

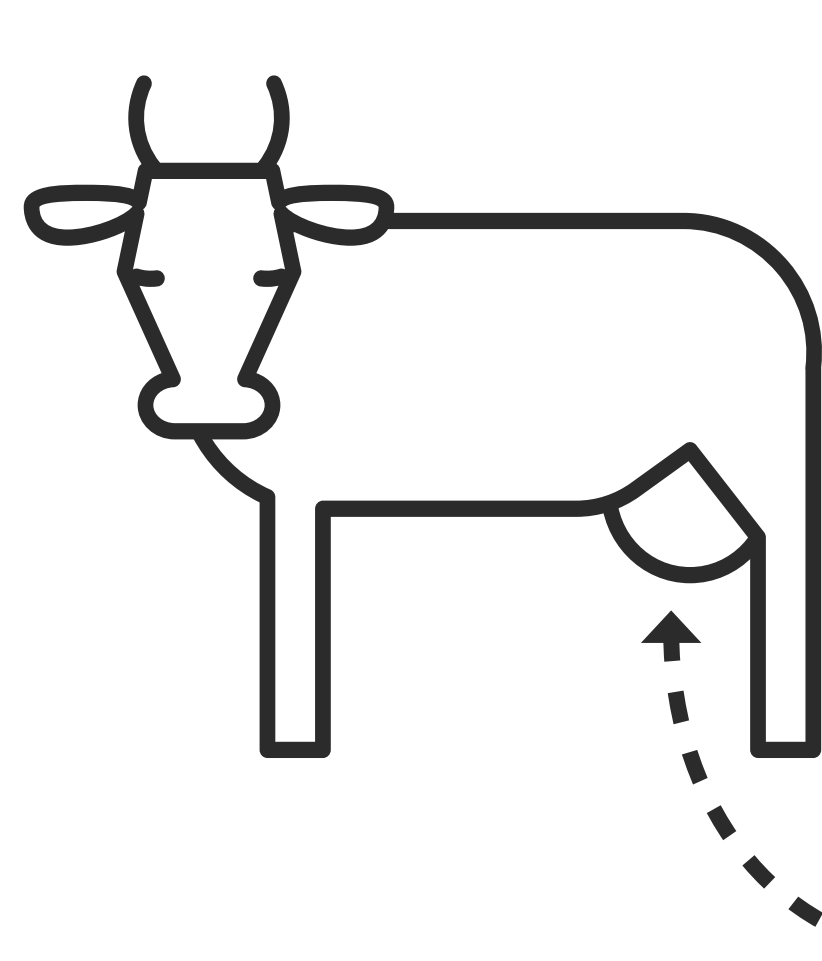
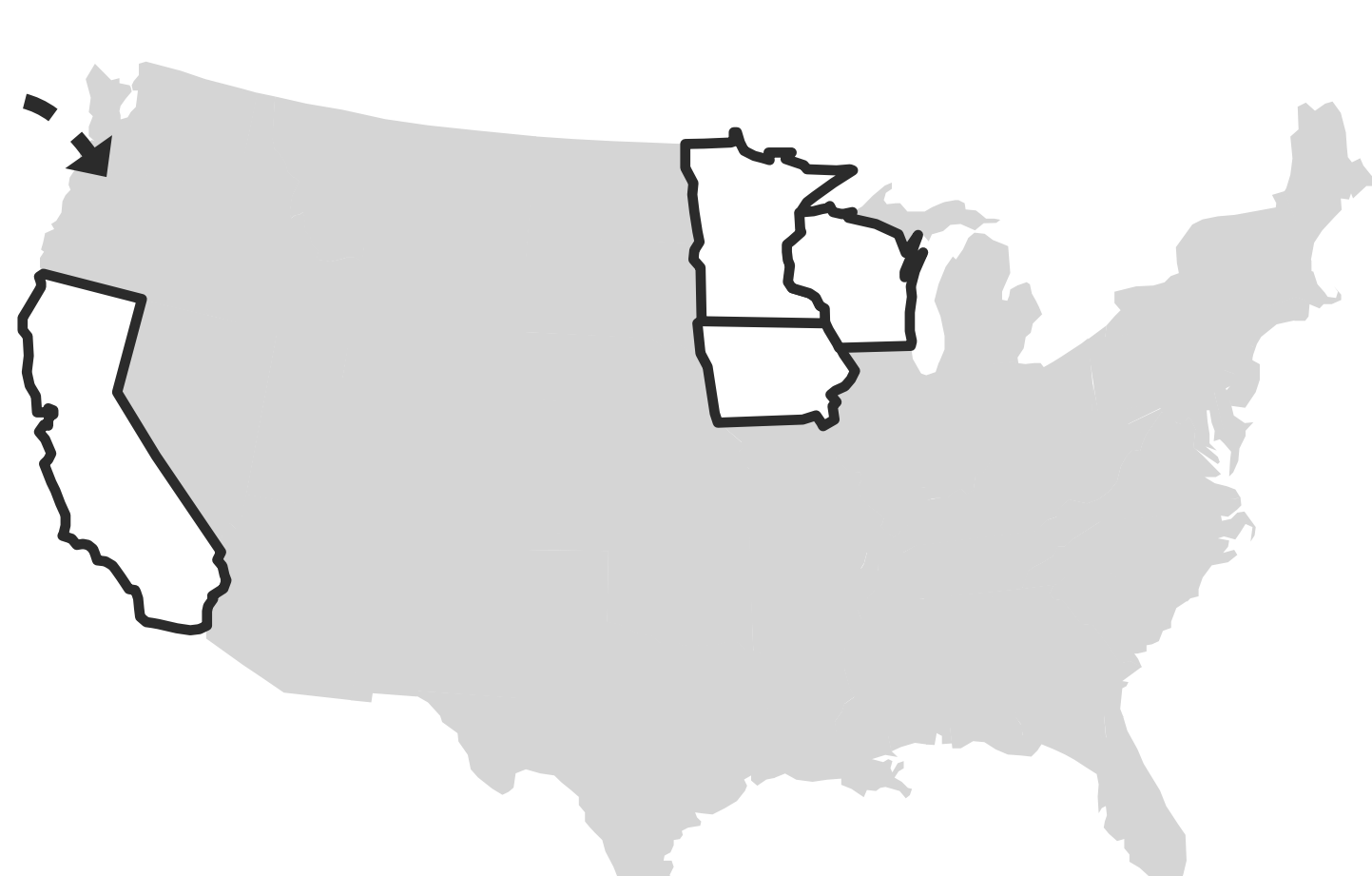
Molecular epidemiology of coagulase-negative *Staphylococcus* species isolated at different lactation stages from dairy cattle in the United States

INTRODUCTION

Coagulase negative *Staphylococcus* (CNS) species are currently the most prevalent intramammary pathogens causing subclinical mastitis and occasional clinical mastitis or persistent infection in lactating dairy cattle. More than 10 CNS species are known, however, they are generally managed as one group on most US dairies. **Improved management decisions and treatment outcomes may be achieved with better understanding of each prevalent species in order to further our understanding of the differences in their pathogenicity and strain diversity** within and across dairies.

METHODOLOGY

A total of **604 CNS species were isolated from milk samples** collected during a dry-cow treatment clinical trial conducted on 6 dairy herds from 4 states in the US. Study cows were randomized to receive one of three intra-mammary antimicrobial infusions at dry-off.



Milk samples were collected at dry-off, calving (0 to 6 days in milk, DIM), post-calving (7-13 DIM) and at first mastitis event within the first 100 DIM.

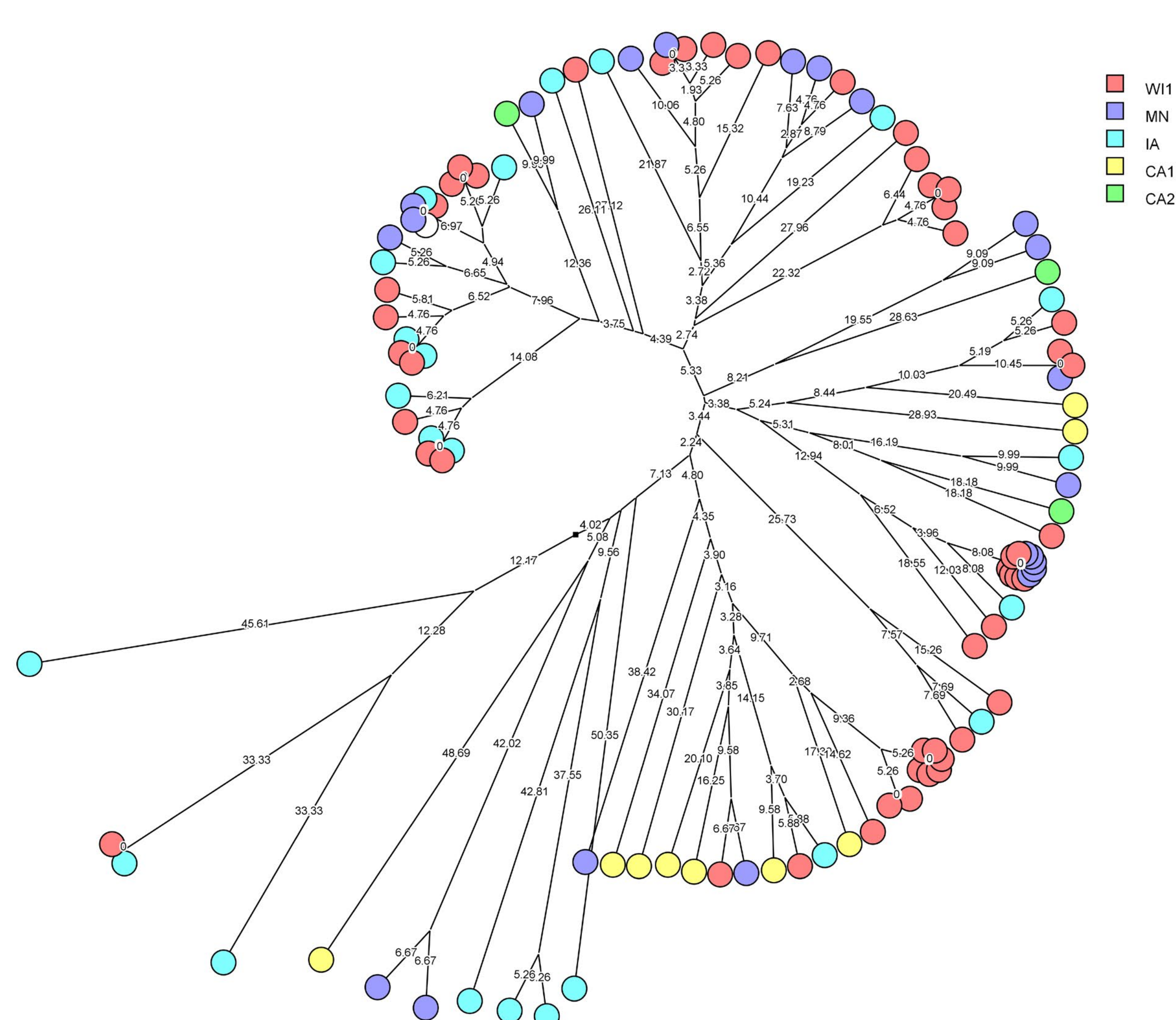
The **CNS species were identified** by partial *rpoB* gene sequencing, and genetic relatedness within species was investigated by phylogenetic analysis of the pulse-field gel electrophoresis profiles of the isolates.



RESULTS

The major CNS species identified were ***S. chromogenes* (48.3%), *S. haemolyticus* (17.9%), *S. simulans* and *S. epidermidis* (each at 6.5%)**. Genetic relatedness was associated with the epidemiological distributions of *S. chromogenes*, *S. simulans*, *S. haemolyticus* and *S. auricularis*. In addition, identical strains of *S. chromogenes* and *S. simulans* were isolated from the same udder quarter of several cows at consecutive sample stages. The rest of the minor species had no deducible genetic-epidemiological link.

Phylogenetic cluster analysis of *Staphylococcus haemolyticus* strains isolated from US dairies



CONCLUSION

The different CNS species and strains circulating on US dairy herds were genetically diverse. Four species had deducible genetic-epidemiological link, 2 of which (*S. chromogenes* and *S. simulans*) caused persistent infection, suggesting possible host-adapted and environmental transmission of these species. Multi-stage isolation of the same udder quarter strain was evidence for persistent intra-mammary infection for the 2 species. Distinguishing between the most frequent CNS species, specifically *S. chromogenes*, *S. simulans*, *S. haemolyticus*, is the first step in the designing of effective mastitis control strategies which is long overdue.

