 3;165		Kaempferol	1	(Li et al., 2014; Dimitrova-dyulgerova et al., 2015)
25 <sup>a</sup>	33.565	345 267	300	258;2 86	256 284	Diosmetin	1	(Li et al., 2014; Marengo et al., 2017a)

370 <sup>a</sup>Compounds identified by comparison with reference standards.

371 <sup>b</sup>The Identification Confidence value is in agreement with the CAWG (2007) guidelines and indicates: Level 1: Identified  
372 compound (a minimum of two independent orthogonal data (such as retention time and mass spectrum) compared directly  
373 to an authentic reference standard; Level 2: Putatively annotated compound (similarity of chromatographic and spectral  
374 data to published data); Level 3: Putatively characterized class of compounds

375



376 **References**

377

378 Al-Shammari, L.A., Hassan, W.H.B., Al-Youssef, H.M., 2015. Phytochemical and biological  
379 studies of *Carduus pycnocephalus* L. J. Saudi Chem. Soc. 19, 410–416.

380 Atzei, A.D., 2003. Le piante nella tradizione popolare della Sardegna. Carlo Delfino Ed.

381 Barres, L., Sanmartín, I., Anderson, C.L., Susanna, A., Buerki, S., Galbany-Casals, M., Vilatersana,  
382 R., 2013. Reconstructing the evolution and biogeographic history of tribe *Cardueae*  
383 (compositae). Am. J. Bot. 100, 867–882.

384 Bohlmann, F., Rao, N., Schwarz, H., 1974. Über zwei neue Sesquiterpene aus *Ptilostemon*  
385 *chamaepeuce* (L.) Less. Chem. Ber. 107, 650–653.

386 Bohlmann, F., Ziesche, J., 1980. Neue guajanolide und acetylenverbindungen aus *Ptilostemon-*  
387 *arten*. Phytochemistry 19, 692–696.

388 Braunberger, C., Zehl, M., Conrad, J., Wawrosch, C., Strohbach, J., Beifuss, U., Krenn, L., 2015.  
389 Flavonoids as chemotaxonomic markers in the genus *Drosera*. Phytochemistry 118, 74–82.

390 Bruno, M., Maggio, A., Paternostro, M.P., Rosselli, S., Arnold, N.A., Herz, W., 2001.  
391 Sesquiterpene lactones and other constituents of three *Cardueae* from cyprus. Biochem. Syst.  
392 Ecol. 29, 433–435.

393 Clifford, M.N., Marks, S., Knight, S., Kuhnert, N., 2006. Characterization by LC-MS<sup>n</sup> of Four New  
394 Classes of p-Coumaric Acid-Containing Diacyl Chlorogenic Acids in Green Coffee Beans. J.  
395 Agric. Food Chem. 54, 4095–4101.

396 Di Stefano, V., Pitonzo, R., 2012. Phytochemical Studies on *Ptilostemon greuteri* Raimondo &  
397 Domina (Compositae). Rec. Nat. Prod. 6, 390–393.

398 Dimitrova-dyulgerova, I., Zhelev, I., Mihaylova, D., 2015. Phenolic profile and in vitro antioxidant  
399 activity of endemic Bulgarian *Carduus* species. Pharmacogn. Mag. 11, 575–579.

400 Djordjevic, I., Tesevic, V., Milosavljevic, S., Menkovic, N., Vajs, V., Jadranin, M., Jovanovic, A.,  
401 Djokovic, D., 2008. Composition of the essential oil of *Ptilostemon gnaphaloides* 44, 538–  
402 539.

403 Dong, W., Cheng, T., Li, C., Xu, C., Long, P., Chen, C., Zhou, S., 2014. Discriminating plants  
404 using the DNA barcode rbcLb : an appraisal based on a large data set. Mol. Ecol. Resour. 14,  
405 336–343.

406 Emerenciano, V.P., Militão, J.S.L.T., Campos, C.C., Romoff, P., Kaplan, M.A.C., Zambon, M.,  
407 Brant, A.J.C., 2001. Flavonoids as chemotaxonomic markers for Asteraceae. Biochem. Syst.  
408 Ecol. 29, 947–957.

409 Ferrauto, G., Costa, R., Pavone, P., 2016. Pollen diversity in the genus *Ptilostemon* (Asteraceae,  
410 Cardueae) from Italy and its taxonomic and palynoecological implications. *Plant Biosyst.* - An  
411 Int. J. Deal. with all Asp. Plant Biol. 3504, 1–15.

412 Galimberti, A., Mattia, F. De, Losa, A., Bruni, I., Federici, S., Casiraghi, M., Martellos, S., Labra,  
413 M., 2013. DNA barcoding as a new tool for food traceability. *Food Res. Int.* 50, 55–63.

414 Garcia-Jacas, N., Garnatje, T., Susanna, A., Vilatersana, R., 2002. Tribal and subtribal delimitation  
415 and phylogeny of the *Cardueae* (Asteraceae): a combined nuclear and chloroplast DNA  
416 analysis. *Mol. Phylogenet. Evol.* 22, 51–64.

417 Gnani, G., Berteà, C.M., Maffei, M.E., 2010. PCR , sequencing and PCR –RFLP of the 5S-rRNA-  
418 NTS region as a tool for the DNA fingerprinting of medicinal and aromatic plants. *Flavour*  
419 *Fragr. J.* 25, 132–137.

420 González-Tejero, M.R., Casares-Porcel, M., Sánchez-Rojas, C.P., Ramiro-Gutiérrez, J.M., Molero-  
421 Mesa, J., Pieroni, A., Giusti, M.E., Censorii, E., de Pasquale, C., Della, A., Paraskeva-  
422 Hadjichambi, D., Hadjichambis, A., Houmani, Z., El-Demerdash, M., El-Zayat, M.,  
423 Hmamouchi, M., ElJohrig, S., 2008. Medicinal plants in the Mediterranean area: Synthesis of  
424 the results of the project Rubia. *J. Ethnopharmacol.* 116, 341–357.

425 Ha, I.J., Lee, M.Y., Kwon, Y.-K., Jung, Y., Kim, H.K., Hwang, G.-S., 2015. Metabolite profiling to  
426 discriminate different species and genus from thistles in Korea using liquid chromatography  
427 with quadrupole time-of-flight mass spectrometry. *J. Sep. Sci.* 38, 502–510.

428 Hebert, P.D.N., Cywinska, A., Ball, S.L., Jeremy, R., 2003. Biological identifications through DNA  
429 barcodes. *Proc. R. Soc. London* 270, 313–321.

430 Janačković, P., Tešević, V., Marin, P.D., Milosavljević, S.M., Petković, B., Soković, M., 2002.  
431 Polyacetylenes and a sesquiterpene lactone from *Ptilostemon strictus*. *Biochem. Syst. Ecol.* 30,  
432 69–71.

433 Jeong, D.M., Jung, H.A., Choi, J.S., 2008. Comparative antioxidant activity and HPLC profiles of  
434 some selected Korean thistles. *Arch. Pharm. Res.* 31, 28–33.

435 Jordon-Thaden, I.E., Louda, S.M., 2003. Chemistry of *Cirsium* and *Carduus*: A role in ecological  
436 risk assessment for biological control of weeds? *Biochem. Syst. Ecol.* 31, 1353–1396.

437 Kress, W.J., 2017. Plant DNA barcodes: Applications today and in the future. *J. Syst. Evol.* 55,  
438 291–307.

439 Kuklev, D. V., Domb, A.J., Dembitsky, V.M., 2013. Bioactive acetylenic metabolites.  
440 *Phytomedicine* 20, 1145–1159.

441 Labra, M., Miele, M., Ledda, B., Grassi, F., Mazzei, M., Sala, F., 2004. Morphological

442 characterization , essential oil composition and DNA genotyping of *Ocimum basilicum* L .  
 443 cultivars 167, 725–731.

444 Li, J.-H., Nesumi, A., Shimizu, K., Sakata, Y., Liang, M.-Z., He, Q.-Y., Zhou, H.-J., Hashimoto, F.,  
 445 2010. Chemosystematics of tea trees based on tea leaf polyphenols as phenetic markers.  
 446 *Phytochemistry* 71, 1342–1349.

447 Li, R., Liu, S., Song, W., Wang, Y., Li, Y., Qiao, X., Liang, H., Ye, M., 2014. Chemical analysis of  
 448 the Tibetan herbal medicine *Carduus acanthoides* by UPLC/DAD/qTOF-MS and simultaneous  
 449 determination of nine major compounds. *Anal. Methods* 6, 7181.

450 Liu, J., Shi, L., Han, J., Li, G., Lu, H., Hou, J., Zhou, X., Meng, F., Downie, S.R., 2014.  
 451 Identification of species in the angiosperm family Apiaceae using DNA barcodes. *Mol. Ecol.*  
 452 *Resour.* 14, 1231–1238.

453 Liu, Z., Liu, Y., Liu, C., Song, Z., Li, Q., Zha, Q., Lu, C., Wang, C., Ning, Z., Zhang, Y., Tian, C.,  
 454 Lu, A., 2013. The chemotaxonomic classification of *Rhodiola* plants and its correlation with  
 455 morphological characteristics and genetic taxonomy. *Chem. Cent. J.* 7, 118.

456 Ma, Q., Wang, L.-H., Jiang, J.-G., 2016. Hepatoprotective effect of flavonoids from *Cirsium*  
 457 *japonicum* DC on hepatotoxicity in comparison with silymarin. *Food Funct.* 7, 2179–2184.

458 Marengo, A., Fenu, G., Gennai, M., Cogoni, D., Fois, M., Bacchetta, G., 2015. Schede per una Lista  
 459 Rossa della Flora vascolare e crittogamica italiana. *Ptilostemon casabonae* (L.) Greuter. *Inf.*  
 460 *Bot. Ital.* 47, 245–289.

461 Marengo, A., Fumagalli, M., Sanna, C., Maxia, A., Piazza, S., Cagliari, C., Rubiolo, P.,  
 462 Sangiovanni, E., Dell’Agli, M., 2018. The hydro-alcoholic extracts of Sardinian wild thistles  
 463 (*Onopordum* spp.) inhibit TNF $\alpha$ -induced IL-8 secretion and NF- $\kappa$ B pathway in human gastric  
 464 epithelial AGS cells. *J. Ethnopharmacol.* 210, 469–476.

465 Marengo, A., Maxia, A., Sanna, C., Bertea, C.M., Bicchi, C., Ballero, M., Cagliari, C., Rubiolo, P.,  
 466 2017a. Characterization of four wild edible *Carduus* species from the Mediterranean region via  
 467 phytochemical and biomolecular analyses. *Food Res. Int.* 100, 822–831.

468 Marengo, A., Piras, A., Falconieri, D., Porcedda, S., Caboni, P., Cortis, P., Foddis, C., Loi, C.,  
 469 Gonçalves, M.J., Salgueiro, L., Maxia, A., 2017b. Chemical and biomolecular analyses to  
 470 discriminate three taxa of *Pistacia* genus from Sardinia Island (Italy) and their antifungal  
 471 activity. *Nat. Prod. Res.* 6419, 1–9

472 Marrelli, M., Loizzo, M.R., Nicoletti, M., Menichini, F., Conforti, F., 2013. Inhibition of Key  
 473 Enzymes Linked to Obesity by Preparations From Mediterranean Dietary Plants: Effects on  $\alpha$ -  
 474 Amylase and Pancreatic Lipase Activities. *Plant Foods Hum. Nutr.* 68, 340–346.

475 Martini, S., Conte, A., Tagliazucchi, D., 2017. Phenolic compounds profile and antioxidant  
476 properties of six sweet cherry (*Prunus avium*) cultivars. Food Res. Int. 97, 15–26.

477 Médail, F., Verlaque, R., 1997. Ecological characteristics and rarity of endemic plants from  
478 Southeast France and Corsica: Implications for biodiversity conservation. Biol. Conserv. 80,  
479 269–281.

480 Míka, V., Kubáň, V., Klejdus, B., Odstrčilová, V., Nerušil, P., 2005. Phenolic compounds as  
481 chemical markers of low taxonomic levels in the family Poaceae. Plant, Soil Environ. 51, 506–  
482 512.

483 Navaz Kharazian, 2014. Chemotaxonomy and flavonoid diversity of *Salvia* L. (Lamiaceae) in Iran.  
484 Acta Bot. Brasilica 28, 281–292.

485 Pignatti, S., 1982. La flora d'Italia. Edagricole.

486 Rahali, F.Z., Lamine, M., Gargouri, M., Rebey, I.B., Hammami, M., Sellami, I.H., 2016. Metabolite  
487 profiles of essential oils and molecular markers analysis to explore the biodiversity of *Ferula*  
488 *communis*: Towards conservation of the endemic giant fennel. Phytochemistry 124, 58–67.

489 Rubiolo, P., Matteodo, M., Bicchi, C., Gnavi, G., Bertea, C., Maffei, M., 2009. Chemical and  
490 Biomolecular Characterization of *Artemisia umbelliformis* Lam., an Important Ingredient of  
491 the Alpine Liqueur “Genepi#.” J. Agric. Food Chem. 57, 3436–3443.

492 Sarangowa, O., Kanazawa, T., Nishizawa, M., Myoda, T., Bai, C., Yamagishi, T., 2014. Flavonol  
493 glycosides in the petal of *Rosa* species as chemotaxonomic markers. Phytochemistry 107, 61–  
494 68.

495 Sun, Y., Kang, H., Kim, Y., Baek, J., Zheng, S., Xiang, J., Hong, S.-K., 2014. Tomato (*Solanum*  
496 *lycopersicum*) variety discrimination and hybridization analysis based on the 5S rRNA region.  
497 Biotechnol. Biotechnol. Equip. 28:3, 431–437.

498 Susanna, A., Garcia-Jacas, N., 2009. *Cardueae* (Carduoideae). In: Funk VA, Susanna A, Stuessy  
499 TF, Bayer RJ, editors. Systematics, evolution and biogeography of the Compositae. Vienna  
500 IAPT 293–313.

501 Susanna, A., Hidalgo, O., Vilatersana, R., Cienfuegos, M. De, 2006. The *Cardueae* (Compositae)  
502 revisited: insights from a combined ITS, trnL-trnF and matK nuclear and chloroplast DNA  
503 analysis. Annu. Missouri Bot. Gard. 93, 150–171.

504 Švehlíková, V., Mráz, P., Piacente, S., Marhold, K., 2002. Chemotaxonomic significance of  
505 flavonoids and phenolic acids in the *Hieracium rohacsense* group (*Hieracium* sect. *Alpina*;  
506 *Lactuceae*, *Compositae*). Biochem. Syst. Ecol. 30, 1037–1049.

507 Tacchini, M., Spagnoletti, A., Marieschi, M., Caligiani, A., Bruni, R., Efferth, T., Sacchetti, G.,

508 Guerrini, A., 2015. Phytochemical profile and bioactivity of traditional ayurvedic decoctions  
509 and hydro-alcoholic macerations of *Boerhaavia diffusa* L. and *Curculigo orchioides* Gaertn.  
510 Nat. Prod. Res. 29, 2071–2079.

511 Tutin, T.G., Heywood, V.H., Burges, N.A., Valentine, D.H., Walters, S.M., Webb, D.A., 1968.  
512 Flora europaea. Cambridge Univ. Press.

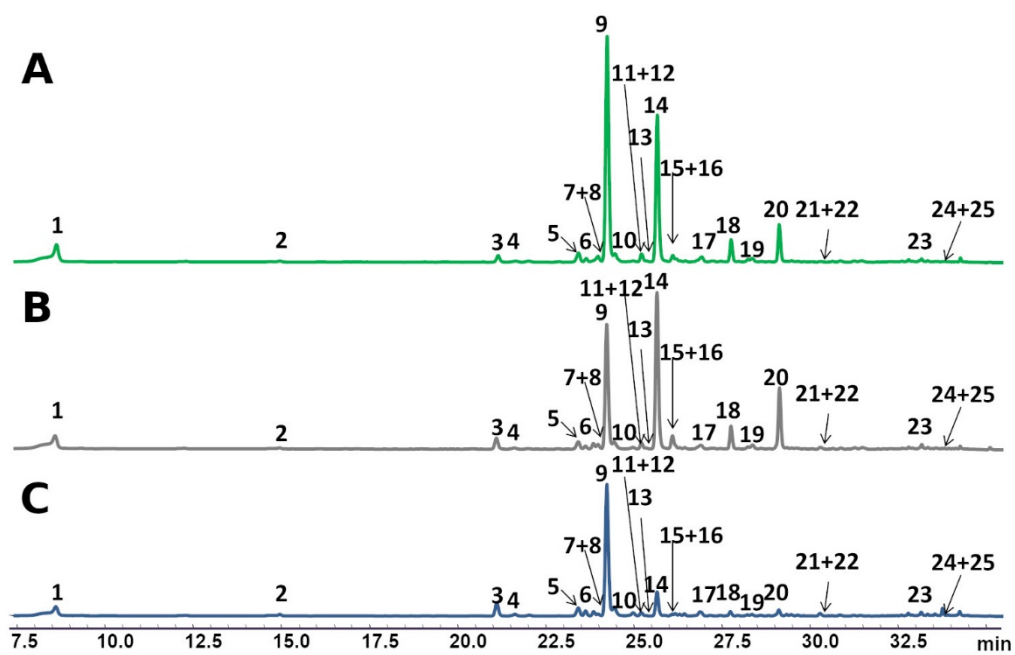
513 Vilatersana, R., Garcia-Jacas, N., Garnatje, T., Molero, J., Sonnante, G., Susanna, A., 2010.  
514 Molecular Phylogeny of the Genus *Ptilostemon*(Compositae: *Cardueae*) and its Relationships  
515 with *Cynara* and *Lamyropsis*. Syst. Bot. 35, 907–917.  
516 <https://doi.org/10.1600/036364410X539952>

517 Wu, P.K., Tai, W.C.S., Choi, R.C.Y., Tsim, K.W.K., Zhou, H., Liu, X., Jiang, Z.H., Hsiao, W.L.W.,  
518 2011. Chemical and DNA authentication of taste variants of *Gynostemma pentaphyllum* herbal  
519 tea. Food Chem. 128, 70–80.

520 Zhang, Z., Schwartz, S., Wagner, L., Miller, W., 2000. A greedy algorithm for aligning DNA  
521 sequences. J. Comput. Biol. 7, 203–214.

522

523 Figure 1

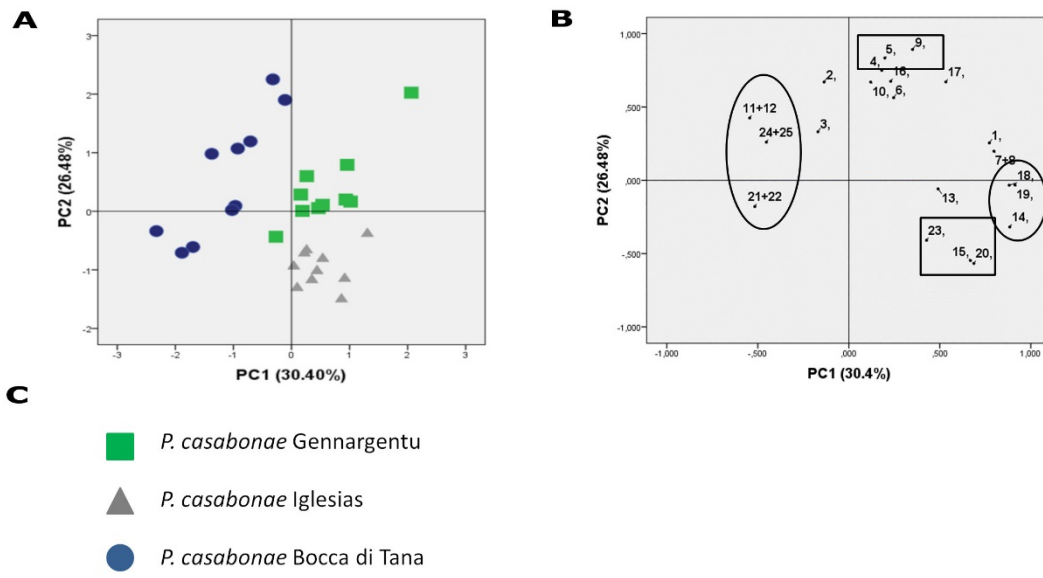


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527 Figure 2



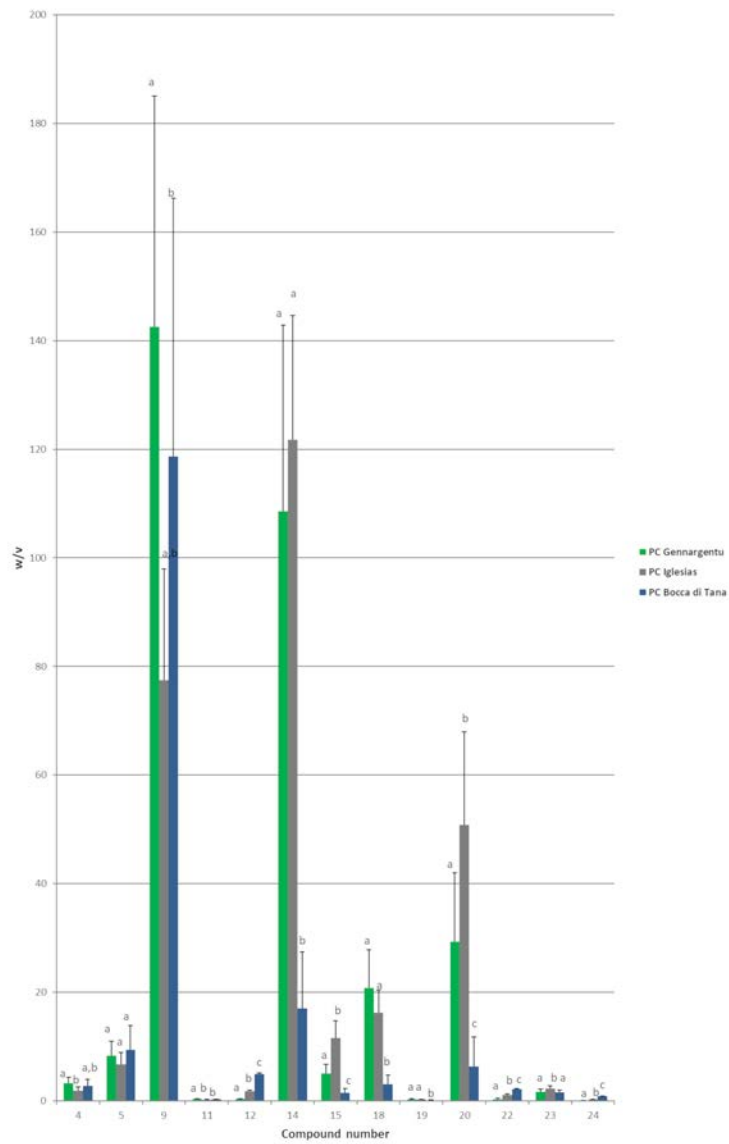
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531 Figure 3

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