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CORRIGENDUM

Corrigendum to Wagner *et al.*: Natural soil microbes alter flowering phenology and the intensity of selection on flowering time in a wild Arabidopsis relative

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The authors would like to correct a bioinformatics error, discovered after publication, in the microbial abundance data presented in Wagner *et al.* (2014a). The error has no effect on any of the paper's biological conclusions, as we demonstrate below. Briefly, a systematic glitch in the processing of the raw MiSeq sequences led to an apparently random duplication of some sequences. This in turn increased the number of total sequences and affected OTU counts reported in the paper. After discovery of the glitch, we repeated all processing and analysis using the corrected pipeline. The revised data set has been uploaded to Dryad as a new version of the preexisting package (Wagner *et al.* 2014b).

The total number of OTUs in our soil samples is 4991 (down from 7844), with a mean 16S copy number of 2.7175 (down from 2.8057). PCo1 now explains 48.0% of the variance, up from 40.5%; PCo2 remains unchanged (Fig. S3; corrected online Supporting Information was posted with this corrigendum). The ordination of soil samples by Bray–Curtis distance is largely unchanged (Fig. 3a) and sample ordination is still controlled by site ($P = 0.017$, $R^2 = 0.27$; compare to originally reported $P = 0.003$, $R^2 = 0.29$) but not by year ($P = 0.097$, $R^2 = 0.07$; compare to originally reported $P = 0.56$, $R^2 = 0.03$). There were no changes to the linear regression of flowering time on PCo2 (Fig. 3b; $P = 0.304$, $R^2 = 0.23$, estimate = 1.4988 days/unit; compare to original result $P = 0.26$, $R^2 = 0.31$, estimate = 1.5028 days/unit). The OTU best correlated with flowering time is in the family Bradyrhizobiaceae rather than Hyphomicrobiaceae (Table S6). There were no major changes to the linear regression of flowering time on the major OTU (Fig. 3c; Benjamini–Hochberg adjusted $P = 0.07$, $R^2 = 0.98$, estimate = 0.0043 days/individual; compare to original adjusted $P = 0.37$, $R^2 = 0.89$, estimate = 0.0182 days/individual).

Comparisons of relative abundances of phyla and families between sites are generally unchanged, with a few exceptions: Crenarchaeota are enriched in JAM rather than MAH soil (Table 3b); the enrichment of Gemmatimonetes in the top 5% of OTUs associated with PCo2 is no longer statistically significant (Table 3c); minor changes to the distributions of families between sites in Table S7 and Fig. S4.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

STATEMENT OF AUTHORSHIP

SGT coordinated data reprocessing through the corrected bioinformatics pipeline. MRW and DSL re-analysed data and wrote the corrigendum with input from SGT, JLD and TMO.

REFERENCES

Wagner, M.R., Lundberg, D.S., Coleman-Derr, D., Tringe, S.G., Dangl, J.L. & Mitchell-Olds, T. (2014a). Natural soil microbes alter flowering phenology and the intensity of selection on flowering time in a wild Arabidopsis relative. *Ecol. Lett.*, 17, 717–726.

Wagner, M.R., Lundberg, D.S., Coleman-Derr, D., Tringe, S.G., Dangl, J.L. & Mitchell-Olds, T. (2014b). Data from: Natural soil microbes alter flowering phenology and the intensity of selection on flowering time in a wild Arabidopsis relative. Dryad Digital Repository. Available at: http://dx.doi.org/10.5061/dryad.1t6s5.2. Last accessed 13 November 2014.

SUPPORTING INFORMATION

Additional Supporting Information may be downloaded via the online version of this article at Wiley Online Library (www.ecologyletters.com).

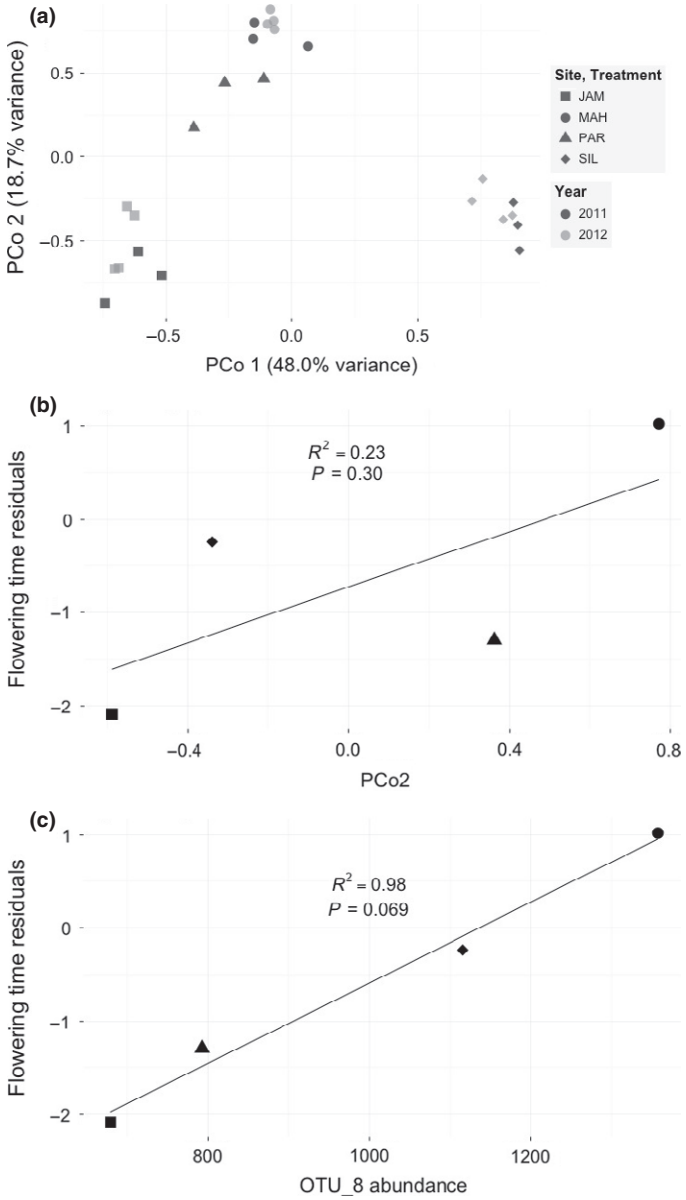

Figure 3 (a) Ordination of Bray–Curtis dissimilarities of rarefied microbial abundances (using 16S data generated with the corrected bioinformatics pipeline) shows clustering of soil samples by field site of origin (ADONIS $P = 0.017$), but not by collection year (ADONIS $P = 0.097$). (b) Flowering time response of western genotypes (residuals, after controlling for block effects, genetic differences, and growth rate) to a gradient of soil microbiome PCo2, a candidate predictor of flowering time. (c) Flowering time response of western genotypes [residuals, as in (b)] to abundance of candidate microbe OTU_8, chosen for its high loading onto PCo2 (Table S6; Appendix S3). (d) Relative abundances of dominant phyla in natural soil communities and the top 5% of taxa most strongly correlated with PCo2. Statistical comparisons of these distributions are in Table 3b,c. Family-level distributions are summarised in Fig. S4 and Table S7.

Table 3 (a) Mean flowering time of western genotypes (residuals after controlling for genetic differences and growth rates), mean PCo2 score and mean abundance of OTU 8 in each microbial community, using 16S data generated with the corrected bioinformatics pipeline. Flowering time data come from the greenhouse experiment, community composition data come from soil samples taken from the same field sites as the inocula for the greenhouse experiment. This set of data can be informative for finding subsets of the microbial community associated with change in flowering time (Fig. 3; Appendix S3). (b) Copy number-adjusted relative abundances of dominant phyla in slow-flowering MAH and late-flowering JAM soils. (c) Copy number-adjusted relative abundances in the full data set ('All OTUs') and the subset of 5% of OTUs most strongly correlated with PCo2, a putative predictor of flowering time. Significance of enrichment/depletion was determined by Wilcoxon Rank Sum tests and adjusted using the Benjamini–Hochberg false discovery rate.

(a) Site	Flowering time (residual)	PCo2	OTU 8 (individuals, ± 1 SE)
JAM	−2.088 ± 0.856	−0.589 ± 0.077	679.08 ± 52.47
MAH	1.022 ± 1.057	0.772 ± 0.027	1358.05 ± 74.90
PAR	−1.298 ± 0.848	0.362 ± 0.093	792.5 ± 137.48
SIL	−0.238 ± 0.819	−0.338 ± 0.050	1116.1 ± 70.43

Phylum	(b) JAM (%)	MAH (%)	P_{FDR}	(c) All (%)	PCo2 (%)	P_{FDR}
Proteobacteria	17.2	26.7	**0.002**	24.9	25.5	0.9
Acidobacteria	21.9	15.6	**0.002**	18.0	18.9	0.6
Verrucomicrobia	18.8	15.5	0.057	16.9	22.0	**0.005**
Actinobacteria	16.0	17.9	0.13	16.0	13.7	**0.005**
Gemmatimonadetes	9.5	9.4	1	7.7	8.9	0.14
Chloroflexi	5.8	7.3	0.057	6.1	6.3	0.9
Planctomycetes	3.5	2.7	0.057	4.0	0.5	**< 0.0001**
Bacteroidetes	2.9	2.7	1	3.6	1.9	**0.0005**
Crenarchaeota	1.4	0.2	**0.002**	0.7	1.0	0.6