# Identification of potential vaccine targets in livestock-associated Staphylococcus aureus

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Propositions accompanying the thesis

## Identification of potential vaccine targets in livestock-associated *Staphylococcus aureus*

1. A few lineages of *S. aureus* are responsible for causing bovine mastitis in the north of Mexico (Chapter 2).
2. The high frequency of benzylpenicillin resistance in Mexican *S. aureus* isolates from cows with mastitis is consistent with the recurring use of this antibiotic to treat/control mastitis in Mexico (Chapter 2).
3. The *S. aureus* CC1 isolate described in Chapter 3 of this thesis does not contain features related to human adaptation, suggesting that the ancestral host switch from human to cow occurred a long time ago.
4. The high-level expression of the virulence genes, such as *seh*, *cna* and *fnpB*, by the CC1 isolate described in Chapter 3 may explain its high virulence in the *G. mellonella* infection model.
5. Most MGEs identified in *S. aureus* isolates from Mexican cows with mastitis are diverse, except for two genomic islands (GIs) and insertion sequences (IS), which suggests ancestral co-existence in the same host (Chapter 3).
6. The observation that exoproteome profiles of human-originated ST398 strains are more similar to each other than the ones of LA-ST398 strains, even though the LA-strains are genetically more closely related, is suggestive of specific adaptations enforced by the human host (Chapter 4).
7. The correlation of exoproteome data to larval killing and toxicity towards HeLa cells highlights the critical roles of the staphylococcal Sbi, SpA, SCIN and CHIPS proteins in virulence (Chapter 4).
8. IgGs from patients with epidermolysis bullosa, healthy human volunteers and immunized mice target the cell wall-binding domain of Sle1 and the catalytic domains of LytM and Aly (Chapter 5).
9. IgGs from mice immunized with Sle1, LytM and/or Aly are not protective against *S. aureus* bacteraemia (Chapter 5).
10. Low-abundant IgGs against the catalytic domain of Sle1 and the N-terminal domains of LytM and Aly are almost exclusively detected in sera from EB patients and healthy human volunteers and may protect against *S. aureus* infection (Chapter 5).
11. Implementing a reverse vaccinology pipeline approach allows the multidimensional immunological representation of peptidoglycan hydrolases, especially the antigens Sle1, LytM, Aly and IsaA (Chapter 6).
12. The expression levels of the genes encoding 23 conserved surface proteins in *S. aureus* isolates involved in mastitis in Mexican cows correlate with two MLST groups (Chapter 6).
13. The surface-associated protein Sle1 of *S. aureus* is a likely candidate target protein for inclusion in a sub-unit vaccine against bovine mastitis.

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