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## 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).

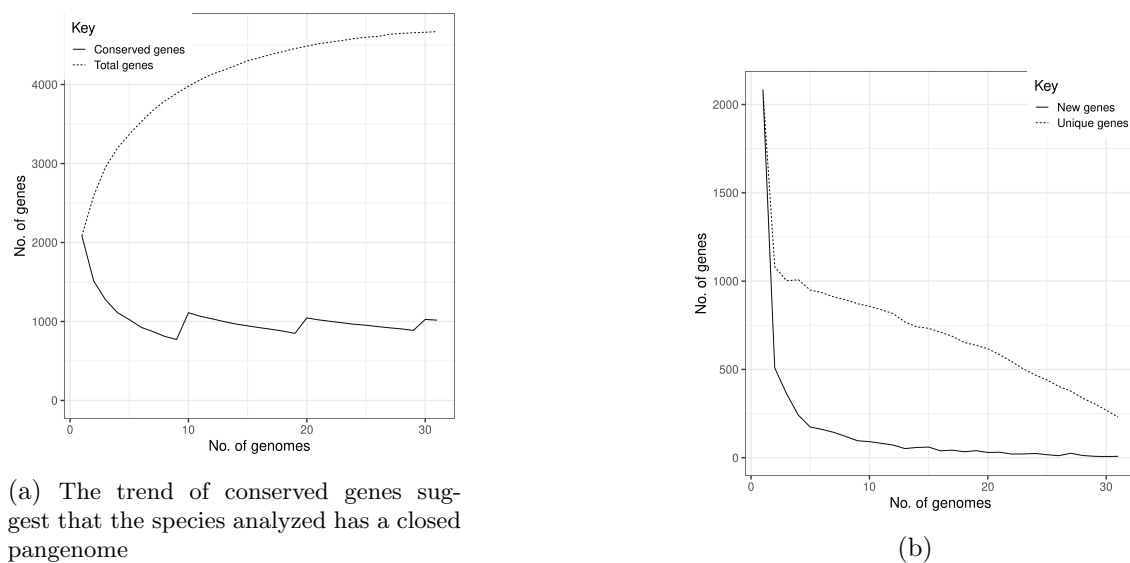


Figure 1

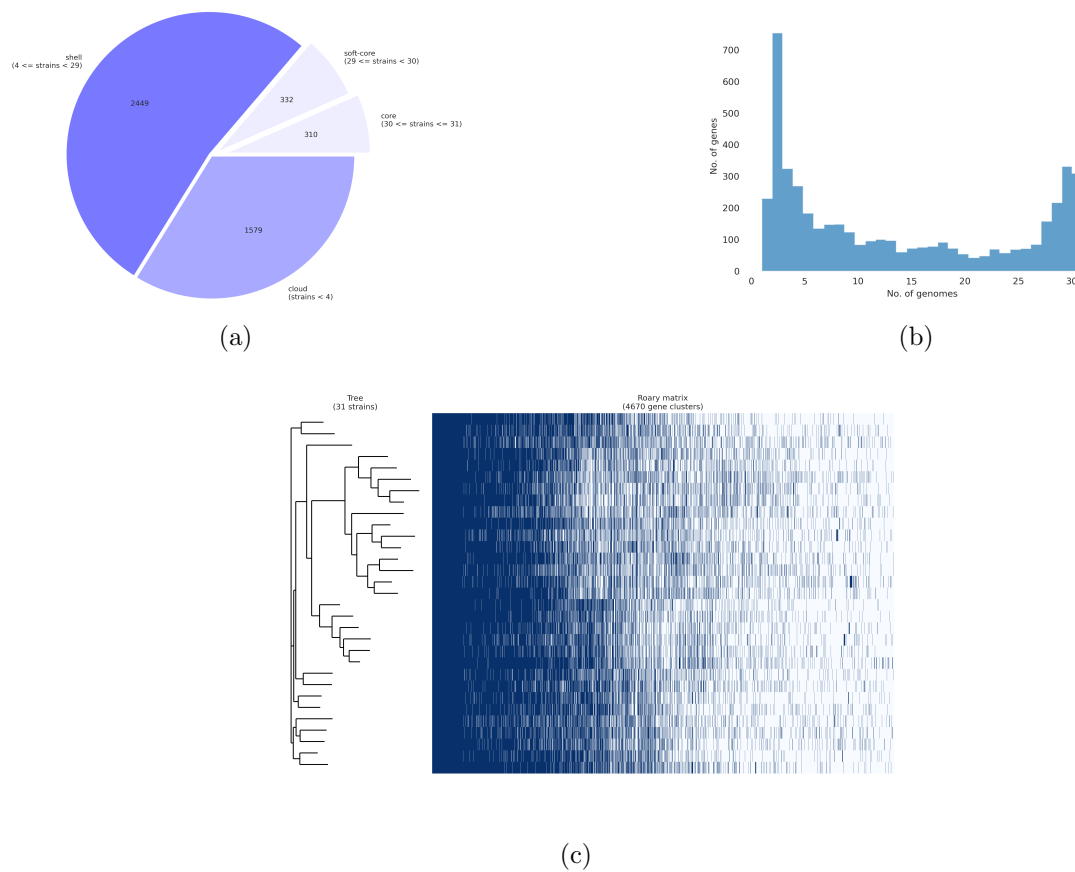


Figure 2: Three simple graphs

Phylogenetic Structure

Taxonomic Annotation

Conclusion

## Supplementary data

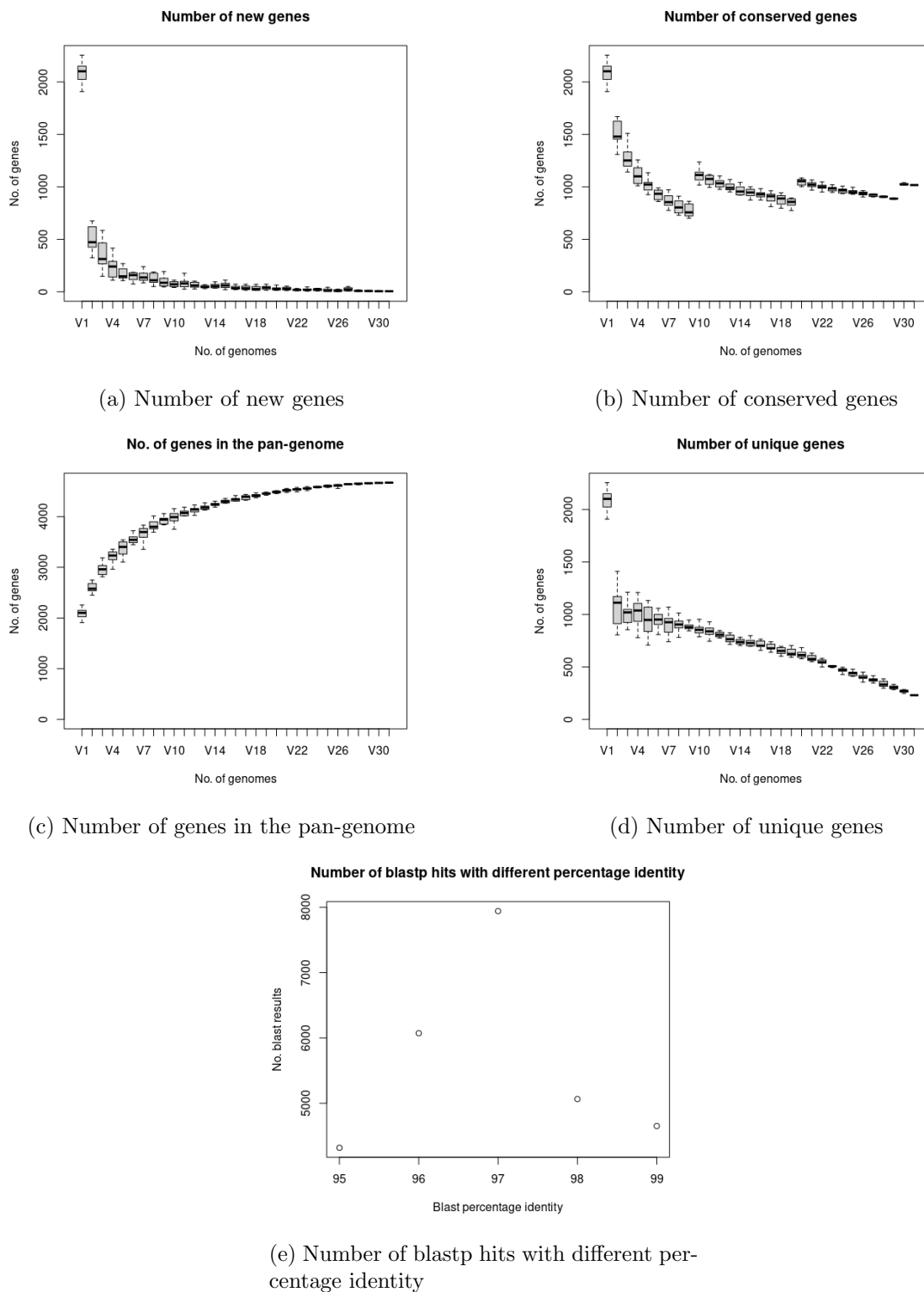


Figure 3: Three simple graphs

## 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>.