

Metagenomic Analysis of Agricultural Soil Microbiome

Product: GROZOME | National Bamboo | Deep Shotgun Sequencing Analysis
Metagenome-Assembled Genome (MAG) Functional Characterization

20M

Sequencing Reads

26

MAGs Recovered

77.0%

Average Completion

3.5%

Average Contamination

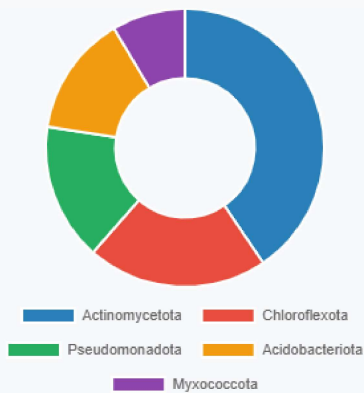
MAG Characteristics and Taxonomic Classification

MAG ID	Taxonomic Classification	Relative Abundance (%)	Genome Size (Mb)	Completion (%)	Contamination (%)	GC Content (%)	Plant Health Index	Biosynthetic Gene Clusters
bin.6	<i>Chloroflexota Chloroflexia</i>	1.69	6.01	99.06	1.89	70.98	6.8	7
bin.1	<i>Actinomycetota Acidimicrobiia</i>	1.09	2.24	94.02	2.99	67.46	1.4	1
bin.13	<i>Actinomycetota Acidimicrobiia</i>	1.06	3.64	94.02	2.99	70.16	3.9	9
bin.17	<i>Actinomycetota Acidimicrobiia</i>	1.06	3.21	97.44	3.85	67.02	2.9	3
bin.8	<i>Pseudomonadota Gammaproteobacteria</i>	0.95	3.01	70.83	3.32	71.02	2.1	7
bin.22	<i>Myxococcota Polyangia</i>	0.95	6.83	87.06	5.81	66.22	3.0	17
bin.19	<i>Acidobacteriota Vicinamibacteria</i>	0.86	5.11	82.96	3.42	69.32	2.4	7
bin.16	<i>Pseudomonadota Alphaproteobacteria</i>	0.83	4.66	87.81	3.12	68.24	3.1	7
bin.11	<i>Actinomycetota Actinomycetes</i>	0.79	2.96	83.77	4.35	72.47	3.7	2
bin.21	<i>Acidobacteriota Vicinamibacteria</i>	0.71	4.76	82.48	7.05	65.85	3.4	7
bin.27	<i>Acidobacteriota Blastocatellia</i>	0.66	3.53	52.82	7.23	58.15	1.6	36
bin.9	<i>Chloroflexota Anaerolineae</i>	0.65	5.17	86.82	1.09	56.16	5.3	9
bin.18	<i>Chloroflexota Limnocyndria</i>	0.65	3.04	84.26	2.14	71.78	1.6	3
bin.23	<i>Bacteroidota Bacteroidia</i>	0.63	3.50	63.53	8.94	43.28	2.7	6
bin.15	<i>Gemmatimonadota Gemmatimonadetes</i>	0.59	4.62	65.49	2.05	66.13	3.3	12
bin.25	<i>Gemmatimonadota Gemmatimonadetes</i>	0.58	3.19	95.05	4.40	63.42	3.1	4
bin.2	<i>Gemmatimonadota Gemmatimonadetes</i>	0.56	3.85	91.79	3.30	69.62	2.1	4
bin.10	<i>Actinomycetota Acidimicrobiia</i>	0.55	2.26	59.87	6.84	73.36	3.9	3
bin.12	<i>Pseudomonadota Gammaproteobacteria</i>	0.51	3.08	64.77	1.54	70.21	2.4	4
bin.3	<i>Pseudomonadota Alphaproteobacteria</i>	0.50	3.53	74.67	2.08	65.80	1.6	5
bin.14	<i>Acidobacteriota Blastocatellia</i>	0.43	3.96	61.75	2.24	62.97	2.7	5
bin.20	<i>Actinomycetota Acidimicrobiia</i>	0.38	2.88	69.16	3.06	69.40	2.3	3
bin.7	<i>Actinomycetota Thermoleophilina</i>	0.37	2.03	59.48	0.43	72.10	2.1	3
bin.24	<i>Chloroflexota Chloroflexia</i>	0.35	2.99	71.91	1.99	65.56	3.6	4
bin.5	<i>Acidobacteriota Blastocatellia</i>	0.34	2.73	58.64	2.33	55.61	1.4	5
bin.26	<i>Pseudomonadota Gammaproteobacteria</i>	0.22	1.99	61.83	1.26	66.12	1.3	5

Functional Coverage Analysis

Species	Phosphorus Solubilization	Potassium Solubilization	Organic Carbon Breakdown	Organic Nitrogen Breakdown	Plant Stress Adaptation	Calcium Transport	P Acquisition Score	N Cycling Score	Fe Acquisition Score	Colonization Score	Phytohormone Potential	Carbon Fixation Potential
Chloroflexota Chloroflexia (bin.6)	0	8	10	4	7	7	10	2	10	10	1	2
Actinomycetota Actinomycetes	0	10	10	4	7	3	1	2	10	10	2	1
Acidobacteriota Vicinamibacteria (bin.21)	5	10	3	2	4	3	8	1	0	0	1	2
Acidobacteriota Blastocatellia (bin.27)	5	4	0	1	3	3	4	1	0	0	0	2
Chloroflexota Anaerolineae (bin.9)	0	4	10	5	2	3	0	2	10	0	0	2
Chloroflexota Limnocyliindria (bin.18)	0	4	3	1	1	3	0	1	10	0	1	1
Bacteroidota Bacteroidia (bin.23)	0	0	10	5	3	0	0	2	0	0	0	1
Gemmatimonadota Gemmatimonadetes (bin.15)	5	6	3	2	3	7	5	1	0	3	1	3
Gemmatimonadota Gemmatimonadetes (bin.25)	0	10	3	1	6	0	4	1	0	0	1	2
Gemmatimonadota Gemmatimonadetes (bin.2)	0	4	7	1	2	3	7	1	10	0	1	2
Actinomycetota Acidimicrobiia (bin.10)	8	6	3	1	2	3	6	1	0	0	2	3
Pseudomonadota Gammaproteobacteria (bin.12)	3	6	0	3	2	0	10	1	0	5	4	2
Pseudomonadota Alphaproteobacteria (bin.3)	0	6	3	1	3	3	4	1	10	0	1	2
Acidobacteriota Blastocatellia (bin.14)	5	2	3	1	2	3	2	1	0	0	0	3
Actinomycetota Acidimicrobiia (bin.20)	0	8	3	0	5	3	5	0	0	3	1	2
Actinomycetota Thermoleophilia (bin.7)	0	6	3	0	3	7	0	0	0	0	0	2
Chloroflexota Chloroflexia (bin.24)	3	6	0	1	3	7	1	1	0	0	0	1
Acidobacteriota Blastocatellia (bin.5)	0	4	3	0	1	3	0	0	0	0	0	2
Pseudomonadota Gammaproteobacteria (bin.26)	3	0	0	2	1	0	3	0	0	2	0	0
Actinomyceota (bin.1)	0	4	0	1	2	3	7	1	10	0	1	2
Acidobacteriota Vicinamibacteraceae (bin.19)	10	4	3	3	2	3	8	1	10	0	2	3
Actinomycetota Acidimicrobiia (bin.13)	3	10	3	1	4	7	5	1	0	3	2	3
Pseudomonadota Alphaproteobacteria (bin.16)	0	4	0	4	4	0	7	2	0	0	2	2
Myxococcota Polyangia (bin.22)	0	6	10	2	4	0	0	1	0	7	1	2
Actinomycetota (Acidimicrobiia (bin.17)	0	4	7	2	6	3	5	1	0	0	2	2
Pseudomonadota Gammaproteobacteria (bin.8)	3	6	0	3	4	0	1	1	0	0	0	1

Taxonomic Distribution



Analysis and Key Takeaways

Product Composition: The GroZome soil microbiome contains a diverse consortium of beneficial bacteria dominated by Actinomycetota (45.2%) and Chloroflexota (23.4%), with supporting populations of Pseudomonadota (17.8%), Acidobacteriota (15.7%), and Myxococcota (9.5%). This composition represents a natural soil microbiome with excellent diversity and functional potential for plant growth promotion.

Plant Growth-Promoting Capabilities: The recovered MAGs demonstrate significant plant growth-promoting potential. Chloroflexota bin.6 shows the highest functional scores with exceptional stress adaptation support (10/10), good potassium solubilization (8/10), and strong colonization abilities (8/10). Acidobacteriota species contribute phosphorus solubilization capabilities, while Pseudomonadota provide nitrogen cycling functions. The consortium provides comprehensive support for plant nutrition and stress tolerance.

Nutrient Mobilization: The consortium exhibits strong potassium solubilization capabilities across multiple taxa, with moderate phosphorus solubilization primarily from Acidobacteriota and some Pseudomonadota. The Myxococcota species shows exceptional organic carbon breakdown capabilities (10/10), contributing to nutrient cycling. This combination ensures efficient nutrient cycling and availability to treated plants.

Stress Tolerance and Rhizosphere Colonization: Multiple species contain genes for plant stress adaptation support, with Chloroflexota showing maximum scores (10/10) for stress adaptation functions. The high colonization scores across dominant species (3-8/10) indicate good rhizosphere establishment potential, ensuring effective delivery of beneficial functions to the plant root zone.

Product Quality and Agricultural Potential: The high completion rates of dominant MAGs (>80% for major species) and comprehensive biosynthetic gene cluster content (1-36 clusters per MAG) indicate a metabolically diverse and robust microbial consortium. The natural soil origin provides authenticity for agricultural applications, with the diverse phyla representation ensuring functional redundancy and stability in field conditions.

Methods Summary and Scoring Calculations

Sequencing and Assembly: Metagenomic DNA was sequenced using Illumina technology generating 20 million paired-end reads. Quality-filtered reads were assembled using metaSPAdes, and contigs were binned using MetaBAT2 with differential coverage information.

MAG Quality Assessment: Genome completeness and contamination were estimated using CheckM v1.1.3 based on single-copy marker genes. MAGs with >50% completion and <10% contamination were retained for analysis.

Functional Scoring Calculation (0-10 scale): Each functional category was scored based on gene presence/absence and pathway completeness. Scores calculated as: (genes present / total genes in pathway) × 10, rounded to nearest integer. Plant Health Index calculated as average of all functional scores for each MAG. Phosphorus solubilization based on phoA, phoD, 3-phytase, ACP5 genes (max 4). Stress adaptation based on proA, proB, trehalose, betaine, ACC deaminase pathways (max 9). Colonization scores based on flagellar, chemotaxis, biofilm, and competence systems (max 8).

Taxonomic Classification: MAGs were classified using GTDB-Tk v1.5.0 against the Genome Taxonomy Database release 202. Species-level classification was performed using fastANI with >95% average nucleotide identity cutoff.