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Publisher Correction: A short exposure to a semi-natural habitat alleviates the honey bee hive microbial imbalance caused by agricultural stress

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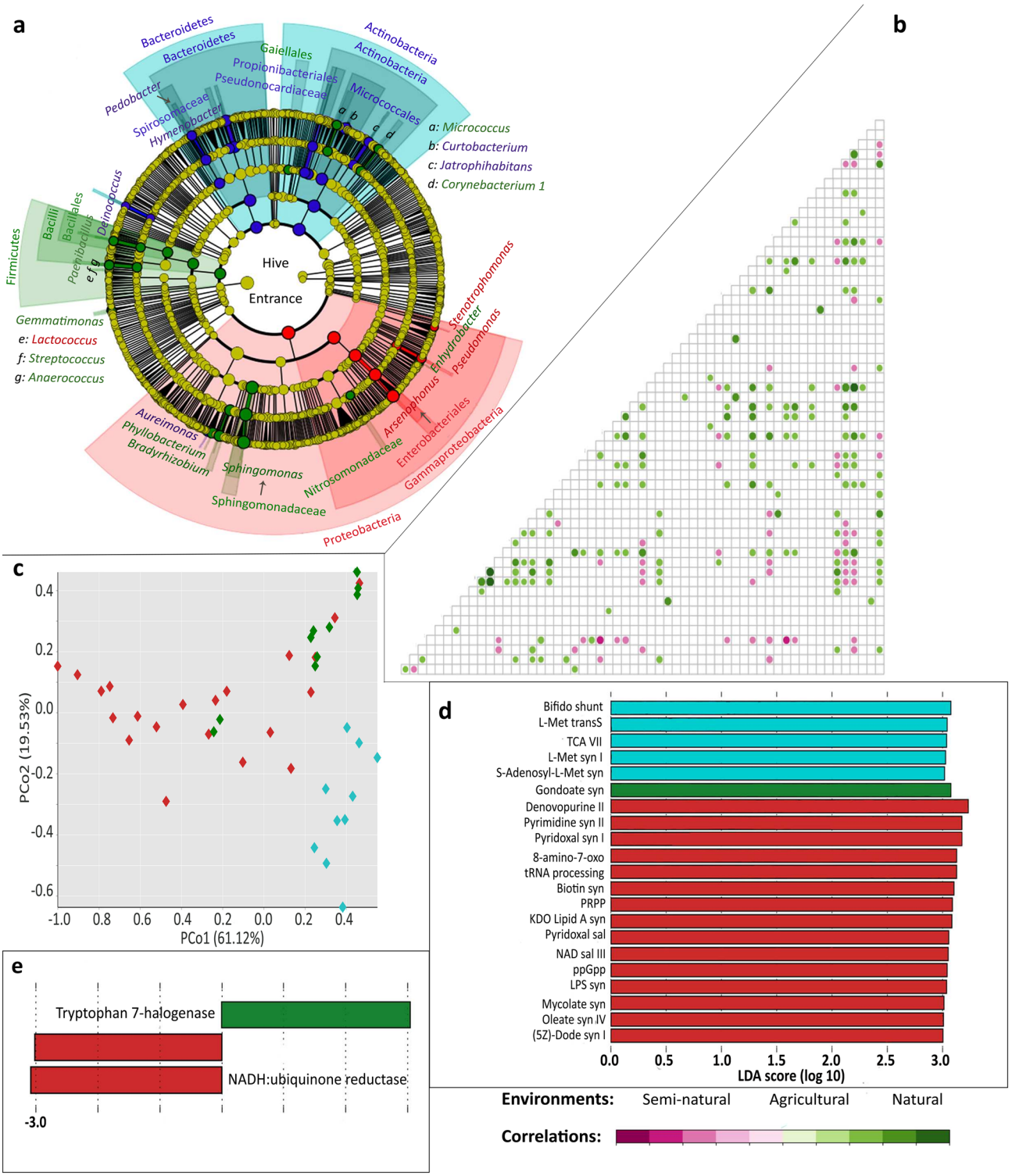
Correction to: *Scientific Reports* https://doi.org/10.1038/s41598-022-23287-6, published online 06 November 2022

The original version of this Article contained a typographical error.

Figure 5 did not display correctly.

The original Figure 5 and accompanying legend appears below.


a
Bacteroidetes
Bacteroidetes
Actinobacteria
Actinobacteria
Gaiellales
Propionibacteriales
Pseudonocardiaceae
Micrococcales
Pedobacter
Spirosomaceae
Hymenobacter
a
b
c
d
a: Micrococcus
b: Curtobacterium
c: Jatrophihabitans
d: Corynebacterium 1
Hive
Entrance
Firmicutes
Bacilli
Bacillales
Paenibacillus
Deinococcus
e f g
Gemmatimonas
e: Lactococcus
f: Streptococcus
g: Anaerococcus
Stenotrophomonas
Enhydrobacter
Pseudomonas
Arsenophonus
Enterobacteriales
Gammaproteobacteria
Aureimonas
Phyllobacterium
Bradyrhizobium
Sphingomonas
Nitrosomonadaceae
Sphingomonadaceae
Proteobacteria
b
c
PCo2 (19.53%)
PCo1 (61.12%)
0.4
0.2
0.0
-0.2
-0.4
-0.6
-1.0
0.8
0.6
0.4
0.2
0.0
0.2
0.4
d
Bifido shunt
L-Met transS
TCA VII
L-Met syn I
S-Adenosyl-L-Met syn
Gondoate syn
Denovopurine II
Pyrimidine syn II
Pyridoxal syn I
8-amino-7-oxo
tRNA processing
Biotin syn
PRPP
KDO Lipid A syn
Pyridoxal sal
NAD sal III
ppGpp
LPS syn
Mycolate syn
Oleate syn IV
(5Z)-Dode syn I
0.0
0.5
1.0
1.5
2.0
2.5
3.0
LDA score (log 10)
Environments:
Semi-natural
Agricultural
Natural
Correlations:
e
Tryptophan 7-halogenase
NADH:ubiquinone reductase
-3.0

◂**Figure 5.** Characterization of the bacterial communities in hive entrance samples. (**a**) Significantly enriched bacteria in each environment, according to LEfSe. Agricultural hives were rich in Gammaproteobacteria and *Lactococcus*. The classes Actinobacteria and Bacteroidia were prevalent in natural samples. Semi-natural samples were enriched in the *Sphingomonas* genus (*LDA* > 5.0), the Bacilli class, genera from the Alphaproteobacteria (*Bradyrhizobium, Phyllobacterium*) and Gammaproteobacteria (*Enhydrobacter*) classes, as well as genera from the Firmicutes, Gemmatimonadetes (*Gemmatimonas* and an uncultured genus), and Actinobacteria phyla. (**b**) Spearman correlation analysis at $p < 0.05$. Positive values were particularly high for *Curtobacterium/Hymenobacter*, *Phyllobacterium/Sphingomonas* and *Phyllobacterium/Bradyrhizobium* interactions ($R > 0.80$, $p < 0.0001$). The most negative interactions were found between *Arsenophonus/Spirosoma* and *Arsenophonus/Nocardioides* ($R \backsimeq -0.6$, $p < 0.001$). (**c**) Principal Coordinate Analysis (PCoA) of samples according to the predictive functional profile (MetaCyc pathways). (**d**) Significantly recruited functions according to LEfSe. (**e**) Significantly enriched enzymes according to LEfSe. The enzymes Endo X3 (EC 3.1.22.4) and coenzyme Q reductase (EC 7.1.1.2, formerly EC 1.6.5.3) were agricultural representatives, while tryptophan 7-halogenase (EC 1.14.19.9) was enriched in semi-natural samples. Bifido shunt: Bifidobacterium shunt, L-Met transS: L-methionine biosynthesis (transsulfuration), TCA VII: TCA cycle VII (acetate-producers), L-Met syn I: L-methionine biosynthesis I, S-Adenosyl-L-Met: S-adenosyl-L-methionine biosynthesis, Gondoate syn: gondoate biosynthesis (anaerobic), Denovopurine II: purine nucleotides de novo biosynthesis II, Pyrimidine syn II: pyrimidine deoxyribonucleotides de novo biosynthesis II, Pyridoxal syn I: pyridoxal 5′-phosphate biosynthesis I, 8-amino-7-oxo: 8-amino-7-oxononanoate biosynthesis I, tRNA processing: tRNA processing, Biotin syn: biotin biosynthesis I, PRPP: histidine, purine, and pyrimidine biosynthesis, KDO *Lipid* A syn: (Kdo)2-lipid A biosynthesis, Pyridoxal sal: pyridoxal 5′-phosphate biosynthesis and salvage, NAD sal III: NAD salvage pathway III (to nicotinamide riboside), ppGpp: ppGpp metabolism, LPS syn: lipopolysaccharide biosynthesis, Mycolate syn: mycolate biosynthesis, Oleate syn IV: oleate biosynthesis IV (anaerobic), (5Z)-Dode syn I: (5Z)-dodecenoate biosynthesis I. Plotting: Cladograms and histograms of LEfSe results were plotted in Galaxy (web application, https://huttenhower.sph.harvard.edu/galaxy/) and taxa names cleaned with INKSCAPE (v0.92.3-1, https://inkscape.org/). PCoAs were plotted using Vega editor (v5.22.1, https://vega.github.io/editor/#/).

The original Article has been corrected.