

Effects of asphalt on microbial diversity in Prince Edward County

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Background

- Studies have found that pavement is linked to less microbial diversity in soil (Chang-Po Chen et al. 2014).
- It has been previously found that different environments such as pavements can change the nutritional composition of soils (Xin Yu et al. 2012).

The goal of this study was to investigate and analyze the microbial diversity in Prince Edward County, Virginia, specifically differentiating between bacteria located near asphalt and bacteria located in a natural environment.

Specific Aim

- **Question:** How does the proximity to asphalt change the diversity of the microbial colonies in Longwood's Lancer Park, located in Prince Edward County?
- **Hypothesis:** Soil located closer to the parking lot will have less microbial diversity in comparison to soil located near a creek.

Materials and Methods

Bacterial collection, physical analysis and data collection

Polymerase Chain Reaction (PCR) of 16s rRNA, MspI restriction digest, gel electrophoresis

Data analysis through Basic Local Alignment Search Tool (BLAST) and identification of bacteria

Conclusion

- The asphalt sample was shown to be more microbial diverse in comparison to the creek sample. Thus, the hypothesis was rejected.
- For future studies, it is suggested that the permeability of different types of pavements should be tested to see if it impacts microbial diversity and asphaltene levels in comparison to others (Marczewski and Szymula 2002).

References

- Chang-Po Chen, Lan-Feng Fan, Hwey-Lian Hsieh, Sih-Fu Wang. 2014. Microbial community structure and activity under various pervious pavements. 140.3.
- Marczewski A, Szymula M. 2002. Absorption of asphaltene from toluene on typical soils of Lublin region. Elsevier Science. 68.45.301-311.
- Xin Yu, Wang YH, Wang Yu-hong, Wu, D. 2012. Effects of asphalt on the enzymatic activity and bacterial community in soil. 6.34. 6399-6406.

Results

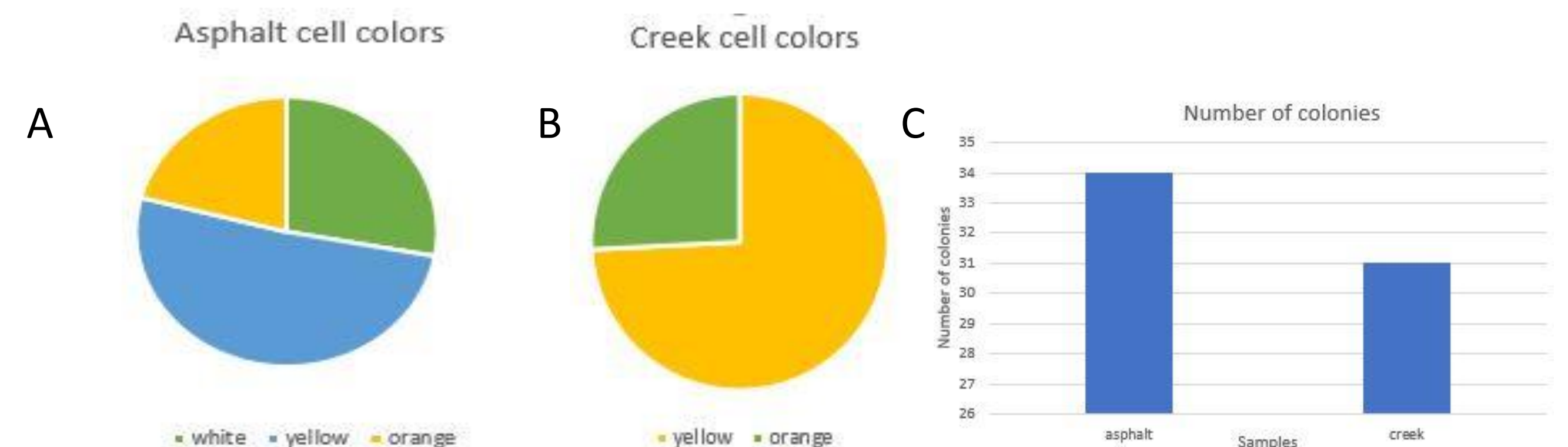


Figure 1. Abundance and diversity of samples from both sites. This figure is the comparison of abundance and diversity of the samples from plate 1:10 of both locations. As shown in Figure 1A, there was a wide variety of colors in the asphalt colonies. As shown in Figure 2A, the creek colonies were not as diverse. As shown in Figure 3A, the samples had a different abundance of colonies.

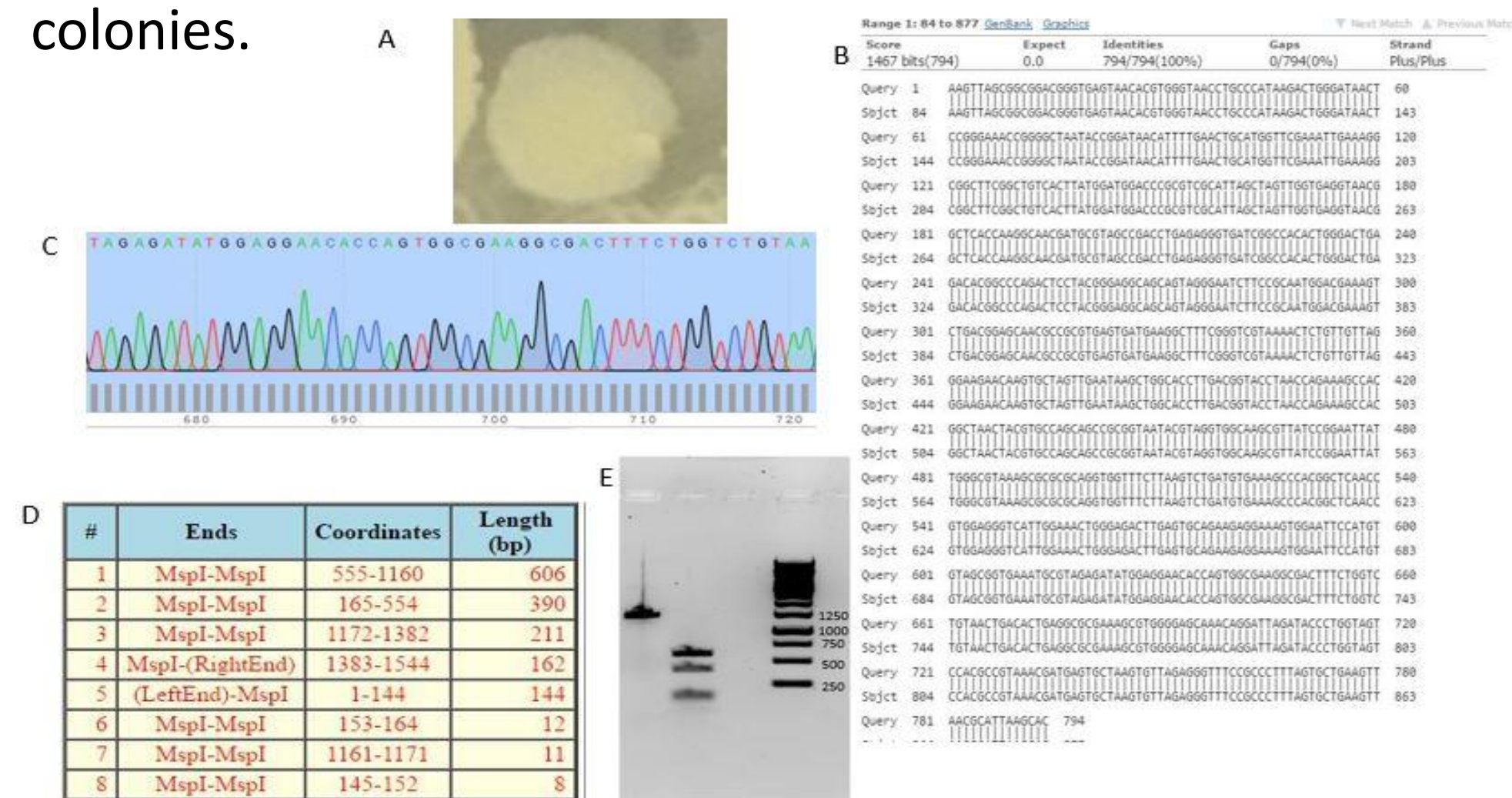


Figure 2. Identification of asphalt sample. As shown in this figure, the asphalt sample cell was identified as *Bacillus toyonensis*. As shown in Figure 2A, an individual microbial colony was selected. As shown in Figure 2B, BLAST was used to obtain a match with the sequence that resulted from the PCR product. Figure 2C was used to show the sequence for *Bacillus toyonensis*. Figure 2D was the MspI digest of the *Bacillus toyonensis*. Figure 2E reflected the results of the gel electrophoresis.

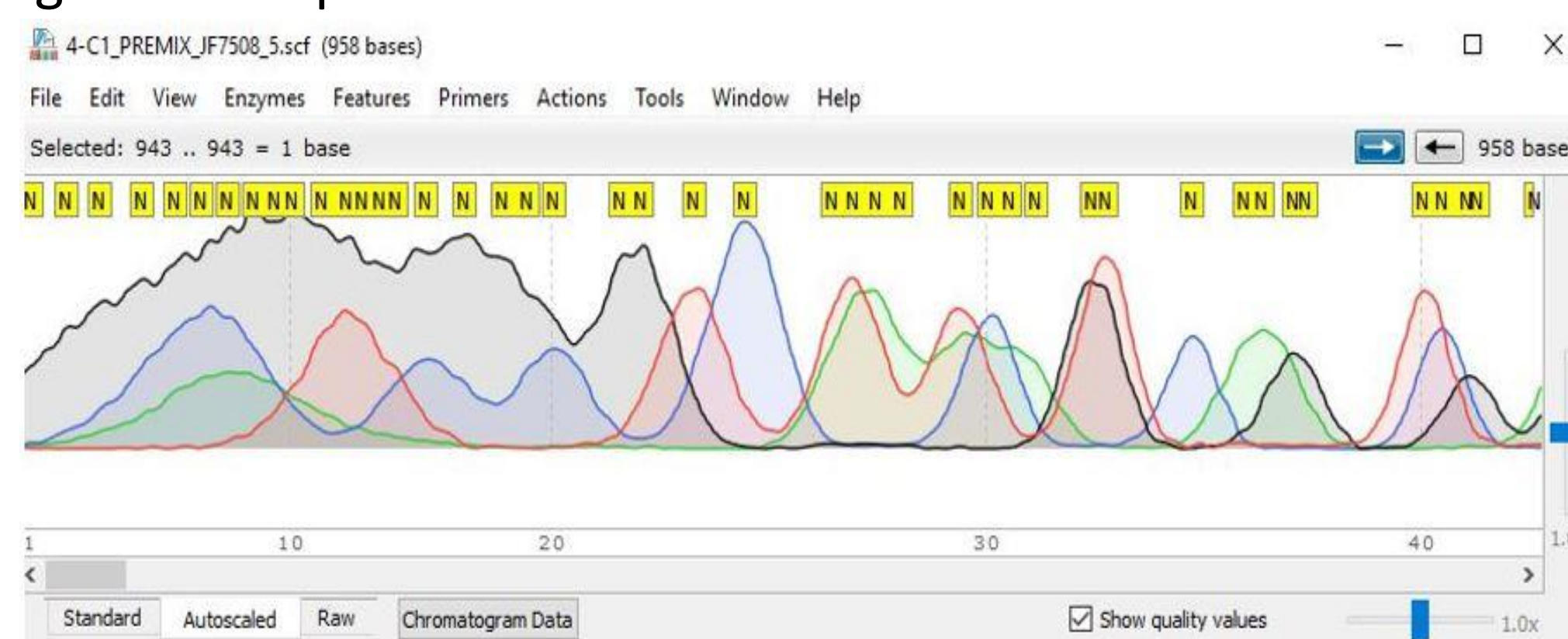


Figure 3. PCR amplification of the creek sample.

- The asphalt sample was identified as *Bacillus toyonensis*.
- The creek sample PCR was of two sets of 16s rRNA and is uninterpretable.