

Supplementary Figures and Tables

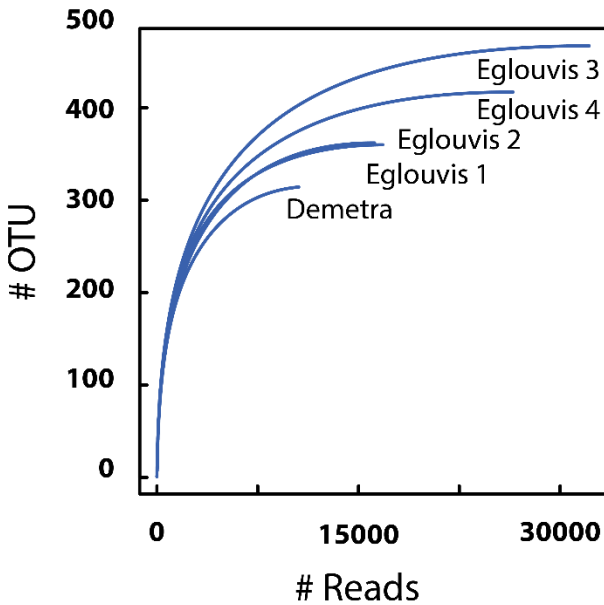


Figure S1. Rarefaction curves of lentil samples.

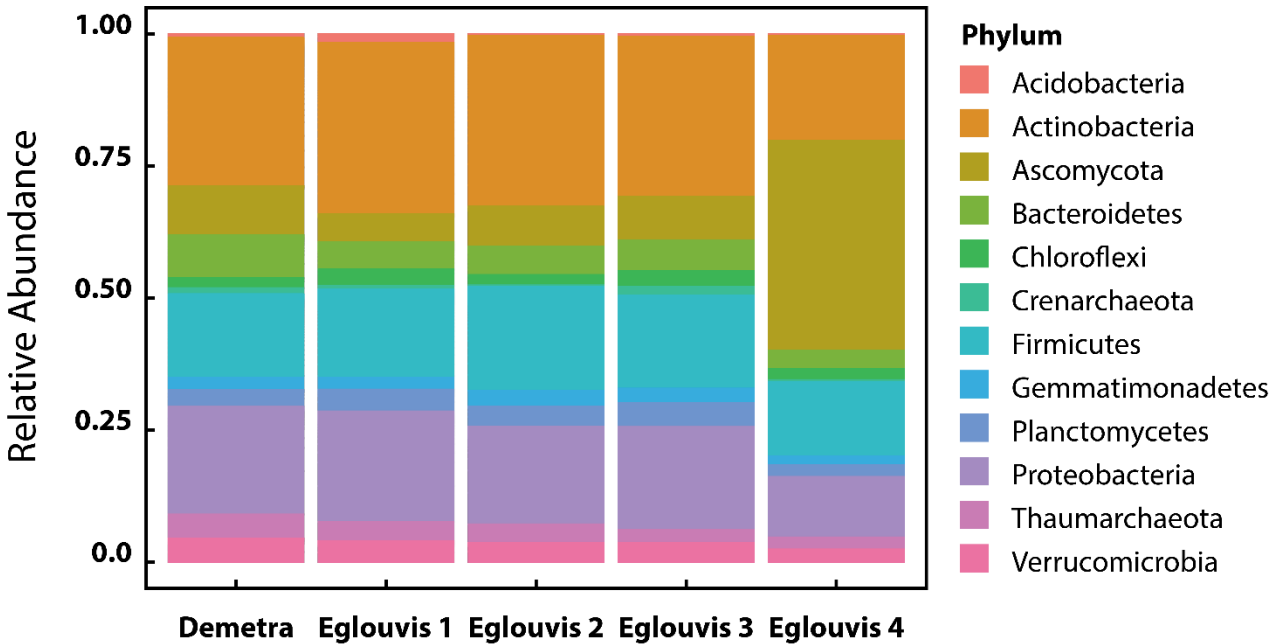


Figure S2: Relative abundances of lentil samples for the 12 most abundant phyla including pathogen *Kabatiella microsticta*.

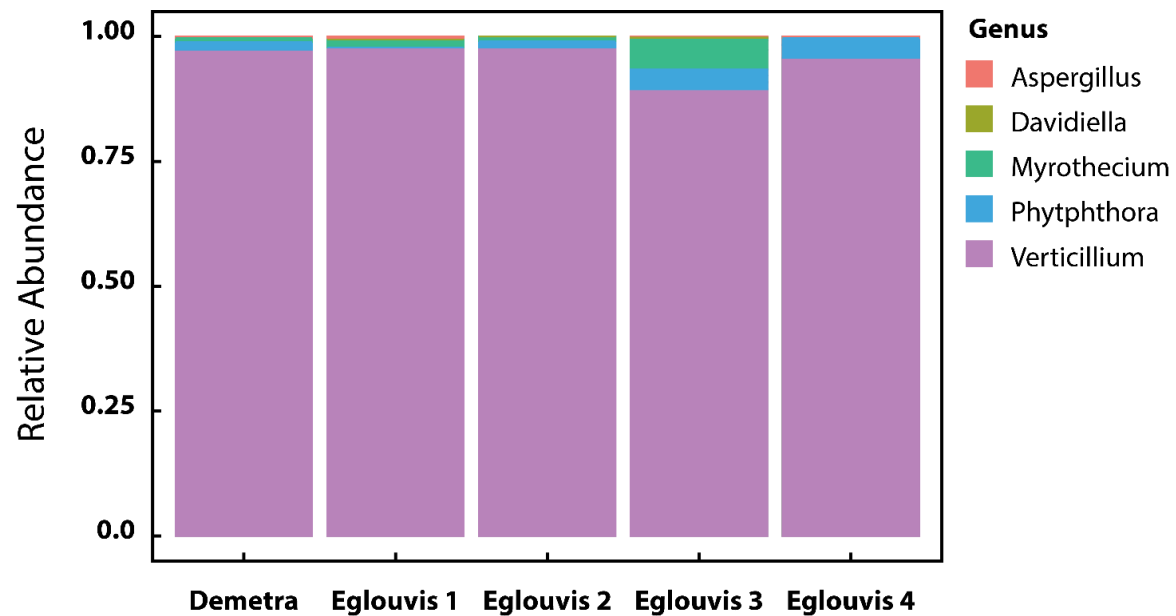


Figure S3. Relative abundances of lentil samples for the pathogens at genus level.

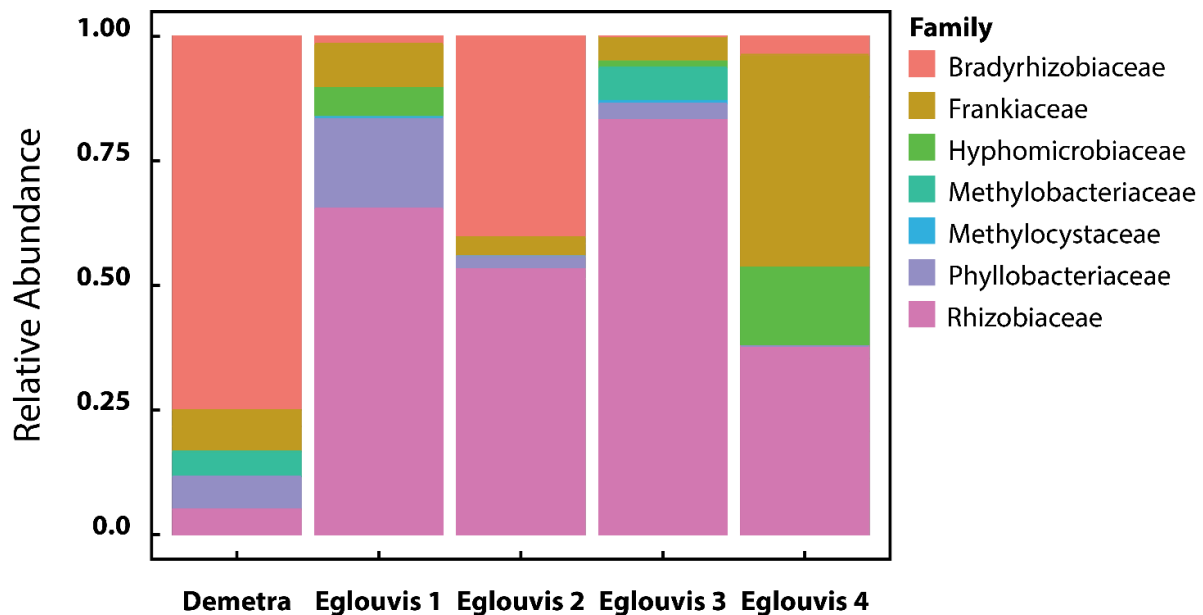


Figure S4. Relative abundances of lentil samples for N₂-fixation bacteria at family level.

Table S1. Amplicon primers, PCR reagents, and PCR cycling program.

	PCR for 16S amplicons	PCR for ITS2 amplicons
Amplicon primers		
Forward primer	515F 5'-GTGCCAGCMGCCGCGGTAA-3'	ITS4 5'-TCCTCCGCTTATTGATATGC-3'
Reverse primer	806R 5'-GGACTACHVHHHTWTCTAAT-3'	ITS9 5'-GAACGCAGCRAAIIIGYGA-3'
PCR reagents' recipe		
gDNA template (10 ng.µL)	3 µL	3 µL
Forward primer (10 µM)	1 µL	1 µL
Reverse primer (10 µM)	1 µL	1 µL
2x Platinum II Hot-Start Master Mix	25 µL	25 µL
Molecular water	10 µL	10 µL
1x Platinum™ GC Enhancer	10 µL	10 µL
Total volume	50 µL	50 µL
PCR cycling conditions		
Initial denaturation	94°C for 120 s	94°C for 120 s
Denaturation	94 °C for 15 s	94°C for 15 s
Annealing	52°C for 15 s	60°C for 15 s
Extension	68°C for 15 s	68°C for 15 s
Cycles	35	35
Final Hold	4 °C	4 °C

Table S2. Metrics of α diversity among the studied genotypes; Eglouvis landrace (Eglouvis 1–4) and the commercial cultivar Demetra.

Sample	Observed	Chao1	ACE	Shannon	Simpson	InvSimpson	Fisher
Eglouvis 1	360	360	360	4.490	0.978	46.1	64.6
Eglouvis 2	362	362	362	4.453	0.977	43.5	65.7
Eglouvis 3	467	467	467	4.590	0.979	48.4	77.4
Eglouvis 4	417	417	417	4.492	0.976	41.6	70.3
Demetra	315	315	315	4.344	0.972	35.4	59.6

Table S3. Relative abundances of common taxa at phylum level for (a) Demetra, Eglouvis 1, and Eglouvis 2, and (b) Demetra, Eglouvis 3, and Eglouvis 4.

(a)

Sample	Demetra	Eglouvis 1	Eglouvis 2
Acidobacteria	0.109	0.729	0.162
Actinobacteria	0.238	0.387	0.375
Ascomycota	0.353	0.274	0.374
Bacteroidetes	0.358	0.330	0.312
Crenarchaeota	0.450	0.394	0.156
Firmicutes	0.212	0.380	0.407
Gemmatimonadetes	0.260	0.352	0.388
Planctomycetes	0.220	0.412	0.368
Proteobacteria	0.276	0.409	0.315
Thaumarchaeota	0.311	0.357	0.332
Verrucomicrobia	0.287	0.371	0.342

(b)

Sample	Demetra	Eglouvis 3	Eglouvis 4
Acidobacteria	0.217	0.408	0.375
Actinobacteria	0.167	0.469	0.364
Ascomycota	0.184	0.315	0.501
Bacteroidetes	0.233	0.451	0.316
Chloroflexi	0.123	0.444	0.433
Crenarchaeota	0.150	0.714	0.137
Firmicutes	0.146	0.457	0.397
Gemmatimonadetes	0.155	0.476	0.370

Planctomycetes	0.140	0.546	0.315
Proteobacteria	0.188	0.469	0.343
Thaumarchaeota	0.239	0.358	0.403
Verrucomicrobia	0.192	0.440	0.368

Table S4. Top 10% of key species (31/158) after degree centrality analysis

Species	Degree Centrality (Links)
<i>Actinoplanes liguriensis</i>	20
<i>Arthrobacter</i> sp. 'SMCC G965'	20
<i>Arthrobacter</i> sp. 'SMCC ZAT200'	19
<i>Cellulomonas fimi</i>	20
<i>Cryobacterium psychrophilum</i>	18
<i>Glaciibacter superstes</i>	18
<i>Microbacterium oxydans</i>	18
<i>Micromonospora chaiyaphumensis</i>	19
<i>Pimelobacter simplex</i>	18
<i>Pseudonocardia zijingensis</i>	18
<i>Terracoccus luteus</i>	20
<i>Thermobispora bispora</i>	20
<i>Verticillium dahliae</i>	18
<i>Chitinophaga sancti</i>	18
<i>Cytophaga hutchinsonii</i>	20
<i>Hymenobacter</i> sp. VUG-A141a	18
<i>Pedobacter</i> sp. MJ11	18
<i>Salinibacter ruber</i>	18
<i>Bacillus halmapalus</i>	20
<i>Bacillus</i> sp. TA2.A1	20
<i>Coprothermobacter proteolyticus</i>	18
<i>Marvinbryantia formatexigens</i>	20
<i>Paenibacillus polymyxa</i>	18
<i>Ruminococcus flavefaciens</i>	20
<i>Symbiobacterium thermophilum</i>	19
<i>Gemmatimonas aurantiaca</i>	18
<i>Planctomycete Zi62</i>	18
<i>Angiococcus disciformis</i>	18
<i>Corallococcus coralloides</i>	18
<i>Shewanella frigidimarina</i>	20
uncultured proteobacterium	18

Table S5. Top 10% (16 /158) key species after closeness centrality analysis.

Species	Closeness Centrality
<i>Actinomadura pelletieri</i>	0.001892
<i>Actinoplanes missouriensis</i>	0.001769
<i>Amycolatopsis coloradensis</i>	0.001755
<i>Lechevalieria aerocolonigenes</i>	0.001892
<i>Microbispora rosea</i>	0.001901
<i>Streptosporangium roseum</i>	0.001755
<i>Hymenobacter aerophilus</i>	0.001901
<i>Hymenobacter antarcticus</i>	0.001901
<i>Prolixibacter bellariivorans</i>	0.001641
<i>Acetobacterium woodii</i>	0.001892
<i>Bacillus firmus</i>	0.001641
<i>Bacillus niacini</i>	0.00188
<i>Bacillus sp. S207</i>	0.00188
<i>Planctomyces limnophilus</i>	0.001901
uncultured <i>Geobacter</i> sp.	0.001901
uncultured Rhodocyclaceae bacterium	0.001892

Table S6. Top 10% of key species (15/158) after betweenness centrality.

Species	Betweenness
<i>Actinoplanes liguriensis</i>	427.067
<i>Clavibacter michiganensis</i>	530.2385
<i>Rubrobacter xylanophilus</i>	538.571
<i>Streptomyces maritimus</i>	543.7762
<i>Streptomyces virginiae</i>	631.2566
<i>Thermobispora bispora</i>	427.067
<i>Cytophaga hutchinsonii</i>	631.2399
<i>Thermomicrobium roseum</i>	461.6074
<i>Bacillus halmapalus</i>	427.067
<i>Bacillus litoralis</i>	424.3583
<i>Bacillus sp. TA2.A1</i>	631.2399
<i>Desulfitobacterium hafniense</i>	424.3583
<i>Desulfonispora thiosulfatigenes</i>	483.5359
<i>Buchnera aphidicola</i>	541.219
<i>Pseudoxanthomonas dokdonensis</i>	462.2815