

Comparative genomics insights into clinical or environmental methicillin-resistant *Staphylococcus aureus*

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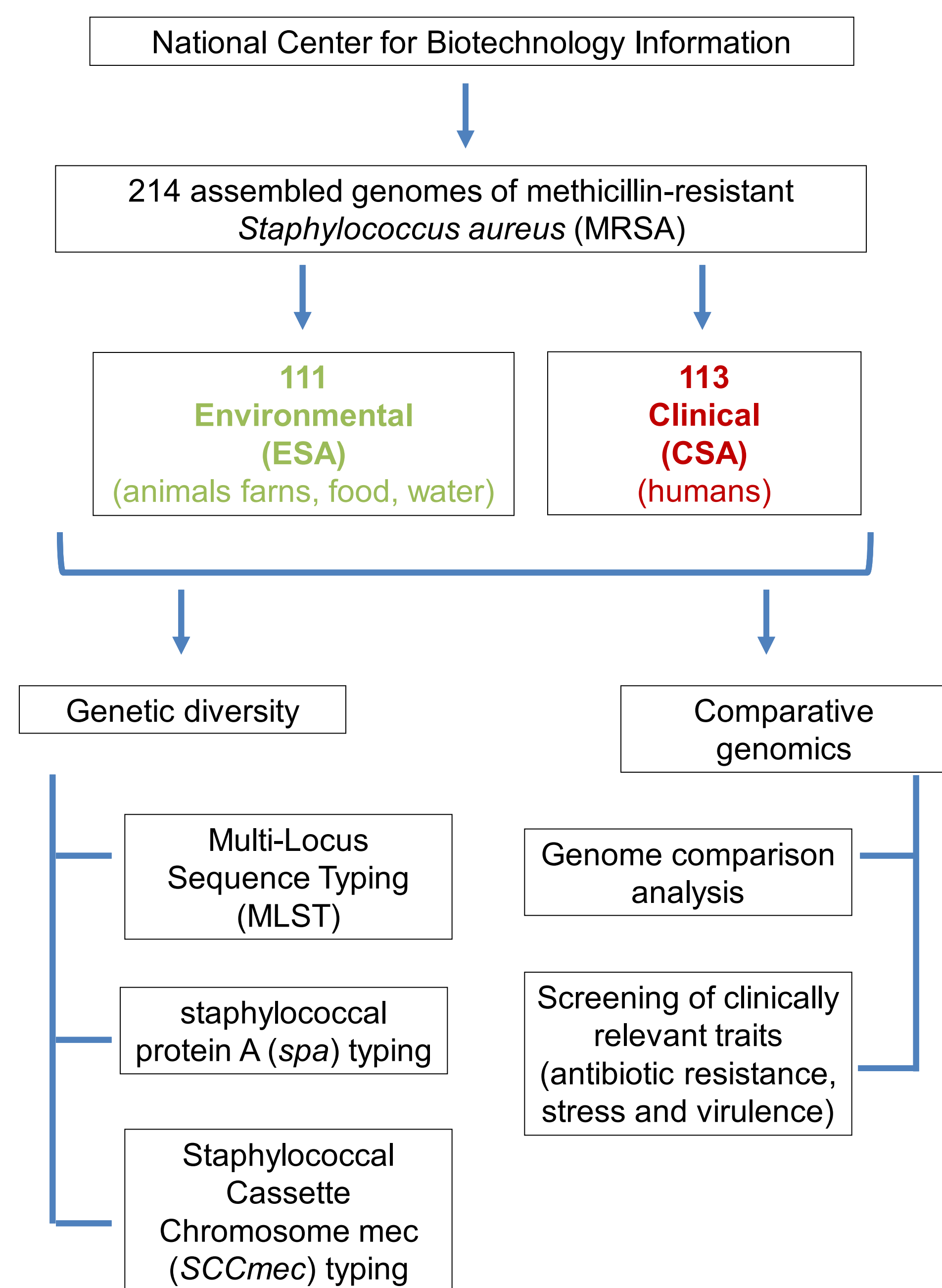
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Introduction

Antibiotic resistant pathogens are frequently ubiquitous bacteria, whose occurrence in the environment represents an opportunity for proliferation, dissemination and to reach the environment-human interfaces, e.g. food-products or leisure areas. *Staphylococcus aureus* is a species that exemplifies that situation. Methicillin resistant *S. aureus* can be found in the environment and in humans, and represent a major public health threat.

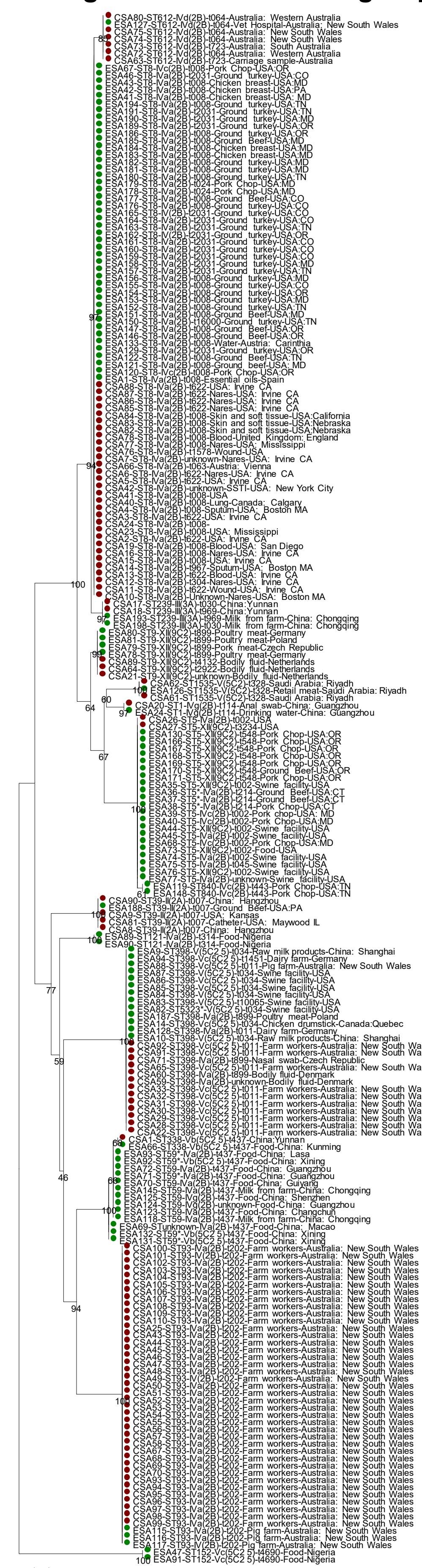
This study aimed at comparing the genomes of strains of distinct origins, in order to explore features that may underlie a specific lifestyle.

Methods



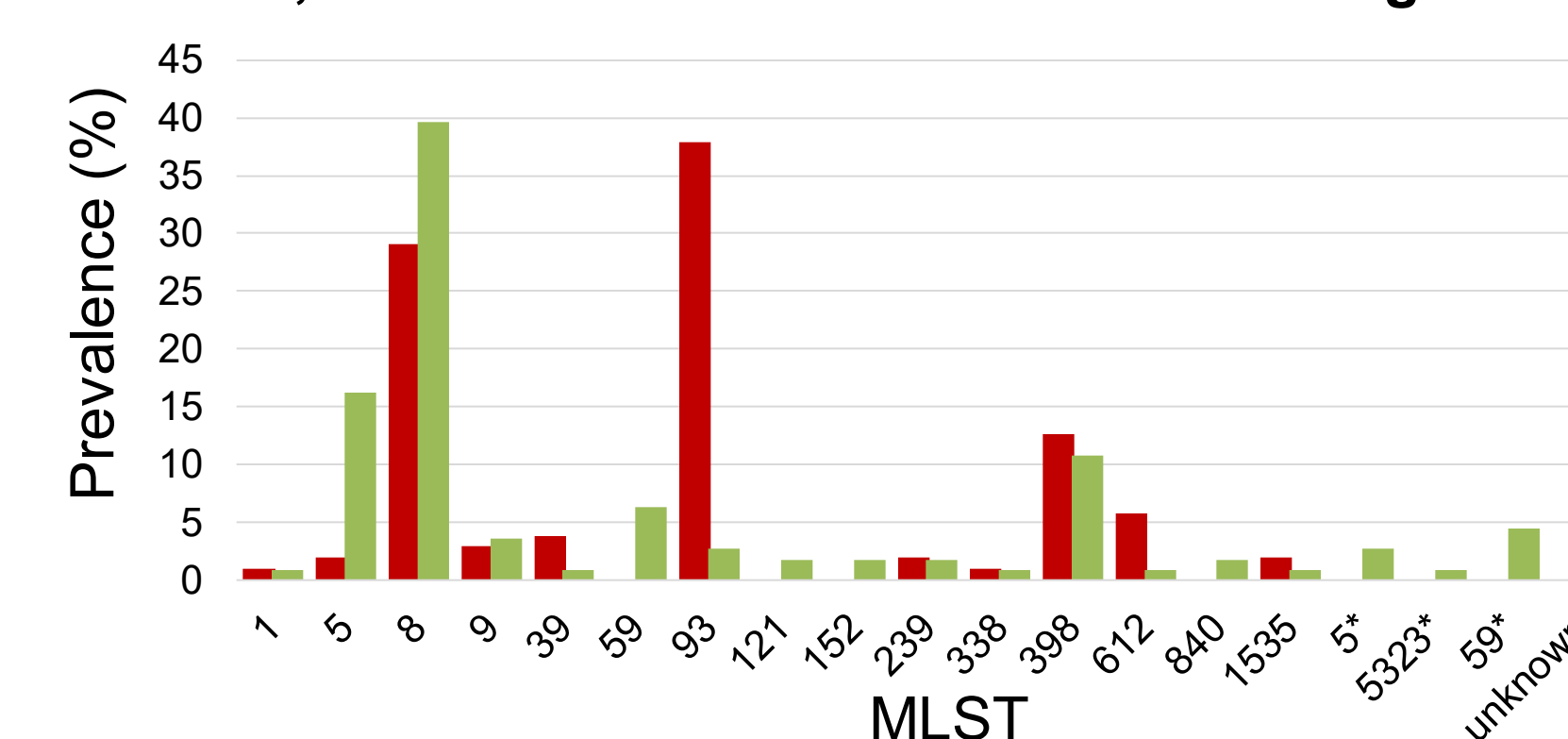
Results

Environmental and clinical MRSA genomes integrated distinct MLST groups

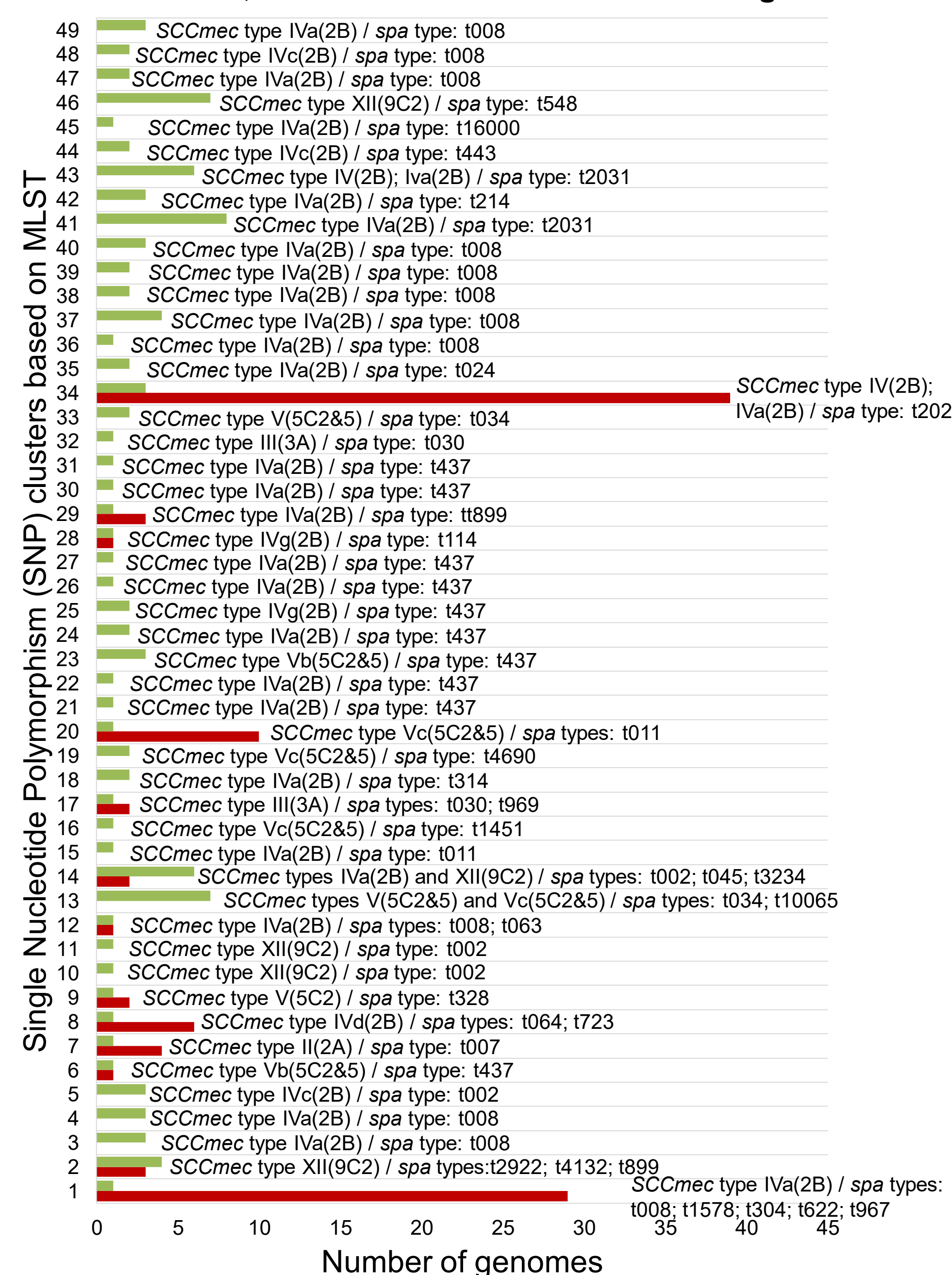


Genetic diversity

The environmental MRSA genomes belonged to 18 MLST, 11 of which were common to clinical genomes



Environmental MRSA genomes were organized in 49 SNP clusters, 13 of which included also clinical genomes



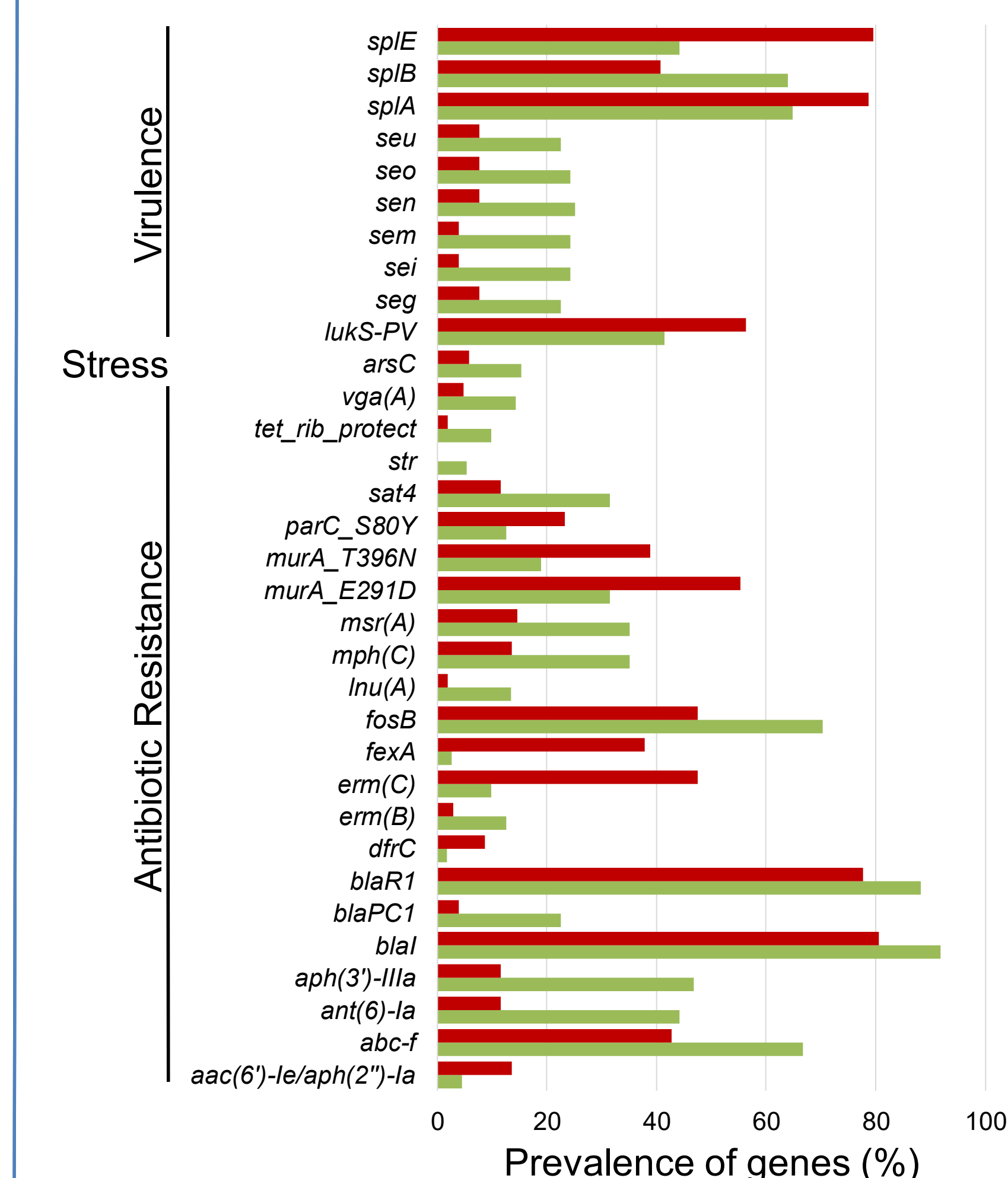
In general, each SNP cluster corresponded to a single SCCmec and spa types

Comparative genomic analysis

Antibiotic resistance, phage and virulence were among the exclusive genes in the environmental genomes, while insertion sequences, transposases and recombinases were among the exclusive genes in the clinical

SNP Cluster	Exclusive in Environmental	Exclusive in Clinical
2	Insertion sequences; Secretion system proteins	-
7	-	-
8	-	Recombinase; Aminoglycoside
9	Recombinases; Toxins, Integrases; Virulence; Phages	-
17	Insertion Sequences	Insertion sequence; Secretion system protein
20	-	-
29	Streptomycin; Mobilization protein	Insertion sequences; transposases

The genes related with resistance to β -lactams, aminoglycosides, macrolides, and enterotoxins were more frequent in the environmental genomes, while the genes related with resistance to fosfomycin and serine proteases were more frequent in the clinical



Conclusions

- Clinical and environmental methicillin-resistant *S. aureus* belong to the same genetic lineages (multi-locus sequence type and staphylococcal cassette chromosome mec type);
- Clinically-relevant traits might suggest specialization to clinical or environmental habitats;
- This work will contribute to improve the knowledge on the characteristics that might differentiate clinical and environmental MRSA.

Acknowledgements

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