

Supplementary Table 1. Average volume percent and standard errors of protein spots depicted in figure 5.

<b>Spot ID</b>	<b>0 mM NaCl non-inoculated</b>	<b>0 mM NaCl inoculated</b>	<b>100 mM NaCl non-inoculated</b>	<b>100 mM NaCl inoculated</b>	<b>300 mM NaCl non-inoculated</b>	<b>300 mM NaCl inoculated</b>
<b>8</b>	0.081 ± 0.017	0.068 ± 0.014	0.044 ± 0.002	0.057 ± 0.004	0.043 ± 0.005	0.044 ± 0.003
<b>11</b>	0.051 ± 0.010	0.018 ± 0.009	0.068 ± 0.022	0.045 ± 0.004	0.020 ± 0.009	0.034 ± 0.012
<b>66</b>	0.103 ± 0.029	0.077 ± 0.007	0.174 ± 0.054	0.157 ± 0.015	0.162 ± 0.033	0.212 ± 0.038
<b>95</b>	0.036 ± 0.005	0.033 ± 0.005	0.043 ± 0.006	0.058 ± 0.006	0.051 ± 0.004	0.060 ± 0.007
<b>117</b>	0.013 ± 0.005	0.010 ± 0.004	0.017 ± 0.002	0.017 ± 0.007	0.041 ± 0.016	0.021 ± 0.003
<b>119</b>	0.020 ± 0.004	0.015 ± 0.005	0.027 ± 0.002	0.029 ± 0.004	0.030 ± 0.004	0.030 ± 0.005
<b>122</b>	0.025 ± 0.008	0.025 ± 0.004	0.033 ± 0.006	0.051 ± 0.004	0.046 ± 0.000	0.038 ± 0.003
<b>140</b>	0.041 ± 0.007	0.041 ± 0.010	0.047 ± 0.003	0.078 ± 0.006	0.058 ± 0.004	0.059 ± 0.012
<b>205</b>	0.033 ± 0.005	0.030 ± 0.008	0.073 ± 0.019	0.081 ± 0.011	0.065 ± 0.009	0.076 ± 0.011
<b>219</b>	0.026 ± 0.011	0.023 ± 0.002	0.051 ± 0.006	0.047 ± 0.011	0.136 ± 0.033	0.127 ± 0.005
<b>301</b>	0.076 ± 0.013	0.071 ± 0.002	0.090 ± 0.010	0.123 ± 0.025	0.140 ± 0.020	0.144 ± 0.017
<b>473</b>	0.035 ± 0.004	0.032 ± 0.005	0.053 ± 0.007	0.046 ± 0.008	0.078 ± 0.019	0.037 ± 0.003
<b>606</b>	0.120 ± 0.006	0.107 ± 0.016	0.082 ± 0.010	0.120 ± 0.017	0.071 ± 0.010	0.093 ± 0.019
<b>621</b>	0.021 ± 0.003	0.035 ± 0.006	0.032 ± 0.006	0.051 ± 0.005	0.087 ± 0.013	0.095 ± 0.025
<b>968</b>	0.015 ± 0.004	0.012 ± 0.005	0.029 ± 0.006	0.026 ± 0.009	0.022 ± 0.002	0.034 ± 0.005
<b>817</b>	0.011 ± 0.001	0.016 ± 0.003	0.007 ± 0.001	0.010 ± 0.003	0.007 ± 0.001	0.010 ± 0.001
<b>884</b>	0.030 ± 0.003	0.031 ± 0.003	0.021 ± 0.002	0.027 ± 0.001	0.021 ± 0.004	0.019 ± 0.003
<b>928</b>	0.027 ± 0.001	0.024 ± 0.003	0.047 ± 0.019	0.032 ± 0.007	0.059 ± 0.006	0.039 ± 0.006

Supplementary Table 2. Protein spot quantification including average volume percent and standard errors as depicted in figure 6.

Spot ID	0 mM NaCl non-inoculated	0 mM NaCl Inoculated	300 mM NaCl non-inoculated	300 mM NaCl Inoculated	Spot ID	0 mM NaCl non-inoculated	0 mM NaCl Inoculated	300 mM NaCl non-inoculated	300 mM NaCl Inoculated
1	0.414 ± 0.031	0.357 ± 0.036	0.226 ± 0.044	0.325 ± 0.023	412	0.042 ± 0.002	0.039 ± 0.008	0.053 ± 0.007	0.064 ± 0.010
8	0.081 ± 0.012	0.068 ± 0.010	0.043 ± 0.005	0.044 ± 0.003	413	0.105 ± 0.009	0.103 ± 0.005	0.077 ± 0.008	0.162 ± 0.018
11	0.051 ± 0.010	0.018 ± 0.009	0.020 ± 0.009	0.034 ± 0.012	441	0.045 ± 0.008	0.040 ± 0.007	0.019 ± 0.004	0.022 ± 0.005
57	0.108 ± 0.007	0.099 ± 0.013	0.212 ± 0.049	0.176 ± 0.024	447	0.015 ± 0.004	0.013 ± 0.003	0.031 ± 0.006	0.021 ± 0.002
66	0.103 ± 0.029	0.077 ± 0.007	0.162 ± 0.033	0.212 ± 0.038	461	0.067 ± 0.005	0.067 ± 0.003	0.037 ± 0.004	0.056 ± 0.007
95	0.036 ± 0.005	0.033 ± 0.005	0.051 ± 0.004	0.060 ± 0.007	473	0.035 ± 0.004	0.032 ± 0.005	0.078 ± 0.019	0.037 ± 0.003
117	0.013 ± 0.005	0.010 ± 0.004	0.041 ± 0.016	0.021 ± 0.003	521	0.051 ± 0.003	0.058 ± 0.002	0.079 ± 0.009	0.076 ± 0.006
119	0.020 ± 0.004	0.015 ± 0.005	0.030 ± 0.004	0.030 ± 0.005	527	0.085 ± 0.011	0.098 ± 0.009	0.049 ± 0.008	0.055 ± 0.006
122	0.025 ± 0.008	0.025 ± 0.004	0.046 ± 0.000	0.038 ± 0.003	549	0.073 ± 0.008	0.093 ± 0.007	0.043 ± 0.009	0.062 ± 0.011
125	0.051 ± 0.005	0.051 ± 0.010	0.088 ± 0.009	0.091 ± 0.011	606	0.120 ± 0.006	0.107 ± 0.016	0.071 ± 0.010	0.093 ± 0.019
166	0.089 ± 0.011	0.119 ± 0.012	0.053 ± 0.019	0.083 ± 0.014	621	0.021 ± 0.003	0.035 ± 0.006	0.087 ± 0.013	0.095 ± 0.025
205	0.033 ± 0.005	0.030 ± 0.008	0.065 ± 0.009	0.076 ± 0.011	636	0.017 ± 0.003	0.017 ± 0.001	0.027 ± 0.002	0.045 ± 0.009
219	0.026 ± 0.011	0.023 ± 0.002	0.136 ± 0.033	0.127 ± 0.005	665	0.076 ± 0.003	0.087 ± 0.007	0.053 ± 0.002	0.081 ± 0.009
221	0.034 ± 0.005	0.038 ± 0.004	0.023 ± 0.007	0.040 ± 0.004	681	0.044 ± 0.007	0.059 ± 0.008	0.028 ± 0.002	0.043 ± 0.007
247	0.024 ± 0.005	0.020 ± 0.005	0.022 ± 0.003	0.013 ± 0.002	691	0.203 ± 0.018	0.250 ± 0.043	0.095 ± 0.029	0.142 ± 0.017
253	0.043 ± 0.009	0.038 ± 0.007	0.013 ± 0.002	0.025 ± 0.002	791	0.039 ± 0.012	0.071 ± 0.006	0.102 ± 0.019	0.073 ± 0.027
301	0.076 ± 0.013	0.071 ± 0.002	0.140 ± 0.020	0.144 ± 0.017	814	0.076 ± 0.008	0.082 ± 0.005	0.045 ± 0.011	0.059 ± 0.009
325	0.081 ± 0.008	0.070 ± 0.015	0.114 ± 0.015	0.122 ± 0.026	817	0.011 ± 0.001	0.016 ± 0.003	0.007 ± 0.001	0.010 ± 0.001
338	0.117 ± 0.005	0.114 ± 0.012	0.053 ± 0.002	0.104 ± 0.010	903	0.035 ± 0.009	0.053 ± 0.005	0.024 ± 0.004	0.052 ± 0.012
339	0.045 ± 0.006	0.035 ± 0.003	0.020 ± 0.003	0.025 ± 0.002	928	0.027 ± 0.001	0.024 ± 0.003	0.059 ± 0.006	0.039 ± 0.006
342	0.031 ± 0.005	0.036 ± 0.004	0.061 ± 0.006	0.056 ± 0.011	947	0.182 ± 0.043	0.234 ± 0.052	0.125 ± 0.027	0.250 ± 0.018
352	0.050 ± 0.006	0.042 ± 0.005	0.073 ± 0.009	0.083 ± 0.017	946	0.143 ± 0.021	0.136 ± 0.015	0.082 ± 0.007	0.168 ± 0.025
377	0.052 ± 0.005	0.049 ± 0.004	0.075 ± 0.012	0.080 ± 0.006	968	0.015 ± 0.004	0.012 ± 0.005	0.022 ± 0.002	0.034 ± 0.005

Supplementary Table 3. List of average percentage proteins showing difference in amount between *Piriformospora indica*-colonized and non-inoculated plants under control (0 mM NaCl).

Spot ID <sup>a</sup>	pI/MW (kDa)		gene no. <sup>d</sup>	Score/ %Cov. <sup>e</sup>	MS/MS -MS <sup>f</sup>	Best matching gene product
	Exp. <sup>b</sup>	The. <sup>c</sup>				
<b>11</b>	6.1/13	5.8/13.3	gi 132107	280/72	11/3	Ribulose biphosphate carboxylase small chain
<b>70</b>	5.2/15	5.3/15.9	gi 1229138	424/47	9/5	low temperature-responsive RNA-binding protein
<b>200</b>	6.4/25	5.9/21.7	gi 58500257	107/26	4/2	Quinone reductase 2 [Triticum monococcum]
<b>586</b>	5.4/41	6.8/40.8	gi 195644252	160/16	4/2	Aspartate-semialdehyde dehydrogenase [Zea mays]
<b>795</b>	6/40	5.7/41.7	gi 162463414	156/29	4/2	Atin [Phaseolus vulgaris]
<b>810</b>	5.5/76	5.3/70.7	gi 27476086	218/24	15/5	Putative heat shock 70 KD protein

a) The numbering corresponds to the 2-D gel in Figure 4. b) Experimental pI and MW. c) Theoretical pI and MW. d) gi number in Gene Bank. e) MASCOT score and percent coverage resulted from combined MS-MS/MS search. f) Number of peptide identified by PMF and MS/MS