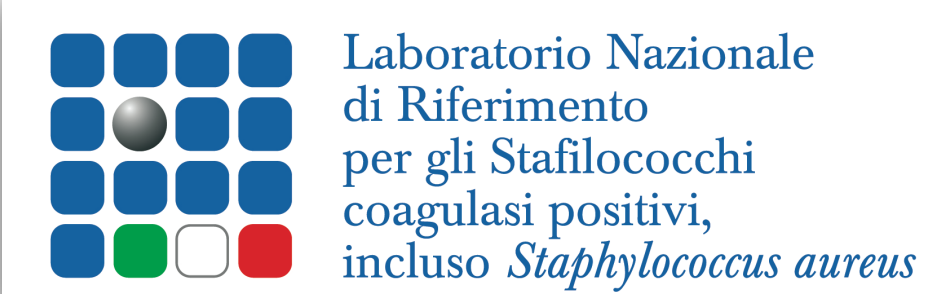


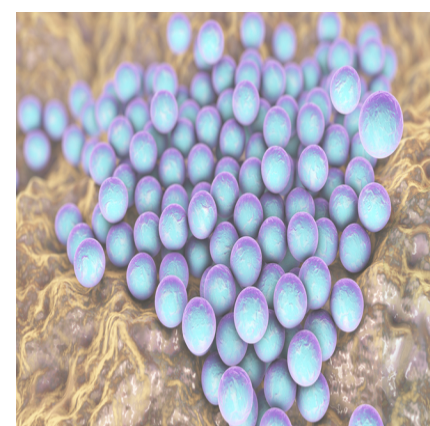


WHOLE GENOME SEQUENCING TYPING TO BUILD OPEN ACCESS STAPHYLOCOCCUS AUREUS DATABASE



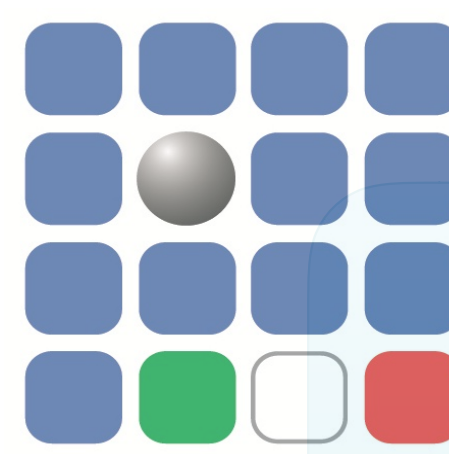
Romano A.¹, Boteva C.¹, Bellio A.¹, Zuccon F.¹, Martucci F.¹, Adriano D.¹, Maurella C.², Bergagna S.³, Chiesa F.⁴, Gallina S.¹, Bianchi M.D.¹ and L. Decastelli¹

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S. aureus model for WGS characterization

- ubiquitous bacteria
- responsible for widespread food borne disease
- direct impact also on animal health



- Biotyping
- mPCR for genes encoding SE
- SpaTyping
- PFGE

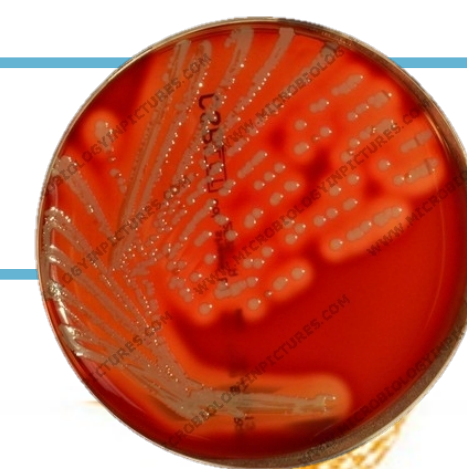
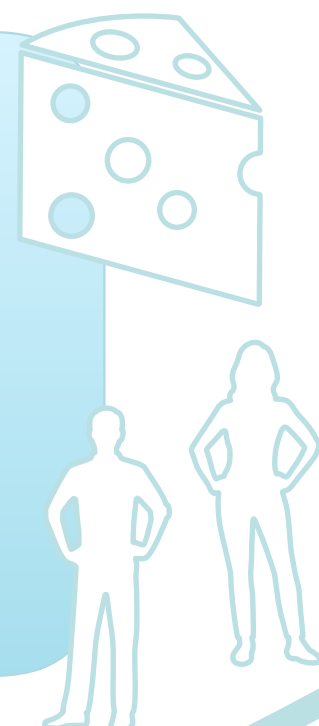
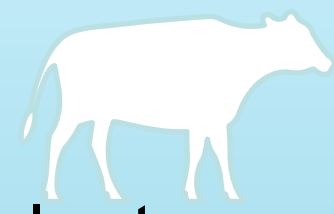


Combining traditional methods with Next Generation Sequencing (NGS) To perform typing and constitute an open access database for *S. aureus*

MATERIAL & METHODS

Strains included:

- 40 encoding SE isolated from food matrices in Piedmont region
- 80 isolated during food borne outbreaks
- 40 isolated from bovine mastitis
- 60 isolated from oropharyngeal swabs to healthy human volunteers

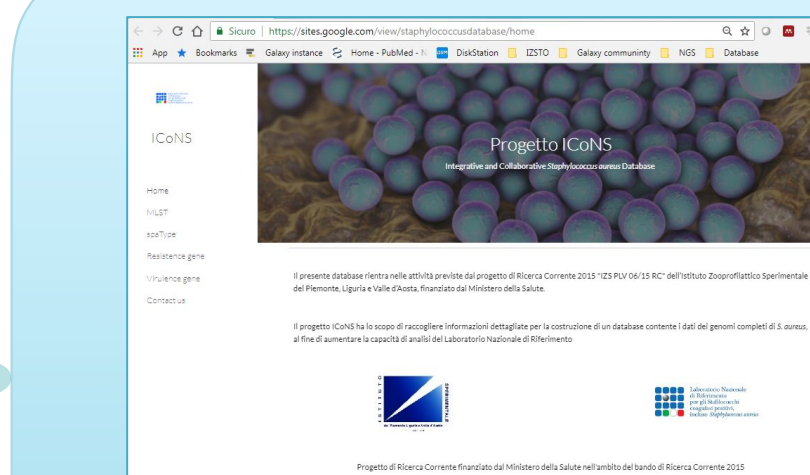
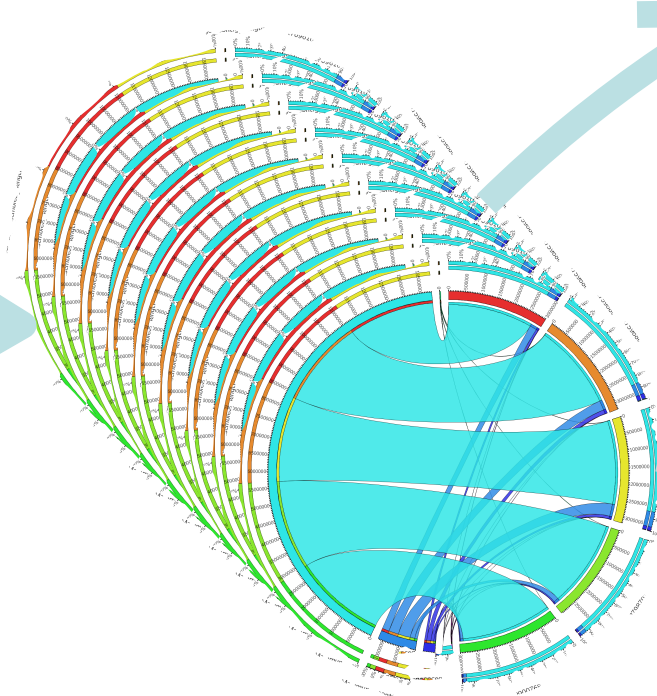


- spaTyper 1.0
- MLST 1.8
- ResFinder 3.0
- CSI Phylogeny 1.2



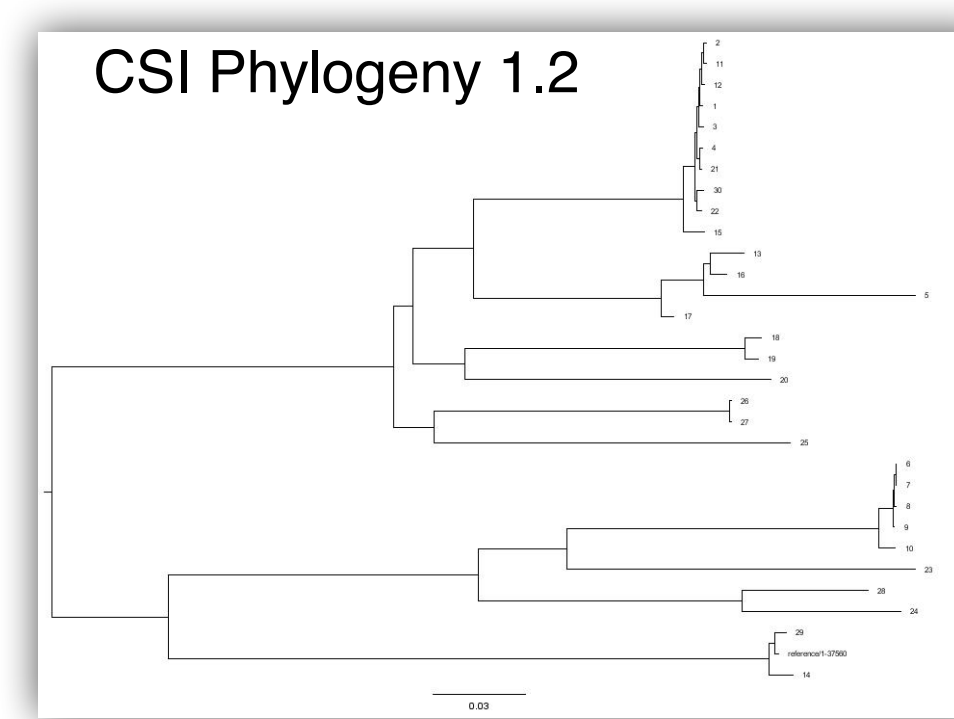
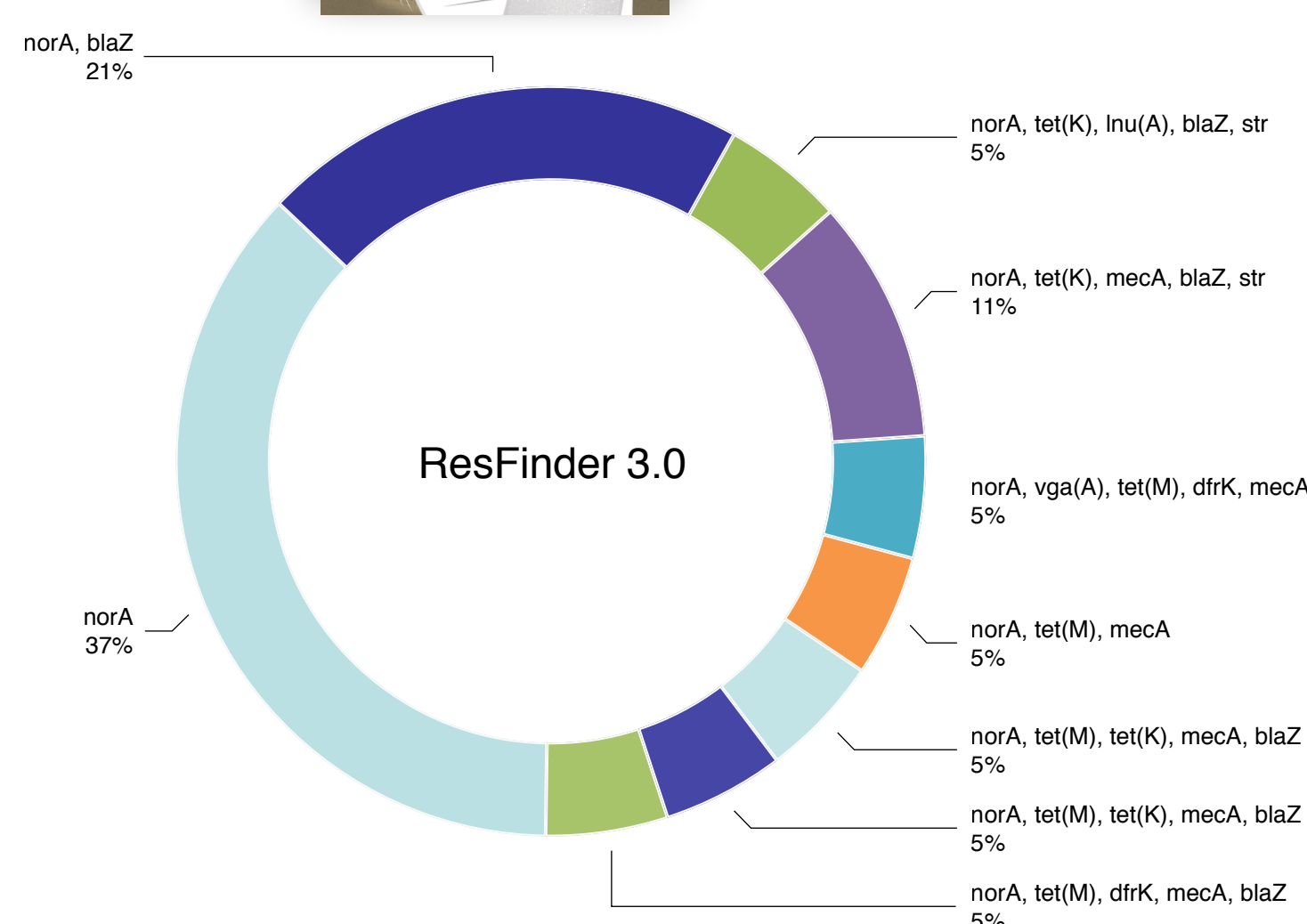
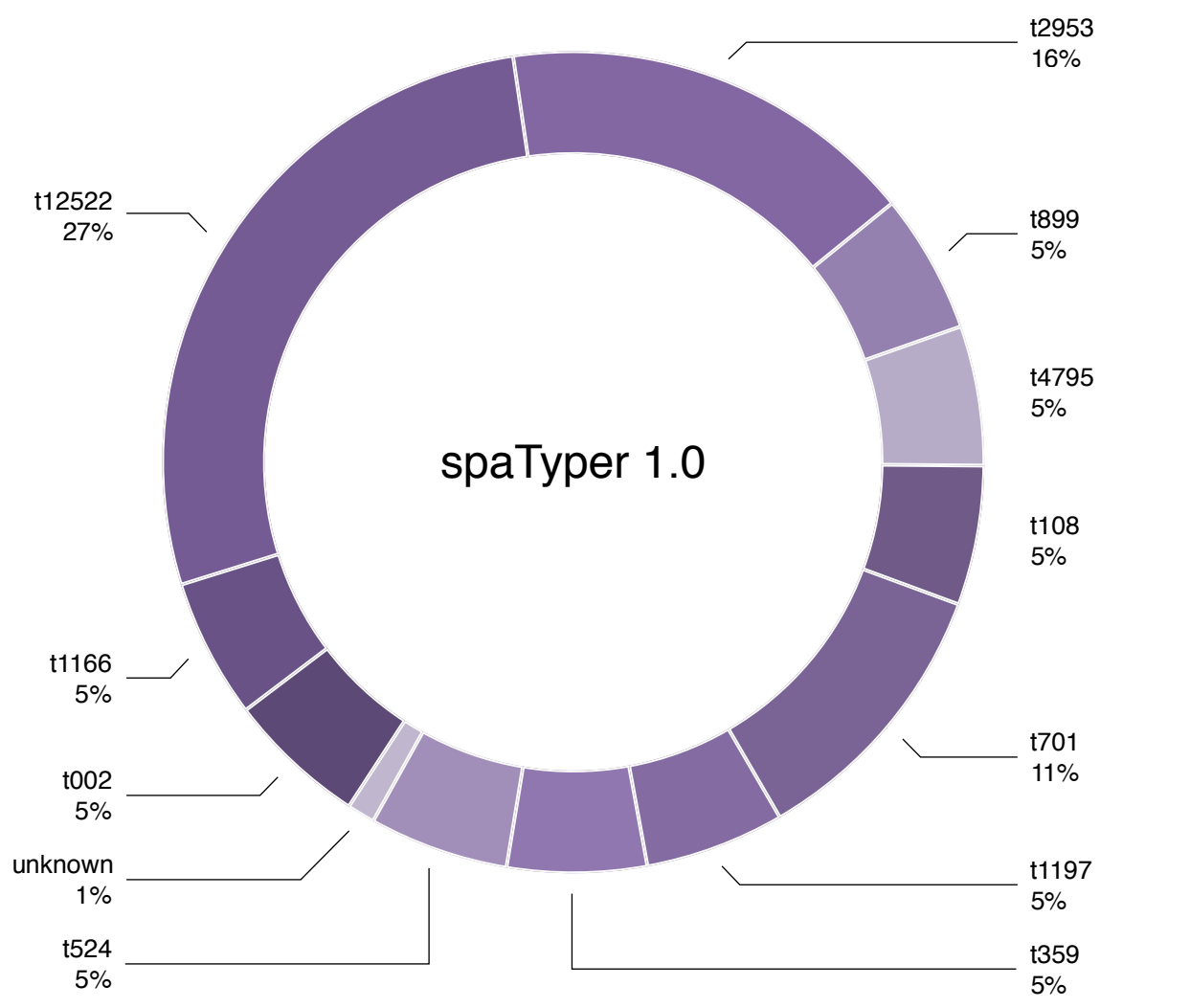
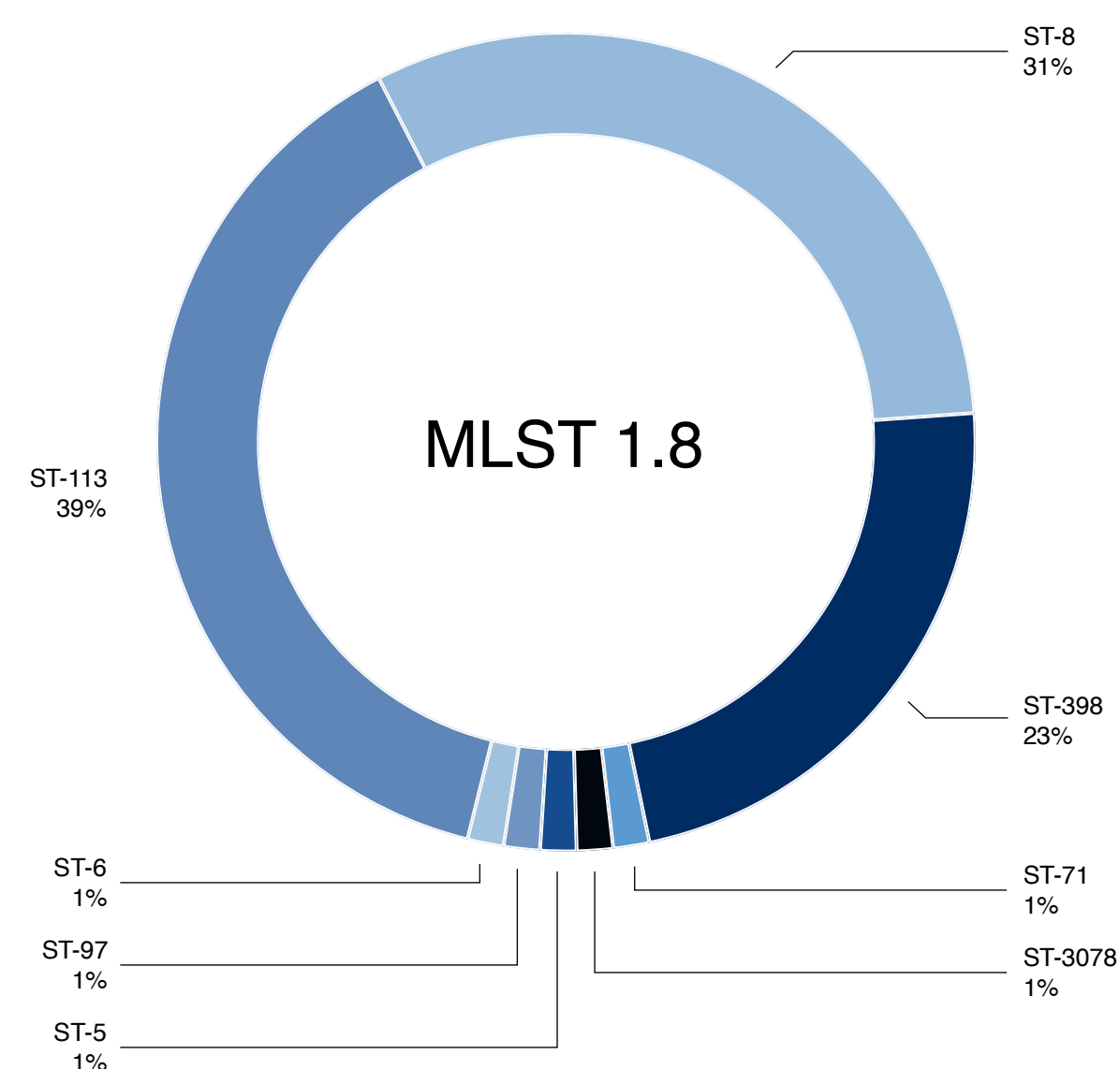
- FastQC
- Trimmomatic
- Unicycler

<https://cge.cbs.dtu.dk/>



<https://sites.google.com/view/staphylococcusdatabase/>

RESULTS & CONCLUSIONS



Whole Genome Sequencing: - large and accurate amount of data
 - allow a deeper characterization

Open access database to provide useful information related to diagnostic and surveillance purpose

