



Metagenomic studies and their applications

Dr. Triastuti Rahayu, S.Si., M.Si
Biology Education Study Program
Faculty of Teacher Training and Education,
Universitas Muhammadiyah Surakarta, Indonesia
Email : tr124@ums.ac.id




WHAT IS METAGENOME ?



A metagenome is comprised of **all the genetic elements** of the host and all those of all the microorganisms (microbiome) that live in or on that host.

Metagenomics is defined as the direct genetic analysis of genomes contained with an environmental sample.

Metagenomic analysis is commonly used to investigate complex microbial communities (MICROBIOME) sampled directly from the environment, without culturing or isolating a single organism.



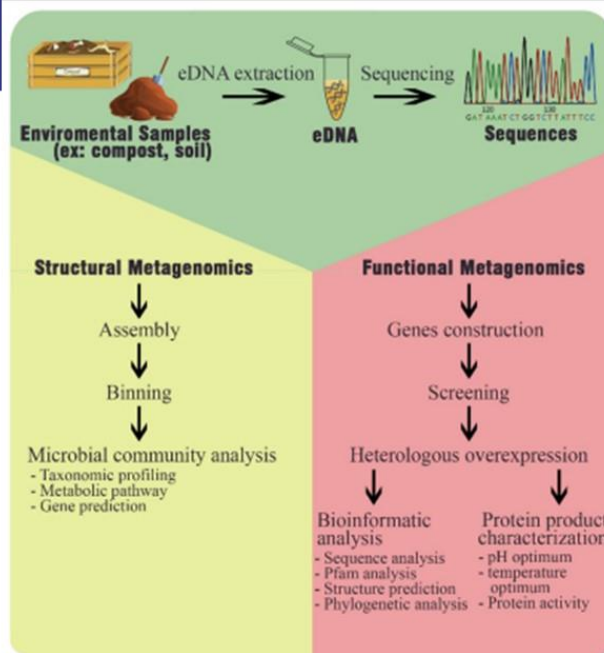


Fig. Framework for metagenomics with two primary studies, structural and functional metagenomics

Prayogo et al. Journal of Genetic Engineering and Biotechnology (2020) 18:39
<https://doi.org/10.1186/s43141-020-00043-9>

Journal of Genetic Engineering and Biotechnology

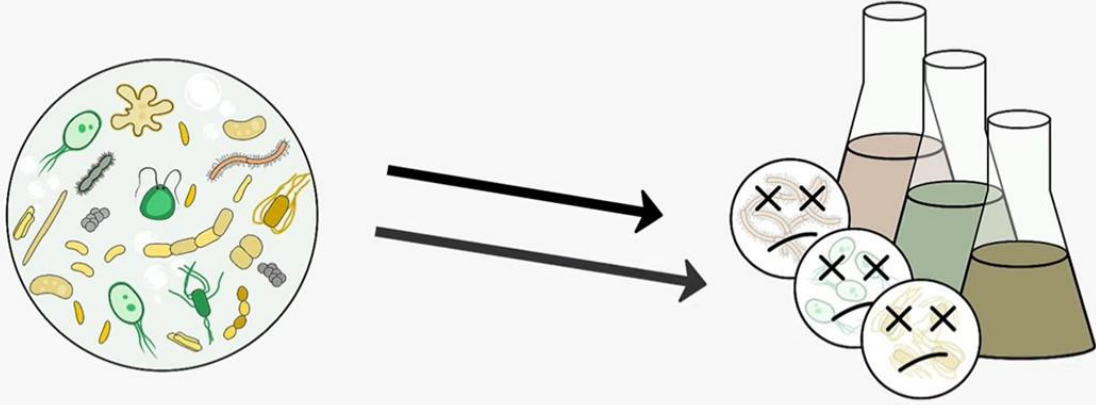
REVIEW **Open Access**

Metagenomic applications in exploration and development of novel enzymes from nature: a review

Fitra Adi Prayogo^{1*}, Anto Budiharjo^{2,3*}, Hermin Pancasakti Kusumaningrum¹, Wijanarka Wijanarka², Agung Suprihadi² and Nurhayati Nurhayati²

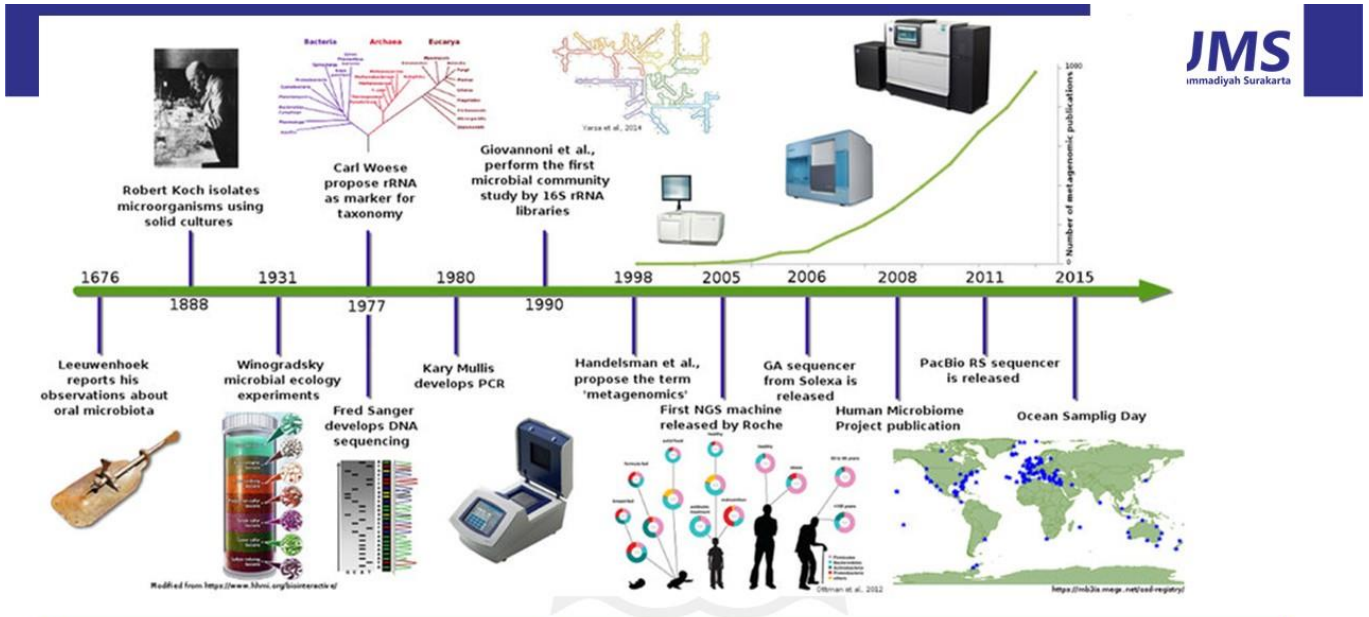
www.ums.ac.id
Humanizing * Liberating * Transcending
3

Why do we study the metagenome?



Only approximately 1% of the community of microbes can be cultivated in artificial media.

ums.ac.id
4



Metagenomics timeline and milestones. Timeline showing advances in microbial communities studies from Leeuwenhoek to NGS (Ottman et al., 2012; Yarza et al., 2014).

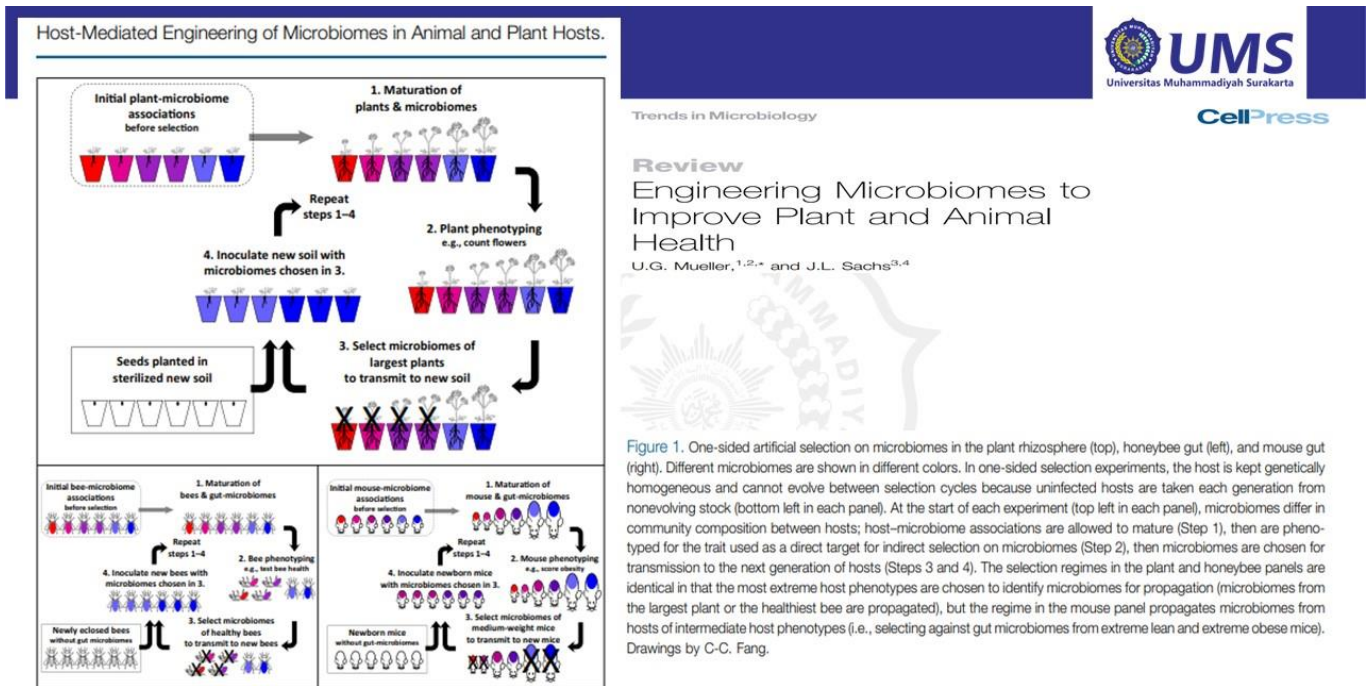


Figure 1. One-sided artificial selection on microbiomes in the plant rhizosphere (top), honeybee gut (left), and mouse gut (right). Different microbiomes are shown in different colors. In one-sided selection experiments, the host is kept genetically homogeneous and cannot evolve between selection cycles because uninfected hosts are taken each generation from non-evolving stock (bottom left in each panel). At the start of each experiment (top left in each panel), microbiomes differ in community composition between hosts; host-microbiome associations are allowed to mature (Step 1), then are phenotyped for the trait used as a direct target for indirect selection on microbiomes (Step 2), then microbiomes are chosen for transmission to the next generation of hosts (Steps 3 and 4). The selection regimes in the plant and honeybee panels are identical in that the most extreme host phenotypes are chosen to identify microbiomes for propagation (microbiomes from the largest plant or the healthiest bee are propagated), but the regime in the mouse panel propagates microbiomes from hosts of intermediate host phenotypes (i.e., selecting against gut microbiomes from extreme lean and extreme obese mice). Drawings by C-C. Fang.

Researchs using the metagenomic approach 1



Research article

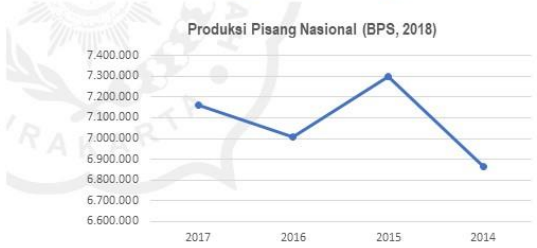
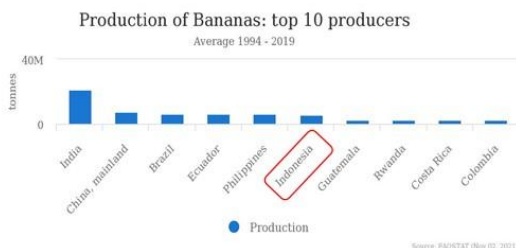
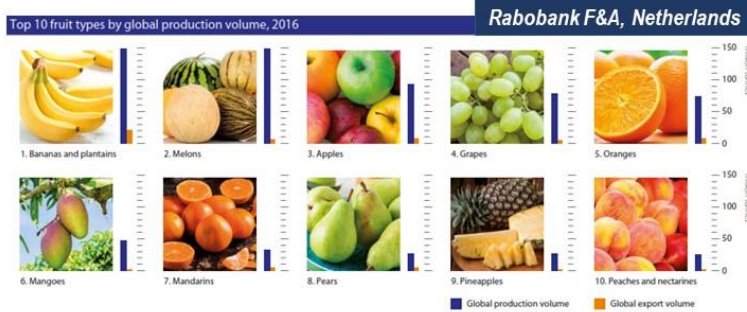
Exploration of core endophytic bacteria from different organs of diploid *Musa balbisiana* and triploid *Musa acuminata*

Triastuti Rahayu^{a,*}, Yekti Asih Purwestri^{b,†}, Siti Subandiyah^{c,†}, Ahmad Suparmin^{d,†}, Donny Widiyanto^{d,*}

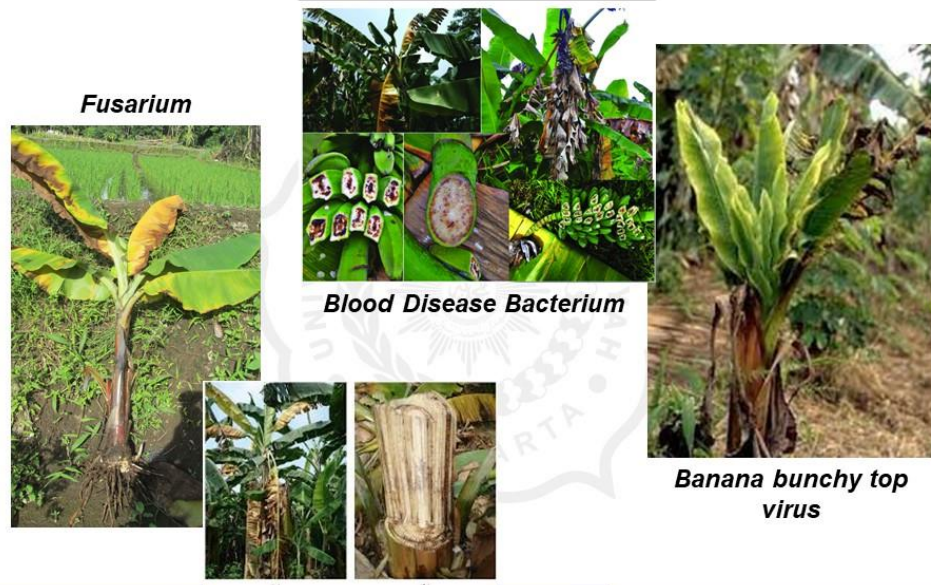
Aims : this study determined the core endophytic bacteria in the Kluthuk and Ambon cultivars

Goal : this report should be valuable for further development of banana resistance through endophytic bacterial amendment based on clear results

Banana production UMS Universitas Muhammadiyah Surakarta

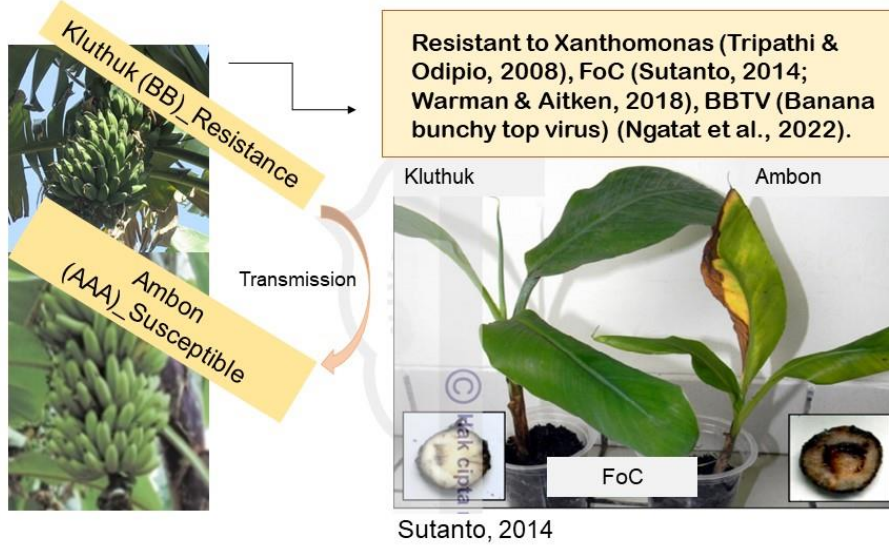


Diseases of banana plants



+ www.ums.ac.id Humanizing * Liberating * Transcending

BANANA PLANT MODEL



+ www.ums.ac.id Humanizing * Liberating * Transcending

Result



Kluthuk



Ambon

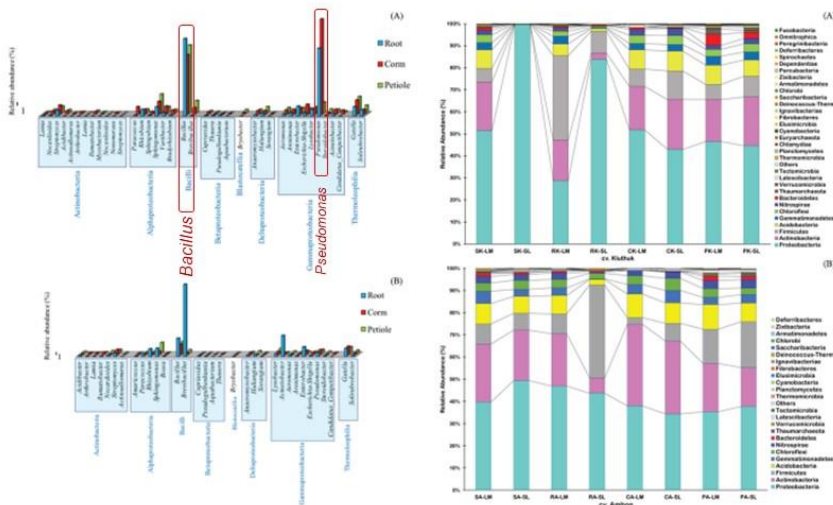


Fig. 5 C cultivars

3 Relative abundance at phylum level of banana cultivars: (A) Kluthuk; (B) Ambon, where x axis label codes are defined in Table S1

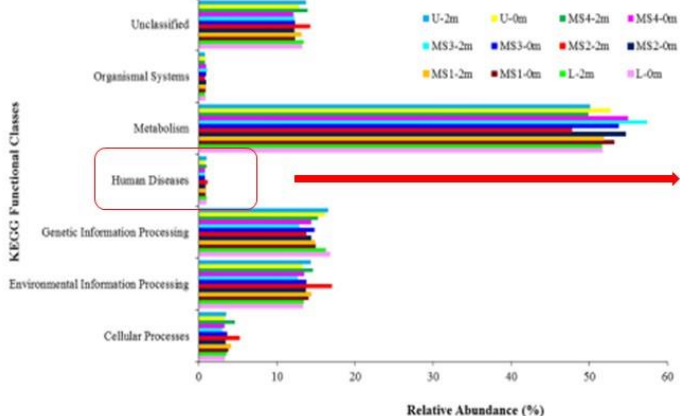
Researchs using the metagenomic approach

2



Metagenomic study in the cemetery

Microbial life beyond the grave: 16S rRNA gene-based metagenomic analysis of bacteria diversity and their functional profiles in cemetery environments
 Akebe Luther King Abia ^{1,2}, Arghavan Alisoltani ^{3,1}, Eunice Ubomba-Jaswa ^{4,1}, Matthys Alois Dippenaar ^{5,1}




OTUs related to human diseases in cemetery soil (relative abundance; %).


Disease	Maitland cemetery (Cape Town)					
	MS1		MS2		MS3	
	0 m	2 m	0 m	2 m	0 m	2 m
Tuberculosis	0.23	0.22	0.22	0.19	0.22	0.18
Alzheimer's disease	0.12	0.13	0.10	0.17	0.10	0.10
Huntington's disease	0.11	0.14	0.11	0.17	0.10	0.09
Vibrio cholerae pathogenic cycle	0.10	0.11	0.09	0.18	0.10	0.10
Type 1 diabetes mellitus	0.08	0.07	0.08	0.06	0.08	0.08
Pathways in cancer	0.07	0.08	0.07	0.10	0.07	0.06
Primary immunodeficiency	0.08	0.07	0.08	0.08	0.08	0.08
Parkinson's disease	0.06	0.08	0.05	0.12	0.05	0.04
Amyotrophic lateral sclerosis (ALS)	0.05	0.06	0.05	0.08	0.04	0.08
Type II diabetes mellitus	0.05	0.05	0.05	0.05	0.05	0.05
Pertussis	0.03	0.05	0.02	0.14	0.02	0.04
Epithelial cell signaling in Helicobacter pylori infection	0.03	0.04	0.03	0.07	0.03	0.03
Renal cell carcinoma	0.03	0.04	0.03	0.04	0.03	0.03
African trypanosomiasis	0.02	0.03	0.02	0.04	0.02	0.04
Amoebiasis	0.03	0.03	0.03	0.02	0.03	0.01
Prostate cancer	0.02	0.02	0.02	0.03	0.02	0.02
Chagas disease (American trypanosomiasis)	0.02	0.02	0.02	0.03	0.02	0.02
Influenza A	0.02	0.02	0.02	0.02	0.01	0.01
Small cell lung cancer	0.02	0.02	0.02	0.02	0.01	0.01
Amoebiasis	0.02	0.02	0.02	0.02	0.01	0.01
Toroplasmosis	0.02	0.02	0.02	0.02	0.01	0.01

Fig. 8. General predicted functional categories of bacterial populations obtained from different cemeteries based on KEGG (Level 1).


Indonesia ??



Universitas Muhammadiyah Surakarta



Bonoloyo Cemetery



Pracimaloyo Cemetery

Rahayu et al., 2023 (unpublished)

Tax_detail

- p_Firmicutes_c_Bacilli_g_Bacillus;
- p_Actinobacteriota_c_Actinobacteria_g_Mammocella;
- p_Actinobacteriota_c_Actinobacteria_g_Nocardioidea;
- p_Proteobacteria_c_Alphaproteobacteria_g_Wolbachia;
- p_Proteobacteria_c_Gammaproteobacteria_g_Buchnera;
- p_Proteobacteria_c_Gammaproteobacteria_g_Pseudomonas;
- k_Archaea_g_Crenarchaeota_c_Nitrososphaeria_g_Nitrososphaeraceae;
- p_Proteobacteria_c_Gammaproteobacteria_g_Escherichia-Shigella;
- p_Actinobacteriota_c_Actinobacteria_g_Pseudarthrobacter;
- p_Actinobacteriota_c_Thermolobos_g_Gaella;
- p_Firmicutes_c_Bacilli_g_Pasteurellales;
- p_Actinobacteriota_c_Actinobacteria_g_Agronomyces;
- p_Firmicutes_c_Bacilli_g_Lactobacillus;
- p_Proteobacteria_c_Alphaproteobacteria_g_Asticcacidia;
- p_Firmicutes_c_Clostridia_g_Romboutsia;
- p_Proteobacteria_c_Gammaproteobacteria_g_Achromobacter;
- p_Proteobacteria_c_Alphaproteobacteria_g_Spiroplasma;
- p_Proteobacteria_c_Alphaproteobacteria_g_Microvaga;
- p_Firmicutes_c_Desulfotomaculum_g_Desulfurispora;
- p_Actinobacteriota_c_Thermolobos_g_Solirubrobacter;
- p_Firmicutes_c_Clostridia_g_Sedimentibacter;
- k_Archaea_g_Crenarchaeota_c_Candidatus_Nitrososphaera;
- p_Nitrososphaeria_c_Nitrososphaera_g_Nitrososphaera;
- p_Firmicutes_c_Bacilli_g_Ammosphaera;
- p_Proteobacteria_c_Alphaproteobacteria_g_Allochrysiaceae-Nectriaceae-Parachrysiaceae-Phialidaceae;
- p_Actinobacteriota_c_Vicinibacteriota_g_Vicinibacteriaceae;
- p_Actinobacteriota_c_Actinobacteria_g_Microthamnia;
- p_Actinobacteriota_c_Actinobacteria_g_Streptomyces;

P12A	P12B	B18A	B18B	B23A	B23B
4631	4911	9577	14392	11338	6670
148	308	132	13206	150	280
250	1162	344	12789	452	980
0	504	7371	0	597	813
0	2528	6658	0	1	6
3	503	1442	4769	1201	1830
1157	556	81	1045	4709	1346
20	184	2605	8	115	217
72	2233	242	1243	771	2454
1383	1734	2136	2366	1635	1616
263	163	2332	689	405	417
40	407	179	2040	199	297
0	1243	1963	393	1466	1711
1	11	1900	0	4	17
23	1018	1647	47	1150	1387
0	0	1615	1	30	3
325	795	578	1174	587	1608
311	1061	354	379	784	1582
2	0	0	1535	0	0
2	42	1530	0	81	85
16	107	572	10	750	1452
84	113	402	1388	141	102
65	395	138	1339	132	403
585	251	153	59	1327	423
108	1204	398	982	414	733
0	1160	1	5	0	2
454	255	7	128	1143	532
1134	539	254	269	726	896
255	104	297	1059	210	170
29	327	258	8	837	1005
952	693	232	946	998	733
94	548	118	0	568	889
841	327	142	863	689	740

+


www.ums.ac.id

Humanizing * Liberating * Transcending

13

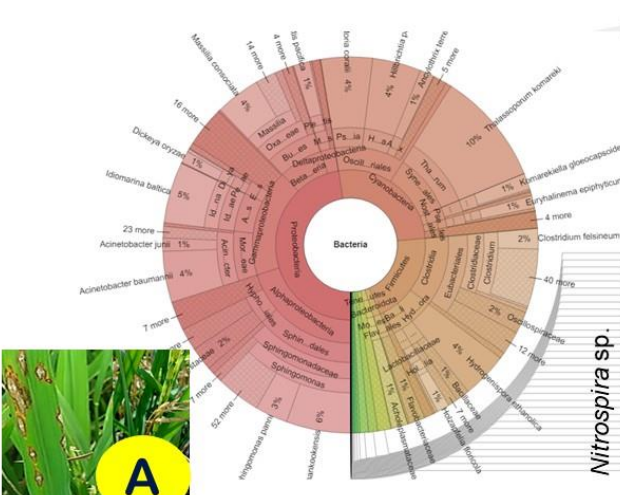
Researchs using the metagenomic approach

3

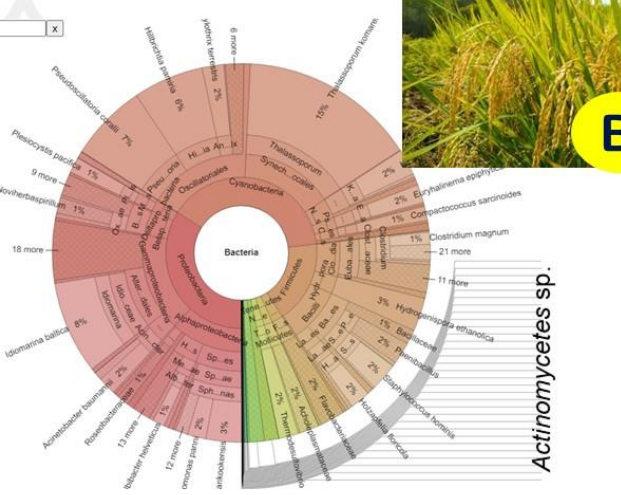


Universitas Muhammadiyah Surakarta



Metagenomic study in paddy (Blast disease – A vs Healthy - B)



Nitrospira sp.



Actinomycetes sp.

+

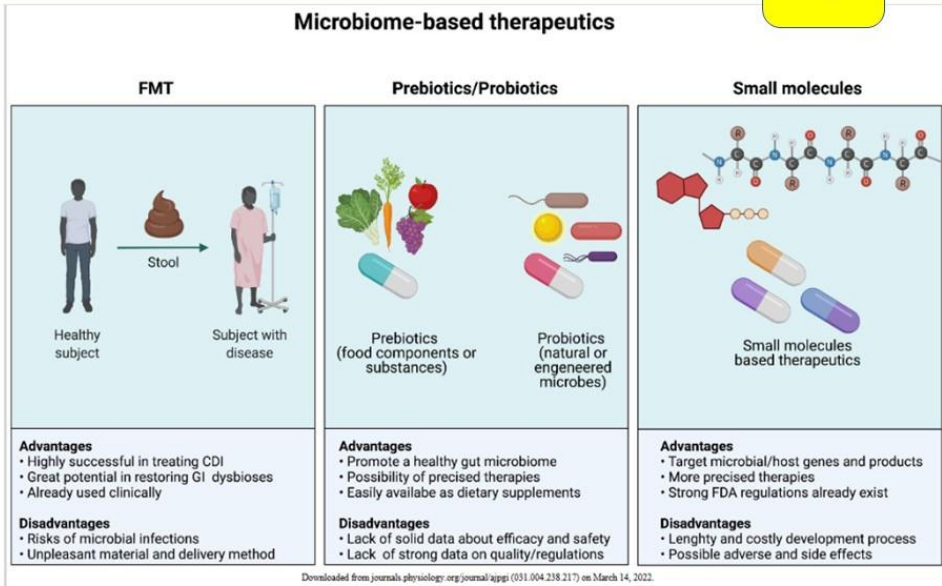
www.ums.ac.id

Humanizing * Liberating * Transcending

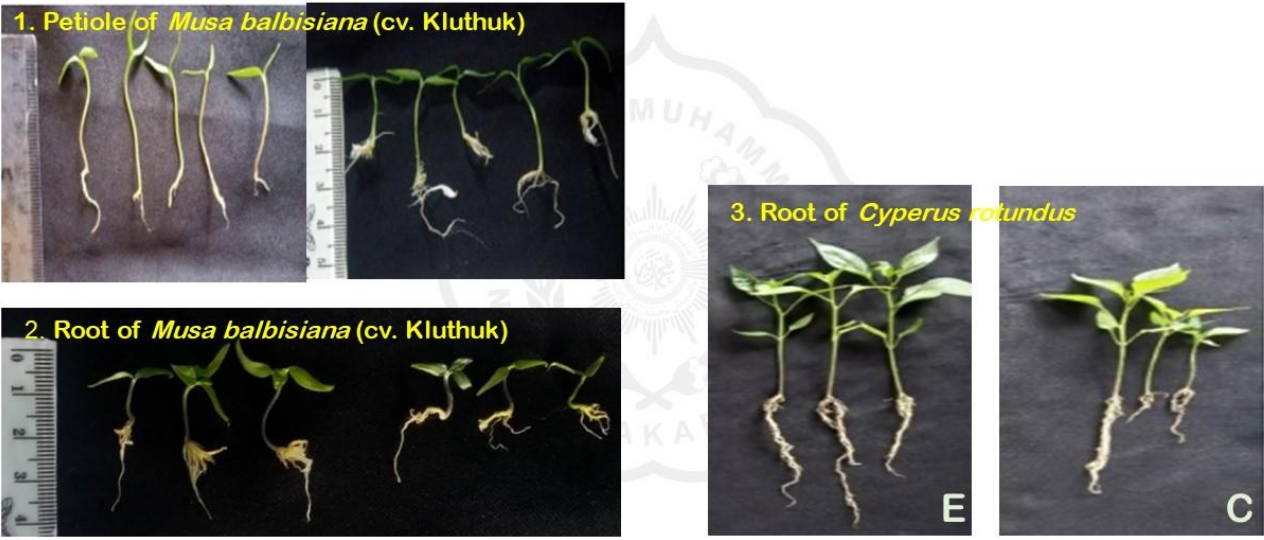
Sidiq et al., 2023, unpublished)

29

Researchs using the metagenomic approach 4 



Application → PLANT EXTRACT

Procedure






Capsicum annum

www.ums.ac.id
Humanizing * Liberating * Transcending

Summary



- Metagenomic studies are essential to know the communities of microorganisms in nature that are related to their respective functions because the microorganisms that can be grown in artificial media are only about 1%.
- Metagenomic approaches can be applied to several fields such as agriculture, environment, and health.

www.ums.ac.id
Humanizing * Liberating * Transcending
18

References



1. Abia ALK, Alisoltani A, Ubomba-Jaswa E, Dippenaar MA. Microbial life beyond the grave: 16S rRNA gene-based metagenomic analysis of bacteria diversity and their functional profiles in cemetery environments. *Sci Total Environ*. 2019 Mar 10;655:831-841. doi: 10.1016/j.scitotenv.2018.11.302. Epub 2018 Nov 22. PMID: 30481710.
2. Escobar A., de Leon A V., Sanchez-Flores A. 2016. The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. *Frontiers in Genetics* 6(104):348. DOI: [10.3389/fgene.2015.00348](https://doi.org/10.3389/fgene.2015.00348).
3. Lopes M., Dia-Filho M B, & Gurge E S C. 2021. Successful Plant Growth-Promoting Microbes: Inoculation Methods and Abiotic Factors. *Front. Sustain. Food Syst.*, 25 February 2021. Sec. Crop Biology and Sustainability. Volume 5 - 2021 | <https://doi.org/10.3389/fsufs.2021.606454>
4. Mueller UG, Sachs JL. Engineering Microbiomes to Improve Plant and Animal Health. *Trends Microbiol*. 2015 Oct;23(10):606-617. doi: 10.1016/j.tim.2015.07.009. Epub 2015 Sep 25. PMID: 26422463.
5. Prayogo, F.A., Budiharjo, A., Kusumaningrum, H.P. *et al*. Metagenomic applications in exploration and development of novel enzymes from nature: a review. *J Genet Eng Biotechnol* 18, 39 (2020). <https://doi.org/10.1186/s43141-020-00043-9>
6. Rahayu T, Purwestri Y A, Subandiyah, Suparmin A, & Widiyanto D. 2021. Exploration of core endophytic bacteria from different organs of diploid *Musa balbisiana* and triploid *Musa acuminata*. *Agr. Nat. Resour*. 55 (2021) 787–797. <https://doi.org/10.34044/j.anres.2021.55.5.09>.