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Coagulase Negative Staphylococci Distribution in Dairy Herds with Automatic Milking System and their Crosstalk with *Staphylococcus Aureus* from IMI and Teat Apex



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BACKGROUND

- Longer milking duration and frequent exposure to teat disinfectants may affect the teat apex microbiota.
- Knowledge of epidemiological characteristics of CNS in automatic milking systems (AMS) herds is sparse
- The role of CNS on the risk to acquire of IMI with *S. aureus* is debated.

OBJECTIVES

 To investigate the distribution of CNS species from aseptically collected quarter milk samples and teat skin in AMS herds,
 To examine if the isolated CNS influence the expression of *S. aureus* virulence factors controlled by the *agr* quorum sensing system.

METHODOLOGY

- ➤ Herd selection: 8 herds: AMS with ≥3 milking robots and bulk tank PCR Ct-values ≤32 for *S. agalactiae*
- Cows selection: 30-40 cows/herd: SCC: ≥ 200,000 cells/mL, and no antibiotic < 4 weeks prior to sampling</p>
- Quarter selection: RH & LF quarters of cows with odd lab number (1,3,5..)
- ➤ Teat skin swabs (modified wet-dry method) and aseptic milk samples collected for bacterial culture using calf blood agar and SA SELECT[™]
- Suspicious CNS colonies were subjected to MALDI-TOF assay for species identification.
- Interaction between S. aureus and CNS investigated with

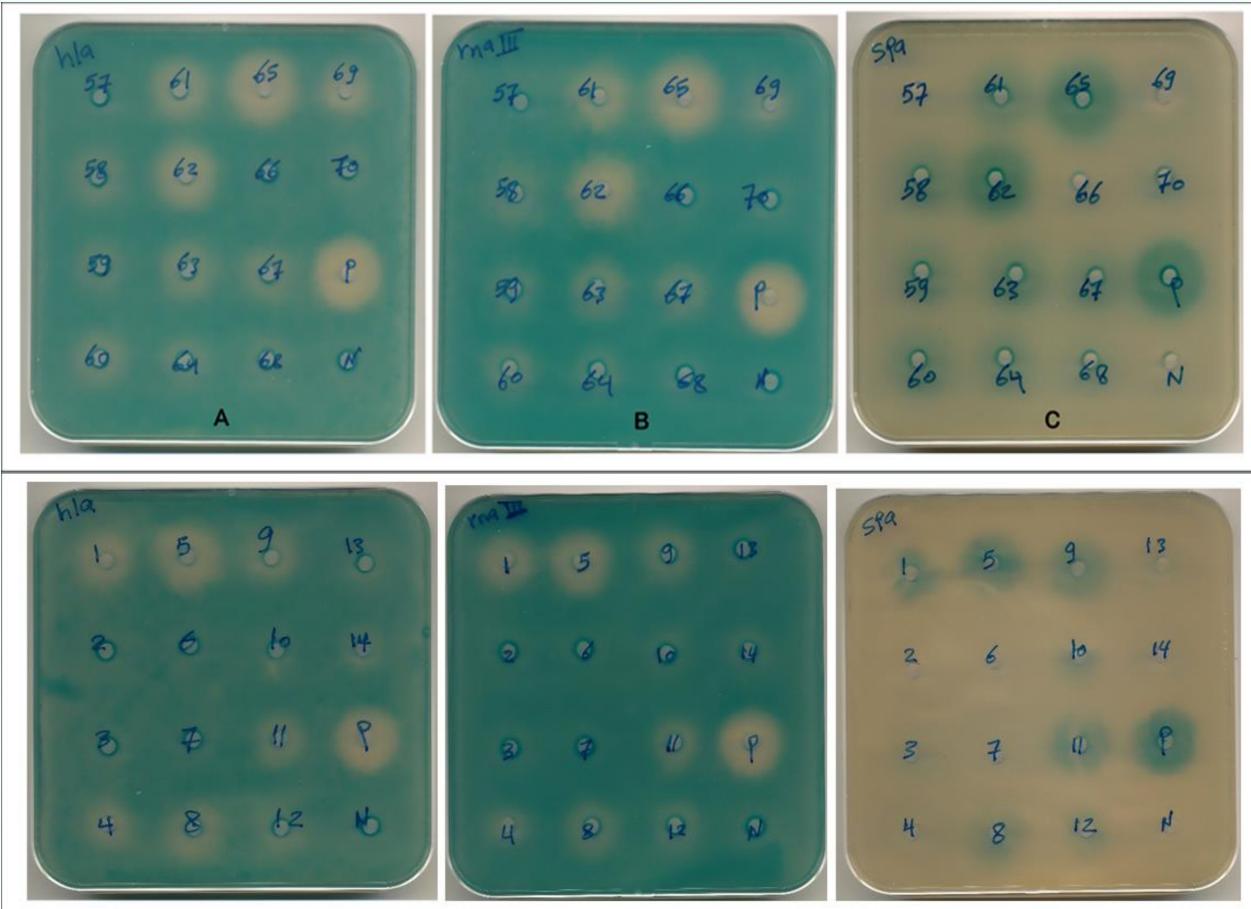
Table 1. Species distribution and association of CNS isolatesfrom aseptic quarter milk and teat skin samples collected from142 cows

CNS species	Sample type (%)		P-value
	Milk (n=105)	Teat (n=268)	
S. arlettae (12)	1 (0.9)	11 (4.1)	0.22 ^{NS}
S. capitis (3)		3 (1.1)	NA*
S. chromogenes (16)	11 (10.5)	5 (1.9)	0.002***
S. cohnii (43)	5 (4.8)	38 (14.2)	0.011**
S. epidermidis (60)	52 (49.5)	8 (3.0)	< 0.0001 ****
S. equorum (122)	6 (5.7)	116 (43.3)	< 0.0001 ****
S. haemolyticus (58)	16 (15.2)	42 (15.7)	0.90 ^{NS}
S. hominis (17)	3 (2.9)	14 (5.2)	0.48 ^{NS}
S. piscifermentans (2)		2 (0.8)	NA*
S. saprophyticus (5)		5 (1.9)	0.36 ^{NS}
S. sciuri (9)		9 (3.4)	0.13 ^{NS}
S. simulans (2)	2 (1.9)		NA*
S. succinus (2)		2 (0.8)	NA*
S. vitulinus (1)		1 (0.4)	NA*
S. warneri (2)	1 (0.9)	1 (0.4)	NA*
S. xylosus (19)	8 (7.6)	11 (4.1)	0.26 ^{NS}

Qualitative Beta-Galactosidase Reporter Plate Assay based on **3** reporter strains of *S. aureus* ; **hla** (a-hemolysin), **RNAIII** (key effector molecule of agr) and **spa** (Protein A).

RESULTS

- ✤ 80% (228/284) quarters (142 cows) had ≥ 1 CNS species.
- ✤ 373 isolates, milk (n=105) and teat skin (n=268).
- 16 CNS species: teat skin (n=15), milk (n=10)
- Coinfections (mixed): 11 quarters from milk samples and 66 quarters from teat samples.
- Downregulation of *S.aureus* by some CNS may be explained by its ability to inhibit *S. aureus* agr system through production of auto-inducing peptide (AIP) molecules.
- Table 1 shows CNS species distribution and Figure 1 shows crosstalk between *S. aureus* and CNS



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CONCLUSIONS

- S. epidermidis and S. chromogenes are milk-associated, while S. equorum and S. cohnii are teat-associated.
- CNS species, habitat type, and herd factors affect CNS and *S. aureus* crosstalk patterns.
- Downregulation of *S.aureus* by some CNS species could explain possible protective effect.

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Downregulation effect

62, 65: *S. arlettae* (teat, H7) 61: *S. chromogenes* (teat, H7) 5: *S. chromogenes* (milk, H3)

Variant effect

1: S.equorum (milk, H1)
2: S.equorum (milk, H2)
6: S.epidermidis (milk,H3)
58: S.epidermidis (teat,H7)

No effect

66: *S. Sciuri* (teat, H7) 7: *S. Sciuri* (teat, H3)

Figure 1. Crosstalk patterns between S. aureus and CNS