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3 **Manipulation of plant primary metabolism by leaf-mining larvae**
4 **in the race against leaf senescence**

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22 *Running head:* Plant nutrient alteration by a leafminer

23
24 **Conflict of interest**

25
26 The authors declare that there is no conflict of interest.

27
28 **Author Contributions**

29
30 MJAB and DG designed the overall study, and set up the analytical protocols for total
31 sugars, starches, and protein-bound and free amino acid analyses. MJAB carried out the
32 experiments and analyzed the data, supervised by DG. The interpretation and writing drafts
33 were done by MJAB, JC and DG.

35 **Abstract**

36

37 Plants are often considered as suboptimal food for phytophagous insects, requiring
38 them to employ various adaptive mechanisms to overcome food nutritional imbalances. This
39 could include host-plant manipulation and/or symbiotic associations. The extensive
40 reconfiguration of plant primary metabolism upon herbivory, as well as its impact on
41 herbivores, have been largely overlooked, while studies investigating secondary metabolites is
42 extensive. Here, we document how the apple leaf-mining caterpillar *Phyllonorycter*
43 *blancardella*, a highly-specialized insect which completes development within a restricted
44 area of a single *Malus domestica* leaf over successive different larval feeding modes,
45 maintains nutrient-rich green tissues in its feeding area on green and senescent leaves. For this
46 purpose, we quantified a large number of compounds involved in plant primary metabolism:
47 starch, total soluble sugars, five individual sugars, twenty protein-bound amino acids and
48 twenty free amino acids. Plant alteration can be observed not only on senescing
49 (photosynthetically inactive) but also normal (photosynthetically active) leaf tissues of its
50 host-plant to compensate for detrimental environmental variations. Our results show a
51 differential control of the primary metabolism depending on the larva developmental stage,
52 itself correlated to the fluid-feeding and tissue-feeding modes. Our results also suggest that
53 leaf amino acid alterations favor a faster insect development. Finally, chemical scores indicate
54 that the most growth-limiting essential amino acids are also common to other phytophagous
55 insects and large herbivores, suggesting that these limitations are a general consequence of
56 using plants as food source. We discuss the possible mechanisms responsible for these
57 different manipulative capacities, as well as their ecological implications.

58

59 **Key words**

60

61 plant-insect interaction; nutrition; nutritional homeostasis; plant primary metabolism; sugars;
62 essential amino acids; herbivorous insect; leaf-miner; feeding strategies; leaf senescence;
63 plant manipulation.

64

65 Introduction

66
67 Plants are abundantly present on Earth and are at the basis of most food webs.
68 However, they are often suboptimal food sources for herbivores for three reasons (Mattson,
69 1980; Schoonhoven et al., 2005; Zhou et al., 2015). First, plant nutrient composition is highly
70 variable according to plant species, organ, season, and other environmental factors (Karasov
71 and Martínez Del Rio, 2007; Schoonhoven et al., 2005; Gündüz and Douglas, 2009). Such
72 variations of plant nutritional quality affect herbivore performance (Karley et al., 2002;
73 Schoonhoven et al., 2005; Larbat et al., 2016). Second, under pathogen infection and
74 herbivore attack, plants mount a defense response and increasing evidence shows an extensive
75 reprogramming of plant metabolism (Schwachtje and Baldwin, 2008; Bolton, 2009; Kerchev
76 et al., 2012). Recent studies demonstrate that hundreds of plant genes involved in defensive
77 pathways are up-regulated during a plant-herbivore interaction and a substantial fraction of
78 them belong to the primary metabolism (Kessler and Baldwin, 2002; Schwachtje and
79 Baldwin, 2008; Kerchev et al., 2012; Zhou et al., 2015). Third, nitrogen is considered to be
80 the most limiting element for the growth of most herbivores (Mattson, 1980; Van Zyl and
81 Ferreira, 2003; Barbehenn et al., 2013; Zhou et al., 2015) and there is ample evidence that
82 amino acid acquisition (including protein-bound and free amino acids) does not match the
83 proportion of essential amino acids (EAAs) they require. Indeed, nitrogen concentration in
84 plants is generally low compared with animal tissues (Bernays and Chapman, 1994; Karasov
85 and Martínez Del Rio, 2007). Thus, the challenge for herbivore is to find and eat foods that
86 contain the best blend of nutrients (specific composition in specific tissues) and at the most
87 adequate concentration (overall plant sugar and/or amino acid content) (Chown and Nicolson,
88 2004; Schoonhoven et al., 2005; Klowden 2007). Otherwise, acquisition of unbalanced food
89 could impair key physiological processes such as protein synthesis, and/or would require
90 sophisticated and costly adaptations (Horie and Watanabe, 1983; Karowe and Martin, 1989;
91 Douglas et al., 2001; Suzuki et al., 2009).

92
93 Because of the major nutritional discrepancy which clearly exists between plant
94 nutrient supply and herbivore nutritional requirements, some species have developed different
95 strategies such as symbioses with microorganisms that supplement insects with limiting EAAs
96 (Douglas, 2006, 2009, 2013, and references therein). Alternatively, many folivorous
97 organisms are selective feeders, consuming certain tissues or cell types and rejecting others.
98 This gives them the unique possibility to consume high-quality tissues in an otherwise low-
99 quality plant or plant organ. Many leaf-mining insects, for example, consume internal
100 mesophyll cells and do not eat epidermis and/or vascular tissues (Hering, 1951; Kimmerer
101 and Potter, 1987; Scheirs et al., 2001; Body et al., 2015). Other insects, such as aphids, are in
102 more privileged position than chewing insects, because nearly all nitrogen-containing
103 compounds in phloem sap can be utilized (Schoonhoven et al., 2005); still, they often, if not
104 always, rely on symbionts to provide them with key EAAs (Douglas et al., 2001; Wu et al.,
105 2006). Finally, other organisms modify the nutritional quality of the host-plant for their own
106 needs by creating specialized tissues to feed on (Hartley, 1998; Nakamura et al., 2003;
107 Koyama et al., 2004; Dardeau et al., 2015), by upregulating protein and/or sugar synthesis *in*
108 *situ* (Saltzmann et al., 2008), and/or by modifying source-sink relationships leading to nutrient
109 translocation towards the insect's feeding site (Larson and Whitham, 1991). The flow of
110 nutrients towards the infection site, which thus behaves as a metabolic sink, has obvious
111 advantages to insects by fueling energetic requirements for growth, survival and reproduction
112 (Stone and Schönrogge, 2003; Giron et al., 2007, 2016; Body et al., 2013). This has been
113 clearly demonstrated, for example, with radioactively labelled nutrients that are preferentially
114 transported and accumulated in specific areas exploited by herbivorous insects (Larson and

115 Whitham, 1991). For example, some gall-inducing insects enhance their nutritional
116 environment by increasing the abundance of plant free amino acids and/or sugars through
117 alteration of their synthesis and/or transport (Larson and Whitham, 1991; Eleftherianos et al.,
118 2006; Saltzmann et al., 2008; Dardeau et al., 2015). Interestingly, improved nutrition does not
119 necessarily imply increased nutrient concentrations, but an adequate composition and/or
120 quantity, leading to a finely tuned regulation of nutrient contents in some biological systems,
121 such as for gall-inducing insects *Neuroterus quercus-baccarum* and *Andricus lignicola*
122 (Hartley and Lawton, 1992; Diamond et al., 2008).

123
124 Although qualitative and quantitative variation in *primary* plant compounds, as
125 opposed to the well know secondary compounds, can have profound effects on phytophagous
126 insect preferences and performances, little is known about plant *primary* metabolism
127 reconfiguration after herbivore attack (Machado et al., 2013, 2015) and data concerning
128 specific feeding-guild with high nutritional constraints are scarce (Schoonhoven et al., 2005).
129 Plant nutrient availability is particularly crucial for endophagous insects such as stem-borers,
130 gall-inducers, and leaf-miners. Their entire life-cycle is indeed usually restricted to the same
131 plant organ without diet switching capacities as observed for free-living external-feeding
132 insects (Hering, 1951; Stone and Schönrogge, 2003; Body et al., 2015). As such, they are the
133 most appropriate feeding-guild in which to examine nutritional constraints imposed by the
134 plant and adaptive strategies adopted by the insect to overcome these constraints.
135 Additionally, changes in the ability and/or need to manipulate the host-plant physiology is
136 expected to vary across insect feeding-mode and developmental stages (Schoonhoven et al.,
137 2005), as herbivorous insects possess a diverse range of feeding habits which differ in the
138 nutritive source they have access to and as nutritional requirements change during the insect
139 development. This prompted us to carry out a detailed biochemical investigation of plant
140 carbohydrate and amino acid profiles in the host-plant *Malus domestica* following attack by
141 the leaf-mining caterpillar *Phyllonorycter blancardella* according to the strongly differing
142 larval feeding-modes.

143
144 *P. blancardella* leaf-mining moth presents an important degree of specialization for its
145 host-plant and a complete development within a restricted area of a single leaf (Hering, 1951;
146 Pottinger and LeRoux, 1971; Connor and Taverner, 1997; Body et al., 2015). In this species,
147 first instars are ‘fluid-feeders’ while the two last instars are ‘tissue-feeders’ due to a
148 hypermetamorphosis of their mouthparts (characteristic changes in morphology and habit
149 between two successive instars) (Body et al., 2015). Previous studies on this biological system
150 focused on later tissue-feeding instars only (Giron et al., 2007; Kaiser et al., 2010; Body et al.,
151 2013; Zhang et al., 2016, 2017). This leaf-miner is able to induce an accumulation of
152 cytokinins in mined tissues which is responsible for the preservation of photosynthetically
153 active green tissues (‘green-island’ phenotype) at a time when leaves are otherwise turning
154 yellow (i.e. senescent leaves) (Engelbrecht et al., 1969; Giron et al., 2007; Kaiser et al., 2010;
155 Body et al., 2013; Zhang et al., 2017). Host-plant physiological alterations occur through an
156 unexpected association with endosymbiotic bacteria (*Wolbachia*) (Kaiser et al., 2010; Body et
157 al., 2013; Giron and Glevarec, 2014; Gutzwiller et al., 2015). The correlation between the
158 green-island phenotype and *Wolbachia* infections has also been highlighted in numerous
159 species of Gracillariidae leaf-mining moths (Gutzwiller et al., 2015). The strong
160 reprogramming of the plant phytohormonal balance (CKs, JA, SA, ABA; Body et al., 2013;
161 Zhang et al., 2016) reported is associated with the regulation of sugar content (Body et al.,
162 2013), inhibition of leaf senescence (Kaiser et al., 2010) and mitigation of plant direct and
163 indirect defense (Giron et al., 2016; Zhang et al., 2016).

164

165 To gain insight into the extend of nutrient regulation and subsequent consequences for
166 *P. blancardella* leaf-miners developing under harsh environmental conditions, we first
167 characterized how larvae with different feeding-modes (fluid- vs. tissue-feeding instars)
168 impact starch, soluble sugar, and protein-bound and free amino acid profiles at their feeding
169 site both on green and on yellow senescing leaves. Senescence is a particularly decisive
170 moment for these insects due to the profound alteration of the plant physiology including the
171 nutrient (sugars and degraded proteins) remobilization to roots. In the Fall, when nutrients
172 become too low, the insect growth usually stops (Edwards and Wratten, 1980). If *P.*
173 *blancardella* fluid-feeding larvae fail to reach the tissue-feeding stage before low Fall
174 temperatures, caterpillars will not be able to complete their development and to pupate which
175 lead to an increased mortality rate (Pottinger and LeRoux, 1971).

176 Sugars and amino acids play a crucial role in life maintenance as a large source of
177 energy for insects, as a structural component of cuticular chitin, and as feeding and
178 oviposition stimulants (Dadd, 1985; Nation, 2002). Estimating if observed plant physiological
179 modifications are beneficial for the insect requires us to measure the impact of various food
180 compositions on insect fitness-related traits. The lack of artificial diet for bioassays with leaf-
181 mining insects impairs such analyses. However, the use of indirect method such as “chemical
182 scores” allows to determine growth-limiting EAAs for herbivores (Van Zyl and Ferreira,
183 2003; Barbehenn et al., 2013). We thus estimated dietary EAA requirements of the leaf-
184 mining larvae by determining the whole-body EAA composition of the insect and confronting
185 these results with plant chemical profiles (Rock, 1972; Van Zyl and Ferreira, 2003; Anderson
186 et al., 2004; Barbehenn et al., 2013). In this study, we expected (*i*) a finely-tuned nutrient
187 accumulation (sugars and amino acids) at the feeding site to meet insect nutritional
188 requirements, and (*ii*) a differential control of the nutritional content depending on the larva
189 developmental stage as the impact of herbivory on plant tissues is correlated to leaf-miner
190 feeding-mode.

191

192 **Materials and Methods**

193

194 *Study species and sampling sites*

195 The experiments were conducted on *Malus domestica* (Borkh. 1803) (Rosaceae)
196 apple-tree leaves naturally infected by the spotted tentiform leaf-miner, *Phyllonorycter*
197 *blancardella* (Fabricius, 1781) (Lepidoptera: Gracillariidae). This leaf-miner species is a
198 polyvoltine microlepidopteran widely distributed in Europe whose first three instars are fluid-
199 feeders and two following instars are selective tissue-feeders (Pottinger and LeRoux, 1971;
200 Body et al., 2015).

201 Both green and yellow mined leaves (only one mine per leaf), and unmined green and
202 yellow leaves (an adjacent neighboring leaf), were simultaneously collected in the field
203 between 08:00 a.m. and 10:00 a.m. in early Falls 2009-2011 on 16-18-year-old apple-trees
204 (“Elstar” varieties), in a biologically managed orchard in Thilouze, France (47° 14' 35” North,
205 0° 34' 43” East). Collected leaves and associated larvae were immediately kept and dissected
206 on ice, and stored at -80 °C until analysis. The synchronization of sampling is crucial as levels
207 of sugars, for example, greatly vary during the day and among trees. This requires collecting
208 green and yellow leaves (mined leaves and their unmined control leaves) simultaneously and
209 on the same tree to make sure that physiological differences observed are due to the impact of
210 the leaf-miner on plant tissues and not to phenological changes in the tree.

211 In order to study spatial (mined vs. unmined areas) and temporal (senescence)
212 variations of starch, total and individual sugar, and protein-bound and free amino acid
213 concentrations, mined tissues (zone M; leaf-mining insects and faeces were removed from the
214 mine), ipsilateral tissues (zone UM¹; leaf tissues on the same side of the main vein as the

215 mine), and contralateral tissues (zone UM²; leaf tissues on the opposite side of the main vein
216 as the mine) were dissected both on green and on yellow leaves (Figure 1.1). Non-infected
217 green and yellow leaves (zone UM³) were also dissected as previously and used as a control
218 (Giron et al., 2007; Body et al., 2013).

219

220 *Sample preparation*

221 Each leaf sample was lyophilized (Bioblock Scientific Alpha 1-4 LD plus
222 lyophilizator) according to the following cycle: primary desiccation of 1 hour at -10°C and 25
223 mbar, and a secondary desiccation overnight at -76°C and 0.0010 mbar. Samples were then
224 ground(ed?) in liquid nitrogen after in order to have an extra-fine leaf powder. Similar
225 amounts (5 mg) of mined (M), ipsilateral (UM¹), contralateral (UM²) and control (UM³) plant
226 tissues were used to allow qualitative and quantitative comparisons (Sartorius micro-balance
227 model 1801-001, Sartorius SA, Palaiseau, France).

228

229 *Carbohydrate quantification*

230 Leaf samples used for this experiment were as follow: *green leaves*: N = 15 for fluid-
231 feeding instars, N = 25 for tissue-feeding instars, N = 120 for unmined green control; *yellow*
232 *leaves*: N = 15 for fluid-feeding instars, N = 25 for tissue-feeding instars, N = 120 for
233 unmined yellow control.

234 *Carbohydrate extraction* – Prior to colorimetric quantifications, chlorophyll and other
235 pigments were removed from leaf tissues (5 mg) with acetone (100 %) until complete
236 elimination of natural coloration. Sugars were then extracted with vortex agitation for 30 sec
237 at room temperature in 1 mL aqueous methanol (80 %) (Fisher Scientific; Hampton, New
238 Hampshire, USA). After centrifugation at 1500 rpm, soluble sugars remained dissolved in the
239 supernatant and were used for: (i) total soluble sugars quantification by colorimetric assays
240 following Van Handel's protocol (1985) as modified by Giron et al. (2002) for microsamples,
241 and (ii) for characterization of individual sugars by capillary electrophoresis using a
242 modification of Rovio's protocol optimizing sugars separation and data reproducibility (Rovio
243 et al., 2007; see Body et al., 2013 for details). Starches remained in the pellet were quantified
244 using a modification of colorimetric techniques developed by Hansen and Møller (1975),
245 Marshall (1986) and Oren et al. (1988). The anthrone reagent consisted of 1.0 g of anthrone
246 (Sigma Aldrich; St. Louis, Missouri, USA) dissolved in 500 mL of concentrated sulfuric acid
247 (Fisher Scientific; Hampton, New Hampshire, USA) added to 200 mL of MilliQ water (Merck
248 Millipore; Billerica, Massachusetts, USA).

249 *Starch quantification* – Leaf material (pellet) kept for starch quantification was
250 suspended in 1 mL of hydrochloric acid 1.1 % (Fisher Scientific; Hampton, New Hampshire,
251 USA), vortexed and placed in a water bath at 90 °C for 30 min to extract and hydrolyze starch
252 into glucose molecules. In a new set of tubes, 1 mL of anthrone reagent was then added to 35
253 µL of the extraction solution for each sample. The tubes were reheated at 90 °C for 15 min,
254 cooled down at 0 °C for 5 min, vortexed. Absorbance was then read in a spectrophotometer at
255 630 nm (DU®-64 spectrophotometer; Beckman, Villepinte, France). For starches, calibration
256 curves that allowed us to transform absorbance into concentrations were made with standard
257 glucose (Sigma Aldrich; St. Louis, Missouri, USA).

258 *Total soluble sugar quantification* – For each sample, 100 µL of initial aqueous
259 methanol supernatant were transferred into a borosilicate tube (16 x 100 mm; Fisher
260 Scientific; Hampton, New Hampshire, USA) and placed in a water bath at 90 °C to evaporate
261 the solvent down to a few microlitres. After adding 1 mL of anthrone reagent, the tubes were
262 placed in a water bath at 90 °C for 15 min, cooled down at 0 °C for 5 min, vortexed and then
263 read in a spectrophotometer at 630 nm (DU®-64 spectrophotometer; Beckman, Villepinte,
264 France). For total soluble sugars, calibration curves were corrected for the underestimation of

265 sugar alcohols using a sugar mixture (sorbitol, trehalose, sucrose, glucose and fructose; Sigma
266 Aldrich; St. Louis, Missouri, USA) (Body et al., 2013; Body et al., 2018) close to the
267 composition of mined and unmined tissues both on green and on yellow leaves (Figure 2).

268 *Individual sugars quantification and capillary electrophoresis conditions* – Remaining
269 supernatants from previous extractions were used for individual sugars assay by capillary
270 electrophoresis (Proteome lab™ PA800, 32Karat data acquisition software; Beckman Coulter;
271 Brea, California, USA) (Rovio et al., 2007). For each sample, 500 µL of supernatant were
272 filtered at 0.45 µm (Whatman®; Maidstone, United Kingdom) and then lyophilized (Bioblock
273 Scientific Alpha 1-4 LD plus lyophilizator). Right before analysis, sugars were resuspended
274 by vortex agitation in 18 µL of MilliQ water (Merck Millipore; Billerica, Massachusetts,
275 USA) and 2 µL melezitose 50 mM (Sigma Aldrich; St. Louis, Missouri, USA), as an internal
276 standard, and then centrifuged briefly. For sugar separation, we used a raw silica capillary of
277 50 µm internal diameter and 67 cm total length (Beckman Coulter; Brea, California, USA).
278 Samples (2.77 nL) were injected and maintained at 15 °C during all the separation which
279 occurred at 16 kV (typical current 90 µA) and lasted for maximum 60 min. The electrolyte
280 was composed of NaOH 130 mM and Na₂HPO₄·12H₂O 36 mM, pH 12.6 (Rovio et al., 2007).
281 The UV detection wavelength was 264 nm. The control solution was composed of 7 standard
282 sugars at 5 mM: D-(+)-xylitol, D-(+)-sorbitol, D-(+)-trehalose, D-(+)-melezitose (internal
283 standard), D-(+)-sucrose, le D-(+)-glucose and D-(+)-fructose. All sugar standards were
284 purchased at Sigma Aldrich (St. Louis, Missouri, USA). Data were processed with the
285 32Karat™ Software (version 7.0) which allowed for the determination of retention times and
286 peak areas for each reference sugars (standards sugars).

287 *Data analysis* – Individual sugar analysis revealed the presence of only five main
288 sugars: sorbitol (retention time: 17.5 min), trehalose (RT: 17.7 min), sucrose (RT: 21.0 min),
289 glucose (RT: 27.8 min), and fructose (RT: 29.3 min) [internal standard, melezitose, RT: 20.3
290 min]. However, as trehalose had a low concentration, was partially co-eluted with another
291 sugar (sorbitol), and highly variable, data were not included in the present study in order to
292 avoid large estimation errors for this sugar. Unlike trehalose, sorbitol was highly concentrated
293 in apple-tree leaves leading to an accurate/reliable quantification with a negligible estimation
294 error due to this partial peak co-elution.

295 In order to compare the biochemical composition of mined and unmined tissues, we
296 had to take into account the withdrawal of sugar-rich mesophyll tissues by leaf-mining insects
297 and the over-representation of sugar-free epidermis in the mined tissue samples. For this
298 purpose, gravimetry was used to estimate the amount of mesophyll eaten by the larva and to
299 correct biochemical data of leaf tissues accordingly (see Supplement 1 for details). All data
300 presented are thus corrected for the amount of tissues eaten by larvae as this parameter was
301 highly significant for all sugars (*Student's paired t-test*: $P < 0.001$ for total sugars, sucrose,
302 glucose and fructose; *Wilcoxon paired test*: $P < 0.01$ for sorbitol).

303
304 *Amino acids quantification*

305 Two sets of leaf samples were used for this experiment (one for protein-bound amino
306 acid and one for free amino acid) and were as follow for each set: *green leaves*: N = 15 for
307 fluid-feeding instars, N = 30 for tissue-feeding instars, N = 135 for unmined green control;
308 *yellow leaves*: N = 15 for fluid-feeding instars, N = 30 for tissue-feeding instars, N = 135 for
309 unmined yellow control.

310 *GC-MS conditions* – Standard physiological amino acids at a concentration of 200
311 nmol.ml⁻¹, norvaline used as internal standard and reagents were supplied in the EZ:faast GC-
312 MS kit for amino acid analysis (Phenomenex; Torrance, California, USA). A Perkin Elmer
313 AutoSystemXL gas chromatograph was directly coupled to a Perkin Elmer TurboMass mass
314 spectrometer (Perkin Elmer; Waltham, Massachusetts, USA). A 10 m x 0.25 mm ZB-AAA

315 column from EZ:faast kit of Phenomenex (Torrance, California, USA) was used. The carrier
316 gas helium (Air Liquide; Paris, France) flow was kept constant at 1.1 mL/min. The oven
317 temperature program was a 30 °C/min ramp from 110 °C to 320 °C. The temperature of the
318 injection port was 250 °C. The MS temperatures were as follows: ion source (electronic
319 impact) 200 °C, and inlet line temperature 310 °C. The scan range was 3.5 scans/s and mass
320 detected between 45 and 450. Under these conditions a 2 µL sample was injected in splitless
321 mode during 30 sec.

322 *Free amino acid extraction* – On a subset of samples, free amino acids from leaf or
323 insect samples were extracted with vortex agitation for 30 sec at room temperature in 1 mL
324 acetonitrile 25 % (Fisher Scientific; Hampton, New Hampshire, USA) in hydrochloric acid
325 0.01 N (1:3, v:v) (Fisher Scientific; Hampton, New Hampshire, USA).

326 *Protein-bound amino acid extraction* – On another subset of samples, proteins were
327 hydrolyzed into their protein-bound amino acids in a sealed glass tube at 150 °C for 2 h with
328 500 µL methanesulfonic acid 4 M (Fisher Scientific; Hampton, New Hampshire, USA) after
329 flushing out air with a gentle stream of nitrogen gas. Unlike HCl hydrolysis, methanesulfonic
330 acid hydrolysis allowed the determination of all residues, including tryptophan (Chiou and
331 Wang, 1988; Fountoulakis and Lahm, 1998). Following hydrolysis, the hydrolysates were
332 partially neutralized with 1 mL sodium carbonate 1 M. Prior analysis, samples were
333 transferred in a 1.5 mL Eppendorf tube and pH were checked to be in the range 1.5-5.0.

334 *Amino acid derivatization and quantification* – One hundred µL of each sample
335 (protein-bound or free amino acid extract) were pipetted into a glass vial and 100 µL of
336 internal standard (norvaline at 200 nmol.mL⁻¹) were added. After solid-phase extraction
337 (SPE), sample derivatization was performed as described in Phenomenex kit protocol.
338 Samples were then concentrated under a gentle stream of nitrogen gas (Air Liquide; Paris,
339 France) under 5 µL and immediately injected into the GC-MS system.

340 *Data analysis* – Chromatograms were analyzed with the TurboMass software (version
341 5.4.2; Perkin Elmer; Waltham, Massachusetts, USA). Retention times and characteristic ions
342 were as follow: alanine (RT: 1.5 min; ions: 130, 70), glycine (RT: 1.6 min; ions: 116, 74),
343 valine (RT: 1.8 min; ions: 158, 72), leucine (RT: 2.0 min; ions: 172, 86), isoleucine (RT: 2.1
344 min; ions: 172, 130), threonine (RT: 2.3 min; ions: 160, 101), serine (RT: 2.3 min; ions: 203,
345 146, 101), proline (RT: 2.4 min; ions: 243, 156), asparagine (RT: 2.5 min; ions: 155, 69),
346 arginine (RT: 3.1 min; ion: 303), aspartate (RT: 3.1 min; ions: 216, 130), methionine (RT: 3.2
347 min; ions: 277, 203), glutamate (RT: 3.5 min; ions: 230, 170, 84), phenylalanine (RT: 3.5
348 min; ions: 206, 190, 148), cysteine (RT: 3.9 min; ions: 248, 206, 162), glutamine (RT: 4.2
349 min; ions: 187, 84), lysine (RT: 4.8 min; ions: 170, 128), histidine (RT: 5.0 min; ions: 282,
350 168), tyrosine (RT: 5.3 min; ions: 206, 107), tryptophan (RT: 5.6 min; ion: 130), and cystine
351 (RT: 6.4 min; ions: 248, 216) [internal standard, norvaline, RT: 1.9 min; ion: 158]. The
352 elution did not allow the separation of all amino acids (threonine was co-eluted with serine,
353 arginine with aspartate, and glutamate with phenylalanine), which prevent from determining
354 accurately their limitation in mined tissues for leaf-mining larvae. The co-eluted peaks are,
355 unfortunately, undistinguishable. In order to determine changes in leaves in essential (EAA)
356 and non-essential (NEAA) amino acids separately, concentrations of co-eluted EAA and
357 NEAA were thus estimated, for simplicity, by dividing co-eluted peaks by two, assuming that
358 both amino acids were present in the same quantities in each sample.

359
360 *Limiting essential amino acids in mined tissues*

361 The plant nutritional quality represented by the amino acid pool available can be
362 estimated based on which EAAs [valine (Val), leucine (Leu), isoleucine (Ile), threonine (Thr),
363 arginine (Arg), methionine (Met), phenylalanine (Phe), lysine (Lys), histidine (His), and
364 tryptophan (Trp), that animals cannot synthesize *de novo*] have the lowest abundance relative

365 to the composition required by an herbivore (growth-limiting EAAs) (Van Zyl and Ferreira,
366 2003; Barbehenn et al., 2013). All calculations were performed using total amino acid content
367 which is composed of protein-bound and free amino acids. The composition of each EAA was
368 calculated as ($\mu\text{g EAA in sample} \div \mu\text{g total amino acids in sample}$) $\times 100$. Total amino acids
369 are composed of protein-bound and free amino acids. The chemical score for each EAA was
370 calculated as the composition of the EAA in mined tissues \div composition of the EAA in the
371 leaf-miner (Barbehenn et al., 2013). Chemical scores were calculated using the mean values
372 from mined tissues and whole leaf-mining insect. For example, the chemical score of histidine
373 for tissue-feeding instars on yellow leaves is calculated as follows: His in the leaf mined
374 tissues (0.59 % of total amino acids) \div His in the body of the leaf-mining insect (62.32 % of
375 total amino acids) = 0.01. The EAAs with chemical scores lower than 1 were defined as
376 limiting EAAs (Barbehenn et al., 2013).

377

378 *Statistical analysis*

379 Statistical analyses were performed using R version 3.2.1 and RStudio version
380 0.99.467 (The R Foundation for Statistical Computing, Vienna, Austria). Preliminary
381 statistical analysis showed that the nutrient content of unmined zones (UM¹, UM², UM³) were
382 identical (*Behrens-Fisher test*: $P > 0.05$), allowing for the statistical analysis of mined (M)
383 versus unmined tissues (UM; ipsilateral + contralateral + non-infected leaf) in the result
384 section. The total soluble sugar, individual sugar, protein-bound and free amino acid contents
385 were analyzed separately using *Kruskal-Wallis test* and *Behrens-Fisher post-hoc test*. The
386 sugar composition from different subsets of leaves/tissues was analyzed using multivariate
387 analysis of variance (*MANOVA*). For *MANOVA* analyses, we used the *Pillai's test statistic*.
388 Where significant effects were observed, post-hoc comparisons were performed. All nutrient
389 quantities are presented in $\mu\text{g per mg}$ of dry weight (DW) as average \pm standard error of the
390 mean (S.E.M.).

391

392 *Abbreviations*

393 EAAs essential amino acids, NEAAs non-essential amino acids, *Ala* alanine, *Arg*
394 arginine, *Asn* asparagine, *Asp* aspartate, *Cys* cysteine, *Gln* glutamine, *Glu* glutamate, *Gly*
395 glycine, *His* histidine, *Ile* isoleucine, *Leu* leucine, *Lys* lysine, *Met* methionine, *Phe*
396 phenylalanine, *Pro* proline, *Ser* serine, *Thr* threonine, *Trp* tryptophan, *Tyr* tyrosine, *Val*
397 valine.

398

399 **Results**

400

401 *Alteration of primary metabolism in mined tissues*

402 To evaluate the impact of leaf-mining larvae on the nutritional value of plant tissues,
403 we conducted experiments investigating carbon and nitrogen contents (starch, total soluble
404 and individual sugars, and protein-bound and free amino acids) of mined tissues compared to
405 unmined control tissues. See Supplement 2 for a detailed statistical analysis concerning
406 carbohydrates and Supplements 3 and 4 concerning amino acids. The data are presented in
407 Figures 1 and 2 for carbohydrates and in Figures 3, 4 and 5 for amino acids.

408 *Sugars* – Individual sugar analysis revealed the presence of five main sugars: sorbitol,
409 trehalose, sucrose, glucose, and fructose. Trehalose data were not included (see Material and
410 Methods section). Senescence leads to a drastic reduction of the total amount of sugars (*green*
411 *control*: $104.0 \pm 2.4 \mu\text{g.mg}^{-1}$ DW; *yellow control*: $50.6 \pm 1.3 \mu\text{g.mg}^{-1}$ DW; *Behrens-Fisher*
412 *test*: $P < 0.001$) and an alteration of the specific sugar composition (*MANOVA*: $F_{4,75} = 18.49$,
413 $P < 0.001$; Figures 1 and 2 – green controls vs. yellow controls; Supplement 2A, left column).
414 Amounts of total and individual sugars in tissues mined by fluid-feeders are similar but not

415 statistically identical on green and on yellow leaves (Supplement 2A, middle column),
416 whereas tissues mined by tissue-feeders remain statistically similar during senescence
417 (Supplement 2A, right column).

418 Composition analysis (Figure 2) showed that, on green leaves, tissues mined by fluid-
419 (Supplements 2B and 2D, left column) and tissue-feeders (Supplements 2C and 2D, left
420 column) are similar to unmined green controls for both total sugar content and specific sugar
421 composition. By contrast, on yellow leaves, the sugar composition of tissues mined by fluid-
422 feeders is identical to the composition of unmined yellow controls (Supplement 2B, right
423 column), whereas for tissues-feeders, the sugar composition of mines is similar to unmined
424 green controls (Supplement 2C, right column).

425 *Starch* – Senescence leads to the decrease of starch content from $73.54 \pm 3.00 \mu\text{g.mg}^{-1}$
426 DW in green controls to $53.28 \pm 2.27 \mu\text{g.mg}^{-1}$ DW in yellow controls (Supplement 2A, left
427 column). Starch amounts in leaf tissues mined by fluid-feeders (*green leaves*: 34.57 ± 4.25
428 $\mu\text{g.mg}^{-1}$ DW; *yellow leaves*: $40.42 \pm 3.96 \mu\text{g.mg}^{-1}$ DW) are similar both on green and on
429 yellow leaves (Supplement 2, middle column), whereas in leaf tissues mined by tissue-
430 feeders, starch quantities (*green leaves*: $77.31 \pm 5.10 \mu\text{g.mg}^{-1}$ DW; *yellow leaves*: $48.76 \pm$
431 $5.01 \mu\text{g.mg}^{-1}$ DW) differ on green and on yellow leaves (Supplement 2A, right column) and
432 are close to their respective controls (Supplement 2C).

433 *Amino acids* – Senescence leads to a metabolic reconfiguration of the leaves with a
434 drastic reduction of the protein-bound amino acid content (from 1.98 ± 0.20 to 0.65 ± 0.06
435 $\mu\text{g.mg}^{-1}$ DW) and an increase of free amino acid content (from 0.17 ± 0.01 to 0.39 ± 0.03
436 $\mu\text{g.mg}^{-1}$ DW) (Figures 3, 4 and 5; Supplements 3 and 4, left columns). In mined tissues, both
437 on green and on yellow leaves, the protein-bound amino acid content remains stable and
438 similar to unmined green controls (Figures 3A and 3B; Supplement 3A, middle and right
439 columns; Supplements 3B and 3C, left columns; Supplement 3D). This pattern can be
440 observed for both fluid- and tissues-feeders and for almost each individual protein-bound
441 amino acid (Figure 4). Contrary to protein-bound amino acids, free amino acid content is
442 closely associated to larvae developmental stages (Figures 3C and 3D; Supplement 4A,
443 middle and right columns; Supplements 4B, 4C and 4D) with pattern observed in leaf tissues
444 mined by tissue-feeding larvae being different from fluid-feeders. Indeed, leaf tissues mined
445 by fluid-feeding larvae show a strong increase of free amino acids on yellow leaves whereas
446 the level remains low on green leaves (Figure 3C; Supplement 4A, middle column;
447 Supplement 4B). However, tissue-feeders induce a strong increase of free amino acid content
448 in mined tissues both on green and on yellow leaves (Figure 3D; Supplement 4C). As a
449 consequence, amino acid content of mined tissues differs between green and yellow leaves for
450 fluid-feeding larvae (Figure 3C; Supplement 4A, middle column), but is similar on green and
451 on yellow leaves for tissue-feeding larvae (Figure 3D; Supplement 4A, right columns).
452 Changes observed in free amino acid content in mined tissues are mostly due to alteration of
453 non-essential amino acid concentrations (Figure 3C). In tissues mined by fluid-feeders, the
454 strong increase of the most abundant non-essential free amino acid, glutamine (50 %) (and
455 asparagine (10 %) to a lesser extent) is responsible for these changes (Figure 5). Moreover,
456 apple-tree leaves appear to provide very low amounts of methionine (~0.5 % of total amino
457 acids), histidine (~1 %), and tryptophan (~1 %).

458
459 *Essential amino acid composition of the leaf-mining larva and limiting amino acids*

460 The whole-body amino acid composition (Table 1) of *P. blancardella* larvae was used
461 to estimate their essential amino acid requirements. It appears that larvae have a strong
462 demand in histidine (EAA; ~50 % of their amino acid pool; Table 1A) for both larval feeding
463 modes, in cysteine for fluid-feeders (NEAA; ~20 %; Table 1B), and in lysine for tissue-
464 feeders (EAA; ~12 %; Table 1A).

465 The relative limitation of EAAs was quantified with chemical scores, with the lowest
466 scores indicating that His was the first most limiting EAA for both fluid- and tissue feeding
467 instars and both on green and on yellow leaves (chemical scores between 0.01 and 0.05)
468 (Table 2). Therefore, His would be the first EAA to be depleted during protein synthesis in *P.*
469 *blancardella*.

470 Moreover, senescence induces changes in amino acid limitation. Indeed, arginine (+
471 aspartate) and tryptophan appear to be limiting only for larvae developing on green leaves,
472 primarily due to their higher availability on yellow leaves (Figures 5.8 and 5.14; Table 2). It is
473 also important to note changes in amino acid requirements according to the development stage
474 of larvae. Tissue-feeding larvae are indeed limited by lysine whereas fluid-feeders are not
475 (Table 2). This limitation is mostly due to an increased demand for this amino acid in later
476 stages (Table 1A). Moreover, methionine seems to be limiting only for fluid-feeders
477 developing on yellow leaves (Table 2). Finally, on yellow leaves, the second most limiting
478 EAA is less limiting for fluid-feeders (0.86 for methionine) than for tissue-feeders (0.19 for
479 lysine) (Table 2). More generally, *P. blancardella* larvae living on yellow leaves appear to be
480 less limited (2 limiting EAAs) than larvae on green leaves (3-4 limiting EAAs) (Table 2).

481

482 Discussion

483

484 *Strong alteration of plant primary metabolism in mined tissues – Are they becoming*
485 *functionally independent areas?*

486 According to our predictions, primary metabolism was altered in the tissue mined by
487 the feeding activity of the insect, with a modification of the total amount of sugars, the
488 specific sugar composition and the protein-bound and free amino acid contents. We
489 hypothesized that mines would act as active nutrient sinks and preferentially accumulate
490 nutrients (Schwachtje and Baldwin, 2008; Bolton, 2009; Kerchev et al., 2012). However, the
491 nutritional content of mined tissues was indeed modified, but in the opposite direction. Sugars
492 and protein-bound amino acids are less (fluid-feeders, for sugars only) or equally (tissue-
493 feeders) concentrated in mined tissues both on green and on yellow leaves than in unmined
494 green controls (Figures 1, 3, 4 and 5). Free amino acids, by contrast, accumulate into mined
495 tissues as predicted.

496 Our results show that protein composition in mined tissues does not seem to be altered
497 neither as part of the senescing process, as a plant defensive mechanism, nor as a leaf
498 manipulation by the insect for its own benefit. Indeed, the protein-bound amino acid
499 composition experienced by caterpillars feeding on senescing leaves (i.e. mined tissues
500 displaying a green-island) is close to the composition of mined tissues on green leaves, and
501 mined tissues both on green and on yellow leaves have a similar composition to unmined
502 green control tissues (Figures 3 and 4). Free amino acid levels, by contrast, are altered in
503 mined tissues with a pattern closely associated with larval development stages. Free amino
504 acid content is higher in tissues mined by tissue-feeding instars both on green and on yellow
505 leaves, whereas this increase is greater and only visible on yellow leaves for fluid-feeding
506 instars. This change of free amino acid content observed for younger larvae on senescing
507 leaves is essentially due to a strong increase of glutamine. For later instars, it is mainly due to
508 an increase of glycine, arginine + aspartate, asparagine and glutamine (Figures 3 and 5).

509 Our results thus strengthen the hypothesis that mines are functionally independent
510 areas, operating a metabolic machinery of their own and providing a “dietary buffer” to the
511 insect, especially in an otherwise senescent autumnal environment (Engelbrecht et al., 1969;
512 Giron et al., 2007, Body et al., 2013). The higher amounts of sugar in mines inhabited by
513 tissue-feeding larvae on yellow leaves (compared to unmined yellow controls; Supplement
514 2C, right column) are not the outcome of an accumulation process, but of a localized

515 continuous renewal. The absence of remobilization of sugars and amino acids by the plant
516 from the insect's feeding area in the Fall (similar nutrient content in unmined zones UM¹,
517 UM² and UM³) and the similar composition of mined tissues both on green and on yellow
518 leaves strongly reinforce the concept of nutritional homeostasis within mined tissues. Similar
519 results have been found in the gall-inducing insects *Neuroterus quercus-baccarum* and
520 *Andricus lignicola* for which induced gall tissues contain less nutrient than surrounding
521 tissues (Hartley and Lawton, 1992; Diamond et al., 2008).

522

523 *Insect manipulation rather than plant defense*

524 Nutritional requirements of any leaf-mining insect were completely unknown before
525 this study, and the lack of artificial diets, preventing manipulative experiments, is a real
526 bottleneck. Changes in plant primary metabolism after biotic infestations have often been
527 interpreted as a necessary requirement to satisfy the increased demand for energy and carbon
528 skeletons to sustain the direct defense machinery and corresponding physiological adaptations
529 (Kerchev et al., 2012). It is also suggested that primary metabolites could function as
530 signaling molecules in plant defense pathways or could act as direct plant defensive
531 compounds (Augner, 1995; Berenbaum, 1995; Schwachtje and Baldwin, 2008). Primary
532 metabolism reconfiguration could also potentially allow the plant to tolerate herbivory while
533 minimizing impacts on fitness traits by supporting necessary physiological adjustments plants
534 must make (Fornoni, 2011). Changes observed in amino acid abundance may not directly
535 impact larval nutrition, but may also be associated with the changing physiological process in
536 the host-plant as it senesces and/or adapts to the leaf-mining larvae (plant tolerance or
537 defense). Indeed, asparagine and glutamine, major components of the free amino acid pool
538 (Figure 5), are known as important nitrogen carriers in plants and involved in remobilization
539 of leaf nitrogen during leaf senescence or infection by pathogens (Lea and Mifflin, 1980;
540 Siciechowicz et al., 1988; Lam et al., 1996; Lea et al., 2007). When plant leaves are attacked
541 by fungi or bacteria, asparagine levels rapidly increase in infected leaves (Siciechowicz et
542 al., 1988; Pérez-García et al., 1998; Scarpari et al., 2005). An increase in the level of
543 asparagine is usually interpreted as a plant reaction against the pathogen due to recovery of
544 leaf protein from attacked leaves (Pérez-García et al., 1998; Scarpari et al., 2005). Insect
545 growth may also strongly depend on the effects of secondary plant substances and/or
546 carbon:nitrogen ratios in the diet (Berenbaum, 1995; Schoonhoven et al., 2005). Thus, even
547 though the physiological function of altered amino acids in mined tissues remains unclear, our
548 results suggest that such alterations of leaf amino acid profiles contribute to enhance the
549 nutritional quality of plant tissues ingested by larvae and may specifically contribute to
550 increase larval fitness under senescing conditions (Table 2). Additionally, in the insect's
551 feeding area, the concomitant inhibition of classical plant defenses (plant secondary
552 compounds such as phenolics – Giron et al., 2016) also strongly suggest the ability of leaf-
553 mining insects to manipulate their host-plant to improve their nutritional environment, leading
554 to a high survival rate in the absence of natural enemies (90 %; Pottinger and LeRoux, 1971;
555 Giron, personal communication).

556

557 *Mechanisms of plant manipulation*

558 The morphological impact of larvae on leaf tissues could be, at least partially,
559 responsible for the differential modulation of the leaf physiological response according the
560 larval feeding-mode. Such differential control of plant sugars (Figure 2, pie chart #4) could
561 also potentially be explained by changes in insect saliva composition (including level and
562 composition of cytokinins; Zhang et al., 2017) and/or in endosymbiotic bacteria levels over
563 the course of the insect development. Indeed, *P. blancardella* and other Gracillariidae moths
564 prevent mined tissues from senescing (inducing a “green-island” phenotype) through

565 endosymbiotic bacteria mediated release of cytokinins which are known to positively impact
566 plant sugar metabolism (Giron et al., 2007; Kaiser et al., 2010; Body et al., 2013; Gutzwiller
567 et al., 2015; Zhang et al., 2017). *P. blancardella* seems thus to take advantage of its intimate
568 association with the plant by controlling nutrient levels in mined tissues for its own benefit
569 (Body et al., 2013; this study). This is consistent with previous results showing the capacity of
570 this insect to alter the plant hormonal balance (Engelbrecht et al., 1969; Giron et al., 2007;
571 Kaiser et al., 2010; Body et al., 2013; Zhang et al., 2016), directly impacting plant primary
572 metabolism (Ehneß and Roitsch, 1997; Lara et al., 2004; Roitsch and González, 2004; Walters
573 and McRoberts, 2006).

574

575 *Leaf-mining larvae make the best out of senescing plant tissues*

576 For *P. blancardella*, the fitness consequences of the sugar content regulation, allowing
577 survival under adverse conditions to complete an additional generation in the Fall, are
578 significant (Kaiser et al., 2010; Body et al., 2013). However, fluid-feeding instars appear to
579 partially suffer from leaf senescence due to their limited abilities to control the sugar content
580 of mined tissues on yellow leaves (Figure 2, pie chart #4; Supplement 2B, right column, sugar
581 composition). In fact, by closely estimating qualitative and quantitative sugar composition of
582 leaf tissues for the two distinct larval stages, we show that the nutritional landscape
583 experienced by fluid-feeding caterpillars feeding on senescing leaves is not dissimilar to
584 unmined yellow leaves, indicative of a lack of control by the fluid-feeding larvae. By contrast,
585 tissue-feeding larvae have acquired extended capacities to regulate the sugar content (for both
586 sugar quantities and composition) in order to ‘delay’ the leaf senescing process (Figure 2,
587 scenarii B and D; Supplement 2C) and eventually sometimes ‘reversing’ the senescing
588 process already engaged (Figure 2, scenarii C and E; Supplements 2B vs. 2C, right columns,
589 sugar composition). This allows insects to generate a nutritional environment similar to green
590 leaves for sugars (except for fluid-feeders on yellow leaves; Figure 2, pie chart #4). Analyzing
591 specific sugars, one notes that sorbitol represents a qualitatively and quantitatively important
592 part of the sugar content in mined tissues (Figures 1 and 2). Its up-regulation on yellow leaves
593 for tissue-feeders may allow larvae to overcome freezing in late Fall. Sugar alcohols are
594 indeed often involved in thermal tolerance, particularly in cryoprotection (Sømme, 1965;
595 Wyatt, 1967; Miller and Smith, 1975; Wolfe et al., 1998; Salvucci et al., 2000). In summary,
596 the manipulation of sugar content at the feeding site most likely allows for better insect
597 performances, as observed for the forest tent caterpillar *Malacosoma disstria* for which a
598 sugar regulation increases caterpillar survival rate (Noseworthy and Despland, 2006).

599

600 *Beyond leaf-miners*

601 While fitness consequences of an increase availability of amino acids for *P.*
602 *blancardella* are still unknown, a recent study on another leaf-miner, *Tuta absoluta*, showed
603 that nutrition on nitrogen-deficient plant tissues impaired the leaf-miner development by
604 notably decreasing pupal weight and lengthening the development period from egg to adult
605 (Mattson, 1980; Larbat et al., 2016). Transposed to our system, a nitrogen-enriched food
606 source on yellow leaves could thus favor a faster development to reach the tissue-feeding
607 stage before climatic conditions become detrimental for insect survival (Pottinger and
608 LeRoux, 1971; Edwards and Wratten, 1980). Some leaf-miners are able to change from one
609 mine (or one leaf) to another in case of inadequate food supply (Needham et al., 1928) – such
610 as the Diptera larva *Scaptomyza flava* (Whiteman et al., 2011), the Coleoptera larva *Neomycta*
611 *rubida* (Martin, 2010) and the micro-Lepidoptera *Coleophora klimeschiella* (Khan and
612 Baloch, 1976) – but such strategies are very rare and only restricted to certain groups. Unlike
613 these temporary miners, *P. blancardella* larvae are constrained to their mine.

614 The lack of comparative work on the EAA requirements of herbivores, and more
615 specifically of leaf-feeding insects, and the amino acid composition of the plant consumed
616 (see for an exception: Barbehenn et al., 2013) has hampered the understanding of many plant-
617 herbivore interactions, with implications ranging from insect behavioral ecology to
618 adaptation, speciation, and population dynamics. In our system, the use of chemical scores
619 allowed us to show that leaf-mining larvae experience a lower EAA limitation when feeding
620 on yellow leaves than on green leaves. Improved nitrogen availability is thus experienced by
621 these insects during the senescence process. Our results are consistent with other studies that
622 have identified histidine, methionine and arginine as the most limiting amino acids for
623 herbivore species. Histidine and methionine were indeed the first or second most limiting
624 EAAs for the caterpillar *Lymantria dispar* throughout the growing season (Barbehenn et al.,
625 2013). Several vertebrate herbivores follow the same pattern. Springboks (*Antidorcas*
626 *marsupialis*), blesboks (*Damaliscus dorcas phillipsi*) and impalas (*Aepyceros melampus*) have
627 also been shown to be limited by these same three amino acids: methionine, histidine, and
628 arginine (Van Zyl and Ferreira, 2003). These similarities between caterpillars and large
629 herbivores suggest that these amino acid limitations are a direct consequence of using plants
630 as food source in general.

631

632 **Synthesis**

633

634 *Nutritional intimate interactions between a leaf-miner and its senescing leaf*

635 The following putative scheme synthesizes the observed sequence of mechanisms at
636 play in the interaction between a leaf-miner and its leaf during Fall. First, symbiont-mediated
637 increase of cytokinin profiles would induce an accumulation of sugar at the leaf-miner feeding
638 site (Giron et al., 2007; Kaiser et al., 2010; Body et al., 2013; Zhang et al., 2016, 2017; this
639 study). Then, to maintain nutritional homeostasis at the feeding site, carbohydrates in excess
640 would be instead degraded by the plant to fuel the amino acid biosynthetic pathways. Indeed,
641 they are costly to process for the larva and could bridge sugar and amino acid metabolisms.
642 This is a key assumption, requiring further investigation on biochemical pathways in this
643 biological system. However, such degradation of excess carbohydrates and their conversion
644 into intermediates for amino acid synthesis has been observed for the Hessian fly *M.*
645 *destructor* (Liu et al., 2007). The observed partial manipulation of plant tissue nutritional
646 value mitigates the detrimental effects of senescent leaves as food source for *P. blancardella*
647 in the race against time for completing an extra-generation.

648

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650

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658

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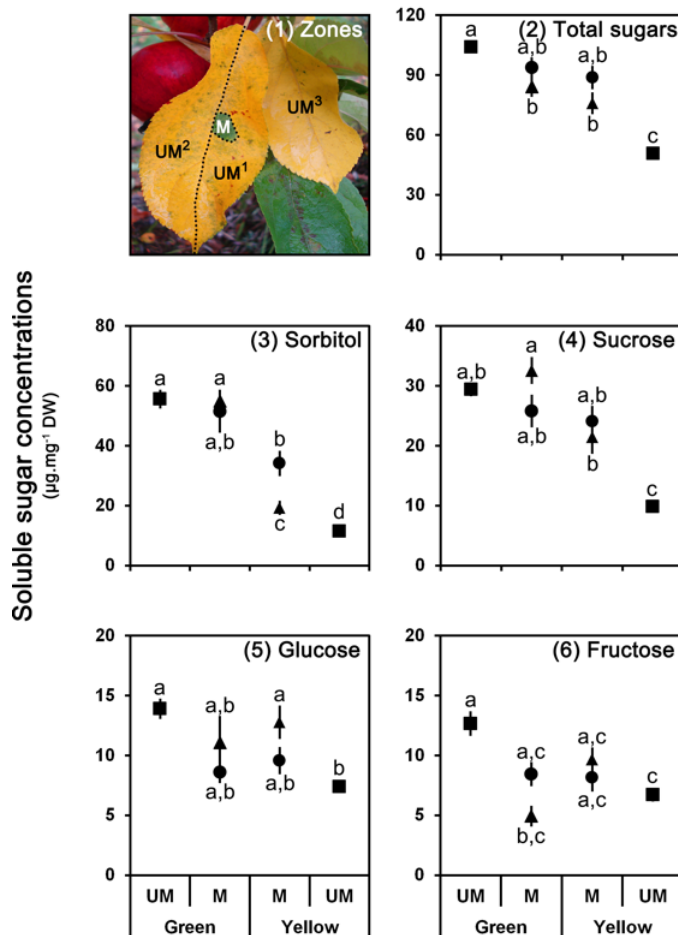
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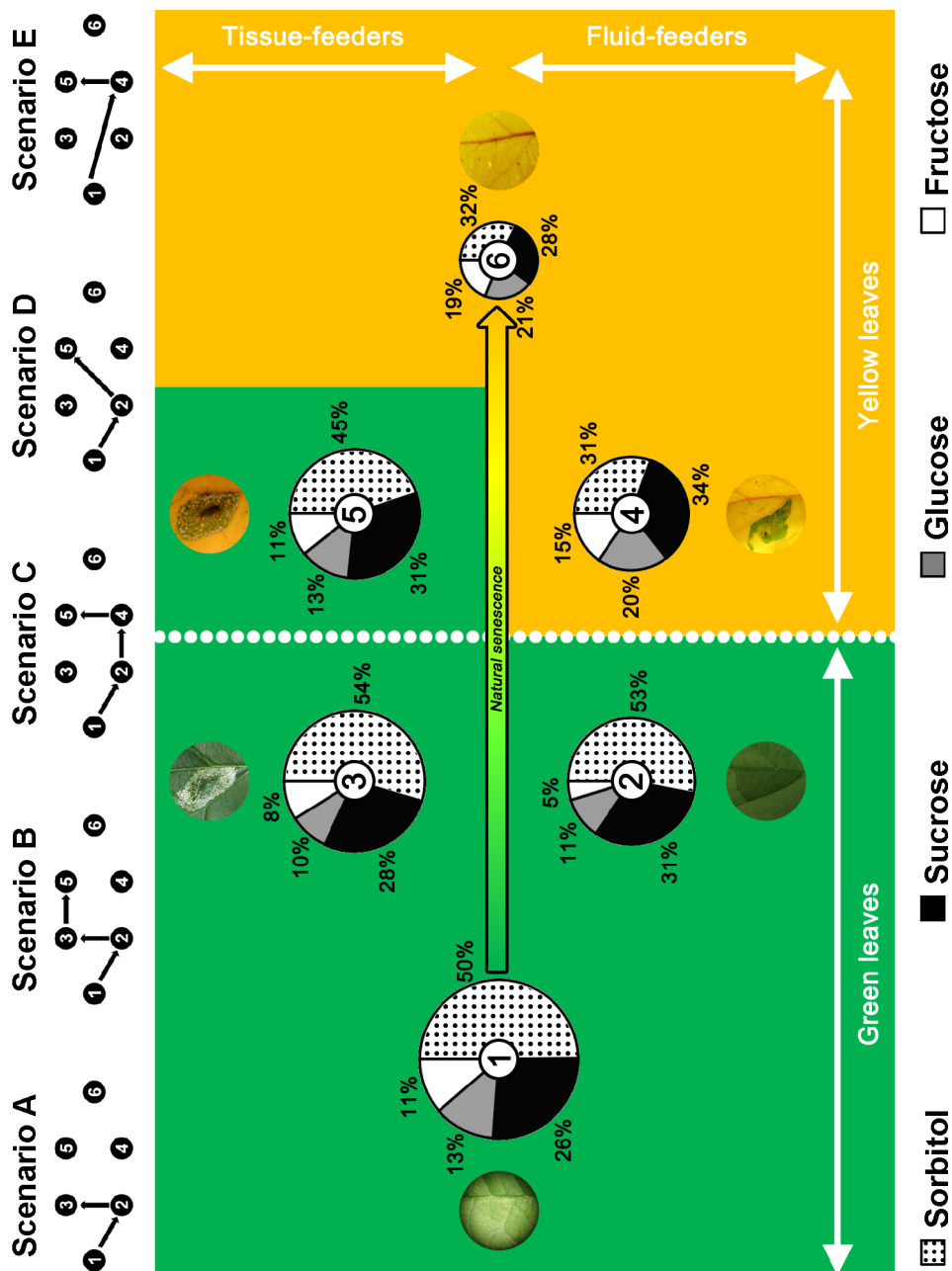
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- 906

907 **Figure 1.** Amounts of sugars in leaf tissues. (1) Picture of a yellow mined leaf: mined tissues
 908 (M zone), ipsilateral unmined tissues (UM¹ zone), contralateral unmined tissues (UM² zone),
 909 and unmined control leaf (UM³ zone). Amounts of (2) total soluble sugars, (3) sorbitol, (4)
 910 sucrose, (5) glucose and (6) fructose in unmined tissues (UM; squares) and mined tissues (M)
 911 for fluid-feeding (L3 instar; triangles) and tissue-feeding (L5 instar; circles) larvae both on
 912 green and on yellow leaves. Data are expressed as μg per mg of leaf dry weight (DW) and
 913 presented as average \pm S.E.M. Statistical differences between averages are shown by different
 914 letters (a, b, c, d) (see Supplement 2 for details).
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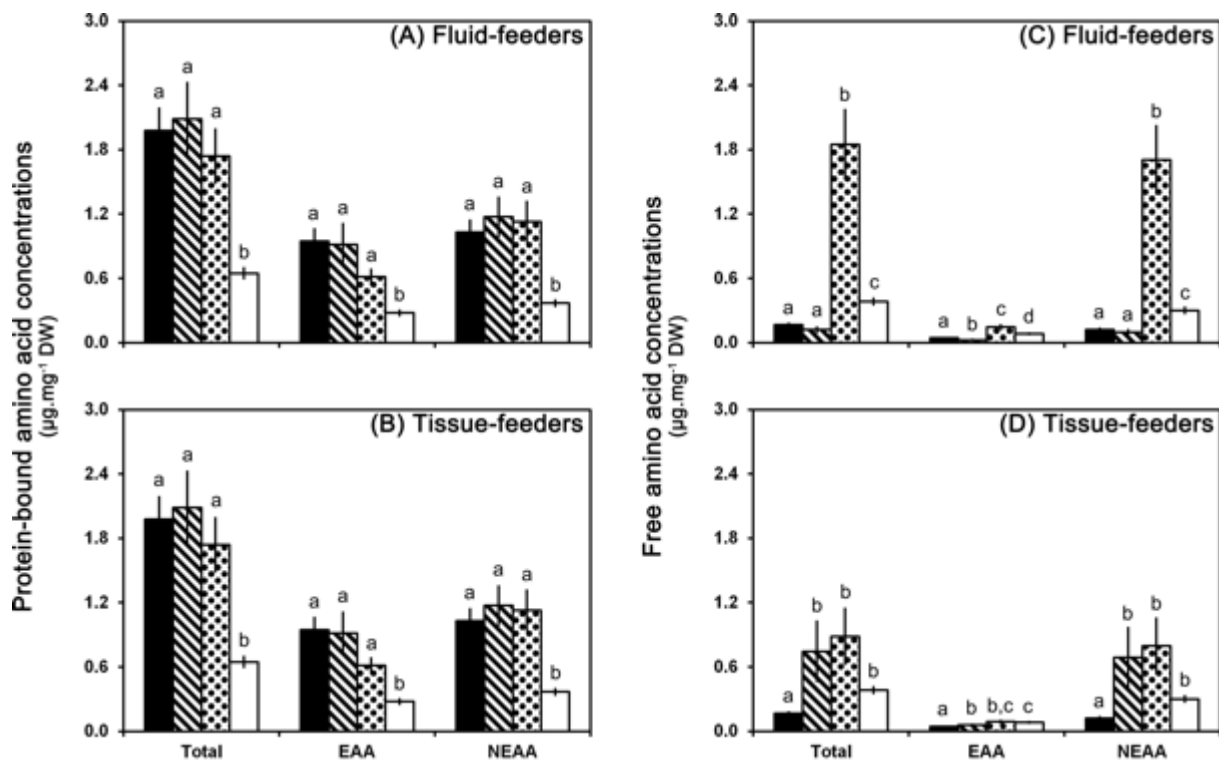
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919 **Figure 2.** Sugar composition of leaf tissues according to the leaf-mining process. Sugar
 920 composition of unmined (1 and 6) and mined tissues for fluid-feeding (2 and 4) and tissue-
 921 feeding (3 and 5) larvae both on green (1 to 3) and on yellow (4 to 6) leaves. Size of pies
 922 represents the total amount of sugars. The green background symbolizes similarities of sugar
 923 quantities and compositions with an unmined green leaf. The yellow background symbolizes
 924 similarities of sugar quantities and compositions with an unmined yellow leaf. The dynamic
 925 of the leaf-mining process is presented through five possible scenarii, eggs being always laid
 926 on green leaves and yellowing of leaves occurring at different possible larval development
 927 stages. Status 1: Unmined green leaf. Status 2: Fluid-feeding larva on green leaf. Status 3:
 928 Tissue-feeding larva on a green leaf. Status 4: Fluid-feeding larva on a yellow leaf. Status 5:
 929 Tissue-feeding larva on a yellow leaf. Status 6: Unmined yellow control. See Supplement 2
 930 for statistical analysis.
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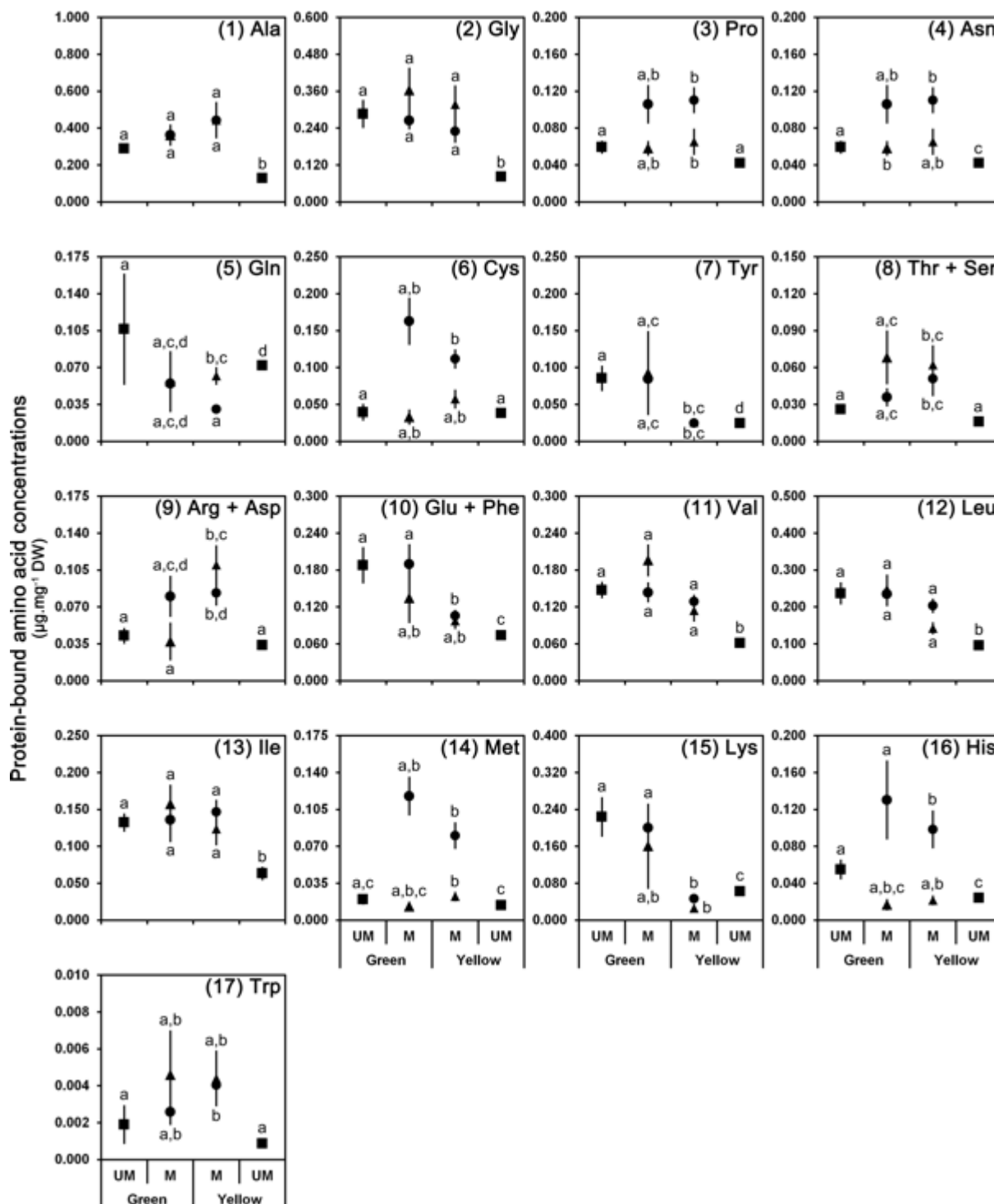
935 **Figure 3.** Amino acid composition (total, essential and non-essential amino acids) of mined
 936 and unmined tissues both on green and on yellow leaves. Upper panels (**A** and **C**) show data
 937 obtained for fluid-feeding instars of the leaf-mining insect *Phyllonorycter blancardella*.
 938 Lower panels (**B** and **D**) show data obtained for tissue-feeding instars. Left panels (**A** and **B**)
 939 show data for protein-bound amino acids. Right panels (**C** and **D**) show data for free amino
 940 acids. Mined tissues on green leaves are represented by the stripe pattern and on yellow leaves
 941 by the dot pattern. Unmined green controls are in black and unmined yellow controls are in
 942 white. Data are presented as average \pm S.E.M. and expressed in μg per mg of leaf dry weight.
 943 Statistical differences between averages are shown by different letters (a, b, c, d) (see
 944 Supplements 3 and 4 for statistical analysis).
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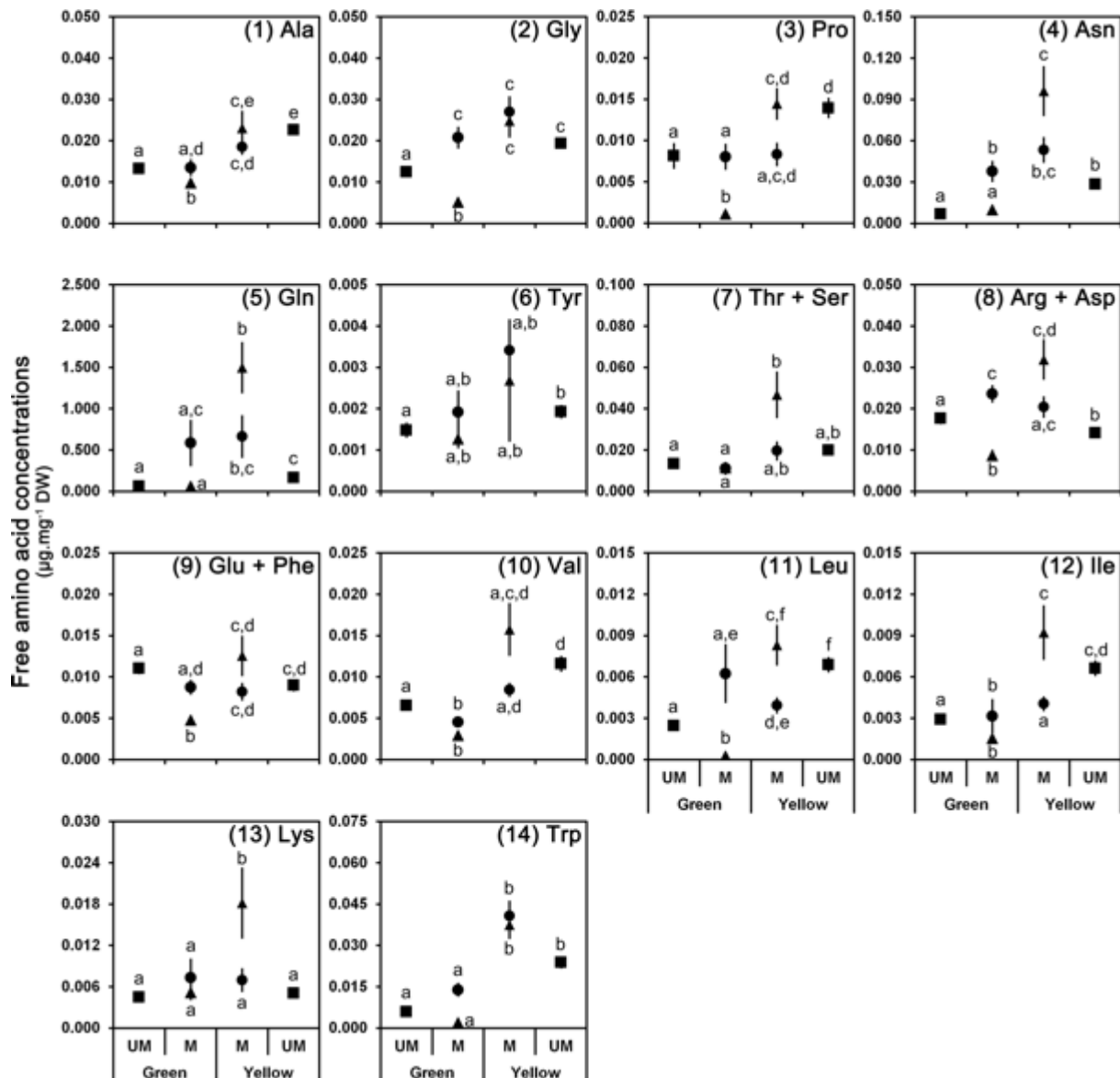
948 **Figure 4.** Protein-bound amino acid profiles in mined (M) and unmined (UM; squares) tissues
 949 both on green and on yellow leaves infected by the leaf-mining insect *Phyllonorycter*
 950 *blancardella* (fluid-feeding (triangles) vs. tissue-feeding (circles) instars). Panels 1-7 are
 951 NEAA, panels 8-10 are co-eluted NEAA and EAA, panels 11-17 are EAA. Data are presented
 952 as average \pm S.E.M. and expressed in μg per mg of leaf dry weight. Statistical differences
 953 between averages are shown by different letters (a, b, c, d) (see Supplement 3 for statistical
 954 analysis).
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958 **Figure 5.** Free amino acid profiles in mined (M) and unmined (UM; squares) tissues both on
 959 green and on yellow leaves infected by the leaf-mining insect *Phyllonorycter blancardella*
 960 (fluid-feeding (triangles) vs. tissue-feeding (circles) instars). Panels 1-6 are NEAA, panels 7-9
 961 are co-eluted NEAA and EAA, panels 10-14 are EAA. Data are presented as average \pm
 962 S.E.M. and expressed in μg per mg of leaf dry weight. Statistical differences between
 963 averages are shown by different letters (a, b, c, d, e, f) (see Supplement 4 for statistical
 964 analysis).
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968 **Table 1. (A)** Essential and **(B)** non-essential amino acid (protein-bound + free) content of
 969 whole body of fluid- and tissue-feeding leaf-mining insects both on green and on yellow
 970 leaves. Data are presented as average \pm S.E.M. and expressed in μg per mg of caterpillar dry
 971 weight. Values in rows with different letters (a, b) are significantly different ($P < 0.05$).
 972

973 **A. Essential amino acids**
 974

	Green leaves		Yellow leaves	
	Fluid-feeders	Tissue-feeders	Fluid-feeders	Tissue-feeders
Val	12.48 \pm 0.67 a	10.39 \pm 1.69 a	10.75 \pm 1.78 a	8.74 \pm 1.55 a
Leu	25.72 \pm 1.42 a	13.18 \pm 2.23 b	20.64 \pm 5.92 a,b	11.65 \pm 2.58 a,b
Ile	8.98 \pm 0.83 a	3.73 \pm 0.71 b	9.84 \pm 2.33 a,b	3.48 \pm 0.75 a,b
Thr (+ Ser)	2.52 \pm 0.93 a	1.46 \pm 0.29 a	2.57 \pm 0.90 a	1.33 \pm 0.24 a
Arg (+ Asp)	18.15 \pm 2.75 a	14.29 \pm 1.94 a	19.62 \pm 1.23 a	12.03 \pm 1.59 a
Met	2.01 \pm 0.29 a	0.54 \pm 0.08 b	5.65 \pm 1.60 c	0.48 \pm 0.12 b
Phe (+ Glu)	12.75 \pm 0.89 a	13.47 \pm 1.84 a	7.65 \pm 0.89 a	12.63 \pm 2.01 a
Lys	14.95 \pm 1.78 a	54.48 \pm 9.49 b	10.96 \pm 6.31 a	42.27 \pm 5.86 b
His	234.06 \pm 45.73 a	140.67 \pm 45.64 a	464.42 \pm 204.74 a	243.82 \pm 112.25 a
Trp	1.63 \pm 0.55 a	11.88 \pm 9.79 a	3.70 \pm 1.53 a	1.01 \pm 0.29 a

975 **B. Non-essential amino acids**
 976
 977

	Green leaves		Yellow leaves	
	Fluid-feeders	Tissue-feeders	Fluid-feeders	Tissue-feeders
Ala	5.35 \pm 0.88 a	5.07 \pm 0.94 a	7.07 \pm 0.81 a	3.96 \pm 0.67 a
Gly	11.80 \pm 0.63 a	8.68 \pm 1.52 a	9.02 \pm 1.82 a	8.00 \pm 1.55 a
Pro	11.81 \pm 0.21 a	8.91 \pm 1.32 a	7.64 \pm 0.58 a	8.01 \pm 1.20 a
Asn	7.15 \pm 1.79 a	1.28 \pm 0.45 b	10.00 \pm 2.43 a	1.72 \pm 0.75 b
Cys	88.88 \pm 8.83 a	24.43 \pm 9.55 b	180.52 \pm 59.49 a	24.71 \pm 9.88 b
Gln	2.72 \pm 0.33 a	1.38 \pm 0.35 a	4.55 \pm 1.53 a	1.29 \pm 0.42 a
Tyr	1.86 \pm 0.62 a	15.84 \pm 4.95 a	1.60 \pm 0.64 a	6.11 \pm 2.52 a

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980 **Table 2.** Chemical scores of essential amino acids (EAAs) in mined tissues both on green and
 981 on yellow leaves based on the EAA compositions of the whole body of *Phyllonorycter*
 982 *blancardella* leaf-miner. When EAAs were co-eluted with NEAAs, the name of the NEAA is
 983 in brackets. Chemical scores were calculated as (μg of EAA in mined leaf tissues / μg of total
 984 AA in mined leaf tissues) / (μg of EAA in insect/ μg of total AA in insect). Limiting essential
 985 amino acids are in bold for both fluid- and tissue-feeding instars. A value lower than 1
 986 indicates an excess of EAA available in the foliar amino acid pool. *Val* valine, *Leu* leucine, *Ile*
 987 isoleucine, *Thr* (+ *Ser*) threonine (+ serine), *Arg* (+ *Asp*) arginine (+ aspartate), *Met*
 988 methionine, *Phe* (+ *Glu*) phenylalanine (+ glutamate), *Lys* lysine, *His* histidine, *Trp*
 989 tryptophan.

990
 991

	Green leaves		Yellow leaves	
	Fluid-feeders	Tissue-feeders	Fluid-feeders	Tissue-feeders
Val	3.34	1.67	2.61	2.35
Leu	2.01	2.14	1.58	2.66
Ile	3.71	4.35	2.92	6.47
Thr (+ Ser)	6.63	3.76	9.15	7.93
Arg (+ Asp)	0.53	0.85	1.56	1.29
Met	1.37	3.50	0.86	7.11
Phe (+ Glu)	2.29	1.72	3.10	1.35
Lys	2.32	0.45	1.52	0.19
His	0.02	0.05	0.01	0.01
Trp	0.84	0.16	2.44	6.60

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