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1 **Genotypic variation of flavonols and antioxidant capacity in broccoli**

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39 **ABSTRACT**

40 Flavonols are gaining increasing interests due to their diverse health benefits for humans.
41 Broccoli is a main flavonol source in our diet, but the genetic variation of flavonols and their
42 correlation with antioxidant capacity remain to be understood. Here, we examined variations
43 of the two major flavonols kaempferol and quercetin in florets and leaves of 15 diverse
44 broccoli accessions by **Ultra-Performance Liquid Chromatography (UPLC)**. Broccoli
45 accumulated more kaempferol than quercetin in most of the accessions tested, with the ratios
46 varying from 4.4 to 27.9 in leaves and 0.4 to 4.4 in florets. Total flavonoids showed 2.5-fold
47 and 3.3-fold differences in leaves and florets of these accessions, respectively. Principle
48 components analysis revealed that flavonols, along with key biosynthetic genes, correlated
49 with antioxidant capacity related indicators. This study provides important information for
50 broccoli flavonol genotypic variations and correlation with antioxidant capacity, and will
51 facilitate the development of flavonol enriched cultivars in broccoli.

52

53 **Keywords:** Broccoli; Flavonols; Kaempferol; Quercetin; Antioxidant capacity; Flavonol
54 synthase gene; Selenium

55

56 **1. Introduction**

57 Flavonoids are a class of naturally occurring secondary metabolites, which are
58 synthesized in plants through the phenylpropanoid pathway. Flavonoids are widely distributed
59 in plants and fulfil many important functions for plant growth and development (Cecilia,
60 Alessio, Federico, Antonella, & Massimiliano, 2018; Ferreyra, Rius, & Casati, 2012). Based on
61 their chemical structures, flavonoids are categorized into various subclasses. Flavonols belong
62 to a subgroup of flavonoids with 3-hydroxyflavone backbone, and represent the most
63 ubiquitous and abundant flavonoids in plant foods. In general, kaempferol and quercetin are the
64 main representatives and have been widely studied due to their health-promoting functions.
65 Both kaempferol and quercetin are known to have unique biological properties of
66 anti-carcinogenic, antimicrobial, antidiabetic, and anti-inflammatory activities (Chen & Chen,
67 2013; Li et al., 2016). Epidemiological studies suggest that intake of foods enriched with
68 kaempferol and quercetin can reduce the risk of some chronic diseases, such as cardiovascular
69 diseases and cancers (Chen & Chen, 2013; Imran et al., 2019; Li et al., 2016).

70 Flavonoids, especially the flavonols, are important antioxidants that are associated with
71 their abilities to suppress free radical formation, scavenge free radicals, and upregulate or
72 protect antioxidant systems (Kumar & Pandey, 2013). They inhibit the enzymes associated
73 with free radical production, reduce lipid peroxidation, and chelate metal ions in reducing free
74 radical generation (Leopoldini, Russo, Chiodo, & Toscano, 2006). In plants, flavonoids
75 contribute significantly to the antioxidant activity (Gu, Howell, Dunshea, & Suleria, 2019).
76 Flavonols like quercetin was found to be associated with high antioxidant activity in vegetables
77 (Fronde et al., 2019). Kaempferol can also activate antioxidant enzymes (Doronicheva, Yasui, &

78 Sakurai, 2007). Considering the structure-activity relationship, flavonols that contains a galloyl
79 moiety usually have higher antioxidant activity than those without, and a B-ring
80 3',4',5'-trihydroxyl group can further improve their efficiency (Wolfe & Liu, 2008).

81 Broccoli (*Brassica oleracea* L. *italica*) is a cruciferous vegetable that contains copious
82 quantities of many nutrients and phytonutrients, including flavonols (Vasanthi, Mukherjee, &
83 Das, 2009). Its consumption has been steadily increasing year over year, in part due to its
84 containing of many health-promoting compounds (Herr & Buchler, 2010; Kaczmarek et al.,
85 2019). Investigation of genotypic variation is known to be an effective strategy for efficient
86 breeding crops with target traits. Large genetic variations of some health beneficial compounds
87 such as glucosinolates and *Se*-methylselenocysteine were reported in broccoli germplasm
88 (Kushad et al., 1999; Ramos, Yuan, Faquin, Guilherme, & Li, 2011). Broccoli is one of the
89 main flavonol sources in our diet. Kaempferol and quercetin in the glycoside forms represent
90 the main flavonols in broccoli (Vallejo, Tomás-Barberán, & Ferreres, 2004). Their stability
91 under different growth conditions and during marketing has been studied
92 (Gliszczyńska-Świąło, Kałużewicz, Lemańska, Knaflewski, & Tyrakowska, 2007; Molmann,
93 et al., 2015). However, the ability of different genotypes of broccoli in accumulating flavonols
94 and the correlation with total flavonoids and antioxidant capacity have not been fully
95 investigated.

96 In this study, we evaluated the variations of the two major flavonols kaempferol and
97 quercetin in leaves and florets of 15 broccoli accessions. We also examined the effects of
98 selenium (Se) treatment on these flavonol accumulations to see whether it is possible to
99 simultaneously accumulate multiple health-promoting compounds, because *Se*-biofortified

100 broccoli is known to synthesize functional forms of Se with enhanced chemopreventive
101 activities. In addition, the total flavonoids, antioxidant capacity, and antioxidant enzyme
102 activity were also investigated. The principal component analysis (PCA) and Pearson
103 correlation were employed to reveal the correlations of flavonol levels with these associated
104 indicators. The expression of genes involved in kaempferol and quercetin biosynthesis was
105 investigated for a better understanding of the key genes controlling flavonols biosynthesis in
106 broccoli.

107

108 **2. Materials and methods**

109

110 *2.1. Plant materials*

111

112 Fifteen accessions and varieties of broccoli (*Brassica oleracea* L. *italica*) were obtained
113 from Plant Genetic Resources Unit at Geneva, NY, USA or as a gift (Superbroccoli)
114 (Supplementary Table S1). For the production of leaf samples, seeds were surface-disinfected
115 with 0.25% sodium hypochlorite and germinated by putting in the moistened roll sheets for 7
116 days at 25°C with a photoperiod of 16-h light and 8-h dark in an incubator. The young
117 seedlings were then transferred to a container with Hoagland solution for conditioning in a
118 greenhouse (Tian, Hui, Thannhauser, Pan, & Li, 2017). One week later, uniform seedlings
119 were transferred to 2.2 L black pots containing the Hoagland solution and grown in the same
120 greenhouse at 25°C with a 14-h light and 10-h dark photoperiod under constant aeration. The
121 nutrient solution was changed every four days. After 12 days of culture, 60 plants (15 varieties

122 x 4 biological replicates) were harvested individually, and each replicate was weighed. The top
123 three young leaves were collected. All the collected samples were immediately frozen in liquid
124 nitrogen and stored at -80 °C for various analyses.

125 For the generation of floret samples, 60 plants (15 varieties x 4 biological replicates)
126 were germinated in pots filled with soil mix and grown in a greenhouse. Florets were harvested
127 individually when heads were fully formed and at market harvest maturity. The top center head
128 samples were collected, ground into fine powder with mortars and pestles in liquid nitrogen,
129 and stored at -80 °C for subsequent analyses.

130 In addition, three varieties that included Packman in the accession panel and Marathon
131 and Diploma were grown in pots each filled with 6 dm³ of soil mix for Se treatment at floret
132 stage as described (Avila et al., 2013). When floral primordia began to form, 100 mL of 1.5
133 mM Na₂SeO₄ solution (equivalent to 25 μM) was applied to each pot. The application was
134 performed twice a week for three weeks. When heads were fully formed and at market harvest
135 maturity, the top center head samples were then harvested, ground into fine powder with
136 mortars and pestles in liquid nitrogen, and stored at -80 °C.

137

138 *2.2. Analysis of flavonols by Ultra-Performance Liquid Chromatography (UPLC)*

139

140 Flavonols were extracted and analyzed following the methods as described
141 (Rybarczyk-Plonska, Wold, Bengtsson, Borge, Hansen, & Hagen, 2016; Watkins, Hechler, &
142 Muday, 2014) with some modifications. To extract flavonols, 150 mg of the powdered tissues
143 were weighed out into a microcentrifuge tube and extracted with 450 μL of 80% methanol by

144 vortexing for 10 min and sonicating for 5 min. Following centrifugation at 14,000 g for 10 min,
145 450 μ L of 2 M HCl were added to the supernatant and incubated for 45 min in a water bath at
146 70 °C to hydrolyze the glycosylated flavonoids and form aglycone flavonols. After hydrolysis,
147 equal volume of ethyl acetate was added, vortexed for 5 min, and centrifuged at 14,000 g for
148 10 min. The upper organic layer was collected, speed-vacuum dried, and resuspended in
149 acetone.

150 The extracted flavonol samples were analyzed using an ACQUITY UPLC equipped
151 with a BEH C18 column (2.1 \times 50 mm, 1.7 μ m) (Waters, Milford, MA, USA). Samples (2 μ L)
152 were injected into the column and eluted using the mobile phases consisting of solvent A
153 (0.1% aqueous formic acid) and solvent B (0.1% formic acid in acetonitrile) in a linear gradient
154 of 15-85% solvent B over 4 min at flow rate of 0.6 mL min⁻¹. The column effluent was
155 monitored at 360 nm. Pure quercetin and kaempferol were obtained commercially (Sigma
156 Aldrich[®] Chemical Co., St. Louis, MO, USA) and used as standards for quantification.

157

158 2.3. DPBA staining of kaempferol

159

160 Kaempferol accumulation in roots was observed via diphenylboric acid 2-aminoethyl
161 ester (DPBA) staining according to the method as described (Vu et al., 2015). Briefly, 5-d old
162 seedlings were stained in a solution containing saturated DPBA (0.25%, w/v) and 0.02% (v/v)
163 Triton X-100 for 45 min, followed by three times of rinsing with distilled water. The
164 fluorescence of kaempferol in the samples was visualized under a Leica TCS SP5 laser
165 scanning confocal microscope (Leica Microsystems, Buffalo Grove, IL, USA).

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2.4. RNA extraction, reverse transcription and quantitative PCR analysis

Total RNA was isolated from 100 mg of leaves using TRIzol reagent and reverse-transcribed into cDNA using PrimeScript cDNA Synthesis Kit according to the instruction of manufacturer (Takara Bio USA, Inc. Mountain View, CA, USA). Quantitative real-time polymerase chain reaction (qRT-PCR) was performed with SYBR Green Master Mix (Bio-Rad, Hercules, CA, USA) on CFX384 Touch Realtime PCR Detection System (Bio-Rad) using gene-specific primers (Supplementary Table S2) as described previously (Cao et al., 2019). The gene expression analysis was performed with three technical trials for each of the three biological replicates.

2.5. Cloning of flavonol synthase gene (FLS)

The flavonol synthase gene was cloned from leaves of two high- and two low-kaempferol varieties. Full-length *BoFLS* cDNAs were amplified using primers listed in Supplementary Table S2 and cloned into pENTR vector (ThermoFisher Scientific, Waltham, MA, USA) for sequencing. Their sequences were aligned using Molecular Evolutionary Genetics Analysis (MEGA) (Tamura, Dudley, Nei, & Kumar, 2007).

2.6. Measurement of total flavonoid, antioxidant capacity, and total anthocyanin levels

188 Total flavonoids and antioxidant capacity were analyzed according to the methods
189 described previously (Abu Bakar, Mohamed, Rahmat, & Fry, 2009) with some modifications.
190 To prepare the extracts, powdered broccoli tissues (100 mg) were mixed with 1 mL of 80%
191 methanol, vortexed for 10 min, and centrifuged at 12,000 g for 15 min. The supernatants were
192 collected and the pellets were extracted again. The combined supernatants were used for the
193 measurements.

194 To analyze total flavonoids, 50 μL of extracts were mixed with 225 μL of ddH₂O and
195 15 μL of 5% NaNO₂. The mixture was incubated at room temperature for 6 min, added with 30
196 μL of 10% AlCl₃, and incubated at room temperature for another 5 min, followed by addition
197 of 100 μL 1 M NaOH. The absorbance at wavelength of 510 nm was read. The total flavonoid
198 content was calculated against rutin standard with a gradient concentration series (0, 0.25, 0.50,
199 0.75, 1.0, 1.5 and 2.0 mg mL⁻¹), and expressed as mg rutin equivalents per 1 g sample (mg RE
200 g⁻¹).

201 The antioxidant capacity was determined by both 2,2-diphenyl-1-picrylhydrazyl (DPPH)
202 and ferric reducing/antioxidant power (FRAP) methods. The DPPH free radical scavenging
203 assay was performed according to the methods described (Abu Bakar et al, 2009). Aliquot (60
204 μL) of extracts or control (80% methanol) were mixed with 600 μL of 500 μM DPPH* in
205 ethanol. The mixture was vortexed vigorously, incubated in the dark for 30 min, and measured
206 spectrophotometrically at 517 nm. The free radical scavenging activity was calculated
207 according to the equation: Scavenging effect (%) = $[1 - (A_{\text{sample}}/A_{\text{control}})] \times 100$. A gradient series
208 of ascorbic acid at concentrations from 0.05 to 0.25 mg mL⁻¹ was also measured to generate a

209 standard curve and used to calculate antioxidant capacity. The data was expressed as mg
210 ascorbic acid equivalent antioxidant capacity per 1 g of sample (mg AEAC g⁻¹).

211 The FRAP assay was carried out using the method as described (Benzie & Strain, 1996)
212 with slight modifications. The FRAP reagent, prepared prior to use, contained a mixture of 300
213 mM acetate buffer (pH 3.6), 10 mM 2,4,6-tripyridyl-*s*-triazine (TPTZ), and 20 mM FeCl₃ in a
214 10:1:1 ratio. One milliliter of 37 °C preheated FRAP reagent was mixed with 30 µL of plant
215 extracts and 90 µL of water, and incubated at 37 °C for 90 min. The absorbance at 593 nm was
216 read using a spectrophotometer. The absorbance difference between sample and blank control
217 was used to calculate the FRAP value against the standard curve, which was constructed with a
218 series of Fe²⁺ concentrations ranging from 100 to 1000 µM. The data was expressed as ferric
219 reducing ability per 1 gram of sample (µM Fe²⁺ g⁻¹).

220 Total anthocyanin content was extracted and measured following a previously reported
221 method (Tian, Xu, Liu, Xie, & Pan, 2016). Powdered broccoli leaf and floret samples (0.5 g
222 each) were added with 5 mL of acidified ethanol (85:15 of 95% ethanol: 1.5 M HCl) and
223 vortexed for 10 min. After centrifugation at 12,000 g for 10 min, the supernatants were
224 collected and measured spectrophotometrically at 535 nm. Anthocyanin content was calculated
225 using the equation: Amount (µg g⁻¹ FW) = (A₅₃₅ × V)/(98.2 × W) × 1000. *V* and *W* represent
226 extract volume and sample weight, respectively. The value 98.2 represents the molar
227 absorptivity of cyaniding 3-galactoside at 535 nm.

228

229 *2.7. Antioxidant enzyme activity assays*

230

231 Plant extracts were prepared using the method described previously (Ramos et al, 2011).
232 Briefly, powdered broccoli sample (100 mg) was mixed with 1 mL of ice-cold extraction
233 buffer containing 50 mM phosphate-buffered saline (PBS) (pH 7.8), 0.2 mM
234 ethylenediaminetetraacetic acid (EDTA), and 0.3% (w/v) Triton X-100. The mixture was
235 vortexed well, kept on ice for 10 min, and centrifuged at 12,000 g for 10 min at 4°C. The
236 supernatant was quantified for protein levels by the Bradford method.

237 The antioxidant enzyme activity assays were performed essentially as described
238 previously (Ramos et al, 2011; Tian et al, 2017). To detect ascorbate peroxidase (APX) activity,
239 the reaction mixture (1 mL) contained 50 mM PBS (pH 7.0), 0.25 mM of reduced ascorbate,
240 12 mM H₂O₂ and 100 µL of plant extract. The reaction was started by addition of H₂O₂. The
241 reaction mixture with 100 µL of PBS solution to replace plant extract was used as the blank
242 control. The absorbance at 290 nm was recorded at an interval of 30 s for 2 min. The decrease
243 of A₂₉₀ was used to calculate the APX activity.

244 To detect catalase (CAT) activity, the reaction reagent (1 mL) contained 50 mM PBS
245 (pH 7.6), 0.1 mM EDTA, 100 mM H₂O₂, and 100 µL of plant extract. The reaction was
246 initiated by addition of H₂O₂. The reaction mixture with 100 µL of PBS solution to replace
247 plant extract was used as the blank control. The absorbance at 240 nm was recorded at an
248 interval of 30 s for 2 min. The decrease of A₂₄₀ was calculated and used to calculate the CAT
249 activity.

250 To detect superoxide dismutase (SOD) activity, the reaction mixture (1 mL) contained
251 50 mM PBS (pH 7.8), 0.1 mM EDTA, 13 mM methionine, 75 µM nitroblue tetrazolium (NBT),
252 2 µM riboflavin, and 100 µL of plant extract. Following addition of riboflavin, the reaction

253 mixture was illuminated for 15 min at the light intensity of 5000 lux. Two additional reaction
254 mixtures with 100 μ L of PBS solution instead of plant extract were used as controls, with one
255 protected from light as blank control and the other illuminated for 15 min at the light intensity
256 of 5000 lux. A_{560} was read and used to calculate the SOD activity following subtraction of the
257 absorbance of illuminated control from sample. All experiments were performed with three
258 biological replicates.

259

260 *2.8. Statistical analysis*

261

262 The data were presented as the means \pm SD of three biological replicates for each
263 sample. The significance difference among treatments was determined using IBM SPSS
264 Statistics 20.0 with Duncan's multiple-range test ($p < 0.05$). The heatmap was performed to
265 evaluate the relationship among the physiological and biochemical parameters with the Pearson
266 correlation coefficients ($p < 0.05$). The "corrplot" package was accessed to generate the heatmap
267 using the functions "corr" and "cor.mtest" to create coefficient and p -values matrices,
268 respectively. Analysis of variance (ANOVA) was conducted to present the statistically
269 significant correlations by inserting asterisks into heatmap cells.

270

271 **3. Results**

272

273 *3.1 Plant growth varied greatly among the broccoli accessions*

274

275 The broccoli accessions used consisted of both landraces and improved entries (Stansell
276 et al., 2018). To compare growth characteristics, these accessions were grown hydroponically
277 in the nutrient solution and their growth was evaluated by measuring plant biomass. The fresh
278 biomass of 4-weeks old young plants ranged from 1.3 to 7.1 g per plant with over 5-fold
279 difference between the highest and lowest accession (Supplementary Fig. S1). This data shows
280 that the experimental broccoli materials represented a diverse collection of accessions with
281 different growth.

282

283 *3.2. Broccoli florets existed large variations in kaempferol and quercetin levels*

284

285 Broccoli is known to accumulate kaempferol and quercetin in their glycoside forms
286 (Vallejo et al, 2004). Their levels in leaves and florets of the broccoli accessions were
287 evaluated after acid hydrolysis of glycosides. Large variations in kaempferol and quercetin
288 content were observed among these accessions. The range of kaempferol accumulation varied
289 from 108.0 to 274.3 $\mu\text{g g}^{-1}$ FW, showing a 2.5-fold difference in leaves (Fig. 1A). The
290 kaempferol levels were from 0.8 to 87.7 $\mu\text{g g}^{-1}$ FW in florets, showing a much large variation
291 (109-folds) in the edible tissue among these accessions (Fig. 1B). Broccoli accumulated higher
292 levels of kaempferol in leaves than florets. The quercetin accumulation ranged from 8.0 to 32.2
293 $\mu\text{g g}^{-1}$ FW in leaves with 4-fold difference, and from 1.8 to 29.0 $\mu\text{g g}^{-1}$ FW in florets with
294 16-fold variations among these accessions (Fig. 1A and 1B). Overall, broccoli plants
295 accumulated much more kaempferol than quercetin in leaves of all 15 accessions, though this
296 was not the case in florets for some accessions. The ratios of kaempferol to quercetin amounts

297 varied from 4.4 to 27.9 in leaves and 0.4 to 4.4 in florets, indicating no correlations of
298 accumulation of these two flavonoid compounds in these broccoli accessions.

299 DPBA staining of root tissue is often used to visually detect kaempferol in plants (Vu et
300 al., 2015). The DPBA staining was also utilized in roots of two accessions with highest and
301 lowest kaempferol levels in leaves (i.e. accession 8 and 12, respectively). A much stronger
302 kaempferol-specific fluorescence intensity was detected in roots of accession 8 that with more
303 kaempferol than accession 12 with less kaempferol (Fig. 1C). The result indicates a rough
304 correlation between kaempferol levels in different tissues of a plant. Taken together, these
305 findings show different capacity of these broccoli accessions in accumulation of these
306 health-beneficial flavonol compounds and suggest DPBA staining of roots as a rough screen for
307 high kaempferol accumulating varieties.

308

309 *3.3. Flavonol accumulation was directly associated with flavonol biosynthetic gene expression*

310

311 Flavonol biosynthetic pathway is well established (Fig. 2A). To gain a better
312 understanding of flavonol accumulation in broccoli, the transcript levels of several major genes
313 in the biosynthetic pathway and a regulator (i.e. *CHS*, *DFR*, *F3H*, *F3'H*, *FLS*, and *MYB2*) were
314 examined. Four accessions with two high (2 and 8) and two low (12 and 14) levels of
315 kaempferol in leaves were utilized for gene expression analysis. As shown in Figure 2B,
316 significant differences in expression of *F3H*, *F3'H*, and *FLS* were observed between both
317 accessions that accumulated high and two accessions that contained low levels of kaempferol.
318 *FLS* showed a largest 6-fold difference. Since *FLS* is responsible for kaempferol and other

319 flavonol synthesis (Fig. 2A), *FLS* CDS from these four accessions was cloned and its sequence
320 difference among these four accessions was examined. A total of 24 SNPs in *FLS* CDS were
321 observed among these four accessions (Supplementary Fig. 2A), suggesting abundant genetic
322 variation in *FLS* gene at DNA level. Among the 24 SNPs, only one caused an amino acid
323 change with Val or Ala between different accessions (Supplementary Fig. 2B). However, this
324 variation does not correlate with kaempferol accumulation. The results suggest that the
325 difference in kaempferol accumulation was likely caused at transcription level of *FLS*.

326

327 3.4. Kaempferol and quercetin levels were not influenced by selenium treatment

328

329 Broccoli as a selenium (Se) secondary accumulator synthesizes and accumulates
330 anticarcinogenic compounds such as *Se*-methylselenocysteine when grown in media containing
331 Se (Avila et al., 2013; Lyi, Heller, Rutzke, Welch, Kochian, & Li, 2005; Ramos et al, 2011).
332 To examine whether Se treatment affected flavonol accumulation, kaempferol and quercetin
333 levels were quantified in florets and leaves of three broccoli cultivars treated with or without
334 25 μM Na_2SeO_4 , a concentration and form of Se that promote *Se*-methylselenocysteine
335 production and cause no adversative impact on plant growth and development (Avila et al.,
336 2013; Lyi et al, 2005; Tian et al., 2018). As shown in Figure 3A, Se treatment did not reduce
337 kaempferol levels in both leaf and floret tissues of these broccoli cultivars, indicating a
338 potential to enhance bioactive Se compounds without impact on kaempferol level.
339 Consistently, leaves contained more kaempferol than florets (Fig. 3A).

340 The level of quercetin was also examined in these cultivars. No significant difference in
341 quercetin levels were observed among these cultivars (Fig. 3B). When treated with Se, the
342 cultivar Marathon showed a significantly reduced content of quercetin in leaves ($p<0.05$),
343 while the other two cultivars did not give statistically significant change. In contrast, Se
344 treatment showed no reduced quercetin levels and with a significant increase in florets of one
345 variety (Fig. 3B). Slightly lower levels of quercetin were detected in florets than leaves for
346 these cultivars (Fig. 3B). Taken together, these results show that kaempferol and quercetin
347 levels in general were not greatly affected by Se application, indicating the possibility of
348 simultaneous enrichment of health-beneficial flavonol and Se compounds.

349
350 *3.5. Total flavonoids, anthocyanins and antioxidant capacity showed different levels of*
351 *genotypic variations*

352
353 In addition to flavonols kaempferol and quercetin, the total flavonoid levels were also
354 examined in leaves and florets of the 15 broccoli accessions. The total flavonoid content varied
355 across the two tissues and different accessions, ranging from 115.7 to 310.9 $\mu\text{g RE g}^{-1}$ FW in
356 leaves and 31.1 to 103.9 $\mu\text{g RE g}^{-1}$ FW in florets (Fig. 4A). A difference of 2.5-folds and
357 3.3-folds was detected in leaves and florets, respectively, among accessions with low and high
358 levels of total flavonoids. Interestingly, the variations in total flavonoid levels showed no
359 apparent correlations with the variation in kaempferol and quercetin content among these
360 accessions (Fig. 1 and Fig. 4A), indicating that the high level of total flavonoids does not
361 necessarily reflect high kaempferol or quercetin content in a particular variety.

362 Anthocyanins are a subgroup of flavonoid compounds and give plant tissues color.
363 Examination of total anthocyanin content revealed that all accessions contained similar levels
364 in leaves, while a 3.5-fold difference was observed in florets between accessions with the
365 highest and lowest content (Fig. 4B). This result shows that anthocyanin content did not vary
366 greatly in green leaves but in florets among different broccoli accessions. These findings
367 suggest that florets are responsive to the environmental and growth influences for anthocyanin
368 production in broccoli.

369 The total antioxidant capacity in leaves and florets of broccoli accessions was
370 determined by both DPPH and FRAP methods. The DPPH values showed over 2-fold changes,
371 ranging from 1.6 to 3.5 mg AEAC g⁻¹ FW in leaves of broccoli accessions, while much high
372 DPPH values were observed in a few accessions than others in florets (Fig. 4C). The FRAP
373 values also showed over 2-fold changes in leaves, but very similar in florets among these
374 broccoli accessions (Fig. 4D). A general coincidence in total antioxidant capacity measured by
375 the two DPPH and FRAP methods was observed in leaves, but not in florets of some
376 accessions.

377

378 *3.6. Antioxidant enzyme activities varied in broccoli accessions*

379

380 The activities of antioxidant enzymes, i.e., APX, CAT, and SOD, in these broccoli
381 accessions were examined. Overall, the activities of these enzymes varied depending on
382 accessions. The APX value was 6.2 and 19.4 $\mu\text{mol min}^{-1} \text{mg}^{-1}$ proteins in leaves of accessions
383 1 and 2, respectively, showing a 3-fold difference between the lowest and highest accessions,

384 while it varied from 1.7 to 11.3 $\mu\text{mol min}^{-1} \text{mg}^{-1}$ proteins in florets with a 6-fold difference
385 (Fig. 5A). APX activity was generally lower in florets, though there were some accessions with
386 similar activity in leaves and florets (Fig. 5A). For CAT, approximately 2-fold activity
387 difference was observed in leaves, but not much variation was found in florets among these
388 broccoli accessions (Fig. 5B). There was about 2-fold difference for SOD activity in leaves,
389 and a 5-fold difference in florets with the lowest and highest accessions (Fig. 5C).
390 Interestingly, APX and CAT activities were generally higher in leaves, while SOD activity was
391 lower in leaves than florets. These results indicate the complexity in antioxidant enzymes
392 between leaves and florets of a specific accession or among accessions.

393

394 *3.7 Flavonol accumulation was correlated with antioxidant-related attributes*

395

396 The correlations between flavonols and various parameters analyzed in florets and leaves
397 of these accessions were examined and shown in Figure 6. In florets, positive correlation was
398 observed between anthocyanins and FRAP, and between total flavonoids, DPPH, APX, and
399 SOD ($p < 0.05$), while CAT was negatively correlated with quercetin and anthocyanins ($p < 0.05$)
400 (Fig. 6A). For broccoli leaves, anthocyanins were positively correlated with quercetin, FRAP
401 and SOD, and total flavonoids were correlated with kaempferol, DPPH and FRAP ($p < 0.05$).
402 Moreover, the expression of genes controlling flavonol biosynthesis presented a very strong
403 correlation with kaempferol, flavonoid and antioxidant capacities ($p < 0.05$) (Fig. 6B).
404 Comparing kaempferol and quercetin, there was a weak negative correlation in florets and a
405 weak positive correlation in leaves, but both failed to pass the statistical significance level

406 ($p>0.05$) (Fig. 6A and B), indicating that accumulation of these two flavonols does not interact
407 with each other in either florets or leaves. Between two tissues of leaves and florets, a positive
408 correlation was observed in kaempferol to give a correlation coefficient of 0.586 ($p<0.05$), but
409 not in quercetin and total flavonoids (with a correlation coefficient of -0.100 and 0.101,
410 respectively) ($p>0.05$). These results suggest that flavonols, as well as key biosynthesis
411 pathway genes, exist correlations with antioxidant capacity-related attributes at different
412 extents in broccoli tissues.

413 Principal component analysis (PCA) is a broadly used multivariate technique that
414 extracts important information from a data table with observations of several inter-correlated
415 variables and displays the pattern of similarity of different variables (Abdi & Williams, 2010).
416 PCA revealed that PC1 and PC2 explained 25.9 and 23.1% of total variations (Fig. 6C and D),
417 and these components were mainly the flavonols and antioxidant capacity related indicators
418 (Supplementary Table S3). When the expressions of flavonol biosynthesis genes were included
419 for PCA, the PC1 accounted for 62.57% of total variations between high and low kaempferol
420 accessions (Supplementary Fig. 3, Supplementary Table S4).

421

422 **4. Discussion**

423

424 The flavonols kaempferol and quercetin have gained increasing interests due to their
425 health-promoting properties (Chen & Chen, 2013; Li et al., 2016). Broccoli is known to mainly
426 accumulate these two flavonols (Gliszczynska-Świgło et al, 2007; Molmann et al., 2015;
427 Vallejo et al, 2004). Thus, this attribute along with its multiple health-benefit nutrients and

428 phytonutrients makes broccoli an excellent functional food. In this study, 15 broccoli
429 accessions consisted of both landraces and improved entries (Stansell et al., 2018) were
430 examined for their flavonol levels and antioxidant associated attributes.

431 In broccoli, flavonol content was reported to be affected by floret developmental stage
432 (Krumbein, Saeger-Fink, & Schonhof, 2007), temperature (Molmann et al., 2015), and
433 radiation treatments (Gliszczyńska-Świgło et al, 2007; Molmann et al., 2015;
434 Rybarczyk-Plonska et al, 2016). Here, we showed that great genotypic variations in flavonol
435 content existed in florets among these broccoli accessions (Fig. 1). The kaempferol levels
436 varied over 100-folds, and the quercetin amounts differed over 16-folds. The
437 kaempferol-quercetin ratios ranged between 0.4 to 5.5 in broccoli florets, consistent with
438 previous reports (Gliszczyńska-Świgło et al, 2007; Krumbein et al, 2007). In addition, we
439 examined flavonols in leaves and found that broccoli leaves accumulated much higher levels of
440 kaempferol, but similar quercetin, with less genotypic variation (≤ 4 -folds) than florets (Fig. 1).
441 As a result, there were much higher kaempferol to quercetin ratios in leaves varying between
442 4.4 to 27.9 among different accessions. While kaempferol was the predominant flavonol in
443 leaves, both kaempferol and quercetin accumulated at relatively comparable amounts in florets
444 of various accessions. In addition, DPBA staining of roots showed a good correlation with
445 kaempferol accumulation in other plant tissues, which may provide a good indicator for
446 identifying high kaempferol accumulating varieties at early stages of breeding.

447 Flavonol biosynthesis shares the upstream biosynthetic pathway with other flavonoids
448 and separates at dihydroflavonol (Fig. 2A). Thus, it shares some common key enzymes that
449 include chalcone synthase (CHS), chalcone isomerase (CHI), flavanone 3-hydroxylase (F3H),

450 and flavonoid 3'-hydroxylase (F3'H). FLS catalyzes the conversion of dihydroflavonols into
451 flavonols. In *Brassica napus*, flavonol biosynthesis was found to be promoted by high sucrose,
452 mannitol and NaCl (Vu et al., 2015), similarly as shown in other plants (Fini, Brunetti, Di
453 Ferdinando, Ferrini, & Tattini, 2011). The flavonol accumulation in the *B. napus* is correlated
454 with the *BnFLS* gene expression (Vu et al., 2015). This implies that the *FLS* gene plays a key
455 role in flavonol biosynthesis in *Brassica* crops. Consistently, when examining the expression
456 of flavonol biosynthetic genes, we observed significant difference in *FLS* gene expression
457 along with *F3H* and *F3'H* between high and low kaempferol producing accessions. The much
458 high level of *FLS* transcription in the high kaempferol accession shows its important role for
459 flavonol accumulation in broccoli as in *B. napus* (Vu et al., 2015). Interestingly, while *FLS*
460 gene expression correlated with kaempferol or total flavonol levels, it showed less correlation
461 with the accumulation of quercetin, indicating that additional factors contribute to the
462 regulation of other individual flavonol content in broccoli.

463 Many flavonoids are strong antioxidants (Kumar & Pandey, 2013; Terao, 2009). While
464 the total antioxidant capacity as measured by DPPH and FRAP showed no great differences in
465 both leaves and florets among these broccoli accessions, kaempferol and total flavonoids were
466 generally consistent with the antioxidant capacity and activities of antioxidant enzymes as
467 revealed by Pearson correlation and PCA (Fig. 6). It has been documented that antioxidant
468 capacity is contributed by many biologically active biomolecules, such as vitamin C, phenolic
469 compounds, and carotenoids in plants (Apak, Ozyurek, Guclu, & Capanoglu, 2016). The
470 antioxidant capacity was to some extent correlated with flavonoids and kaempferol, implying

471 that total flavonoid and kaempferol contribute partly and the antioxidant capacity is a
472 composite result of complex factors.

473 Se-biofortified broccoli is a promising approach to supply bioactive forms of Se with
474 strong anticarcinogenic activity (Avila et al., 2013; Lyi et al, 2005; Ramos et al, 2011). We
475 observed that Se-biofortification did not compromise the accumulation of major flavonols
476 kaempferol and quercetin in the broccoli varieties tested (Fig. 3). Thus, it is possible to
477 simultaneously produce bioactive Se compounds and maintain the flavonol levels in edible
478 parts of broccoli to further enhance its chemopreventive properties.

479 In summary, we present a comprehensive evaluation of broccoli germplasm for
480 genotypic variations with flavonols along with total flavonoids and antioxidant capacity. We
481 found great genetic variation in those major flavonols kaempferol and quercetin among the
482 broccoli accessions tested. The information would be useful in selecting and developing
483 broccoli cultivars for high flavonol content with enhanced health-promoting properties.

484

485 **CRedit authorship contribution statement**

486 **Yongbo Duan:** Conceptualization, Investigation, Methodology, Validation, Writing –
487 original draft. **Franklin Eduardo Melo Santiago:** Investigation, Methodology, Validation.
488 **Andre Rodrigues dos Reis:** Data analysis. **Marislaine A. de Figueiredo:** Methodology.
489 **Suping Zhou:** Methodology. **Theodore W. Thannhauser:** Methodology, Writing - review &
490 editing. **Li Li:** Conceptualization, Validation, Supervision, Writing- review & editing.

491

492 **Declaration of Competing Interests**

493 The authors declare that they have no known competing financial interests or personal
494 relationships that could have appeared to influence the work reported in this paper.

495

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502

503 **Supplementary data**

504 Supplementary data to this article can be found online

505

506

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635

636 **Figure legends**

637 **Fig. 1.** Kaempferol and quercetin levels in various broccoli accessions. (A) Kaempferol and
638 quercetin levels in leaves. (B) Kaempferol and quercetin levels in florets. (C) Representative
639 images of DPBA staining on roots of 5 days old broccoli plants from genotype 8 and 12. The
640 numbers indicate the germplasm ID numbers listed in Supplementary Table S1. Bars
641 represent 3 mm.

642

643 **Fig. 2.** Flavonol biosynthetic pathway and relative expression of the pathway genes. (A)
644 Outline of flavonol biosynthetic pathway. (B) qRT-PCR analysis of expression of flavonol
645 biosynthetic genes in two high (2 and 8) vs two low (12 and 14) kaempferol genotypes. Error
646 bars indicate standard error of the mean ($n=3$). The different lowercases stand for significant
647 difference between accessions for each gene ($p<0.05$). CHS, chalcone synthase; DFR,
648 dihydroflavonol 4-reductase; F3H, flavanone hydroxylase; F3'H, flavonoid 3'-hydroxylase;
649 FLS, flavonol synthase; Myb2, MYB transcription factor 2.

650

651 **Fig. 3.** Effect of selenium on kaempferol and quercetin levels. (A) Effect of selenium on
652 kaempferol levels in leaves and florets of three broccoli cultivars treated with or without 25
653 $\mu\text{M Na}_2\text{SeO}_4$. (B) Effect of selenium on quercetin levels. Error bars indicate standard error of
654 the mean ($n=3$). * Represents significant difference ($p < 0.05$)

655

656 **Fig. 4.** Total levels of flavonoids, anthocyanins, and antioxidant capacities in leaves and florets of
657 different broccoli accessions. (A) Flavonoid levels. (B) Anthocyanin levels. (C) Antioxidant capacity

658 by DPPH assay. (D) Antioxidant capacity by FRAP assay. Error bars indicate standard error of the
659 mean ($n=3$).

660

661 **Fig. 5.** Antioxidant enzyme activities in leaves and florets of different broccoli accessions. (A)
662 Ascorbate peroxidase (APX) activity. (B) Catalase (CAT) activity. (C) Superoxide dismutase
663 (SOD) activity. Error bars indicate standard error of the mean ($n=3$).

664

665 **Fig. 6.** Heatmap of Pearson correlation coefficients obtained from variables of broccoli plants.
666 (A) Corresponds to physiological parameters analyzed in florets, and (B) analyzed in leaves. *
667 indicates significant correlation ($p < 0.05$). (C) PCA triplot showing the loading of each
668 genotype score (points) and groups (circles). (D) PCA triplot showing the loading of plant
669 attributes (arrows). Nearby points correspond to observations with similar scores in the PCA
670 components. The length of the arrows indicates the variation of attributes in the component,
671 while the points between them indicate their correlations. Kaemp: kaempferol, Quer: quercetin,
672 Anth: anthocyanin, Fla: flavonoids, FRAP: ferric reducing antioxidant power, DPPH:
673 2,2-diphenyl-1-picryl-hydrazyl-hydrate, SOD: superoxide dismutase, CAT: catalase, APX:
674 ascorbate peroxidase.











