Methicillin-resistant *Staphylococcus aureus* (MRSA) has been recognized for over 40 years and has become a global issue in the medical and veterinary setting. This pathogen continues to evolve with the recent emergence of livestock-associated strains belonging to sequence type (ST) 398; which poses a significant risk to both farming industry as well as persons in contact with food-producing animals.

In this study, a panel of MRSA ST398 isolates was subjected to comparative genetic characterisation to identify molecular markers that distinguish the strains from other lineages of *S. aureus*.

### Methods

- Total of 56 isolates were characterised:
  - 18 veterinary and human clinical MRSA (ST398), all isolated in Belgium.
  - 18 veterinary clinical (cattle only) MSSA, isolated in the UK.
  - 20 human clinical MSSA and MRSA, isolated in the UK.
- All strains were subjected to spa typing, DNA microarray characterisation using IdentiHib MRSA Array (Figure 1) and clonal complex assignment.
- MRSA strains only were SCCmeC typed, screened for presence of additional antimicrobial resistance genes (tetL, ermA, tetK, dfrK) and subjected to MIC testing by broth microdilution method according to CLSI.
- Total of 30 different spa types were identified with an overall 87.12% identity (Figure 2).
- Based on microarray data the following ST/CCs were identified among non-ST398 strains (Figure 2):
  - Veterinary MSSA: CC97, CC151, CC130, ST42
  - Human MSSA: ST30, ST121, CC15, CC5, CC8, CC9, CC78
- Virulence genes (all strains analysed, Figure 3):
  - The majority of strains carried *hla*, *hld, hldg, seL, seT, lukF, lukS* and *sarA*.
  - No additional virulence factors were detected in MRSA ST398 strains.
- Resistance genes (MRSA strains only, Figure 4):
  - All strains were negative for *msrA*, *vanA*, *vanB*, *vanC*, *vga*, *far1*, *cat, cfr, apha3* (data not shown).
  - Novel resistance genes *tetL*, *ermA* and *dfrK* were detected among ST398 strains only.
- MIC testing (Figure 4):
  - All isolates were susceptible to apramycin, vancomycin and teicoplanin (data not shown).
  - Erythromycin resistance was common among all MRSA strains.
  - All ST398 strains were resistant to tetracycline.
  - All CC22 and CC30 strains were resistant to ciprofloxacin.

### Results

- **Figure 3**: Comparative genotypic and phenotypic characterisation of human and animal isolates of methicillin-resistant *Staphylococcus aureus* sequence type (ST) 398 using DNA microarrays.

### Conclusions

- MRSA ST398 strains appear to lack significant virulence factors in comparison to other lineages of both animal and human derived *S. aureus* strains.
- MRSA ST398 displays high frequency of antimicrobial resistance elements including presence of novel resistance genes such as *ermA*, *tetK* and *tetL*.
- The multi-drug resistance detected among MRSA ST398 strains could pose a considerable clinical challenge whereas the apparent lack of significant virulence genes would suggest low pathogenic potential.

### References


Acknowledgments: This work has been funded by the Department for Environmental Food and Rural Affairs, presenting author attendance at the 21st ECCMID/27th ICC has been funded by the Society for General Microbiology. Correspondence: d.jamezo@lva.defra.fs