

Title

Subtitle

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.

Genome Annotation

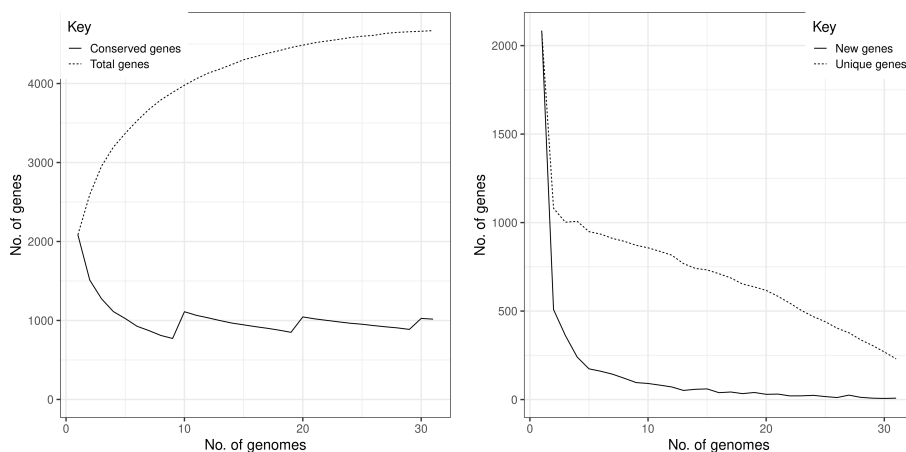
Pangenome Analysis

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