

Article

Effects of Microplastic on Human Gut Microbiome: Detection of Plastic-Degrading Genes in Human Gut Exposed to Microplastics—Preliminary Study

Husna Nugrahapraja ^{1,2}, Pramudya Wisnu Wicaksono Sugiyo ³, Balqis Qonita Putri ³, Ni'matuzahroh ^{3,4}, Fatimah ^{3,4}, Li Huang ⁵, Nourhane Hafza ⁶, Friedrich Götz ⁶, Heri Santoso ⁷, Anjar Tri Wibowo ^{3,*} and Arif Luqman ^{8,*}

¹ University Center of Excellence for Nutraceuticals, Bioscience and Biotechnology Research Center, Institut Teknologi Bandung, Bandung 40132, Indonesia

² School of Life Sciences and Technology, Institut Teknologi Bandung, Bandung 40132, Indonesia

³ Department of Biology, Faculty of Science and Technology, Airlangga University, Surabaya 60115, Indonesia

⁴ University CoE Research Center for Bio-Molecule Engineering, Universitas Airlangga, Surabaya 60115, Indonesia

⁵ Department of Preventive Veterinary Medicine, College of Animal and Veterinary Science, Southwest Minzu University, Chengdu 610093, China

⁶ Microbial Genetics Department, Eberhard Karls University of Tuebingen, 72076 Tuebingen, Germany

⁷ Generasi Biologi Indonesia (Genbinesia) Foundation, Gresik 61171, Indonesia

⁸ Biology Department, Institut Teknologi Sepuluh Nopember, Surabaya 60111, Indonesia

* Correspondence: anjar.tri@fst.unair.ac.id (A.T.W.); arif.luqman@its.ac.id (A.L.)

Table S1. Accession numbers of the reference genes for read count analyses.

| No. | Gene | Product | Accession number |
|--|--------------|--|---------------------|
| 1 | <i>rpoB</i> | RNA Polymerase subunit beta | NZ_QRKQ01000009.1 |
| Gut health-related genes | | | |
| 2 | <i>scpC</i> | Propionate production from succinate | NC_000913.3 |
| 3 | <i>bglX</i> | beta-glucosidase | NZ_QRKQ01000013.1 |
| 4 | <i>but</i> | butyryl-CoA:acetate CoA-transferase (butyrate production) | NZ_VWSY01000001.1 |
| 5 | <i>Ato</i> | butyryl-CoA:acetoacetate CoA-transferase subunit alpha | NC_014633.1 |
| 6 | <i>buk</i> | butyrate kinase (butyrate production) | NZ_VVYQ01000024.1 |
| 7 | <i>adhE</i> | bifunctional acetaldehyde-CoA/alcohol dehydrogenase (acetate production) | NZ_CP011663.1 |
| 8 | <i>ilvE</i> | branched-chain-amino-acid aminotransferase | NC_000913.3 |
| 9 | <i>cutD</i> | choline TMA-lyase-activating enzyme | NZ_KE136504.1 |
| 10 | <i>torT</i> | TMAO reductase system periplasmic protein TorT | NZ_JABTBL01000001.1 |
| 11 | | tryptophanase | NC_008593.1 |
| Plastic degrading enzyme-encoding genes | | | |
| 12 | <i>pbsA</i> | poly(tetramethylene succinate) depolymerase (Polybutylene succinate and poly((tetramethylsuccinate)-co-adipate) degradation) | AB066349.1 |
| 13 | <i>cutA</i> | Cutinase A precursor (polyester degradation) | KU695574.1 |
| 14 | <i>alkA</i> | aromatic/alkene/methane monooxygenase hydroxylase/oxygenase subunit alpha (LMWPE degradation) | NZ_CP022562.1 |
| 15 | <i>alkB</i> | aromatic/alkene monooxygenase hydroxylase subunit beta (LMWPE degradation) | NZ_CP022562.1 |
| 16 | <i>cut1</i> | Cutinase | HQ147785.1 |
| 17 | | Lipase/esterase | NC_007333.1 |
| 18 | <i>MNP_1</i> | Manganese peroxidase | LHYA1_G003107 |

| | | | |
|----|-------------|---|-------------------------------|
| 19 | <i>StyC</i> | styrene oxide isomerase | MBR_07180 |
| 20 | <i>feaB</i> | phenylacetaldehyde dehydrogenase | b1385, ECK1382 |
| 21 | | Polyurethenase | HLB40_RS16045, HLB40_16045 |
| 22 | <i>nylA</i> | 6-aminohexanoate-cyclic-dimer hydrolase (Nylon oligomers-degrading enzyme EI) | SALIVA_1117 |
| 23 | <i>phaZ</i> | poly(3-hydroxyalkanoate) depolymerase | HLB40_RS02110, HLB40_02110 |
| 24 | | PHB depolymerase family esterase | AUP70_RS01860 |

Table S2. Microplastic contamination level in human stool samples of coastal and highland populations in Indonesia. Data obtained from previous studies [21, 22].

| Code | Microplastic contamination level (µg/g feces) | | | | | |
|------|---|-------------|-------------|--------------|--------------|-------------|
| | HDPE | LDPE | PE | PP | PS | PET |
| C1 | 13,99 ± 3,95 | nd | nd | nd | nd | nd |
| C2 | nd | nd | nd | nd | nd | nd |
| C3 | nd | nd | nd | nd | nd | nd |
| C4 | 7,19 ± 1,76 | nd | nd | 3,13 ± 0,51 | nd | nd |
| C5 | nd | nd | nd | nd | nd | nd |
| C6 | 12,27 ± 0,21 | nd | 7,00 ± 1,25 | nd | nd | nd |
| C7 | 3,33 ± 1,37 | nd | nd | nd | nd | nd |
| C8 | nd | nd | nd | nd | nd | nd |
| C9 | nd | nd | nd | nd | nd | nd |
| C0 | nd | nd | nd | nd | 11,59 ± 2,56 | 2,44 ± 0,3 |
| C11 | nd | 3,48 ± 1,25 | nd | nd | 8,18 ± 2,41 | nd |
| H1 | nd | nd | nd | nd | nd | 6,94 ± 2,56 |
| H2 | nd | nd | nd | 3,95 ± 2,05 | 4,82 ± 1,41 | nd |
| H3 | 13,77 ± 5,71 | nd | nd | nd | 2,65 ± 1,28 | nd |
| H4 | 0,52 ± 0,17 | nd | nd | 7,86 ± 1,28 | nd | nd |
| H5 | nd | nd | nd | nd | nd | nd |
| H6 | nd | nd | nd | nd | nd | nd |
| H7 | nd | nd | nd | 12,40 ± 3,44 | nd | nd |
| H8 | nd | nd | nd | 16,55 ± 5,96 | nd | nd |
| H9 | nd | nd | nd | nd | nd | nd |
| H10 | nd | nd | nd | nd | nd | nd |
| H11 | 15,62 ± 2,78 | nd | nd | nd | nd | nd |

*nd: not detected.

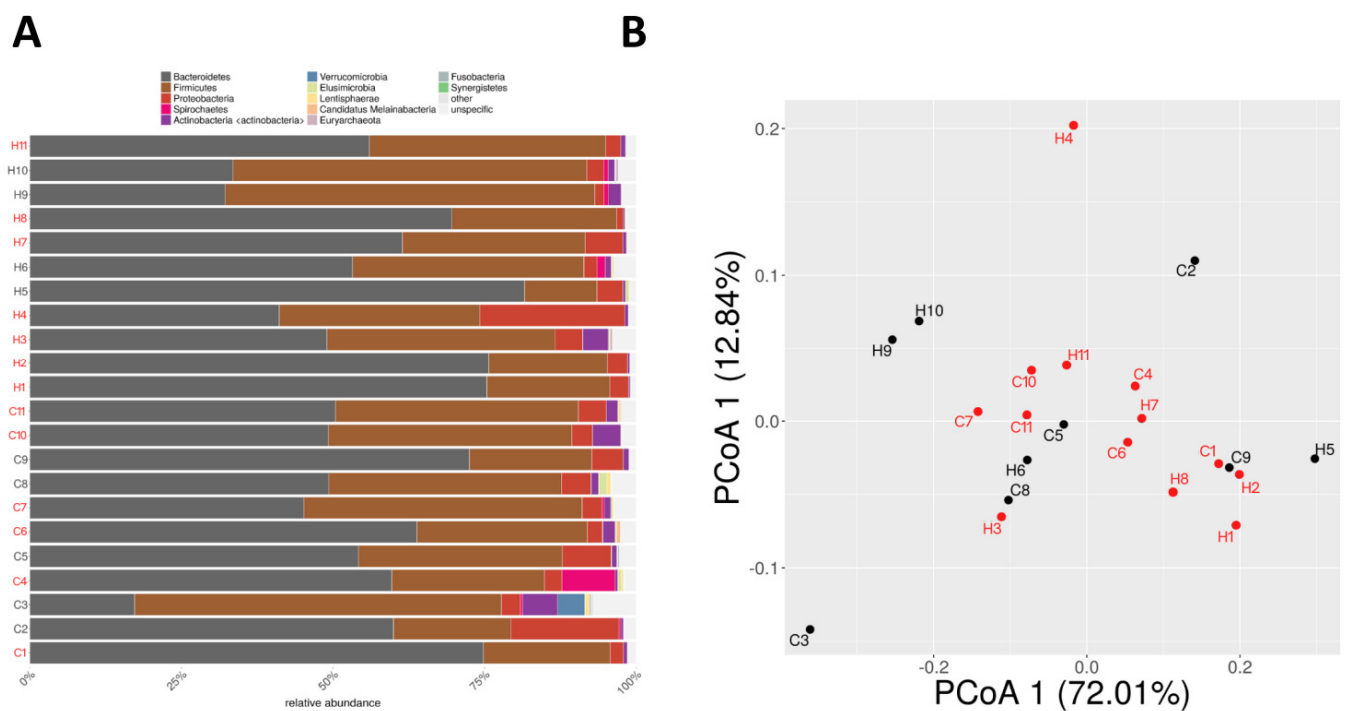


Figure S1. Gut microbiome profiles at the family level of Indonesian coastal and highland population that exposed to microplastics contamination.

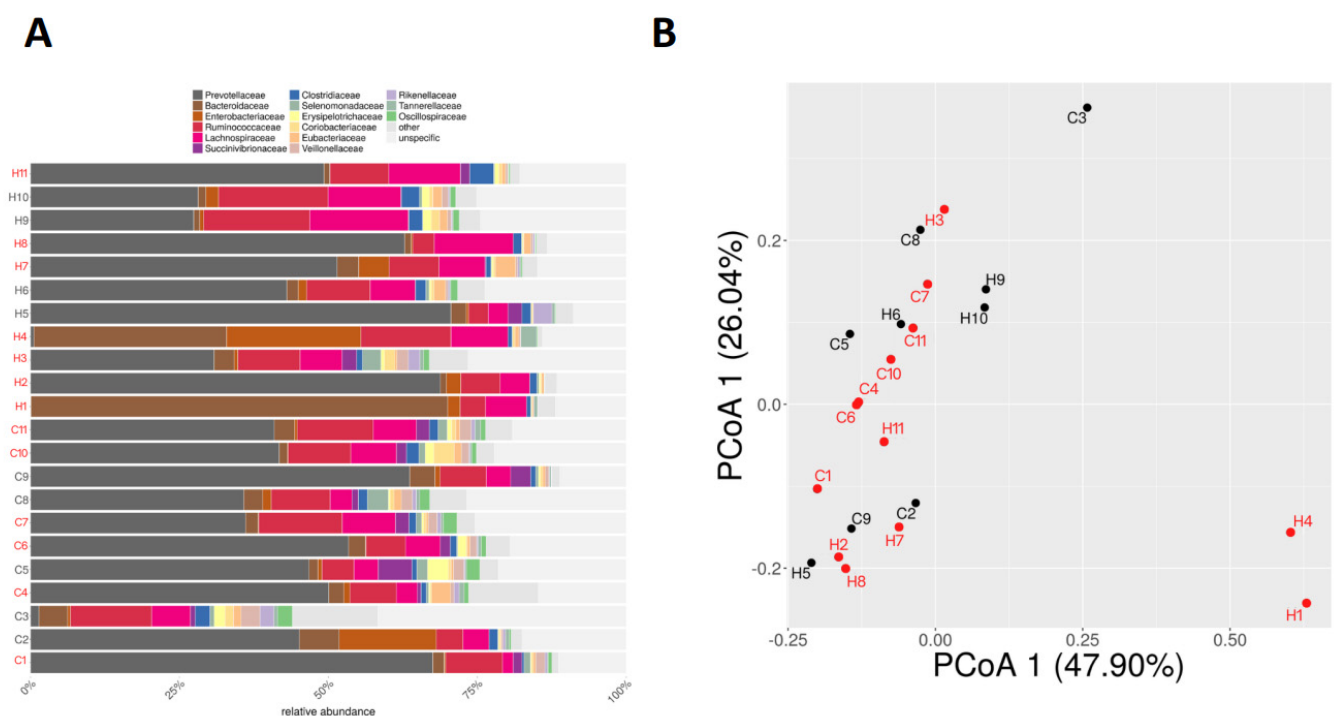


Figure S2. Gut microbiome profiles at the phylum level of Indonesian coastal and highland population that exposed to microplastics contamination.