

Title

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Author Name

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Department Name

University Name

Date

Abstract

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Introduction

Methods

A total of 31 HQ genomes (29 SGBs and 2 reference genome) were used in this study.

The species' pangenome was obtained using Roary (citation) based on Prokka annotation files (.gff).

Results and Discussion

Genome Annotation

Pangenome Analysis

Pangenome analysis found 4670 total genes (figure 2a), among which 1017 were attributed to the *core* (above 90% prevalence in MAGs), 2074 to the *shell* (from 15% to 89% prevalence), and 1579 were classified as *cloud* (from 0% to 15% prevalence). The results were robust with respect to many rounds of computation.

The number of conserved genes appears to reach a plateau (figure 1a) when the number of MAGs increases, suggesting that this species has a closed pangenome. This is further confirmed by the trend of unique genes plotted against the number of genomes (figure 1b).

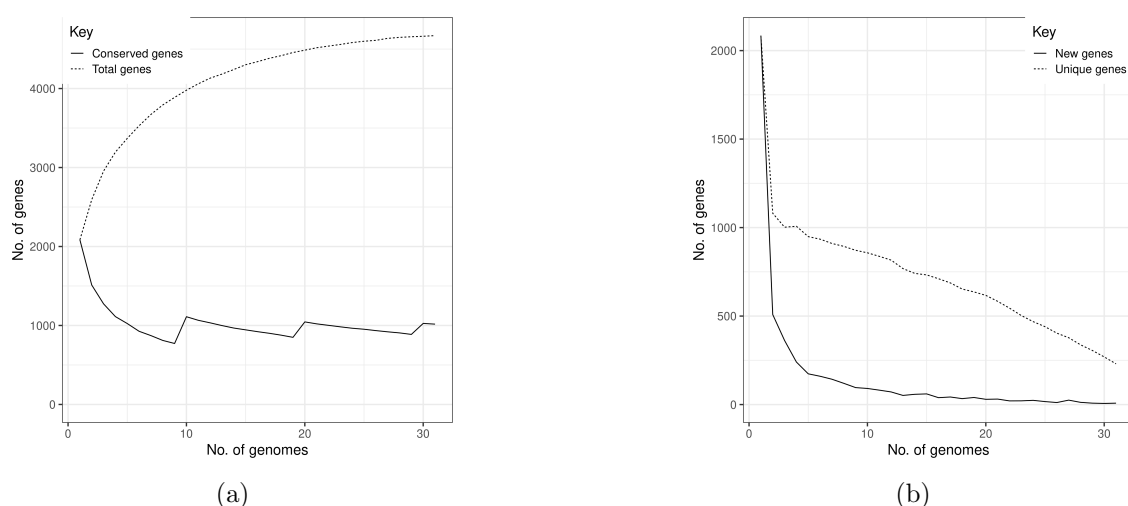


Figure 1

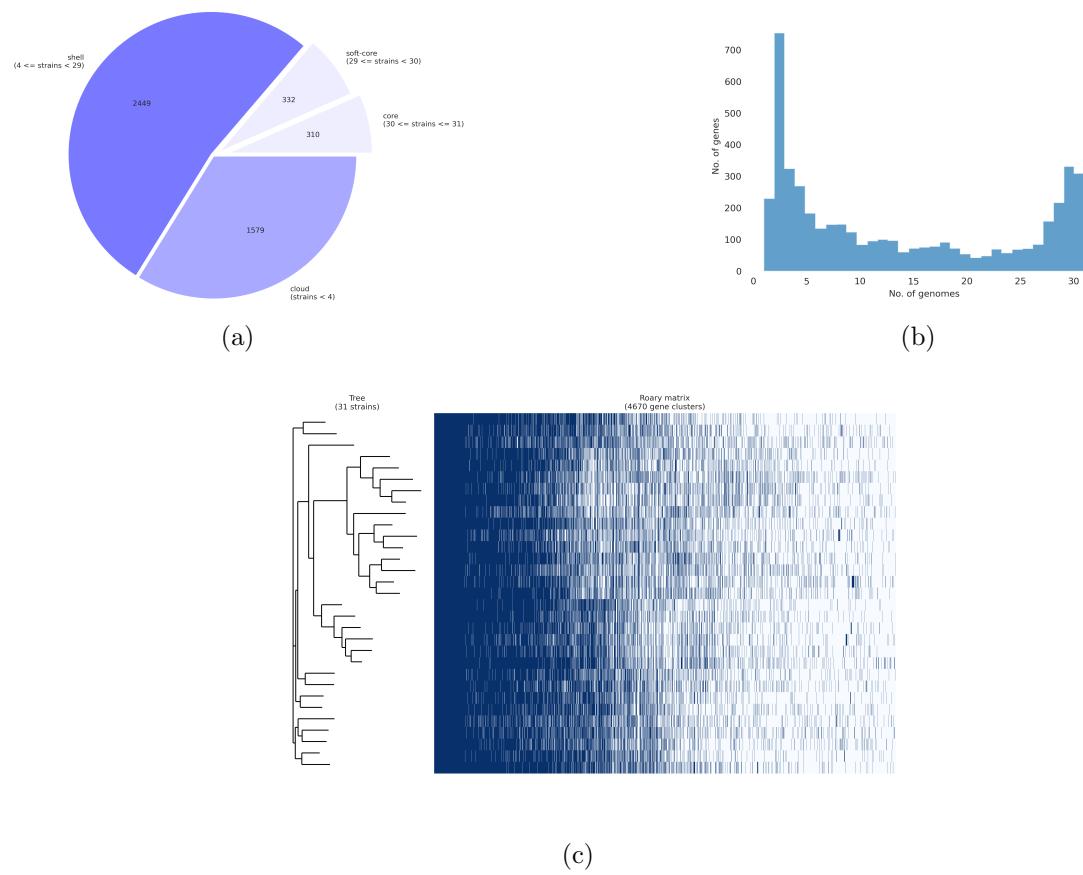


Figure 2: Three simple graphs

Phylogenetic Structure

Taxonomic Annotation

Conclusion

Supplementary data

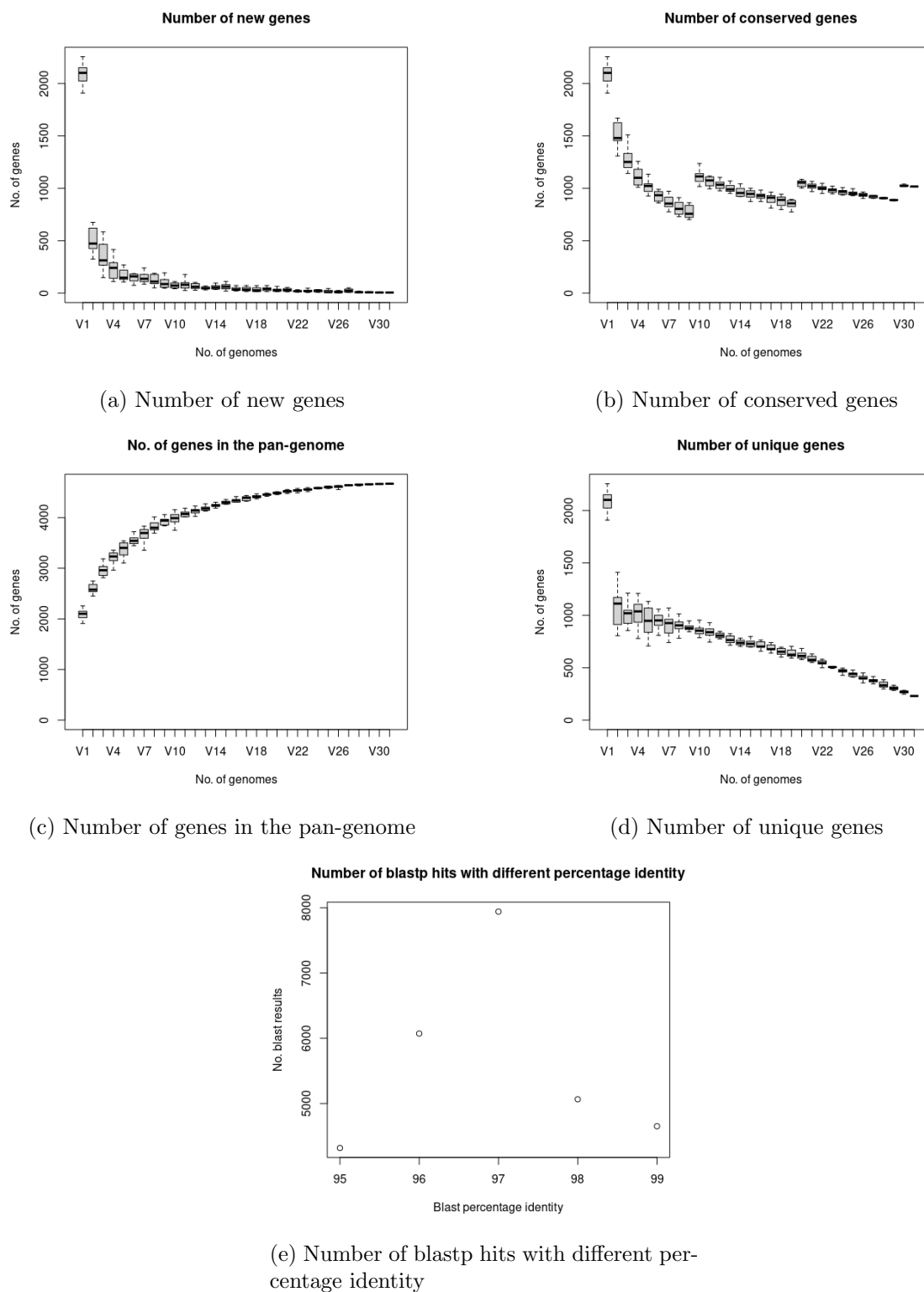


Figure 3: Three simple graphs

References

- [1] O. Tange. “GNU Parallel - The Command-Line Power Tool”. In: *The USENIX Magazine* (2011). DOI: 10.5281/zenodo.16303. URL: <http://www.gnu.org/s/parallel>.