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Proteomic analysis reveals how pairing of a Mycorrhizal fungus with plant growth-promoting bacteria modulates growth and defense in wheat

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► To cite this version:

Candida Vannini, Guido Domingo, Valentina Fiorilli, Daniel García Seco, Mara Novero, et al.. Proteomic analysis reveals how pairing of a Mycorrhizal fungus with plant growth-promoting bacteria modulates growth and defense in wheat. *Plant, Cell and Environment*, 2021, 44 (6), pp.1946-1960. 10.1111/pce.14039 . hal-03238035

HAL Id: hal-03238035

<https://hal.science/hal-03238035v1>

Submitted on 30 Dec 2023

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This is the author's manuscript

Original Citation:

Availability:

This version is available <http://hdl.handle.net/2318/1783474> since 2022-06-22T12:45:51Z

Published version:

DOI:10.1111/pce.14039

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(Article begins on next page)

1 **Proteomic analysis reveals how pairing of a Mycorrhizal Fungus with**
2 **Plant Growth-Promoting Bacteria modulates growth and defense in wheat**

3

4 **Running head:** AMF and PGPB modulate plant growth and defense

5

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24 **Funding**

25 This work was supported by the MIC-CERES (“Microbial eco-compatible
26 strategies for improving wheat quality traits and rhizospheric soil
27 sustainability”) Project (FC Project ID 2013–1888; AF Project ID 1301–003)
28 jointly supported by the Agropolis Foundation (through the “Investissements
29 d’avenir” program, with the reference number ANR-10-LABX-0001-01) and
30 Fondazione Cariplo.

31

32 **Abstract**

33 Plants rely on their microbiota for improving the nutritional status and
34 environmental stress tolerance. Previous studies mainly focused
35 on bipartite interactions (a plant challenged by a single microbe), while plant
36 responses to multiple microbes have received limited attention. Here, we
37 investigated local and systemic changes induced in wheat by two plant growth-
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41 investigate bipartite (wheat–PGPB) and tripartite (wheat–PGPB–AMF)
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43 AMF and *A. brasilense* promoted plant growth by activating photosynthesis
44 and N assimilation which led to increased glucose and amino acid content. The

45 bioprotective effect of the PGPB–AMF interactions on infected wheat
46 plants depended on the PGPB-AMF combinations, which caused specific
47 phenotypic and proteomic responses (elicitation of defense related proteins,
48 immune response, and jasmonic acid biosynthesis). In the whole, wheat
49 responses strongly depended on the inoculum composition (single vs. multiple
50 microbes) and the investigated organs (roots vs. leaf). Our findings showed that
51 AMF is the best-performing microbe, suggesting its presence as the crucial one
52 for synthetic microbial community development.

53

54 **Keywords**

55 *Funneliformis mosseae*, *Azospirillum brasilense*, *Paraburkholderia graminis*,
56 *Xanthomonas translucens*, proteome, pathogens, bi- and tripartite interaction,
57 wheat, growth and defense response.

58

59 **Acknowledgments**

60 V.F., D.G.S., P.B., L.M., and C.V designed the study; V.F., D.G.S., M.N., and
61 D.G. carried out the majority of experiments; G.D., M.M., and C.V performed
62 the bioinformatic analysis of proteomic data; C.V., V.F., P.B. L.M., F.W.-D.,
63 and M.B. interpreted the data and wrote the manuscript.

64

65

66

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96

97 **INTRODUCTION**

98 Like humans, animals, and fungi, plants live among a variety of microbial
99 species, which together comprise the plant microbiota (Schlaeppli & Bulgarelli,
100 2015). Plant root-associated microbes have received increasing attention,
101 starting from their taxonomic description (Bulgarelli et al., 2012; Lundberg et
102 al., 2012) to their role in plant health (Müller, Vogel, Bai, & Vorholt, 2016).
103 Data generated by multiple omics approaches demonstrate that the plant
104 microbiota does not represent a random assembly of microbes living in the soil.
105 On the contrary, plant microbiota composition is determined by an active host
106 plant-driven selection process, which depends on the plant genotype,
107 environmental conditions, and microbial interactions (Durán et al., 2018;
108 Hacquard et al., 2015; Saad, Eida, & Hirt, 2020; Thiergart et al., 2019; Uroz,
109 Courty, & Oger, 2019). The complexity of the microbial community structure
110 parallels the many beneficial functions currently assigned to the plant

111 microbiota: stimulation of plant growth through phytohormone production,
112 improvement of the plant nutrient status through the increased uptake of
113 nutrients such as inorganic phosphate (Pi) and nitrogen (N) and increased
114 availability of nutrients such as iron, greater tolerance to abiotic stress (e.g.,
115 drought) and biotic stress, and increased activation of plant innate immunity
116 (Hacquard, Spaepen, Garrido-Oter, & Schulze-Lefert, 2017). Many of these
117 benefits have been traditionally associated with the so-called plant growth-
118 promoting bacteria (PGPB), as well as with the root symbionts, such as
119 arbuscular mycorrhizal (AM) fungi and N-fixing bacteria (Lugtenberg,
120 Caradus, & Johnson, 2016). Comparison of the data generated by culture-
121 independent approaches with the knowledge obtained from the investigation of
122 controlled binary interactions of bacterial and fungal isolates with their host
123 plant has led to the creation of the so-called synthetic communities (SynComs)
124 (Herrera Paredes et al., 2018; Tsolakidou et al., 2019). Simultaneous
125 inoculation of the host plant with several different beneficial microbes allows
126 the investigation of plant responses under controlled and reproducible
127 conditions. These new tools therefore form the basis of the so-called microbial
128 revolution, defined as the microbe-driven increase in crop productivity, leading
129 to higher sustainability (Baez-Rogelio, Morales-García, Quintero-Hernández,
130 & Muñoz-Rojas, 2017).

131 Together with rice and corn, wheat is one of the most important crops
132 worldwide (Ferne & Yan, 2019). Recently, many studies have been conducted

133 on wheat-associated microbes, providing a detailed list of bacteria and fungi
134 associated with wheat plants under natural conditions (Kuzniar et al., 2020;
135 Mahoney, Yin, & Hulbert, 2017; Naylor, DeGraaf, Purdom, & Coleman-Derr,
136 2017; Pagé, Tremblay, Masson, & Greer, 2019) or describing the core
137 microbiome of wheat (Simonin et al., 2020), thus revealing the ecological rules
138 that regulate microbial assembly (Hassani, Özkurt, Seybold, Dagan, &
139 Stukenbrock, 2019). Ecological studies suggest that higher soil microbial
140 diversity results in a greater resilience of the plant population (van der Heijden
141 et al., 1998). However, the assumption that a mixture of beneficial microbes
142 automatically provides greater plant protection is an oversimplification
143 (Rosier, Bishnoi, Lakshmanan, Sherrier, & Bais, 2016). In this context, the
144 responses of wheat to its microbiota are still unknown.

145 In this study, to disentangle the inherent complexity of plant–microbiota
146 interactions (Vorholt, Vogel, Carlström, & Müller, 2017), we followed a
147 reductionist approach, where we selected two PGPB species, *Azospirillum*
148 *brasiliense* and *Paraburkholderia graminis*, which are associated with wheat
149 plants under natural conditions, as well as an arbuscular mycorrhizal fungus
150 (AMF), *Funneliformis mosseae*. We hypothesized that targeted inoculation of
151 wheat plants with the AMF and one of the two PGPB could provide an
152 experimentally tractable system for evaluating the outcome of the interaction
153 between beneficial microbes. Previously, we demonstrated that inoculation
154 with *F. mosseae* improved plant growth and enhanced bioprotection in wheat

155 (Fiorilli et al., 2018). The current study aimed to investigate the long-term local
156 and systemic effects of *P. graminis* or *A. brasilense* on the wheat proteome in
157 non-mycorrhizal and mycorrhizal plants. We compared the proteomic changes
158 in wheat triggered by co-inoculation of PGPB and *F. mosseae* with those
159 elicited by single inoculations. We also investigated the bioprotective effects
160 of bipartite (wheat–PGPB) and tripartite (wheat–PGPB–AMF) interactions on
161 wheat plants against the leaf pathogen, *Xanthomonas translucens*. While *A.*
162 *brasilense* drastically altered the bioprotective effect of the AMF, *P. graminis*
163 did not affect AMF-induced pathogen resistance. Overall, proteomic changes
164 revealed the molecular mechanisms underlying the tripartite interaction and
165 showed that the beneficial effects of the AMF on plants are differentially
166 modulated by the plant-associated PGPB.

167

168 **MATERIALS AND METHODS**

169 **Bacterial strains, mycorrhizal fungus and wheat genotype**

170 Two plant growth promoting bacteria (PGPB), *Azospirillum brasilense* Sp245
171 (obtained from UMR Ecologie Microbienne, Villeurbanne) and
172 *Paraburkolderia graminis* C4D1M (type strain of the species, LMG collection,
173 Ghent, Belgium), one wheat pathogen, *Xanthomonas translucens* CFBP2054
174 (obtained from CFBP collection), and one mycorrhizal fungus, *Funneliformis*
175 *mosseae* (BEG.12, MycAgro Lab, France) were used in our experiments.

176 In detail, *A. brasilense* strain Sp245 was isolated from wheat roots and was
177 shown to stimulate root development and increase plant dry mass (Kapulnik,
178 Okon, & Henis, 1985), while the strain C4D1M of *P. graminis* was isolated
179 from senescent corn roots and found to positively interact with different species
180 of wheat (L. Moulin, personal communication).

181 Gfp-tagged derivatives were also included for cytology analyses: *A. brasilense*
182 Sp245 eGFP carrying the pMP2444 plasmid eGFP, GmR (Wisniewski-Dyé et
183 al., 2011) and *P. graminis* C4D1M eGFP, constructed by triparental mating
184 (using a Tn7 eGFP construct described in (Norris, Kang, Wilcox, & Hoang,
185 2010) with a single insertion of the Tn7 upstream of the *glmS* gene). *A.*
186 *brasilense* was cultivated at 28°C on LBA medium (Luria Broth low salt, agar)
187 and *P. graminis* in YMA medium (yeast extract, 3 g; mannitol, 10 g; KH₂PO₄,
188 0.5 g; MgSO₄, 0.2 g; NaCl, 0.1 g; agar, 18 g; distilled water, 1 L; pH 6.8) and
189 grown overnight in the same broth medium for inoculation. Strains were stored
190 at -80°C in 20% glycerol. *X. translucens* CFBP 2054 was grown at 28 °C on
191 Peptone sucrose agar (PSA) medium, retrieved from Petri dish with sterile
192 water to reach OD 0.5 for leaf clipping and infiltration assays.

193 The *Triticum aestivum* cv Chinese Spring was used for all experiments (seeds
194 obtained from Valeria Terzi, CREA, Italy).

195

196 **Plant material and plant inoculations**

197 The methodologies have already been described in previous articles on the
198 wheat response to *Xanthomonas* (Garcia-Seco et al., 2017a) and to mycorrhizal
199 fungi (Fiorilli et al., 2018). Twelve combinations were studied: 1). Control
200 plants (C), 2) *A. brasilense*-inoculated plants (Az), 3) *P. graminis*-inoculated
201 plants (P), 4) *F. mosseae*-inoculated plants (M), 5) C+*Xanthomonas*
202 *translucens* (X), 6) Az+X, 7) P+X, 8) M+X, 9) Az+M, 10) P+M, 11) Az+M+X,
203 12) P+M+X. An overview of the experiment is given in Figure S1.

204 Seeds were disinfected by immersing for 40 min in a sodium hypochlorite
205 solution and washed with sodium thiosulfate (Hurek et al., 1994) and
206 pregerminated. The seedlings were transferred to pots containing a mix of
207 sterile quartz sand + either the *F. mosseae* carrier inoculum substrate (the
208 substrate without the fungus) for control and PGPB conditions, or the *F.*
209 *mosseae* inoculum (30% v/v) for mycorrhizal and mycorrhizal+PGPB
210 conditions. PGPB were inoculated directly after seedling transfer to pots, with
211 1 ml per plant at OD 1 from an overnight broth culture washed once and diluted
212 with water.

213 For each inoculated condition, 10 pots containing 1 plant were used for
214 phenotyping of root and fresh weight at 50 dpi, 5 pots were used for proteomic,
215 and 5 pots for leaf-clipping assays with *Xanthomonas translucens*.

216 All plants were maintained under glasshouse conditions under cycles of 12 h
217 of light at 21 °C and 50% relative humidity (RH) and 12 h of dark at 21 °C and
218 50% RH, watered twice a week with water, and once with a modified Long-

219 Ashton solution containing a low phosphorous concentration (32 μM
220 $\text{Na}_2\text{HPO}_4 \cdot 12\text{H}_2\text{O}$).

221 Spikes weight were measured separately in the mature plants at the end of their
222 natural cycle. The spikes were threshed and 1000-kernel weights were
223 determined.

224 For *Xanthomonas* infections, two types of inoculation were performed. A
225 phenotyping leaf-clipping assay with scissors soaked in a 0.5 OD *X.*
226 *translucens* culture was performed at 46 dpi on a first set of plants for
227 phenotyping the length of the symptoms at 4-day post-clipping (dpc; starting
228 point of the lesions) and 26 dpc. A second set of plants dedicated to proteomic
229 analyses was infiltrated at 49 dpi with a 0.5 OD *X. translucens* culture using a
230 microneedle, as described in Garcia-Seco et al. (Garcia-Seco et al., 2017b), and
231 sampled the following day.

232

233 **Evaluation of wheat roots microbial colonization**

234 The mycorrhizal and mycorrhizal+PGPB roots were stained with 0.1% cotton
235 blue and the level of mycorrhizal colonization was assessed as previously
236 described (Trouvelot, Kough, & Gianinazzi-Pearson, 1986).

237 For Colony Forming Unit (CFU) counting from plant roots, root fragments
238 were weighted then pulverized with a FastPrepTM in tubes containing a ceramic
239 bead in 500 μL of sterile water, centrifuged at 1000 rpm for 30 s and drops of
240 20 μL of serial dilutions were plated on bacterial media and counted 24 h later.

241

242 **Proteomic analysis and data processing**

243 Plant samples (root and leaves) were sampled at 50 dpi and pulverized with
244 liquid nitrogen. The used protocol for total protein extraction was based on
245 SDS and phenol extraction (Wu, Xiong, Wang, Scali, & Cresti, 2014). Then,
246 samples were digested and analysed by Liquid Chromatography-Mass
247 Spectrometry (LC-MS/MS) as described previously (Garcia-Seco et al.,
248 2017b). Mass spectrometer raw files were analysed by MaxQuant (version
249 1.6.2.3, default parameters) against UniProt *T. aestivum* (Version 2017-1,
250 150,716 entries), Uniprot *Rhizophagus irregularis* (Version 2015-10, 29,847
251 entries), Uniprot *P. graminis* (Version 2015-10, 6,732 entries) and Uniprot *A.*
252 *brasilense* (Version 2015-10, 7,636 entries). On January 2019, the UniProt *T.*
253 *aestivum* database has been updated. Therefore, we obtained the updated
254 protein IDs by BLAST search of our dataset against the Uniprot *T. aestivum*
255 2019 database (143,020 entries). Unknown proteins were annotated by BLAST
256 search against the Uniprot viridiplantae database (Version 2019-01, 6,913,939
257 entries), taking the first hit with a valid annotation.

258 All MS proteomic data have been deposited in the ProteomeXchange
259 Consortium via PRIDE partner repository with the Username:
260 reviewer04430@ebi.ac.uk and Password: 2vlyEEVZ.

261 MaxQuant output files were processed as described earlier (Vannini et al.,
262 2019). Only proteins detected in at least two of the three biological replicates
263 (75%) sharing the same treatment and tissue were considered.

264 To compare the differences among analytical groups we performed an
265 ANOVA based multiple samples coupled with Tukey test using the *R* package
266 LIMMA. Only proteins with false discovery rate (FDR) below 0.01 were
267 considered Differentially Abundant Proteins (DAPs) within the various
268 comparisons. In order to produce a reliable and robust dataset, all proteins
269 which gave one nonzero and two zero outcomes (two-time imputation) in at
270 least one of the samples in each comparison were considered unreliable and
271 therefore eliminated.

272 In order to use bioinformatic tools available only for *A. thaliana*, a local
273 BLAST of *T. aestivum* proteins against the TAIR10 database (version 2012-
274 05-07) was performed.

275 The enrichment analysis was performed using the Gene Ontology Resource
276 (<http://geneontology.org>), running PANTHER algorithm with *A. thaliana* as
277 background and $FDR < 0.05$ or using the AgriGO Singular Enrichment
278 Analysis (SEA) compare tool
279 (<http://bioinfo.cau.edu.cn/agriGO/analysis.php?method=compare>), with *A.*
280 *thaliana* TAIR10_2017 protein database as background, default parameters
281 and a FDR threshold of 0.05 (Du, Zhou, Ling, Zhang, & Su, 2010).

282

283 **Amino acid analysis**

284 For the amino acids (AAs) extraction, 0.1 g of lyophilized samples were re-
285 suspended in 10 mL of 0.1% (v/v) formic acid in water/methanol (50:50). 10
286 μL of 10 mM deuterated internal standards (L-Phenyl-d5-alanine and L-alanine
287 ^{15}N Met), were added. Free AAs were quantified by Liquid Chromatography
288 Tandem Mass Spectrometry (LC-MS/MS) as described previously (Fiorilli et
289 al., 2018).

290

291 **Total glucose and nitrogen content**

292 Soluble sugars were extracted as described by (Shi, Wang, Yang, Li, & Miao,
293 2016) with minor modifications. Briefly, 0.2 g of leaves material were boiled
294 (80°C) in ethanol 80% for 30 min. After centrifugation (13000g x 5 min) the
295 supernatant was recovered. The extraction was repeated twice and all
296 supernatants were collected. Sucrose in solution was hydrolysed with HCl (2%
297 of HCl concentrated V/V) for 5 min at 90°C. After acid neutralization by KOH
298 (5% of 5N KOH V/V) total glucose was estimated by the dinitrosalicylic (DNS)
299 method (Miller, 1959).

300 Wheat root N content was determined by CHNS elemental analyzer Thermo
301 Fisher Scientific following the manufacturer's specifications. About 2–3 mg of
302 sample for each replicate were weighed and placed in a tin capsule containing
303 9.5 to 10.5 mg of vanadium pentoxide. The N₂ product by sample combustion
304 was quantitatively determined through a separation with a gas chromatograph
305 (GC) followed by a quantification using a thermal conductivity detector. Three
306 tests were prepared for each sample.

307

308 **Statistics**

309 Phenotyping data of plant weight, CFU and lesion length were analyzed,
310 depending on normality of data, by ANOVA followed by Tukey post-hoc test
311 or Kruskal-Wallis test followed by Mann–Whitney pairwise comparisons, in R
312 Environment (rstatix) and figures produced by ggplot.

313 Data from quantification of amino acid, total glucose and nitrogen were
314 subjected to statistical analysis by ANOVA and Tukey post-hoc test.

315

316 **RESULTS**

317 **PGPB and AMF impact plant growth**

318 Wheat plants were inoculated with *A. brasilense* Sp245, *P. graminis* C4D1M,
319 *A. brasilense* Sp245 plus *F. mosseae*, or *P. graminis* C4D1M plus *F. mosseae*
320 (hereafter referred to as Az, P, AzM, and PM plants, respectively) and grown
321 under controlled conditions (Figure S1). The root and shoot biomass of these

322 plants was determined at 50 days post-inoculation (dpi) and compared with that
323 of mock-inoculated control (C) and *F. mosseae* only-inoculated (M) plants. In
324 isolation, *A. brasilense* Sp245 exerted a strong positive effect on the growth of
325 roots and shoots, whereas *P. graminis* C4D1M did not induce statistically
326 significant growth of these organs (Figure 1). Monitoring these plants until
327 seed production revealed that *P. graminis* significantly increased the seed
328 yield, doubling the spike weight (Figure S2).

329 To determine whether the positive impact of the two PGPB on plant
330 growth was associated with an efficient colonization process, bacteria on the
331 root surface were counted at different time points. *A. brasilense* exhibited the
332 greatest colonizing potential, with the bacterial count remaining constant
333 across different time points. Colonization by *P. graminis* decreased with time
334 to 1×10^2 colony forming units (CFU) at 21 dpi (Figure S3). The success of
335 AMF colonization was evaluated at 50 dpi by calculating the total length of
336 colonized roots (F%) and total number of arbuscules (A%) in plants inoculated
337 with AMF alone or AMF plus PGPB (*A. brasilense* or *P. graminis*).
338 Colonization by the AMF resulted in abundant arbuscules in all plants. No
339 differences were detected in F% and A% among plants inoculated with AMF
340 alone or together with PGPB, indicating that the presence or absence of PGPB
341 does not affect mycorrhizal colonization (Figure S3).

342 The shoot weight of AzM and PM plants was significantly higher than
343 that of Az and P plants (Figure 1B) but comparable with that of M plants,

344 indicating that PGPB did not lead to any additional yield benefit compared with
345 the mycorrhizal condition.

346

347 **AMF alone or in combination with a PGPB triggers different responses to**
348 ***X. translucens* infection**

349 Inoculated wheat plants were assessed for protective effect to *X. translucens*
350 leaf infection by leaf-clipping plants with the pathogen at 46 dpi and recording
351 leaf symptoms at 4 and 26 days post-leaf clipping (dpc). Pathogen-infected
352 plants were identified as AzX, PX, MX, AzMX, and PMX and positive control
353 plants as CX. Disease symptoms were evident in CX plants at 4 and 26 dpc
354 (Figure 2). Lesion length in MX plants was significantly less than that in CX
355 plants both at 4 and 26 dpc, consistent with our previous results (Fiorilli et al.,
356 2018).

357 Lesion length appeared extended in AzX and CX plants at both time
358 points. AzMX plants showed reduced symptoms in comparison with AzX
359 plants at 4 dpc but showed extended lesions compared with CX and AzX plants
360 at 26 dpc. This result indicates that the *F. mosseae*-induced bioprotection in
361 wheat is abrogated between 4 and 26 dpc in the presence of *A. brasilense*.

362 At 26 dpc, a significant reduction in symptoms was observed only in MX
363 and PMX plants when compared with CX plants, whereas lesions were
364 significantly increased in AzX and AzMX plants compared with PX, MX, and
365 PMX plants. These results indicate that inoculation with *F. mosseae* alone

366 (Fiorilli et al., 2018) or in combination with *P. graminis* increased protection
367 against *X. translucens*. Overall, this experiment showed that *A. brasilense*
368 inoculation alone did not protect wheat plants against the pathogen, and rather
369 undermined the positive effect exerted by *F. mosseae*.

370

371 **Quantitative overview of proteomics analysis**

372 We conducted proteomic analysis of the roots (R) of Az, P, M, AzM, and PM
373 plants (hereafter referred to as RAz, RP, RM, RAzM, and RPM samples,
374 respectively) as well as the leaves of these plants (hereafter referred to as LAz,
375 LP, LM, LAzM, and LPM samples, respectively). We also performed
376 proteomic analysis of the leaves of these plants following infection with *X.*
377 *translucens* (hereafter referred to as LAzX, LPX, LMX, LAzMX, and LPMX,
378 respectively). Each treatment was analyzed in triplicate.

379 A total of 3,846 and 3,883 wheat proteins were identified and quantified
380 in root and leaf samples, respectively. Samples were clustered by condition
381 according to their protein expression patterns (Figure S4). Replicates within
382 each analytical group clustered together, confirming the high reproducibility of
383 biological replicates. Protein abundance was compared between samples, and
384 differentially abundant proteins (DAPs) were identified using the following
385 thresholds: false discovery rate (FDR) < 0.01 and log₂fold-change (log₂FC) >
386 0.5 (Tables S1–S5 and S7–S15).

387 Functional characterization of DAPs was conducted with Gene Ontology
388 (GO) enrichment analysis to determine the main biological processes
389 stimulated by microbial inoculations.

390 In root samples, approximately 7%, 0.6%, and 0.6% of all identified
391 proteins were assigned to AMF, *A. brasilense*, and *P. graminis* proteomes,
392 respectively, confirming the presence of all three root-associated microbes at
393 harvest.

394

395 **Wheat response to single inoculation: an overview**

396 A large number of significant DAPs ($P < 0.01$) were identified; 639 DAPs (386
397 in leaves and 253 in roots) in the C vs. Az comparison, and 1,085 DAPs (424
398 in leaves and 661 in roots) in the C vs. P comparison (Tables S1–S4). In leaves,
399 approximately 50% of the DAPs were common between the C vs. Az and C vs.
400 P comparisons (Figure S5A). By contrast, in roots, proteomic expression was
401 highly specific, mirroring the stronger impact on the colonized niche; only 12%
402 of the DAPs were common between the C vs. Az and C vs. P comparisons
403 (Figure S5B).

404 To decipher the molecular mechanisms involved in *A. brasilense*-
405 induced plant growth promotion, we performed GO enrichment analysis of
406 LAz vs LC, LP vs LC, Raz vs RC and RP vs RC (Figure 3). In leaf samples,
407 “photosynthesis light harvesting” and “photosynthetic electron transport
408 chain” were the two most enriched GO terms. These data were consistent with

409 the higher total glucose content of LAz samples compared with LC, LP, and
410 LM samples (Figure 4A). Our experiments, therefore, confirmed that *A.*
411 *brasiliense* exhibits a greater ability to drive an increase in the glucose content
412 of shoots than other beneficial microorganisms (*F. mosseae* and *P. graminis*).
413 Moreover, the LAz sample showed a higher abundance of sucrose transporter
414 2D (SUT2D) than the LC sample; SUT2D shows high similarity to rice SUT2
415 (OsSUT2), which is involved in sucrose mobilization to sink cells (Eom et al.,
416 2011).

417 The “amino acid metabolism” GO term was highly enriched in enzymes
418 involved in the synthesis of aspartate, proline, and branched-chain amino acids.
419 The increased content of amino acids both in root and leaf samples validated
420 the proteomics data (Table S6). The presence of *A. brasiliense* on wheat roots
421 also increased the abundance of the phosphate transporter Pht1-10, which is
422 induced by the AMF (Fiorilli et al., 2018) and enhances Pi uptake.
423 Interestingly, the abundance of Pht1-10 was lower in the RP sample vs RC
424 (Figure S6). Moreover, Pht1-10 was among the four proteins whose abundance
425 showed opposite trends between RAz and RP samples (Table S5). Plants
426 assimilate and metabolize ammonium (NH_4^+) provided by diazotrophs,
427 including *Azospirillum* spp. (Carvalho, Balsemão-Pires, Saraiva, Ferreira, &
428 Hemerly, 2014). In LAz samples, we observed an increase in the abundance of
429 ferredoxin-glutamate dehydrogenase, 2-oxoglutarate (2-OxG)/malate
430 translocator, and isocitrate dehydrogenase (ICDH), and a decrease in the

431 abundance of ferredoxin-nitrite reductase; both these trends are indicative of a
432 higher NH_4^+ assimilation rate in the leaves of Az plants. The increase in
433 photosynthesis could contribute to enhanced tolerance to NH_4^+ toxicity by
434 increasing NH_4^+ assimilation (Setién et al., 2013). Higher concentrations of
435 free amino acids and N in RAz samples support these proteomic results (Table
436 S6, Figure 4B).

437 In roots and leaves, inoculation with *A. brasilense* stimulated the
438 mitochondrial electron transport for ATP synthesis, even if the proteins
439 involved were different (Tables S1 and S2).

440 Proteomic data showed that *P. graminis* inoculation also had a substantial
441 impact on primary metabolism (glycolysis, tricarboxylic acid cycle, and
442 aerobic respiration) in roots and leaves (Figures 3, Figure S6, Tables S3–S5).
443 In the LP sample, DAPs related to photosynthesis did not showed a clear
444 pattern (Table S4).

445 Similar to Az plants, *P. graminis*-inoculated plants showed significantly
446 higher concentrations of N and almost all amino acids than C plants,
447 particularly in the roots (Figure 4B, Table S6). In P plants, the more efficient
448 N uptake could be due to the increased abundance of the high-affinity nitrate
449 transporter NAR2 and its activator NRT2. The abundance of the wheat ortholog
450 of rice ammonium-inducible transporter 1-2 (OsAMT1-2) was also increased
451 in RP sample (Figure S6, Table S5).

452 Overall, most of these proteomic changes affecting respiration,
453 photosynthesis, N assimilation, and mineral nutrition mirror the differential
454 growth response of wheat upon PGPB inoculation, as illustrated in Figure 1,
455 with a significant systemic effect of only *A. brasilense* on plant growth.

456

457 **AMF plays a dominant role in plant roots upon binary association with** 458 **PGPB**

459 We previously showed that *F. mosseae* elicits a significant proteomic change
460 in wheat roots and leaves during colonization (Fiorilli et al., 2018). Consistent
461 with this observation, AzM and PM samples showed high numbers of DAPs;
462 RAzM vs. RC and RP vs. RC comparisons revealed 709 and 1055 DAPs,
463 respectively (Tables S7 and S8), whereas LAzM vs. LC and LPM vs. LC
464 comparisons revealed 504 and 808 DAPs, respectively (Tables S9 and S10,
465 Figure S7).

466 Venn diagrams showed a specific contribution by *F. mosseae* in the roots
467 of co-inoculated plants, mainly AzM plants (Figure S7B and S7D). These data
468 are consistent with our previous proteomic data showing that *F. mosseae* has a
469 stronger local but a weaker systemic impact on wheat (Fiorilli et al., 2018). In
470 roots, inoculation with *F. mosseae* alone or together with *A. brasilense* or *P.*
471 *graminis* led to an increased abundance of 196 proteins, several of which have
472 been previously shown to increase in abundance during mycorrhization
473 (Fiorilli et al., 2018). In particular, we found increased levels of key enzymes

474 involved in glycolysis and the pentose phosphate pathway (glyceraldehyde-3-
475 phosphate dehydrogenase, pyruvate kinase, and 6-phosphogluconate
476 dehydrogenase), fatty acid biosynthesis and metabolism (plastid acetyl-CoA
477 carboxylase and 3-oxoacyl-[acyl-carrier-protein] reductase, GDSL
478 esterase/lipase), and mineral nutrition (OsAMT3;1 homolog). We also detected
479 significant up-regulation of some proteins involved in plant defense, including
480 one acidic endochitinase protein, cysteine-rich receptor-like protein kinase 25
481 (CRK25), and some Germin-like proteins (GLPs).

482 Venn diagrams also showed that most DAPs were exclusively expressed
483 in AzM and PM plants. This trend was mainly detected in leaves (Figure S7A
484 and S7C). In fact, GO enrichment analysis showed that oxidative
485 phosphorylation, response to oxidative stress, photosynthesis, and response to
486 abiotic stimulus were among the up-regulated biological processes in the
487 LAzM vs. LPM comparison. Ribosome biogenesis, translation, and gene
488 expression were down-regulated processes (Table S11, Figure S8).

489 Altogether, our results revealed that organ-specific proteomic changes in
490 AMF-inoculated wheat plants (Fiorilli et al., 2018) are mostly maintained upon
491 binary inoculation. This suggests that the AMF plays a dominant role in the
492 root protein profile.

493

494 **Defense proteins are induced locally and systemically during bipartite and**
495 **tripartite interactions**

496 Some rhizosphere-associated beneficial bacteria trigger a plant immunization
497 phenomenon, called induced systemic resistance (ISR), thus priming the plant
498 immune system (C. M. Pieterse et al., 2014). To verify whether *A. brasilense*
499 and *P. graminis* possess the tools to elicit immune system priming in wheat,
500 we first examined the enriched GO terms involved in plant–microbe
501 interactions. Whereas the “response to wounding” was one of the up-regulated
502 GO enriched categories in RAz samples, the DAPs enriched in the category
503 “response to bacterium” showed a decrease, in LAz samples (Figure 3). In
504 particular, we found reduced abundance of two chitinases, two pathogenesis-
505 related (PR) proteins, and one protein (A0A3B6BXY2) highly similar to the
506 Arabidopsis heat stable 1 (HS1) protein, which exhibits antibacterial activity
507 (Park et al., 2007). This decrease in the abundance of defense-related proteins
508 in leaves could at least partly explain the susceptibility of Az plants to *X.*
509 *translucens* infection in leaf-clipping tests (Figure 2). The sucrose transporter
510 SUT2D specifically induced by *Azospirillum* (Table S2) in wheat leaves could
511 also play a role in the susceptibility of Az plants to pathogen infection.
512 *Xanthomonas* TAL effectors usually target SWEET family sugar transporters
513 to sustain pathogen growth (Verdier et al., 2012).

514 In RP samples harvested at 50 dpi, one of the enriched GO terms was
515 “defense response/incompatible interaction” with the induction of several
516 defense proteins (Figure 3, Table S5). Among them, the A0A3B6DGK2
517 protein, which is similar to RPM1-interacting protein 4 (RIN4), a major

518 regulator of plant defense that plays important roles in both pathogen-
519 associated molecular pattern (PAMP)-triggered immunity (PTI) and effector-
520 triggered immunity (ETI) (Ray, Macoy, Kim, Lee, & Kim, 2019). Additionally,
521 lipoxygenase 1 (LOX1), 12-oxophytodienoate reductase 1 (OPR1), OPR3, and
522 allene oxide cyclase 3 (AOC3) point to up-regulation of the biosynthesis of
523 jasmonic acid (JA), a plant hormone that plays a key role in the biotic stress
524 response and overall plant immunity (C. M. J. Pieterse et al., 1998). Moreover,
525 RP samples showed an increased abundance of a protein (A0A3B6KT24) that
526 is similar to the respiratory burst oxidase homolog protein D (RbohD) and is
527 involved in the generation of reactive oxygen species (ROS) during
528 incompatible plant–pathogen interactions (Torres, Dangl, & Jones, 2002), a
529 CERK homolog (A0A3B6RF20), and proteins required for lignin biosynthesis,
530 which are activated in tomato plants associated with native microbiota (M.
531 Chialva et al., 2018). Lastly, *P. graminis*-inoculated plants showed an
532 increased abundance of some proteins involved in isoprene metabolism,
533 suggesting the up-regulation of pathways involved in plant defense. These data
534 support the hypothesis that similar to other PGPB (C. M. J. Pieterse et al., 1998)
535 and unlike *A. brasilense*, *P. graminis* elicits an immune response in the roots
536 but does not elicit strong ISR at 50 dpi in the leaves against *X. translucens*
537 infection (Figure 2).

538 To describe the systemic bioprotective effect of AMF and PGPB co-
539 inoculation in wheat, we performed LAzM vs. LAz and LPM vs. LP

540 comparisons (Tables S12 and S13). Our analysis showed an increase in several
541 DAPs, putatively involved in the biotic stress response, in both LAzM and
542 LPM samples (Figure 5A). Among these DAPs, we found proteins either
543 involved in JA biosynthesis, such as a phospholipase D, three LOXs, and an
544 AOC, or induced by JA, such as a dirigent protein, PR4 (wheat protein)
545 (Desmond et al., 2005), and OsMPK1 (Singh & Jwa, 2013). Moreover, we
546 observed an increase in the abundance of other proteins involved in signaling of
547 the plant immune response, such as the homolog of brassinosteroid (BR)-signaling
548 kinase 1 (BSK1) (Shi et al., 2013) and a calcium-transporting ATPase, whose
549 homolog (ACA8) is required for limiting the growth of virulent bacteria in
550 Arabidopsis (Frei dit Frey et al., 2012). Another protein, whose expression was
551 highly induced in LPM and LAzM samples, was manganese superoxide
552 dismutase 1 (Mn-SOD1), which belongs to the polyphyletic family of enzymes
553 and protect cells from reactive superoxide radical-induced damage, thus
554 conferring increased stress tolerance (S-Wang et al., 2017).

555 Overall, this analysis revealed some unexpected features: *A. brasilense*
556 alone down-regulates plant defense (which is consistent with the observed
557 disease susceptibility phenotype shown in Figure 2), while single inoculations
558 of *P. graminis* and *F. mosseae* trigger a similar number of proteins involved in
559 the plant immune response in an organ-dependent way. Co-inoculation of
560 wheat plants with the AMF and *A. brasilense* or *P. graminis* elicits the plant
561 immune response not only in LPM but also in LAzM samples, at least in the

562 short term, suggesting that both microbial pairs (AMF–*A. brasilense* and
563 AMF–*P. graminis*) induce a priming response at least at the proteome level
564 (Figure 5A).

565

566 **Microbial pairs modulate wheat response to *X. translucens* by inducing**
567 **different proteomic changes**

568 Leaf inoculation of M, Az, P, and C plants with *X. translucens* revealed that
569 pathogen susceptibility detected in the leaves of LAzX plants was alleviated by
570 the presence of mycorrhizal colonization at 4 dpc (based on the LAzMX vs.
571 LAzX comparison) (Figure 2A). To decipher the main proteins responsible for
572 the reduction of symptoms at 4 dpc, we analyzed the DAPs identified in the
573 LAzMX vs. LAzX and LAzMX vs. LMX comparisons (Tables S14 and S15).

574 The up-regulated proteins included those involved in JA biosynthesis and
575 response. Several LOXs and two lipases including phospholipase A1-II and
576 phospholipase D, which generate fatty acid substrates for JA biosynthesis
577 (Browse, 2009), were highly induced in the LAzMX vs. LAzX and LAzMX
578 vs. LMX comparisons (Ishiguro, Kawai-Oda, Ueda, Nishida, & Okada, 2001;
579 Lee & Park, 2019; C. Wang et al., 2000; Wasternack & Hause, 2013) (Figure
580 5A, Tables S14 and S15). In addition, two allene oxide synthase (AOS)
581 enzymes, which catalyze the first step in the JA biosynthesis pathway, and two
582 AOCs, which are committed for the second step in this pathway (Schaller &
583 Stintzi, 2009), were highly induced in LAzMX samples (Figure 5A) compared

584 with LAzX and LMX samples. We also found that two JA-induced dirigent-
585 like proteins, which act downstream of the JA biosynthesis pathway, were
586 induced in LAzMX samples. This increase of proteins involved in JA
587 biosynthesis was also observed in LPMX samples (Figure 5A).

588 Our results showed that *A. brasilense*-AMF and *P. graminis*-AMF
589 interactions amplified JA signaling during pathogen attack. In addition,
590 proteins involved in biotic stress, which were induced during *A. brasilense*-
591 AMF and *P. graminis*-AMF interactions in LAzM and LPM samples,
592 respectively (Figure 5A), were also recruited during *X. translucens* infection,
593 as testified by their higher abundance in LAzMX and LPMX samples,
594 respectively.

595 These proteomic data correlate with the reduced lesion length observed
596 at the early time point (4 dpc) in AzMX plants with respect to AzX plants.
597 However, at 26 dpc, a significant reduction in lesion size resulted only in MX
598 and PMX plants compared with CX plants (Figure 2B). These data suggest that
599 when co-inoculated with *A. brasilense*, the bioprotective effect exerted of *F.*
600 *mosseae* is transient and probably related to prompt induction of the JA
601 response.

602 Further analysis is needed to clarify the molecular changes during the
603 later stage of pathogen attack under different conditions. However, the
604 proteomic profile of LAzMX samples was very different from that of LPMX
605 samples (799 DAPs; Table S16). Among the most abundant proteins identified

606 in the LAzMX vs. LPMX comparison, we found proteins involved in the
607 response to abiotic stimulus and oxidative stress, while those implicated in
608 translation, ribosome biogenesis, gene expression were down-regulated. A
609 similar pattern was already observed in the LAzM vs. LPM comparison (Figure
610 S8).

611 Overall, these data highlight the intricate network of processes that
612 regulate wheat–PGPB–AMF–pathogen interactions (as observed in LAzMX
613 and LPMX samples). However, elicitation of defense priming in the proteome
614 of LAzM and LPM samples does not necessarily lead to better performance
615 once the plant is under pathogen attack.

616

617 **DISCUSSION**

618 Wheat, one of the earliest food crops to be domesticated, is currently the second
619 most widely cultivated crop in the world and one of the most important grain
620 sources for humans. Given the increasing relevance of plant microbiota, many
621 researches have described wheat-associated microbiota by considering the
622 effects in different organs as well as in grain production. The results of this
623 study illustrate how proteomic changes in wheat plants depend on the inoculum
624 composition (single or multiple microbes) and the organ under study, and lead
625 to differential growth effects and pathogen resistance. All analyses revealed
626 that the AMF was the crucial driver of plant growth and defense priming under
627 our growth conditions (low P). However, the overall changes induced by the

628 AMF–PGPB consortium can interfere with the final mycorrhizal-induced
629 resistance (MIR) outcome (Figure 6).

630

631 **Effect of beneficial microbes on wheat growth is organ- and microbial**
632 **identity-dependent**

633 In addition to their N-fixing ability, *Azospirillum* spp. exhibit a remarkable
634 capacity to benefit a wide range of plant species by activating multiple
635 mechanisms (Fukami, Cerezini, & Hungria, 2018); however, the available
636 omics data are limited to the effects of *A. brasilense* inoculation on roots
637 (Drogue et al., 2014; Spaepen, Bossuyt, Engelen, Marchal, & Vanderleyden,
638 2014). In this study, we showed that the higher root and shoot biomass of plants
639 colonized by *A. brasilense* is supported by the sustained activation of the main
640 metabolic processes (respiration, photosynthesis, and N assimilation), while
641 the roots act as a strong sink for nutrients, such as hexoses and amino acids.
642 These results are consistent with the findings of Zeffa and colleagues, who
643 showed that *A. brasilense* promotes plant growth in maize by enhancing the
644 plant photosynthetic potential or by increasing the N use efficiency (Zeffa et
645 al., 2019) On the other hand, *P. graminis* did not efficiently increase the root
646 and shoot biomass of wheat plants but increased the spike biomass.

647 Wheat actively responds to *P. graminis* inoculation by eliciting many
648 metabolic processes, which involve a higher number of DAPs compared with
649 those induced by *A. brasilense*. Some of these processes were, however,

650 common to the two bacterial species (e.g., processes involved in ROS
651 scavenging) as well described for many other PGPB (Fukami et al., 2018).

652 Wheat responds well to AMF, particularly *F. mosseae* (Fiorilli et al.,
653 2018). The wheat–PGPB–AMF tripartite interaction led to intensive proteomic
654 changes where nutrient transporters and many enzymes involved in primary
655 and secondary metabolism, protein biosynthesis, and ROS homeostasis were
656 elicited.

657 Overall, plant growth experiments, nutrient quantification, and
658 proteomic analyses demonstrated that the AMF plays a leading role in tripartite
659 interactions, particularly in the root, while PGBP (at least *Azospirillum*) affects
660 systemic growth, as evident from the leaf proteome.

661

662 **The bioprotective effect of the AMF is modulated by the nature of the co-** 663 **inoculated PGPB**

664 PGPB are considered essential components of the plant microbiota because of
665 their ability to improve plant growth via multiple mechanisms, including plant
666 health protection (Berendsen, Pieterse, & Bakker, 2012; Lugtenberg et al.,
667 2016). *Azospirillum* is not a typical biocontrol agent, despite studies showing
668 its ability to increase pathogen resistance in plants (Bashan & de-Bashan, 2002;
669 Kusajima et al., 2018; Tortora, Díaz-Ricci, & Pedraza, 2012; Yasuda, Isawa,
670 Shinozaki, Minamisawa, & Nakashita, 2009). On the other hand, some
671 *Paraburkholderia* taxa, such as *P. phytofirmans*, induce resistance against a

672 broad range of plant pathogens by inducing plant-mediated responses in aerial
673 organs (Miotto-Vilanova et al., 2016). Proteomic analysis of wheat plants
674 inoculated with a single microbe showed that proteins involved in plant defense
675 were down-regulated in LAz samples. Moreover, according to the “pathogen
676 starvation” model, which links plant resistance with soluble sugars (Bezruczyk
677 et al., 2018), the high sugar and amino acid contents of LAz leaves coupled
678 with an enhanced abundance of sugar transporters could guarantee a nutrient-
679 rich niche for the pathogen. Under these conditions, the plant could not activate
680 any defense mechanisms, notwithstanding a slight improvement in the presence
681 of the AMF at 4 dpc.

682 *P. graminis* induced diverse proteomic changes in roots characterized by
683 an increase in the abundance of proteins involved in microbe-associated
684 molecular pattern (MAMP) perception, PTI and ETI regulation (RIN4), ROS
685 production and detoxification, lignin biosynthesis, and isoprene metabolism.
686 These findings suggest that *P. graminis* elicits an immunomodulatory
687 response; however, this does not lead to ISR.

688 The protein profiles clearly indicate the capacity of mycorrhizal plants,
689 associated with PGPB, to increase the number of defense-related proteins in
690 leaves in the absence of the pathogen, and an augmented capacity to express
691 these proteins upon pathogen infection (Figure 5A). The up-regulation of JA
692 biosynthesis proteins was a key finding because this hormone is considered the
693 first regulator of the plant immune response (Hickman et al., 2017; C. M. J.

694 Pieterse et al., 1998). Several studies reported that AM symbiosis protects
695 plants against pathogens, suggesting that JA defense mechanisms play a key
696 role in MIR (Jung, Martinez-Medina, Lopez-Raez, & Pozo, 2012).

697 AMF are a crucial component of the plant microbiota (Bonfante, Venice,
698 & Lanfranco, 2019) and the first inducers of plant immunity. A previous study
699 showed that co-inoculation of wheat with an AMF and *Pseudomonas* spp.
700 (PGPB) leads to synergistic effects, priming the host immunity through
701 chitosan-induced callose deposition (Pérez-de-Luque et al., 2017). A
702 comparable result has been described in tomato plants grown in native soil
703 containing multiple bacteria and AMF; MAMPs released by various microbes
704 enhance the plant immunity, thus activating PTI markers. When challenged by
705 pathogenic *Fusarium* spp., the tomato plants were strongly protected because
706 of the activation of specific antifungal proteins (Chialva, Zhou, Spadaro, &
707 Bonfante, 2018).

708 According to a previously proposed hypothesis (Cameron, Neal, van
709 Wees, & Ton, 2013), JA could act as a long distance signaling molecule that in
710 mycorrhizal wheat, and also in the presence of both PGPB species, activates
711 the systemic priming of plant defense. However, in our system, lesion length
712 was reduced only at the early time point (4 dpc) in AzMX plants in comparison
713 with AzX plants. At 26 dpc, a significant reduction in lesion length was
714 observed only in MX and PMX plants in comparison with CX plants (Figure
715 2B). We speculate that additional determinants induced by the AMF-PGPB

716 interactions interfere with cellular processes, leading to MIR. Proteomic data
717 showed that in LAzMX samples, the abundance of proteins involved in
718 ribosome biogenesis and gene expression decreased compared with their
719 abundance in LMX and LBMX samples (Figure 5B). Ribosomal genes are
720 highly responsive to stress and signaling molecules, indicating that the encoded
721 proteins play roles in stress amelioration, besides house-keeping. The
722 instantaneous up-regulation of ribosomal genes in response to stress might
723 function as a prompt defense response (Moin et al., 2016). In addition, a
724 reduction in HMGA subfamily transcription factor and H2B and H1 histones
725 could affect the transcription of defense-related genes (Isaac, Hartney, Druffel,
726 & Hadwiger, 2009). Finally, a reduction in the abundance of two proteins
727 involved in stomata regulation, H1.3 and ubiquitin-specific protease 24
728 (Rutowicz et al., 2015; Zhao et al., 2016), and some proteins involved in
729 cuticular wax production, could promote leaf pathogen invasion in AzMX
730 plants.

731

732 **CONCLUSION**

733 Plant-associated microbiota hold great promise for the development of
734 sustainable crop systems, and this can be guaranteed by the use of SynComs
735 (Kong, Hart, & Liu, 2018). However, results obtained from on-field microbiota
736 census and those obtained using reductionist approaches, mostly through
737 laboratory-based experiments, have not yet been fully integrated (Fitzpatrick

738 et al., 2020). Our results suggest that beneficial microbes have different impacts
739 on plants, at least in wheat, and the plant growth-promoting effects of beneficial
740 microbes are not always accompanied by enhanced pathogen resistance, as
741 shown by *A. brasilense* inoculation (Figure 6). On the other hand, a bacterium
742 that does not show strong growth-promoting effect, such as *P. graminis*, may
743 be more effective against pathogen attack, if associated with an AMF (Figure
744 6). Our data highlight the crucial role of AM fungi, which are often absent in
745 SynComs, as well as the potential contrasting effects of different AMF–PGPB
746 consortia on plant defense. In a wider context, these findings suggest that
747 SynCom efficiency should be validated by checking the outcome of the
748 interaction under different conditions (microbe-microbe interactions;
749 nutritional status, plant life cycle and biotic stress) before their exploitation for
750 crop growth.

751

752 **ACKNOWLEDGMENTS**

753 This work was supported by the MIC-CERES (“Microbial eco-compatible
754 strategies for improving wheat quality traits and rhizospheric soil
755 sustainability”) Project (FC Project ID 2013–1888; AF Project ID 1301–003)
756 jointly supported by the Agropolis Foundation (through the “Investissements
757 d’avenir” program, with the reference number ANR-10-LABX-0001-01) and
758 Fondazione Cariplo. The authors thank the Functional Genomics Center Zurich
759 (FGCZ) for providing highly valuable technical support.

760

761 **AUTHOR CONTRIBUTIONS**

762 V.F., D.G.S., P.B., L.M., and C.V designed the study; V.F., D.G.S., M.N., and
763 D.G. carried out the majority of experiments; G.D., M.M., and C.V performed
764 the bioinformatic analysis of proteomic data; C.V., V.F., P.B. L.M., F.W.-D.,
765 and M.B. interpreted the data and wrote the manuscript.

766

767 **CONFLICT OF INTEREST**

768 The authors have no conflict of interest to declare.

769

770 **SUPPORTING INFORMATION**

771 Table S1. Differentially abundant proteins (DAPs) identified by comparative
772 proteomic analysis of the roots (R) of *Azospirillum brasilense*-inoculated (Az)
773 and mock-inoculated (control; C) wheat plants (RAz vs. RC comparison).

774 Table S2. DAPs identified by comparative proteomic analysis of the leaves (L)
775 of Az and C plants (LAz vs. LC comparison).

776 Table S3. DAPs identified by comparing the leaf proteome of
777 *Paraburkholderia graminis*-inoculated (P) and C plants (RP vs. RC
778 comparison).

779 Table S4. DAPs identified by comparing the leaf proteome of P and C plants
780 (LP vs. LC comparison).

781 Table S5. Root-specific DAPs identified by comparing the root proteome of
782 Az or P plants with that of C plants (RAz vs. RC and RP vs. RC comparisons,
783 respectively).

784 Table S6. Amino acid content (ratio).

785 Table S7. DAPs identified by comparing the root proteome of wheat plants co-
786 inoculated with the arbuscular mycorrhizal fungus (AMF), *Funneliformis*
787 *mosseae*, and *A. brasilense* (AzM) with that of C plants (RAzM vs. RC
788 comparison).

789 Table S8. DAPs identified by comparing the root proteome of wheat plants co-
790 inoculated with the AMF and *P. graminis* (PM) with that of C plants (RPM vs.
791 RC comparison).

792 Table S9. DAPs identified by comparing the leaf proteomes of AzM and C
793 plants (LAzM vs. LC comparison).

794 Table S10. DAPs identified by comparing the leaf proteomes of PM and C
795 plants (LPM vs. LC comparison).

796 Table S11. DAPs identified by comparing the leaf proteomes of AzM and PM
797 plants (LAzM vs. LPM comparison).

798 Table S12. DAPs identified by comparing the leaf proteomes of Az plants
799 treated with or without the AMF (LAzM vs. LAz comparison).

800 Table S13. DAPs identified by comparing the leaf proteomes of P plants treated
801 with or without the AMF (LPM vs. LP comparison).

802 Table S14. DAPs identified by comparing the leaf proteomes of Az plants
803 infected with or without the leaf pathogen, *Xanthomonas translucens* (LAzMX
804 vs. LAzX comparison).

805 Table S15. DAPs identified by comparing the leaf proteomes of AzM plants
806 and AMF only-inoculated (M) plants infected with *X. translucens* (LAzMX
807 vs. LMX comparison).

808 Table S16. DAPs identified by comparing the leaf proteomes of AzMX plants
809 and PM plants infected with *X. translucens* (LAzMX vs. LPMX comparison).

810 Figure S1. Overview of the experimental set up.

811 Figure S2. Spike fresh weight.

812 Figure S3. Evaluation of microbial root colonization.

813 Figure S4. Hierarchical clustering analysis of protein intensities.

814 Figure S5. Overlap of differentially abundant proteins (DAPs) between Az vs.
815 C and P vs. C comparisons.

816 Figure S6. Heat map of DAPs belonging to “carbohydrate metabolism”,
817 “photosynthesis”, “ion transport”, and “defense” GO terms in LAz vs. LC, LP
818 vs. LC, RAz vs. RC, and RP vs. RC comparisons.

819 Figure S7. Venn diagrams of DAPs identified by comparing the proteome of
820 mock-inoculated control (C) wheat plants with that of plants inoculated with
821 only plant-growth promoting bacteria (PGPB; single inoculation) or co-
822 inoculated with PGPB and arbuscular mycorrhizal fungus (AMF) (double
823 inoculation).

824 Figure S8. Schematic representation of AgriGO SEA COMPARE function of
825 up/down-regulated in LAzM vs. LPM and LAzMX vs. LPMX comparisons.

826

827 **FIGURE LEGENDS**

828 **Figure 1.** Effect of arbuscular mycorrhizal (AM) symbiosis on the biomass of
829 different organs of wheat plants. (A) Fresh weight of roots (RFW; grams). (B)
830 Fresh weight of shoots (SFW; grams). Plants were either mock-inoculated
831 (control; C) or inoculated with different microbial combinations: *Azospirillum*
832 *brasilense* only (Az), *Paraburkholderia graminis* only (P), *Funneliformis*
833 *mosseae* only (M), *A. brasilense* plus *F. mosseae* (AzM), and *P. graminis* plus
834 *F. mosseae* (PM). Wheat plants were harvested at 50 days post-inoculation
835 (dpi). Data represented as mean \pm standard deviation (SD; $n \geq 6$) were subjected
836 to a one-way analysis of variance (ANOVA). Asterisks indicate significant
837 differences ($P < 0.05$; Tukey's test). Different lowercase letters indicate
838 significant differences.

839

840 **Figure 2.** Phenotypic evaluation of disease symptoms caused by the bacterial
841 pathogen *Xanthomonas translucens*. Lesion length (mm) was assessed on
842 leaves of C, Az, P, M, AzM, and PM plants at 4 (A) and 26 (B) days post-leaf
843 clipping (dpc). Data at 4 dpc (not normally distributed) were analysed using
844 the Kruskal-Wallis test. Asterisks indicate significant differences at the 5%

845 level using Mann–Whitney pairwise comparisons. Data at 26 dpc were
846 subjected to one-way analysis of variance (ANOVA). Asterisks indicate
847 significant differences ($P < 0.05$; Tukey’s test). Different lowercase letters
848 indicate significant differences.

849

850 **Figure 3.** Gene Ontology (GO) enrichment analysis of DAPs identified by
851 comparing Az or P vs. C roots (RAz vs. RC and RP vs. PC) and leaves (LAz
852 vs. LC and LP vs. LC). Enriched GO terms were selected using the following
853 thresholds: false discovery rate (FDR) ≤ 0.05 and fold enrichment > 3.5 . Red
854 and blue indicate the enrichment of GO biological process terms for up- and
855 down- regulated DAPs, respectively.

856

857 **Figure 4.** Total glucose and nitrogen (N) contents of wheat leaves and roots,
858 respectively. (A, B) Total glucose content of leaves (A) and N content of roots
859 (B) of C, Az, P, M, AzM, and PM wheat plants harvested at 50 dpi. Data
860 represented as mean \pm SD ($n \geq 3$) were subjected to a one-way ANOVA.
861 Different lowercase letters indicate significant differences ($P < 0.05$; Tukey’s
862 test).

863

864 **Figure 5.** Heat map of the main DAPs involved in plant defense (A) and in cell
865 wall production, epigenetic regulation, translation (B) found in wheat leaves
866 inoculated with PGPB and/or AM fungus (AMF) and treated with or without

867 *X. translucens*. Log₂fold-change (Log₂FC) values indicate the changes in
868 protein abundance with respect to the control. Red and blue indicate maximum
869 and minimum values, respectively. Asterisks indicate significant differences
870 (ANOVA FDR < 0.01; Tukey's test).

871

872 **Figure 6.** (A) Scheme showing the molecular and phenotypic responses of non-
873 mycorrhizal wheat colonized by *A. brasilence* (left side) and *P. graminis* (right
874 side). (B) Scheme showing the molecular and phenotypic responses of
875 mycorrhizal (*F. mosseae*) wheat alone (center) or colonized by *A. brasilence*
876 (left side) and *P. graminis* (right side). The green boxes include the effects on
877 the leaves while the brown ones include the effects on the roots.

878

879 **Figure S1.** Overview of the experimental set up. Twelve treatments of two
880 different plant growth-promoting bacteria (PGPB) and one arbuscular
881 mycorrhizal fungus (AMF) were tested. Surface-sterilized wheat seeds were
882 pre-germinated for 4 days, transplanted into pots (see Experimental
883 procedures) at t₀, and inoculated with PGPR 1 day after. The AMF was present
884 in the substrate at t₀ (M treatment). The leaf-clipping assay was performed by
885 infecting plants with *Xanthomonas translucens* on day 46, and the length of
886 lesions was monitored at 4 and 26 days post-clipping (dpc; corresponding to
887 day 50 and 72, respectively). To perform proteomics analysis, leaves were

888 infiltrated with a micro needle on day 49, and the infiltrated zone was sampled
889 on day 50 and frozen in liquid nitrogen.

890

891 **Figure S2.** Spike fresh weight of control, Az and P plants evaluated at the end
892 of wheat natural life cycle. Data (means \pm SD, $n \geq 6$) were subjected to one-
893 way analysis of variance (ANOVA). The asterisks indicated significant
894 differences at the 5% level using Tukey's test.

895

896 **Figure S3.**

897 Evaluation of microbial colonization of wheat plants. (A) Quantification of
898 bacterial population (colony forming units [CFU]) per gram of wheat roots at
899 7, 14, and 21 dpi. (B, C) Frequency of mycorrhizal hyphae (F%) (B) and
900 arbuscule abundance (A%) (C) in plant samples stained with trypan blue. One
901 hundred, 1-cm root fragments were analyzed for each sample. Data represent
902 mean \pm standard error (SE) of two biological replicates per treatment. Az,
903 *Azospirillum brasilense* Sp245; P, *Paraburkholderia graminis* C4D1M; M,
904 *Funelliformis mosseae*; AzM, *A. brasilense* Sp245 plus *F. mosseae*; PM, *P.*
905 *graminis* C4D1M plus *F. mosseae*.

906

907 **Figure S4.** Hierarchical clustering analysis of protein intensities in different
908 organs of wheat plants. (A) Leaf dataset; (B) root dataset.

909

910 **Figure S5.** Overlap of differentially abundant proteins (DAPs) between Az vs.
911 C and P vs. C comparisons. (A, B) Venn Diagrams of DAPs in leaves (A) and
912 roots (B). Red and blue values indicate up- and down-regulated proteins,
913 respectively. (C, D) Heat map of DAPs regulated in response to both plant
914 growth-promoting bacteria (PGPB) in leaves (C) and roots (D). Red and blue
915 indicate maximum and minimum values, respectively.

916

917 **Figure S6.** Heat map of DAPs belonging to “carbohydrate metabolism”,
918 “photosynthesis”, “ion transport”, and “defense” GO terms in LAz vs. LC, LP
919 vs. LC, RAz vs. RC, and RP vs. RC comparisons. Log₂fold-change (Log₂FC)
920 values are shown. Red and blue indicate maximum and minimum values,
921 respectively.

922

923 **Figure S7.** Venn diagrams of differentially abundant proteins (DAPs) found in
924 all single and double inoculations vs. control (C) plants. DAPs exclusively and
925 commonly regulated by *A. brasilense* and AMF upon single and double
926 inoculations in leaves (A) and roots (B). DAPs exclusively and commonly
927 regulated by *P. graminis* and AMF upon single and double inoculations in
928 leaves (C) and roots (D).

929

930 **Figure S8.** Schematic representation of AgriGO SEA COMPARE function of
931 up/down-regulated in LAzM vs LPM and LAzMX vs LPMX comparisons. The

932 colored blocks represent the level of regulation of each term, where the degree
933 of color saturation (yellow-to-red) of the corresponding box, was determined
934 by the adjusted P-value of the GO term (red = more significant).

935

936 DATA AVAILABILITY STATEMENT

937 Data available on request from the authors

938

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