Microbial Community Analysis of Indonesia Tempeh Employing Metagenome Galaxy Pipeline

Adi Yulandi[1], Yeremia Jonathan[1], Cecilia Seumahu[2], Antonius Suwanto[1,3]

[1] Faculty of Biotechnology, Atma Jaya Catholic University of Indonesia
[2] Department of Biology, University of Pattimura
[3] Department of Biology, Faculty of Mathematics and Natural Sciences, Bogor Agricultural University

ABSTRACT

Tempeh is a traditional fermented food from Indonesia. It is usually produced by household industry that is spread out all over Indonesia. It is estimated that there are more than 100.000 tempeh producers with many variation in flavor or texture. *Rhizophus oligosporus* or microsporus is commonly used as starter for the tempeh production. However, due to open fermentation technique, naturally-occurring bacteria could grow and contribute in sensory quality of tempeh. Microbial community analysis would be an important tool to study microbial community and dynamic during tempeh production. Next Generating sequencing technologies might contribute significantly to study culture-independent microbial community analysis. Total bacterial genomics DNA was isolated from two tempeh samples from different producers (SDJD and EMP). The V6 hyper-variable region of the 16S rRNA were amplified and sequenced each on a 314 chip Ion Torrent Personal Genome Machine (PGM). Sequencing read were analyzed employing metagenome pipeline in local facility Galaxy server and revealed the different bacterial community that might be responsible in flavor or texture formation from those two tempeh samples.

Keywords: Metagenome, Tempeh, Galaxy, Ion Torrent PGM

PROBLEM

Research to identify diversity of microorganisms besides *Rhizopus* genus in tempeh fermentation process would show the contribution of certain organism(s) in characterizing produced tempeh. Focusing on the contribution of each organism would not help in revealing effects of microorganism diversity in tempeh production. The reason was because in the fermentation process, microorganisms work in consortium (Seumahu 2012). Metagenomic techniques provide the possibility to view microorganism diversity in an ecosystem as these techniques could be used to analyze consortiums of microorganisms without cultivating it first (Teeling & Glockner 2012).

Ion Torrent PGM as a product of Life Technologies offered NGS with affordable price. The success of metagenomics research of bacterial community based on 16S rRNA amplification using Ion Torrent PGM technology had been reported (Jünemann *et al.* 2012; Whiteley *et al.* 2012). Galaxy Project (galaxyproject.org) gave ease of bioinformatics analysis either online through their public server or offline using private facility. Application in the Galaxy Project can be used to analyze metagenomic data (Pond *et al.* 2009).
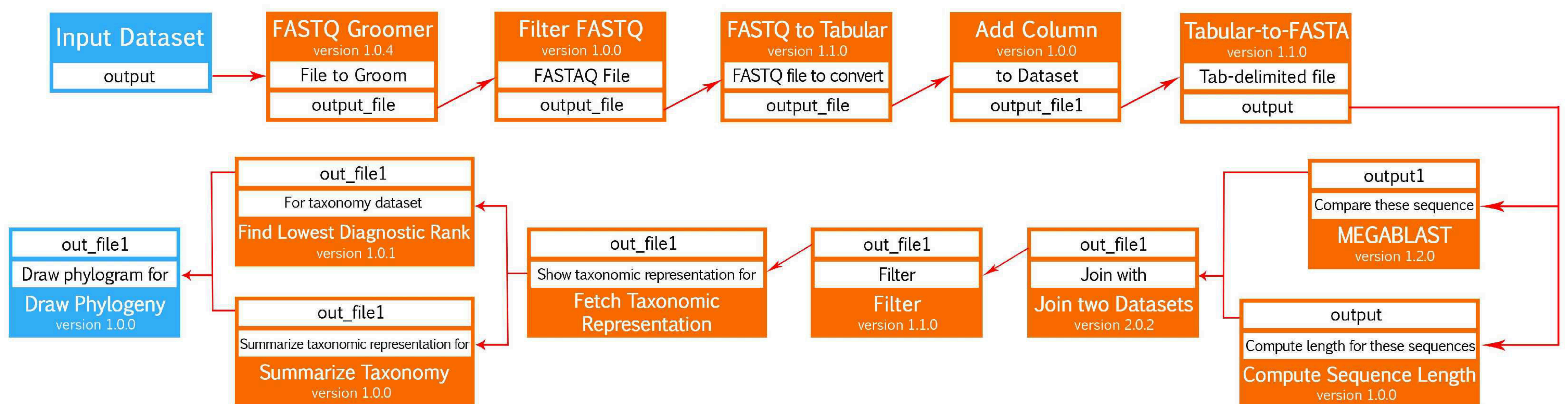
METHOD

Figure 1   Galaxy Metagenome Analysis Workflow for Ion Torrent based on Pond *et al.* (2009)
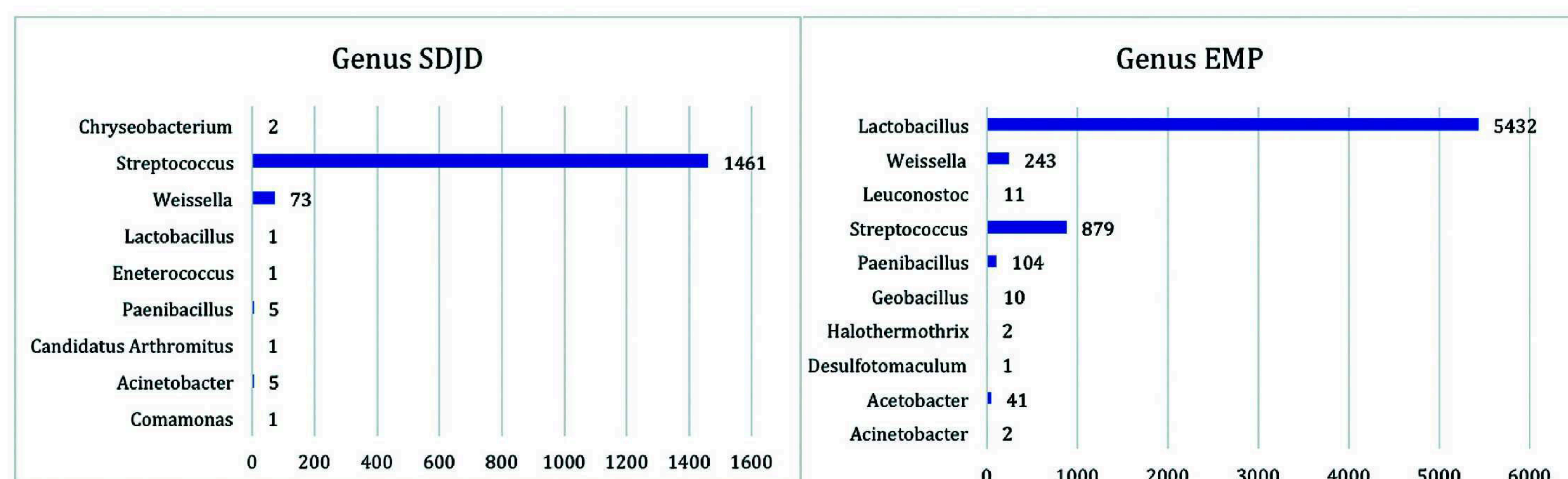
RESULT

Figure 2   A genus level phylogenetic profile of two samples Indonesian tempeh

CONCLUSION

Microbial community analysis from two tempeh samples from different producers in Indonesia using Ion Torrent PGM and modified metagenome analysis workflow revealed the different bacterial community that might be responsible in flavor or texture formation.

REFERENCE

(1) Jünemann S, Prior K, Szczepanowski R, Harks I, Ehmke B, Goesmann A, Stoye J, Harmsen D. 2012. Bacterial community shift in treated peridodontitis patients revealed by ion torrent 16S rRNA gene amplicon sequencing. *PLOS ONE* 7(8):1-8; DOI:e41606.
(2) Pond SK, Wadhawan S, Chiaromonte F, Ananda G, Chung WY, Taylor J, Nekrutenko, The Galaxy Team. 2009. Windshield splatter analysis with the Galaxy metagenomic pipeline. *Genome Research,* 19(11), 2144–2153. DOI:10.1101/gr.094508.109.
(3) Seumahu CA, Suwanto A, Rusmana I, Solihin DD. 2012. Comparison of DNA extraction methods for microbial community analysis in Indonesia tempe employing amplified ribosomal intergenic spacer analysis. HAYATI *J Biosci* 19(2):93-98; DOI:10.4308/hjb.19.2.93.
(4) Teeling H, Glöckner FO. 2012. Current opportunities and challenges in microbial metagenome analysis – a bioinformatic perspective. Brief Bioinfo 13(6):728-742; DOI:10.1093/bib/bbs039.
(5) Whiteley AS, Jenkins S, Waite I, Kresoje N, Payne H, Mullan B, Allcock R, O'Donnel A. 2012. Microbial 16S rRNA ion tag and community metagenome sequencing using the ion torrent (PGM) platform. J *Microbiol Methods* 91:80-88; DOI:10.1016/j.mimet.2012.07.008.

Galaxy Australasia Workshop 2014