Title

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Author Name

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Department Name
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Abstract

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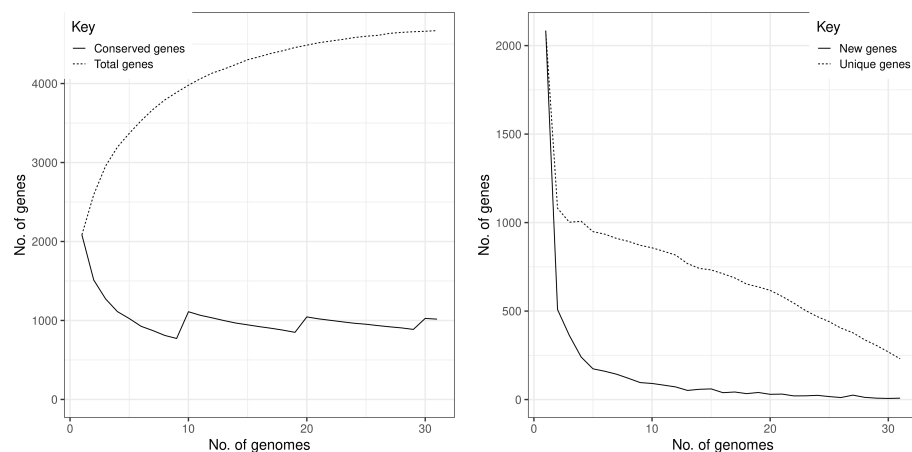
Introduction

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

Phylogenetic Structure

Taxonomic Annotation

Conclusion

Supplementary data

Number of new genes

(a) Number of new genes

Number of conserved genes

(b) Number of conserved genes

No. of genes in the pan-genome

(c) Number of genes in the pan-genome

Number of unique genes

(d) Number of unique genes

Number of blastp hits with different percentage identity
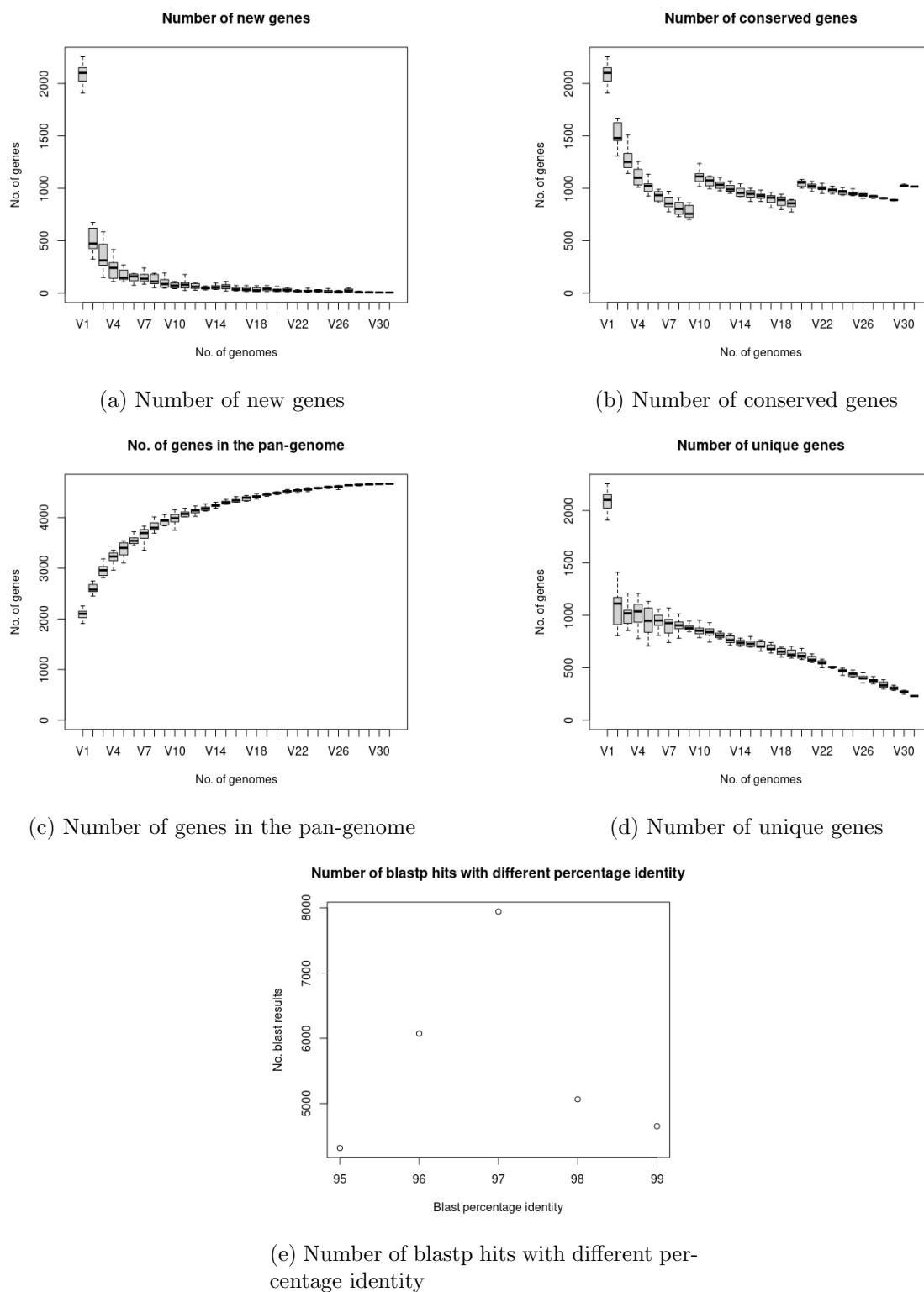

(e) Number of blastp hits with different percentage identity

Figure 1: Three simple graphs