

# Variation in Soil Bacterial Communities Composition in Different Recreational Parks at Hulu Langat Selangor



KEMENTERIAN KESIHATAN MALAYSIA

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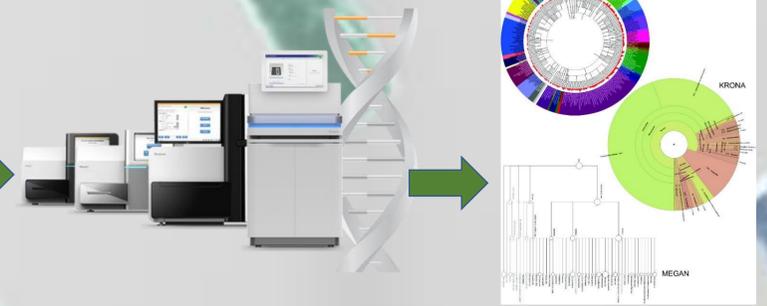
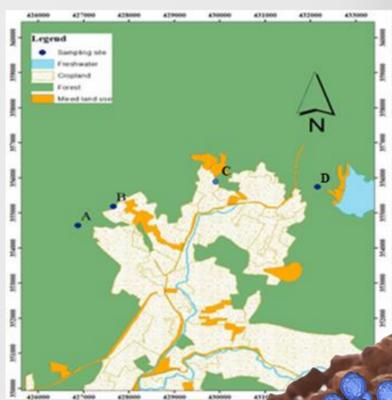


## Introduction

- Soils are natural boundaries between human and various type of organism (Dragon et al. 2021).
- Soil contaminants, including microbes has been reported as a medical importance due to their abilities to cause several diseases (Joshua et al. 2020).
- This study is to identify any microbial community structure in recreational areas in Hulu Langat Selangor. The result will provide a useful information on soil microbial structure which is related with the coinfection with other diseases.

## Method

- Twelve soil samples were collected from four recreational areas (Hulu Perdik\_HP, Sungai Lopo\_SL, Sungai Congkak\_SC and Gunung Nuang\_GN) in Hulu Langat, Selangor.
- The DNA was extracted using NucleoSpin®Soil Kit.
- Microbial DNA were sent to the Illumina for Miseq Illumina Sequencing
- Sample were analyzed using standard protocol for Miseq data, using Qiime package



## Soil Sampling

## Result

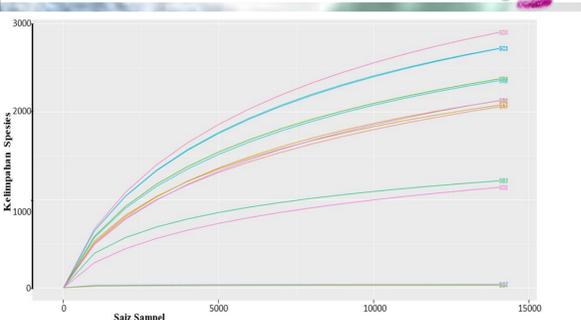


Figure 2. Rarefaction curves showed species richness of the microbial communities in all sampling sites

- The sample collection in all four location were well enough/represented due to the samples attended plateau phase or curvilinear (Zhu et al. 2021) (Figure 2).
- The whole microbial community structure at four study areas is presented through Krona graph plotted by Krona tools (Figure 4).



Figure 3. The abundance of the top ten (a) phyla and (b)

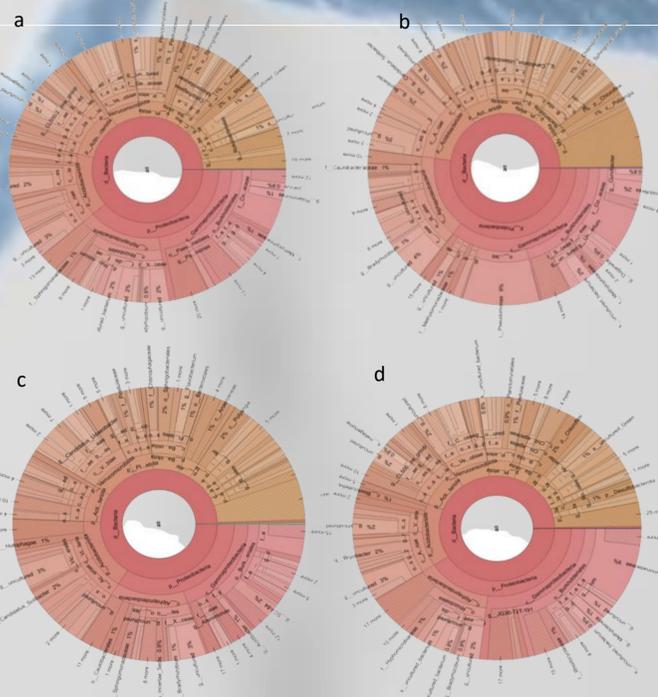


Figure 4. Krona chart showing relative abundance of community bacteria in(a) HP, (b) SL, (c) SC and (d) GN

## Conclusion

- The most common phyla in recreational areas in Hulu Langat, Selangor were identified in Figure 3a. It was observed that the highest abundance phyla in study areas was *Proteobacteria* (41.84%) and *Acidobacteroida* (17.01%).
- Burkholderiales*, *Rhizobiales*, and *Pedospaerales* was the most abundance at the order level (Figure 3b). Their presence in soil environment showed that analysing DNA community bacterial can be used to predict the possibilities of infection and to develop a better treatment solutions.

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