Climatic zone and soil properties determine the biodiversity of the soil microbial communities associated to native plants from desert areas of North-Central Algeria

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Table S1. Information regarding the 14 Algerian autochthonous plant species.

Table S2. Physical-chemical properties of the soils sampled from the rhizosphere of 14 different plant species in North-Central Algeria.

Table S3. Linear discriminant analysis Effect Size (LEfSe) at species level according to sampling site. All the possible comparisons are reported in the table. Light gray indicates species less present in the first sampling site than in the second one and red indicates a presence less than 50%. Dark gray indicates species more present in the first sampling site than in the second one and green indicates a presence more than 200%.

Figure S1. A) Precipitation (mm), B) Wind speed (ms^{-1}), C) Average T (°C) in the year 2018 in the six Algerian sampling sites and Alessandria town in Italy as reference.

Figure S2. A) Minimum temperature (°C), B) Maximum temperature (°C) Temperature difference (°C) in the year 2018 in the six Algerian sampling sites and Alessandria town in Italy as reference.

Figure S3. Phylum abundance (%) in A) plants, B) sampling sites and C) climatic zone.

Figure S4. CORE analysis at phylum level according to sampling site (climatic zone). The Microbiome CORE analysis identifies core taxa that remain unchanged in their composition across the whole microbial community. Two parameters are considered: sample prevalence and relative abundance (%) of a taxa. Core microbiome analysis is adopted from the core function in R package microbiome. The result of this analysis is represented in the form of heatmap of core taxa where Y-axis represent the prevalence level of core features across the detection threshold (Relative abundance) range on X-axis. Two soil sampling sites in the arid region of Ghardaïa (Algeria): Metlili and Beni Isguen. Four soil sampling sites in the semi-arid region of Djelfa (Algeria): Messaad, Ain Naga, Moudjbara and Zaafrane.

Figure S5. CORE analysis at species level according to sampling site.

Figure S6. CORE analysis at phylum level according to climatic zone.

Figure S7. CORE analysis at species level according to climatic zone.

Figure S8. Heat trees at phylum level. Heat trees report the effect of the sampling site on hierarchical structure of taxonomic classifications (median abundance, non-parameter Wilcoxon Rank Sum test).The reported comparisons are **Metlili** *vs* A) Ain Naga, B) Beni Isguen, C) Messaad, D) Moudjbara, E) Zaafrane; **Beni Isguen** *vs* F) Ain Naga, G) Messaad, H) Moudjbara, I) Zaafrane; **Messaad** *vs* J) Ain Naga, K) Moudjbara, L) Zaafrane; **Ain Naga** *vs* M) Moudjbara, N) Zaafrane and finally **Moudjbara** *vs* O) Zaafrane. Comparing Sample 1 *vs* Sample 2, a blue line indicates that one phylum in sample 2 is more abundant than in sample 1, while a red line indicates that one phylum in sample 2 is less abundant than in sample 1. Heat tree analysis was performed using R metacoder package of MicrobiomeAnalyst, a free available on-line software (https://www.microbiomeanalyst.ca).

Table S1. Information regarding the 14 Algerian autochthonous plant species.

Label	Sampling site	Coordinates	Species	Local name	Family	Traditional uses
1	Metlili, Ghardaïa	32°16'49.9"N 3°38'17.1"E	*Cleome arabica*	Khanza (stinker), Dafrah (ذفرة عربية)	Capparaceae	It is used in the treatment of inflammation and rheumatism. It possesses antimicrobial and antioxidant activities [19]. It is also used as diuretic and febrifuge. Furthermore, *Cleome arabica* has cytotoxic effects which are exploited for the production of bioherbicides and larvicides [19,20].
2	Metlili, Ghardaïa	32°16'48.3"N 3°38'15.9"E	*Reseda villosa*	Bliha (بليحاء)	Resedaceae	It is used in medicine for its content in flavonoids with antioxidant power [21]. It is used in the treatment of diarrhea and intestinal pains [22].
3	Beni Isguen, Ghardaïa	32°27'52.0"N 3°41'02.7"E	*Zilla spinosa*	Shibrim (شبرم)	Brassicaceae	It is used for grazing [23] and for medicinal purposes as gastrointestinal disorders, diabetes, urinary tract pains, diarrhea, gall bladder, kidney stones, liver and pancreas pain, respiratory ailments and rheumatism [24].
4	Beni Isguen dam, Ghardaïa	32°27'54.1"N 3°41'04.3"E	*Pulicaria undulata*	Guertoufa (قرطوفة، جثجاث)	Asteraceae	It has been traditionally used to treat diabetes, cardiac disorders, skin diseases, abscesses, inflammations, an insect repellent as well as an herbal tea and tonic. Several investigations have reported the chemical composition, antibacterial and antioxidant activities of the essential oil of *P. undulata* [25-29].
5	Messaad, Djelfa	34°06'07.8"N 3°33'46.4"E	*Arthrophytum scoparium*	Remth (رمث)	Amaranthaceae	It is used as a traditional medicine for the treatment of ocular disorders, against mold, for its hepatoprotective, antioxidant, antitumor and anti-larval properties [30]. It exerts potent anti-amnesic effects [31].
6	Messaad, Djelfa	34°06'02.4"N 3°33'56.1"E	*Astragalus armatus*	Guendal (قندال، قتاد)	Fabaceae	It is used to treat leischamaniose and helminthiasis [22]. It is used against chronic bronchitis, stomach ulcer, cough, hypertension, diabetes, gynecological disorders and poisonous scorpion stings [32].

	Messaad, Djelfa	34°06'12.6"N 3°33'49.8"E	*Retama raetam*	R'tem (رتم)	Fabaceae	Retama species contain alkaloids, flavonoids with antibacterial, antifungal and cytotoxic activities [33]. *Retama raetam* is widely used in dune stabilization and soil fixation. Furthermore, it is capable of producing significant quantities of biomass which are exploited as fodder, an important raw material resource for microfibers production and for the treatment of various human and animal diseases as intestinal worms, scabies, Fever, abortion [22, 34].
8	Ain Naga, Djelfa	34°24'18.1"N 3°28'38.2"E	*Stipa tenacissima*	Halfa (حلفاء)	Poaceae	It is also named Esparto grass and in Algeria it is used as a main source of fiber for paper production [35]. It is used to modulate melancholy, neuralgia and hypercholesterolemia [22].
9	Moudjbara, Djelfa	34°34'19.3"N 3°25'28.2"E	*Artemisia herba-alba*	Shih (شيح)	Asteraceae	It is used in the traditional medicine of the Northern Badia region of Jordan, in the form of a decoction, against fever and menstrual and nervous problems. It is also known as desert wormwood and it has been used in folk medicine by many cultures since ancient times and in Moroccan folk medicine to treat arterial hypertension and/or diabetes [36]. In Algeria, it is used to treat stomach pain and some genital infections [22].
10	Zaafrane, Djelfa	34°52'04.6"N 2°50'56.5"E	*Salsola tetragona*	Djel, Belbel (جل)	Chenopodiaceae	The leaves and sprouts of many *Salsola* species are edible, and sometimes the plants are specially grown and used for salads or to flavor sushi. It is used also as camel forage [37]. Furthermore, it is used for the treatment of indigestion, constipation, belly and stomach pain [38].
11	Zaafrane, Djelfa	34°52'09.7"N 2°50'56.7"E	*Atriplex halimus*	G'taf (قطف)	Chenopodiaceae	It has a high agricultural value: the leaves, available all year round, have an excellent salty taste and can be added to salads or cooked like spinach, while the seeds are used to thicken soups or are mixed with cereals to make bread. It is the common fodder shrub that are used for revegetation of rangelands and to generate plant cover in contaminated soils [39]. The main curative aspect is the treatment of cysts [40].
12	Zaafrane, Djelfa	34°52'19.3"N 2°50'58.3"E	*Peganum harmala*	Harmal, Syrian Rue (حرمل)	Nitrariaceae	It is used for medicinal and psychoactive purposes since ancient times. Its seeds are known to possess hypothermic and hallucinogenic properties, and are used as spices or condiments. Due to its abortive,

						narcotic, aphrodisiac, stimulant, sedative, and emetic properties it is used for the treatment of syphilis, fever, hysteria, malaria, neuralgia, parkinsonism, rheumatism, colic, asthma and ocular disorders [41]. It is used also to alleviate leishmaniasis, rheumatoid arthritis, seizures and depression [22].
13	Zaafrane, Djelfa	34°52'26.9"N 2°50'53.4"E	*Suaeda fruticosa*	Suaeda (سويداء)	Amaranthaceae	It is a source of cardiotonic and anti-infective agents. It could be a valuable source of phenolic and flavonoid compounds with antioxidant, anti-inflammatory and anticancer properties [42].
14	Zaafrane, Djelfa	34°52'01.1"N 2°50'56.6"E	*Thymelaea microphylla*	Methnan (مثنان)	Thymeleaceae	It shows biological activities thanks to the richness of bioactive secondary metabolites such as flavonoids, sterols, terpeness and coumarins [43]. It is used for hair care and the alleviation of hair loss, helminthiasis and depression [22].

Table S2. Physical-chemical properties of the soils sampled from the rhizosphere of 14 different plant species in North-Central Algeria.

Area	Texture	pH	Organic matter (%)	Total $CaCO_3$ (%)	Active $CaCO_3$ (%)	Total Phosphorus (ppm)	Olsen Phosphorus (ppm)	Electrical conductivity (Ms/cm) at 25°C	Total Nitrogen (%)	Plant species
Metlili, Ghardaïa	Sandy-silty	7.2±0.06	0.33±0.01	8.87±0.18	3.31±0.13	102.54±2.88	8.13±0.20	0.525±0.02	0.13±0.01	*Cleome arabica* *Reseda villosa*
Beni Isguen, Ghardaïa	Sandy-silty	8.31±0.10	0.89±0.03	7.26±0.20	5.23±0.11	112.39±4.80	19.88±0.26	0.612±0.03	0.15±0.02	*Zilla spinosa* *Pulicaria undulata*
Messaad, Djelfa	Silty-sandy	8.23±0.07	0.36±0.01	10.89±0.09	4.53±0.09	138.07±3.20	12.27±0.16	0.416±0.01	0.07±0.01	*Arthrophytum scoparium* *Astragalus armatus* *Retama raetam*
Ain Naga, Djelfa	Silty-sandy	7.83±0.05	0.41±0.02	12.19±0.19	6.11±0.05	148.78±3.50	33.22±0.20	0.211±0.01	0.08±0.01	*Stipa tenacissima*
Moudjbara, Djelfa	Silty-sandy	7.23±0.05	0.45±0.04	11.5±0.07	5.65±0.04	168.02±4.11	24.56±0.30	0.287±0.02	0.12±0.02	*Artemisia herba-alba*
Zaafrane, Djelfa	Sandy-silty	7.9±0.07	0.51±0.03	9.56±0.13	4.12±0.05	152.31±3.89	3.54±0.05	0.823±0.02	0.11±0.01	*Salsola tetragona* *Atriplex halimus* *Peganum harmala* *Suaeda fruticosa* *Thymelaea microphylla*
Method*	Soil Survey Staff (1999)	Al-Busaidi et al. (2005)	Baize and Jabiol (2011)	Baize and Jabiol (2011)	Baize and Jabiol (2011)	Rowland and Haygarth (1997)	Maghsoodi et al. (2015)	Thomas (1982)	Bremner and Tabatabai (1972)	

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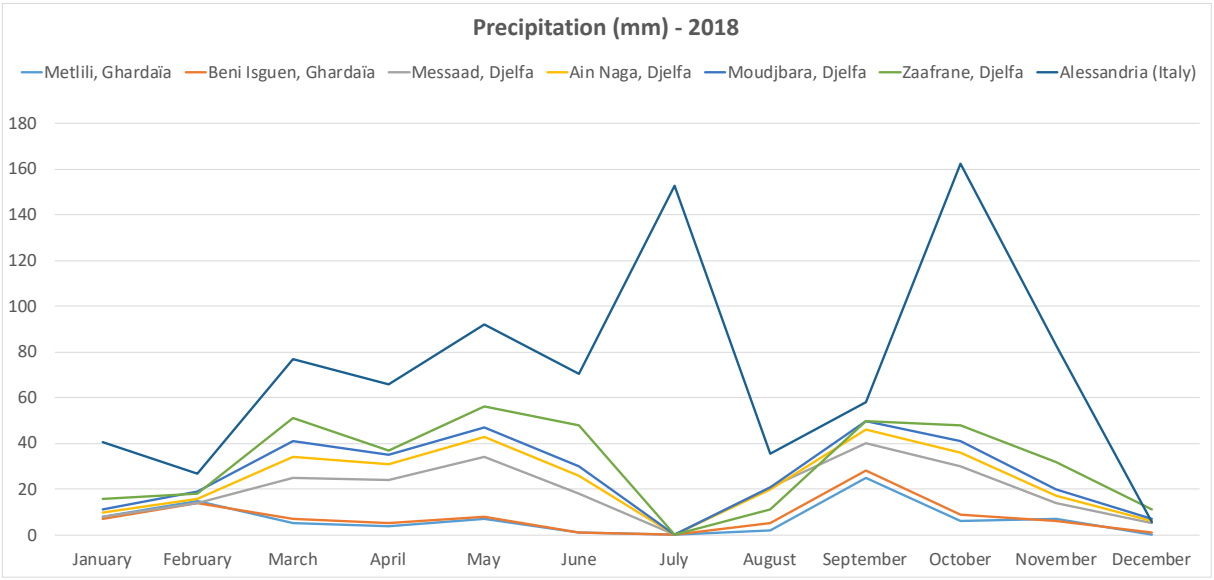
Table S3. Linear discriminant analysis Effect Size (LEfSe) at species level according to sampling site. All the possible comparisons are reported in the table. Light gray indicates species less present in the first sampling site than in the second one and red indicates a presence less than 50%. Dark gray indicates species more present in the first sampling site than in the second one and green indicates a presence more than 200%.

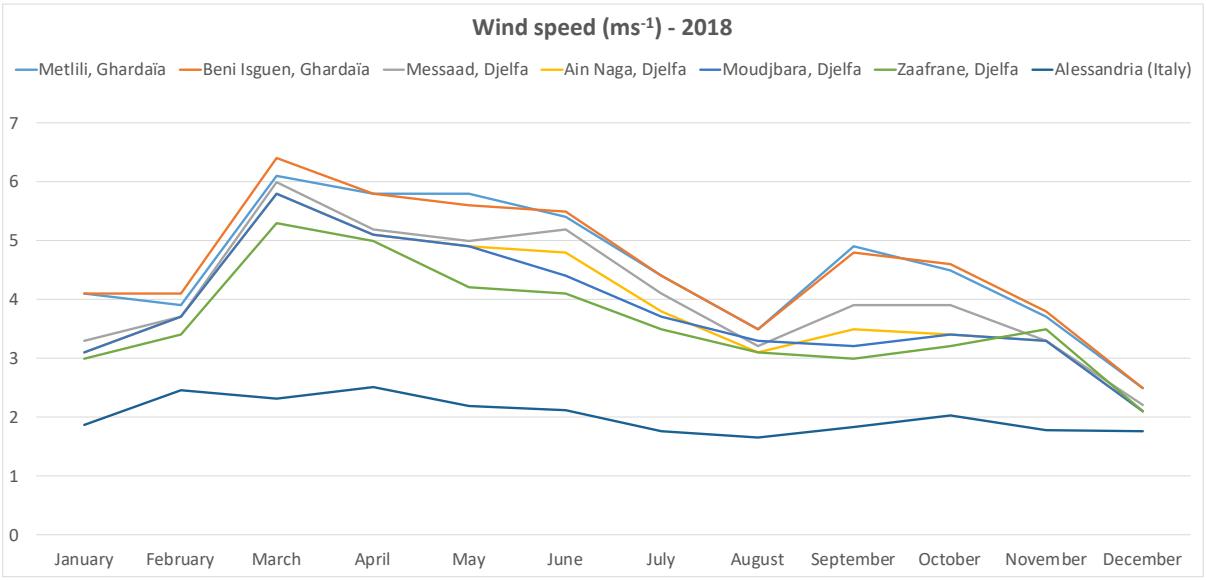
Species	Phylum	P-values	LDA score	Beni Isguen/ Metlili %	Beni Isguen/ Ain Naga %	Beni Isguen/ Messaad %	Beni Isguen/ Moudjbara %	Beni Isguen/ Zaafrane %	Metlili/ Ain Naga %	Metlili/ Messaad %	Metlili/ Moudjbara %	Metlili/ Zaafrane %	Ain Naga/ Messaad %	Ain Naga/ Moudjbara %	Ain Naga/ Zaafrane %	Messad/ Moudjbara %	Messad/ Zaafrane %	Moudjbara/ Zaafrane %
unclassified Acidobacteria	Acidobacteria	0.0002639	4.25	98%	117%	153%	71%	150%	119%	157%	72%	153%	131%	61%	128%	46%	98%	212%
unclassified Acidobacteria Gp3	Acidobacteria	0.0000008	4.27	169%	153%	471%	196%	481%	91%	279%	116%	285%	308%	128%	314%	41%	102%	246%
unclassified Acidobacteria Gp4	Acidobacteria	0.0000001	4.70	23%	71%	21%	10%	29%	316%	92%	46%	127%	29%	15%	40%	50%	138%	276%
unclassified Blastocatella	Acidobacteria	0.0035542	4.11	17%	39%	28%	9%	27%	227%	159%	54%	156%	70%	24%	69%	34%	98%	288%
Rubrobacter radiotolerans	Actinobacteria	0.0040006	3.96	11%	44%	21%	14%	26%	403%	188%	124%	239%	47%	31%	59%	66%	127%	192%
unclassified Acidimicrobiales	Actinobacteria	0.0032255	4.51	177%	157%	160%	211%	157%	89%	90%	119%	89%	102%	134%	100%	132%	98%	74%
unclassified Aciditerrimonas	Actinobacteria	0.0000362	4.57	336%	569%	434%	645%	675%	169%	129%	192%	201%	76%	113%	119%	149%	155%	105%
unclassified Actinobacteria	Actinobacteria	0.0000002	5.74	194%	491%	160%	304%	358%	253%	82%	157%	185%	33%	62%	73%	190%	224%	118%
unclassified Actinomycetales	Actinobacteria	0.0000744	5.08	154%	116%	153%	219%	166%	75%	99%	142%	108%	132%	189%	143%	143%	109%	76%
unclassified Blastococcus	Actinobacteria	0.0000242	4.08	77%	25%	206%	39%	112%	33%	267%	51%	144%	820%	156%	444%	19%	54%	284%
unclassified Euzebya	Actinobacteria	0.0000020	4.06	694%	746%	1657%	1435%	182%	107%	239%	207%	26%	222%	192%	24%	87%	11%	13%
unclassified Gaiella	Actinobacteria	0.0000029	5.31	484%	2824%	346%	420%	2188%	583%	71%	87%	452%	12%	15%	77%	121%	633%	521%
unclassified Geodermatophilaceae	Actinobacteria	0.0032241	3.84	67%	51%	94%	81%	43%	77%	142%	121%	65%	185%	158%	85%	86%	46%	54%
unclassified Geodermatophilus	Actinobacteria	0.0000882	3.94	31%	23%	128%	49%	47%	75%	415%	158%	152%	553%	211%	203%	38%	37%	96%
unclassified Ilumatobacter	Actinobacteria	0.0014008	4.19	65%	27%	53%	15%	36%	41%	80%	23%	55%	196%	55%	134%	28%	68%	243%
unclassified Microbacteriaceae	Actinobacteria	0.0000283	4.20	146%	23%	100%	139%	48%	16%	69%	96%	33%	440%	615%	211%	140%	48%	34%
unclassified Micrococcaceae	Actinobacteria	0.0000402	4.43	172%	312%	307%	147%	93%	181%	178%	85%	54%	99%	47%	30%	48%	30%	63%
unclassified Micromonosporaceae	Actinobacteria	0.0000011	4.64	56%	38%	107%	86%	121%	67%	189%	152%	214%	281%	226%	317%	80%	113%	140%
unclassified Nocardioidaceae	Actinobacteria	0.0000001	4.49	365%	129%	237%	354%	158%	35%	65%	97%	43%	184%	275%	123%	150%	67%	45%
unclassified Nocardioides	Actinobacteria	0.0007040	4.12	250%	85%	247%	266%	195%	34%	99%	106%	78%	290%	312%	228%	108%	79%	73%
unclassified Propionibacteriaceae	Actinobacteria	0.0000991	4.20	9%	37%	25%	22%	81%	420%	282%	254%	933%	67%	60%	222%	90%	331%	368%
unclassified Pseudonocardiaceae	Actinobacteria	0.0024329	4.08	125%	138%	108%	378%	191%	111%	87%	304%	153%	78%	274%	138%	350%	177%	51%
unclassified Rubrobacter	Actinobacteria	0.0000019	5.25	17%	22%	16%	9%	19%	127%	91%	50%	112%	72%	39%	89%	55%	123%	224%
unclassified Solirubrobacter	Actinobacteria	0.0000282	4.10	182%	215%	312%	281%	518%	118%	172%	155%	286%	146%	131%	242%	90%	166%	184%
unclassified Solirubrobacterales	Actinobacteria	0.0000732	4.61	171%	219%	154%	183%	244%	128%	91%	107%	143%	71%	83%	112%	118%	158%	134%
unclassified Streptomycetaceae	Actinobacteria	0.0054961	3.97	191%	184%	65%	293%	200%	96%	34%	153%	105%	36%	160%	109%	448%	305%	68%
unclassified Thermoleophilum	Actinobacteria	0.0000001	4.01	279%	699%	187%	456%	991%	251%	67%	164%	356%	27%	65%	142%	244%	530%	218%
unclassified Archaea	Archea	0.0001193	3.77	105%	115%	168%	97%	301%	109%	160%	92%	286%	147%	85%	262%	58%	179%	310%
unclassified Armatimonadetes gp4	Armatimonadetes	0.0000001	3.97	131%	428%	251%	284%	480%	328%	192%	218%	367%	59%	66%	112%	113%	191%	169%
unclassified Armatimonas1Armatimonadetes gp1	Armatimonadetes	0.0000833	3.92	34%	54%	28%	31%	24%	162%	84%	91%	71%	52%	56%	44%	109%	85%	78%
Adhaeribacter aquaticus (T)	Bacteroidetes	0.0000136	3.95	704%	162%	1430%	704%	274%	23%	203%	100%	39%	884%	436%	170%	49%	19%	39%
unclassified Adhaeribacter	Bacteroidetes	0.0000003	4.14	787%	203%	1593%	592%	341%	26%	203%	75%	43%	783%	291%	168%	37%	21%	58%
unclassified Bacteroidetes	Bacteroidetes	0.0000001	4.98	56%	15%	35%	23%	13%	27%	62%	42%	24%	232%	158%	90%	68%	39%	57%
unclassified Chitinophagaceae	Bacteroidetes	0.0125190	5.02	141%	86%	123%	69%	97%	61%	87%	49%	69%	143%	80%	113%	56%	79%	140%
unclassified Cytophagaceae	Bacteroidetes	0.0000044	3.95	634%	124%	439%	260%	130%	20%	69%	41%	20%	354%	209%	105%	59%	30%	50%
unclassified Cytophagales	Bacteroidetes	0.0000005	3.87	120%	28%	273%	68%	30%	24%	226%	57%	25%	958%	240%	105%	25%	11%	44%
unclassified Flavobacteriaceae	Bacteroidetes	0.0000000	4.49	186%	3%	34%	26%	2%	1%	18%	14%	1%	1258%	973%	62%	77%	5%	6%
unclassified Ohtaekwangia	Bacteroidetes	0.0000037	5.34	47%	11%	71%	40%	31%	23%	151%	85%	65%	655%	370%	284%	56%	43%	77%
unclassified Sphingobacteriaceae	Bacteroidetes	0.0000001	3.99	95%	72%	433%	151%	59%	76%	456%	159%	62%	599%	209%	82%	35%	14%	39%
unclassified Saccharibacteria genera incertae sedis	Candidatus Saccharibacteria	0.0000000	4.97	34%	10%	55%	56%	22%	30%	161%	166%	64%	546%	564%	215%	103%	39%	38%
unclassified Anaerolineaceae	Chloroflexi	0.0000000	5.00	189%	475%	957%	1611%	797%	252%	507%	854%	423%	202%	339%	168%	168%	83%	50%
unclassified Chloroflexi	Chloroflexi	0.0000001	4.83	77%	74%	256%	107%	199%	97%	334%	140%	260%	345%	145%	268%	42%	78%	185%
unclassified Litorilinea	Chloroflexi	0.0000811	3.74	97%	60%	687%	201%	118%	61%	706%	207%	121%	1152%	337%	197%	29%	17%	58%
unclassified Sphaerobacter	Chloroflexi	0.0006056	3.79	82%	78%	223%	245%	151%	96%	273%	301%	185%	286%	315%	194%	110%	68%	62%
unclassified Thermomicrobia	Chloroflexi	0.0006216	4.02	64%	36%	212%	41%	65%	56%	330%	64%	102%	593%	114%	183%	19%	31%	160%
unclassified Bacillales	Firmicutes	0.0000011	4.21	178%	243%	572%	355%	209%	137%	322%	200%	118%	235%	146%	86%	62%	37%	59%
unclassified Gemmatimonas	Gemmatimonadetes	0.0002522	5.13	59%	51%	71%	24%	39%	87%	120%	42%	67%	139%	48%	77%	35%	56%	160%
unclassified Gemmata	Planctomycetes	0.0000377	3.83	65%	118%	136%	45%	208%	181%	208%	70%	319%	115%	38%	176%	33%	153%	458%
unclassified Pirellula	Planctomycetes	0.0000000	4.47	206%	150%	464%	485%	557%	73%	225%	235%	270%	309%	323%	371%	104%	120%	115%
unclassified Planctomyces	Planctomycetes	0.0000026	4.20	16%	9%	42%	37%	15%	53%	261%	231%	95%	492%	434%	179%	88%	36%	41%
unclassified Planctomycetaceae	Planctomycetes	0.0000036	5.14	68%	56%	120%	133%	109%	82%	177%	197%	161%	215%	239%	196%	111%	91%	82%
unclassified Planctomycetes	Planctomycetes	0.0000197	3.65	70%	78%	306%	189%	158%	113%	440%	271%	228%	391%	241%	202%	62%	52%	84%
gamma proteobacterium SA29 B	Proteobacteria	0.0000539	4.08	39%	9%	40%	157%	27%	24%	104%	406%	68%	429%	1678%	283%	392%	66%	17%
unclassified Acetobacteraceae	Proteobacteria	0.0137480	3.79	286%	138%	198%	187%	225%	48%	69%	65%	79%	143%	135%	163%	95%	114%	120%
unclassified Alphaproteobacteria	Proteobacteria	0.0000104	4.84	48%	37%	46%	75%	38%	76%	97%	157%	80%	127%	205%	105%	162%	83%	51%
unclassified Betaproteobacteria	Proteobacteria	0.0009143	4.66	121%	109%	162%	83%	149%	90%	133%	69%	123%	148%	76%	136%	52%	92%	179%
unclassified Bradyrhizobiaceae	Proteobacteria	0.0000009	3.87	16%	15%	16%	19%	33%	97%	100%	120%	206%	103%	123%	213%	120%	207%	172%
unclassified Burkholderiales	Proteobacteria	0.0000374	4.43	75%	201%	360%	188%	207%	269%	482%	252%	278%	179%	94%	103%	52%	58%	110%
unclassified Caulobacteraceae	Proteobacteria	0.0000393	3.91	71%	15%	27%	33%	18%	21%	38%	46%	26%	177%	216%	120%	122%	68%	55%
unclassified Comamonadaceae	Proteobacteria	0.0000071	4.22	430%	221%	406%	132%	133%	51%	94%	31%	31%	184%	60%	60%	33%	33%	101%
unclassified Cystobacteraceae	Proteobacteria	0.0000874	4.11	32%	92%	124%	85%	143%	287%	388%	265%	446%	135%	93%	156%	68%	115%	168%
unclassified Deltaproteobacteria	Proteobacteria	0.0001865	4.11	150%	155%	284%	203%	208%	103%	189%	135%	138%	184%	131%	134%	71%	73%	103%
unclassified Erythrobacteraceae	Proteobacteria	0.0000000	4.34	73%	35%	37%	59%	6%	48%	51%	82%	8%	107%	171%	16%	160%	15%	9%
unclassified Gammaproteobacteria	Proteobacteria	0.0000004	4.79	51%	20%	57%	102%	40%	38%	110%	199%	78%	287%	519%	204%	181%	71%	39%
unclassified Hyphomicrobiaceae	Proteobacteria	0.0002941	3.64	93%	65%	68%	224%	104%	70%	73%	241%	112%	104%	343%	159%	329%	153%	47%
unclassified Microvirga	Proteobacteria	0.0000735	4.45	35%	44%	259%	132%	115%	126%	739%	376%	326%	587%	299%	260%	51%	44%	87%
unclassified Myxococcales	Proteobacteria	0.0005790	4.63	47%	39%	90%	55%	52%	83%	189%	116%	110%	228%	140%	132%	61%	58%	95%
unclassified Nitrospira	Proteobacteria	0.0000002	3.79	128%	149%	187%	142%	475%	116%	146%	110%	370%	125%	95%	318%	76%	254%	335%
unclassified Oxalobacteraceae	Proteobacteria	0.0004758	4.56	695%	274%	580%	434%	281%	39%	83%	62%	40%	212%	159%	103%	75%	48%	65%

Species	Phylum	P-values	LDA score	Beni Isguen/ Metlili %	Beni Isguen/ Ain Naga %	Beni Isguen/ Messaad %	Beni Isguen/ Moudjbara %	Beni Isguen/ Zaafrane %	Metlili/ Ain Naga %	Metlili/ Messaad %	Metlili/ Moudjbara %	Metlili/ Zaafrane %	Ain Naga/ Messaad %	Ain Naga/ Moudjbara %	Ain Naga/ Zaafrane %	Messad/ Moudjbara %	Messad/ Zaafrane %	Moudjbara/ Zaafrane %
unclassified_Phaselicystis	Proteobacteria	0.0000023	3.85	12%	4%	16%	13%	8%	33%	135%	110%	71%	407%	332%	215%	82%	53%	65%
unclassified_Phenylobacterium	Proteobacteria	0.0026468	4.14	114%	23%	139%	127%	127%	20%	123%	112%	112%	619%	564%	563%	91%	91%	100%
unclassified_Phyllobacteriaceae	Proteobacteria	0.0000378	3.95	52%	9%	34%	129%	29%	17%	66%	249%	57%	382%	1449%	329%	379%	86%	23%
unclassified_Proteobacteria	Proteobacteria	0.0006293	4.42	69%	66%	106%	129%	81%	95%	153%	186%	117%	160%	195%	123%	122%	77%	63%
unclassified_Rhizobiales	Proteobacteria	0.0000014	5.05	40%	35%	82%	71%	68%	87%	203%	176%	168%	233%	202%	193%	87%	83%	95%
unclassified_Rhodobacteraceae	Proteobacteria	0.0000389	3.78	264%	222%	485%	543%	122%	84%	184%	206%	46%	218%	245%	55%	112%	25%	23%
unclassified_Rhodospirillaceae	Proteobacteria	0.0000000	4.22	35%	50%	73%	181%	33%	144%	212%	523%	94%	147%	362%	65%	246%	44%	18%
unclassified_Rhodospirillales	Proteobacteria	0.0000069	3.90	69%	73%	142%	284%	120%	106%	206%	410%	173%	194%	386%	163%	199%	84%	42%
unclassified_Rubellimicrobium	Proteobacteria	0.0000026	4.61	443%	302%	1579%	901%	1179%	68%	356%	203%	266%	522%	298%	390%	57%	75%	131%
unclassified_Skermanella	Proteobacteria	0.0030325	4.13	116%	48%	388%	125%	50%	42%	335%	108%	43%	802%	259%	103%	32%	13%	40%
unclassified_Sphingomonadaceae	Proteobacteria	0.0001146	4.70	76%	58%	70%	93%	43%	77%	92%	124%	56%	119%	160%	73%	134%	61%	46%
unclassified_Sphingomonadales	Proteobacteria	0.0000053	4.13	104%	44%	61%	108%	31%	42%	59%	104%	30%	139%	247%	72%	178%	52%	29%
unclassified_Sphingomonas	Proteobacteria	0.0014753	4.07	144%	89%	195%	128%	192%	62%	135%	89%	133%	220%	144%	217%	66%	99%	150%
unclassified_Sphingosinicella	Proteobacteria	0.0027862	4.09	52%	50%	207%	51%	99%	96%	396%	96%	190%	414%	101%	198%	24%	48%	197%
unclassified_Steroidobacter	Proteobacteria	0.0000032	4.42	13%	6%	22%	26%	19%	43%	166%	198%	147%	388%	464%	346%	119%	89%	75%
unclassified_Xanthomonadaceae	Proteobacteria	0.0000000	4.64	33%	5%	30%	90%	10%	14%	91%	270%	29%	632%	1869%	201%	296%	32%	11%
bacterium_Ellin6510	unclassified_Bacteria	0.0000312	4.71	957%	6732%	262%	944%	816%	703%	27%	99%	85%	4%	14%	12%	361%	312%	86%
unclassified_Bacteria	unclassified_Bacteria	0.0001553	5.96	82%	103%	67%	82%	75%	125%	81%	99%	91%	65%	79%	73%	122%	112%	91%
unclassified_Gp10	unclassified_Bacteria	0.0000154	4.15	10%	23%	72%	72%	41%	237%	758%	753%	433%	319%	317%	182%	99%	57%	57%
unclassified_Gp3	unclassified_Bacteria	0.0001731	4.06	200%	200%	321%	270%	254%	100%	160%	135%	127%	161%	135%	127%	84%	79%	94%
unclassified_Gp4	unclassified_Bacteria	0.0001146	4.71	65%	281%	59%	42%	73%	433%	91%	64%	113%	21%	15%	26%	71%	124%	175%
unclassified_Gp7	unclassified_Bacteria	0.0007332	4.28	108%	187%	261%	103%	168%	174%	242%	95%	156%	139%	55%	90%	39%	64%	163%
unclassified_Parcubacteria_genera_incertae_sedis	unclassified_Bacteria	0.0012838	3.66	30%	20%	20%	18%	11%	67%	69%	61%	38%	102%	90%	56%	88%	55%	62%
unclassified_Subdivision3_genera_incertae_sedis	unclassified_Bacteria	0.0005943	4.67	119%	136%	250%	148%	189%	114%	209%	123%	158%	184%	109%	139%	59%	76%	128%
unclassified_WPS_1_genera_incertae_sedis	unclassified_Bacteria	0.0000009	5.32	35%	42%	32%	17%	26%	118%	91%	48%	73%	77%	41%	62%	53%	80%	151%
unclassified_WPS_2_genera_incertae_sedis	unclassified_Bacteria	0.0003330	4.27	131%	360%	220%	189%	259%	275%	169%	145%	198%	61%	53%	72%	86%	117%	137%
unclassified_Opitutus	Verrucomicrobia	0.0023655	4.32	111%	53%	191%	65%	67%	47%	171%	59%	60%	363%	124%	128%	34%	35%	103%
unclassified_Spartobacteria_genera_incertae_sedis	Verrucomicrobia	0.0000780	4.47	49%	45%	43%	14%	38%	91%	88%	28%	78%	97%	31%	86%	32%	88%	275%
unclassified_Verrucomicrobia	Verrucomicrobia	0.0007743	4.37	70%	47%	49%	44%	38%	67%	71%	63%	55%	105%	93%	82%	89%	78%	87%

A)



B)



C)

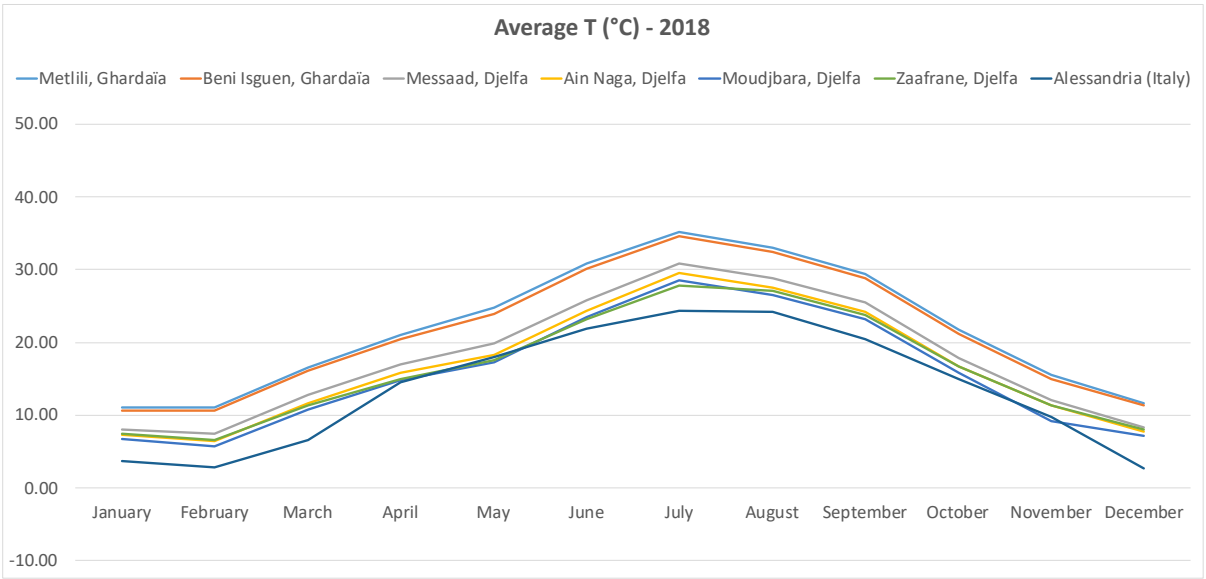
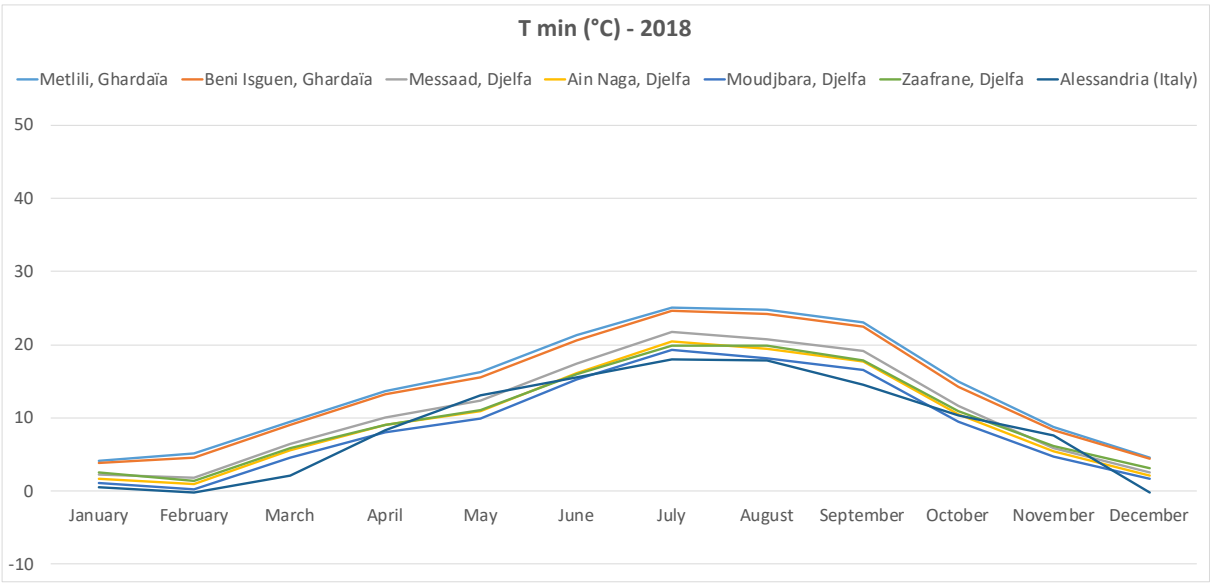
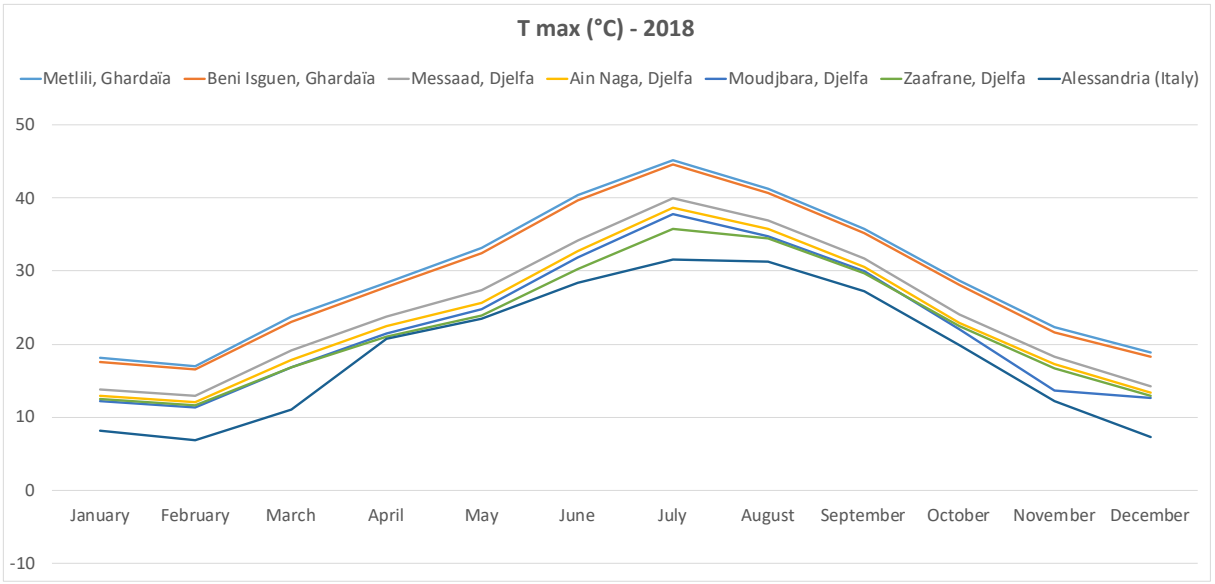


Figure S1.

A)



B)



C)

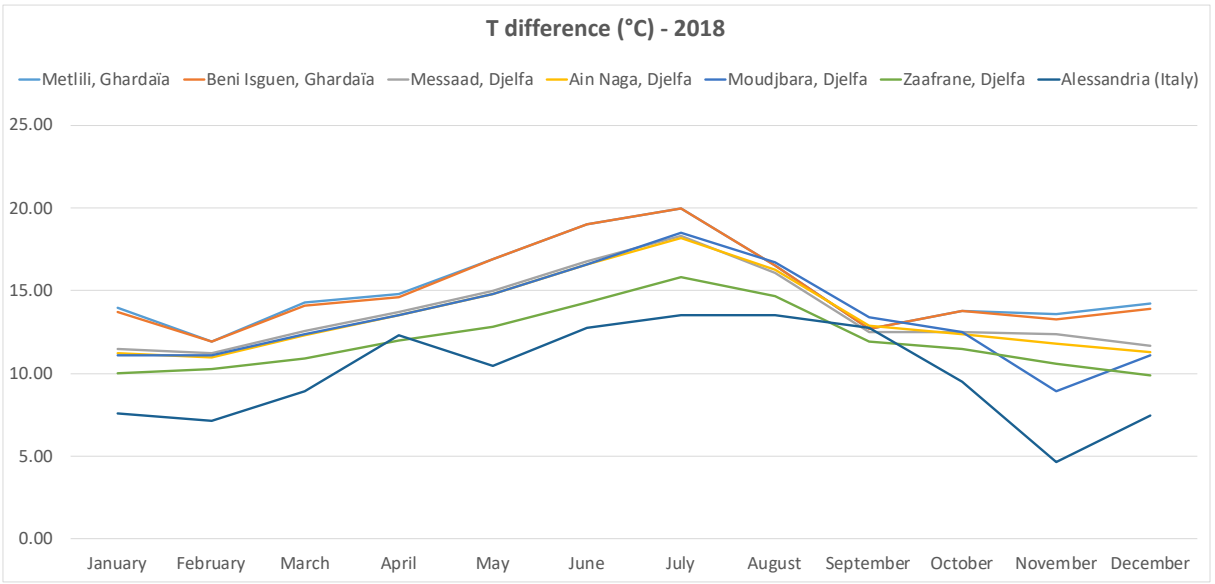


Figure S2.

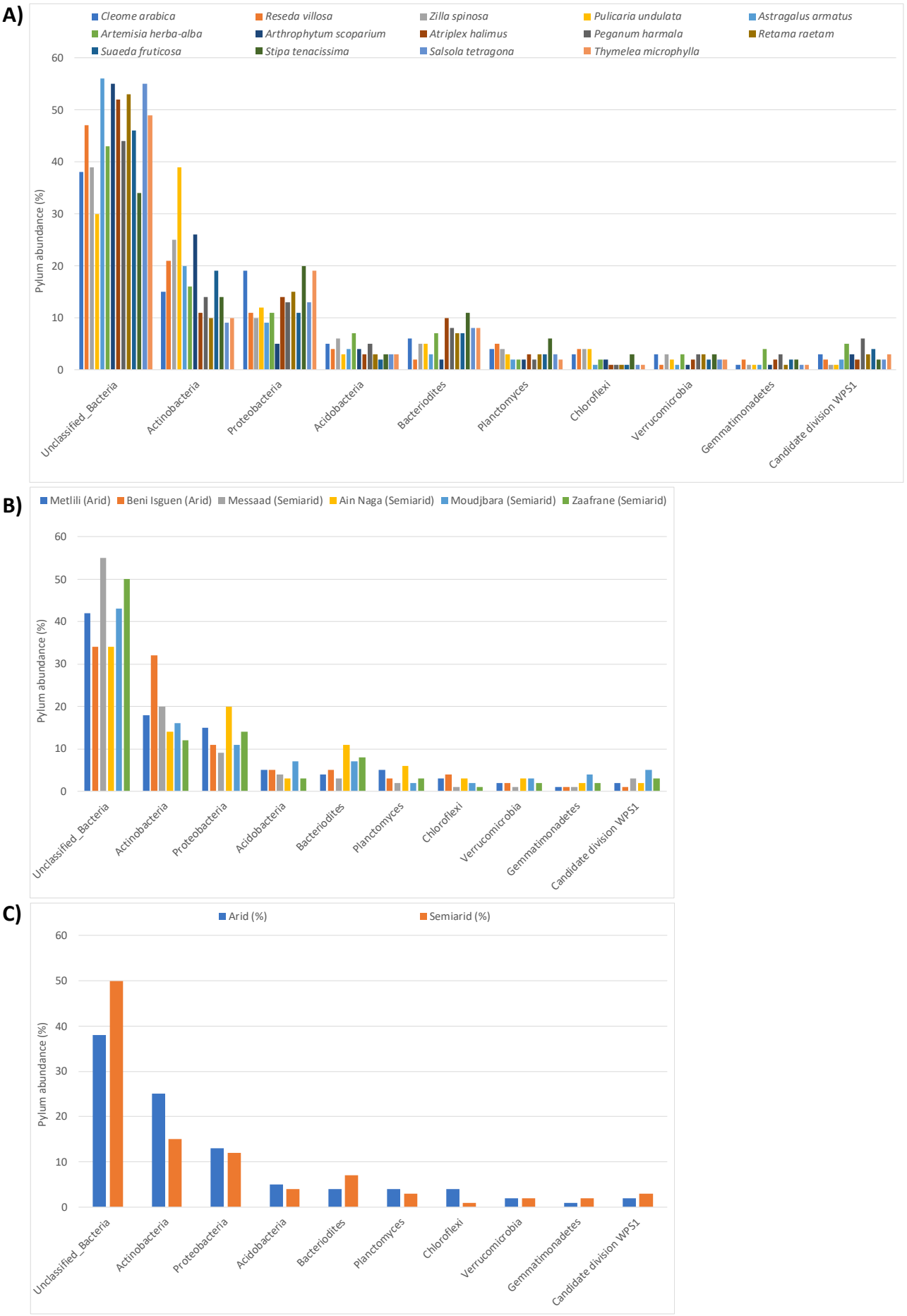

A)
Cleome arabica
Reseda villosa
Zilla spinosa
Pulicaria undulata
Astragalus armatus
Artemisia herba-alba
Arthrophytum scoparium
Atriplex halimus
Peganum harmala
Retama raetam
Suaeda fruticosa
Stipa tenacissima
Salsola tetragona
Thymelea microphylla
Pylum abundance (%)
0
10
20
30
40
50
60
Unclassified_Bacteria
Actinobacteria
Proteobacteria
Acidobacteria
Bacteriodites
Planctomyces
Chloroflexi
Verrucomicrobia
Gemmatimonadetes
Candidate division WPS1
B)
Metlili (Arid)
Beni Isguen (Arid)
Messaad (Semiarid)
Ain Naga (Semiarid)
Moudjbara (Semiarid)
Zaafrane (Semiarid)
Pylum abundance (%)
0
10
20
30
40
50
60
Unclassified_Bacteria
Actinobacteria
Proteobacteria
Acidobacteria
Bacteriodites
Planctomyces
Chloroflexi
Verrucomicrobia
Gemmatimonadetes
Candidate division WPS1
C)
Arid (%)
Semiarid (%)
Pylum abundance (%)
0
10
20
30
40
50
60
Unclassified_Bacteria
Actinobacteria
Proteobacteria
Acidobacteria
Bacteriodites
Planctomyces
Chloroflexi
Verrucomicrobia
Gemmatimonadetes
Candidate division WPS1

Figure S3.

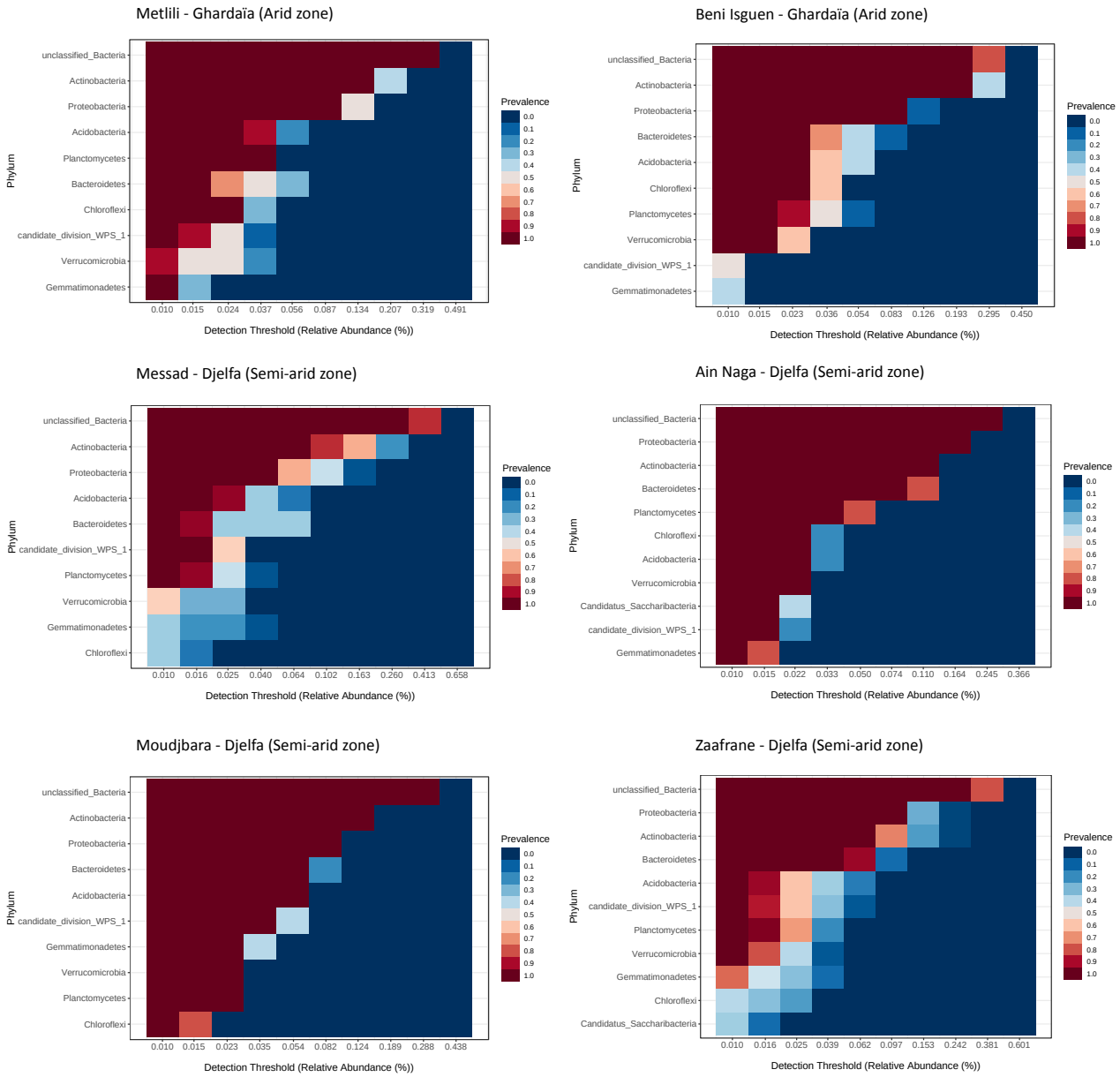

Metlili - Ghardaïa (Arid zone)
Beni Isguen - Ghardaïa (Arid zone)
Messad - Djelfa (Semi-arid zone)
Ain Naga - Djelfa (Semi-arid zone)
Moudjbara - Djelfa (Semi-arid zone)
Zaafrane - Djelfa (Semi-arid zone)
Phylum
Prevalence
Detection Threshold (Relative Abundance (%))
unclassified_Bacteria
Actinobacteria
Proteobacteria
Acidobacteria
Planctomycetes
Bacteroidetes
Chloroflexi
candidate_division_WPS_1
Verrucomicrobia
Gemmatimonadetes
Candidatus_Saccharibacteria

Figure S4.

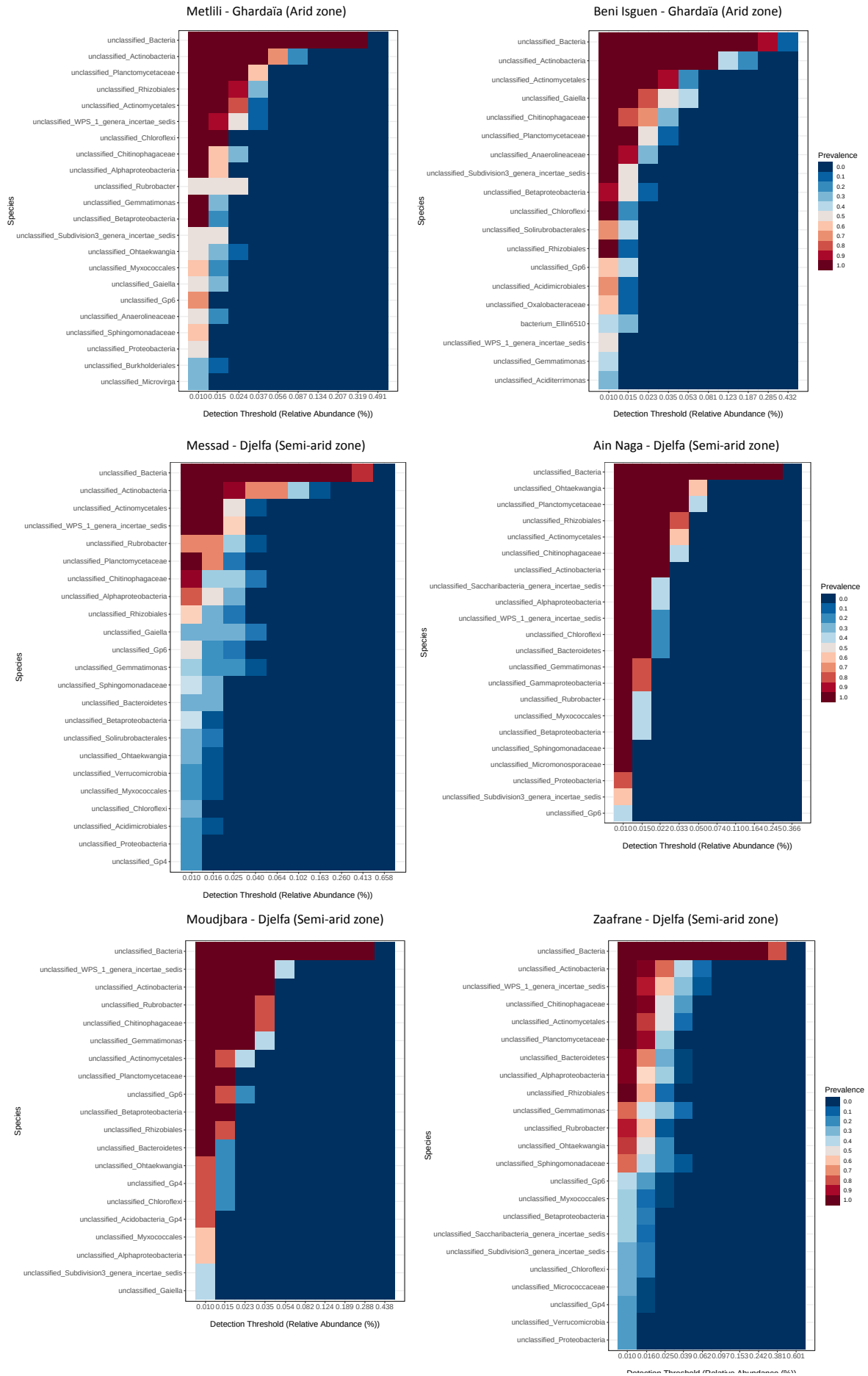

Metlili - Ghardaïa (Arid zone)
unclassified_Bacteria
unclassified_Actinobacteria
unclassified_Planctomycetaceae
unclassified_Rhizobiales
unclassified_Actinomycetales
unclassified_WPS_1_genera_incertae_sedis
unclassified_Chloroflexi
unclassified_Chitinophagaceae
unclassified_Alphaproteobacteria
unclassified_Rubrobacter
unclassified_Gemmatimonas
unclassified_Betaproteobacteria
unclassified_Subdivision3_genera_incertae_sedis
unclassified_Ohtaekwangia
unclassified_Myxococcales
unclassified_Gaiella
unclassified_Gp6
unclassified_Anaerolineaceae
unclassified_Sphingomonadaceae
unclassified_Proteobacteria
unclassified_Burkholderiales
unclassified_Microvirga
Species
0.010 0.015 0.024 0.037 0.056 0.087 0.134 0.207 0.319 0.491
Detection Threshold (Relative Abundance (%))
Beni Isguen - Ghardaïa (Arid zone)
unclassified_Bacteria
unclassified_Actinobacteria
unclassified_Actinomycetales
unclassified_Gaiella
unclassified_Chitinophagaceae
unclassified_Planctomycetaceae
unclassified_Anaerolineaceae
unclassified_Subdivision3_genera_incertae_sedis
unclassified_Betaproteobacteria
unclassified_Chloroflexi
unclassified_Solirubrobacterales
unclassified_Rhizobiales
unclassified_Gp6
unclassified_Acidimicrobiales
unclassified_Oxalobacteraceae
bacterium_Ellin6510
unclassified_WPS_1_genera_incertae_sedis
unclassified_Gemmatimonas
unclassified_Aciditerrimonas
Species
0.010 0.015 0.023 0.035 0.053 0.081 0.123 0.187 0.285 0.432
Detection Threshold (Relative Abundance (%))
Prevalence
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Messad - Djelfa (Semi-arid zone)
unclassified_Bacteria
unclassified_Actinobacteria
unclassified_Actinomycetales
unclassified_WPS_1_genera_incertae_sedis
unclassified_Rubrobacter
unclassified_Planctomycetaceae
unclassified_Chitinophagaceae
unclassified_Alphaproteobacteria
unclassified_Rhizobiales
unclassified_Gaiella
unclassified_Gp6
unclassified_Gemmatimonas
unclassified_Sphingomonadaceae
unclassified_Bacteroidetes
unclassified_Betaproteobacteria
unclassified_Solirubrobacterales
unclassified_Ohtaekwangia
unclassified_Verrucomicrobia
unclassified_Myxococcales
unclassified_Chloroflexi
unclassified_Acidimicrobiales
unclassified_Proteobacteria
unclassified_Gp4
Species
0.010 0.016 0.025 0.040 0.064 0.102 0.163 0.260 0.413 0.658
Detection Threshold (Relative Abundance (%))
Ain Naga - Djelfa (Semi-arid zone)
unclassified_Bacteria
unclassified_Ohtaekwangia
unclassified_Planctomycetaceae
unclassified_Rhizobiales
unclassified_Actinomycetales
unclassified_Chitinophagaceae
unclassified_Actinobacteria
unclassified_Saccharibacteria_genera_incertae_sedis
unclassified_Alphaproteobacteria
unclassified_WPS_1_genera_incertae_sedis
unclassified_Chloroflexi
unclassified_Bacteroidetes
unclassified_Gemmatimonas
unclassified_Gammaproteobacteria
unclassified_Rubrobacter
unclassified_Myxococcales
unclassified_Betaproteobacteria
unclassified_Sphingomonadaceae
unclassified_Micromonosporaceae
unclassified_Proteobacteria
unclassified_Subdivision3_genera_incertae_sedis
unclassified_Gp6
Species
0.010 0.015 0.022 0.033 0.050 0.074 0.110 0.164 0.245 0.366
Detection Threshold (Relative Abundance (%))
Prevalence
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Moudjbara - Djelfa (Semi-arid zone)
unclassified_Bacteria
unclassified_WPS_1_genera_incertae_sedis
unclassified_Actinobacteria
unclassified_Rubrobacter
unclassified_Chitinophagaceae
unclassified_Gemmatimonas
unclassified_Actinomycetales
unclassified_Planctomycetaceae
unclassified_Gp6
unclassified_Betaproteobacteria
unclassified_Rhizobiales
unclassified_Bacteroidetes
unclassified_Ohtaekwangia
unclassified_Gp4
unclassified_Chloroflexi
unclassified_Acidobacteria_Gp4
unclassified_Myxococcales
unclassified_Alphaproteobacteria
unclassified_Subdivision3_genera_incertae_sedis
unclassified_Gaiella
Species
0.010 0.015 0.023 0.035 0.054 0.082 0.124 0.189 0.288 0.438
Detection Threshold (Relative Abundance (%))
Zaafrane - Djelfa (Semi-arid zone)
unclassified_Bacteria
unclassified_Actinobacteria
unclassified_WPS_1_genera_incertae_sedis
unclassified_Chitinophagaceae
unclassified_Actinomycetales
unclassified_Planctomycetaceae
unclassified_Bacteroidetes
unclassified_Alphaproteobacteria
unclassified_Rhizobiales
unclassified_Gemmatimonas
unclassified_Rubrobacter
unclassified_Ohtaekwangia
unclassified_Sphingomonadaceae
unclassified_Gp6
unclassified_Myxococcales
unclassified_Betaproteobacteria
unclassified_Saccharibacteria_genera_incertae_sedis
unclassified_Subdivision3_genera_incertae_sedis
unclassified_Chloroflexi
unclassified_Micrococcaceae
unclassified_Gp4
unclassified_Verrucomicrobia
unclassified_Proteobacteria
Species
0.010 0.016 0.025 0.039 0.062 0.097 0.153 0.242 0.381 0.601
Prevalence
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0

Figure S5.

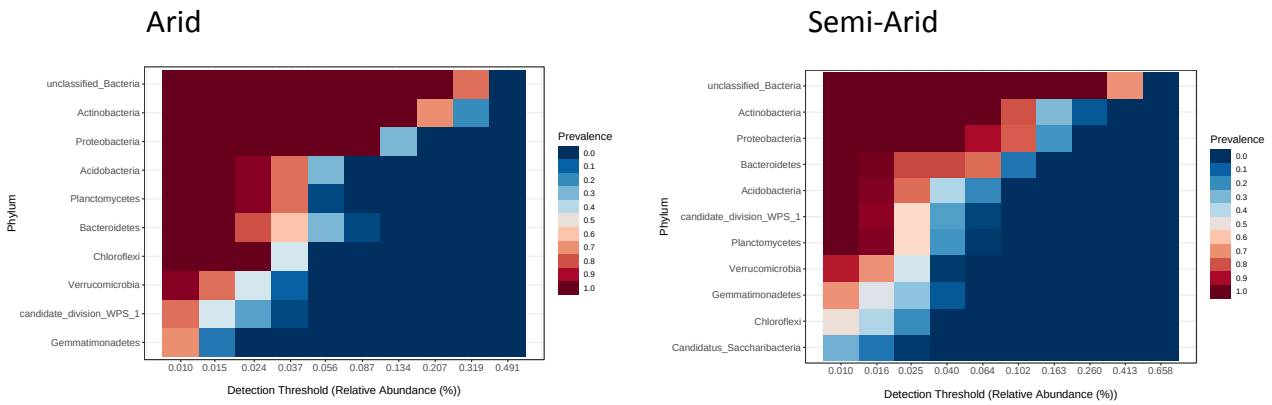


Figure S6.

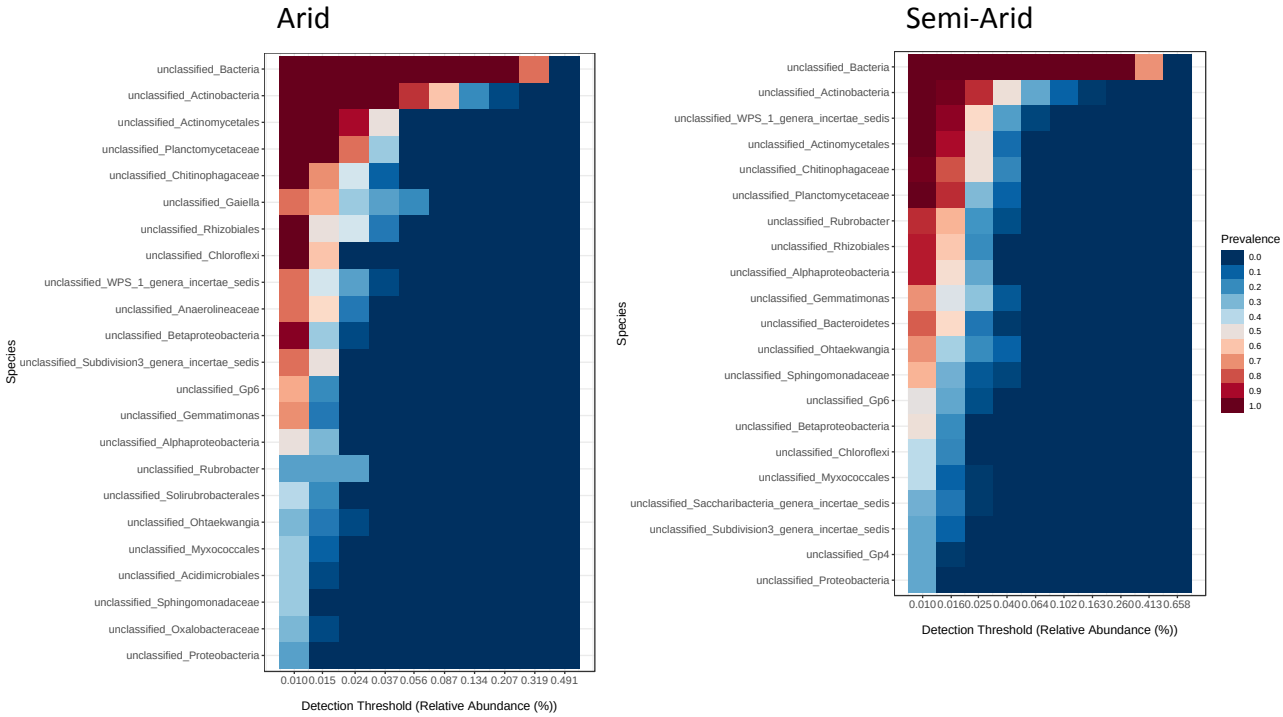


Figure S7.

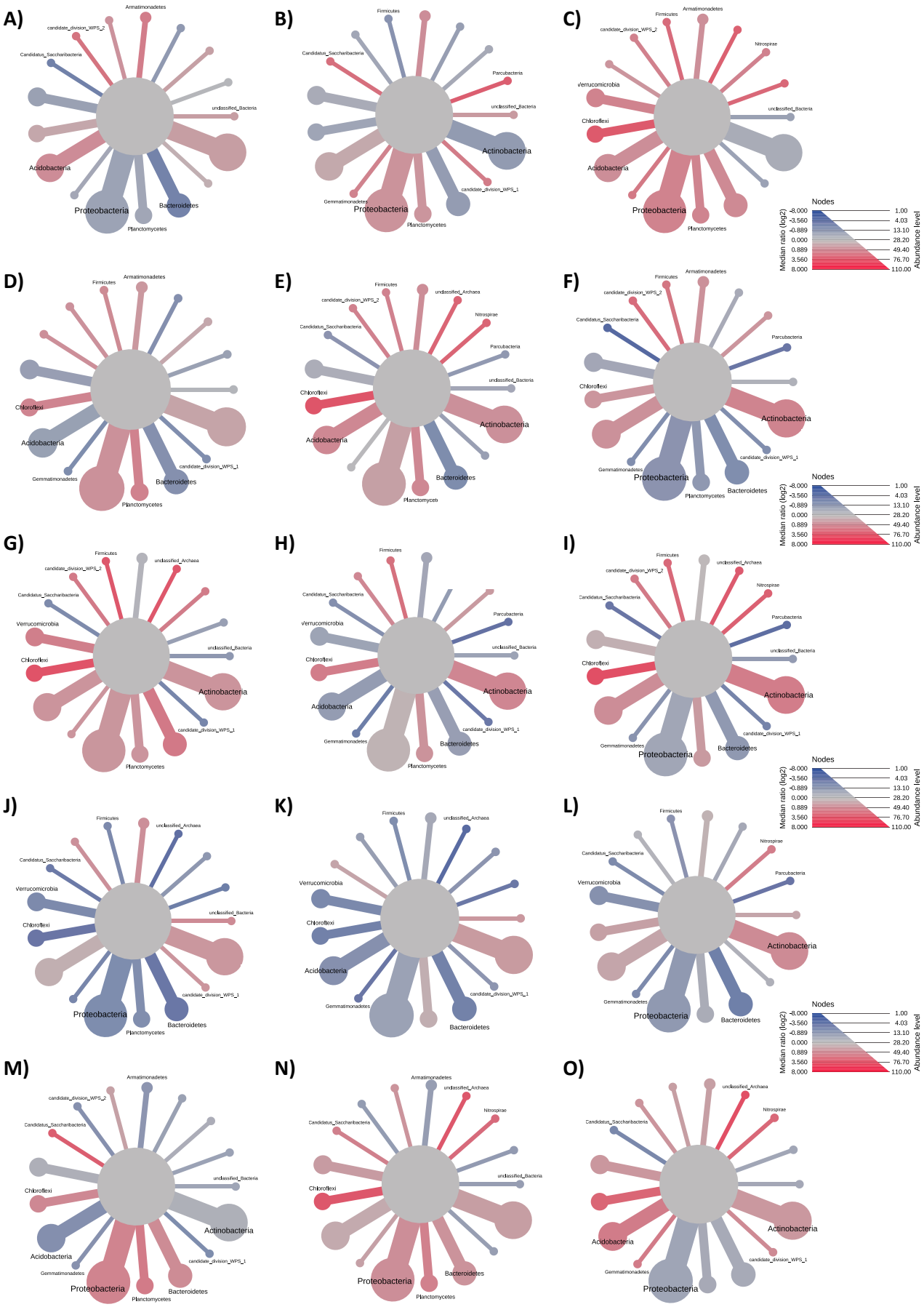

A)
B)
C)
D)
E)
F)
G)
H)
I)
J)
K)
L)
M)
N)
O)
Armatimonadetes
candidate_division_WPS_2
Candidatus_Saccharibacteria
unclassified_Bacteria
Acidobacteria
Proteobacteria
Bacteroidetes
Planctomycetes
Firmicutes
Parcubacteria
Actinobacteria
Gemmatimonadetes
candidate_division_WPS_1
Nitrospirae
Verrucomicrobia
Chloroflexi
unclassified_Archaea
Nodes
Median ratio (log2)
-8.000
-3.560
-0.889
0.000
0.889
3.560
8.000
1.00
4.03
13.10
28.20
49.40
76.70
110.00
Abundance level

Figure S8.