

Microarray based genetic profiling of *Staphylococcus aureus* isolated from abattoir byproducts of pork origin

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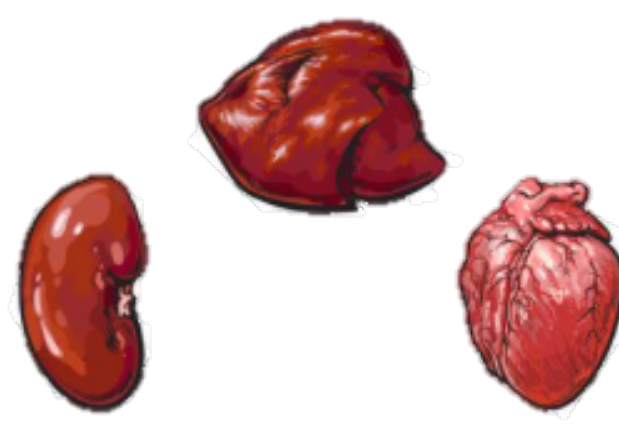
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Background

Many parts of pork meat processing are currently not used for human consumption in Switzerland, although they are of great nutritional value. Therefore, data on the occurrence of pathogenic organisms on byproducts is extremely scarce and the prevalence and population structure of *Staphylococcus aureus* on meat processing sidestreams is unknown.

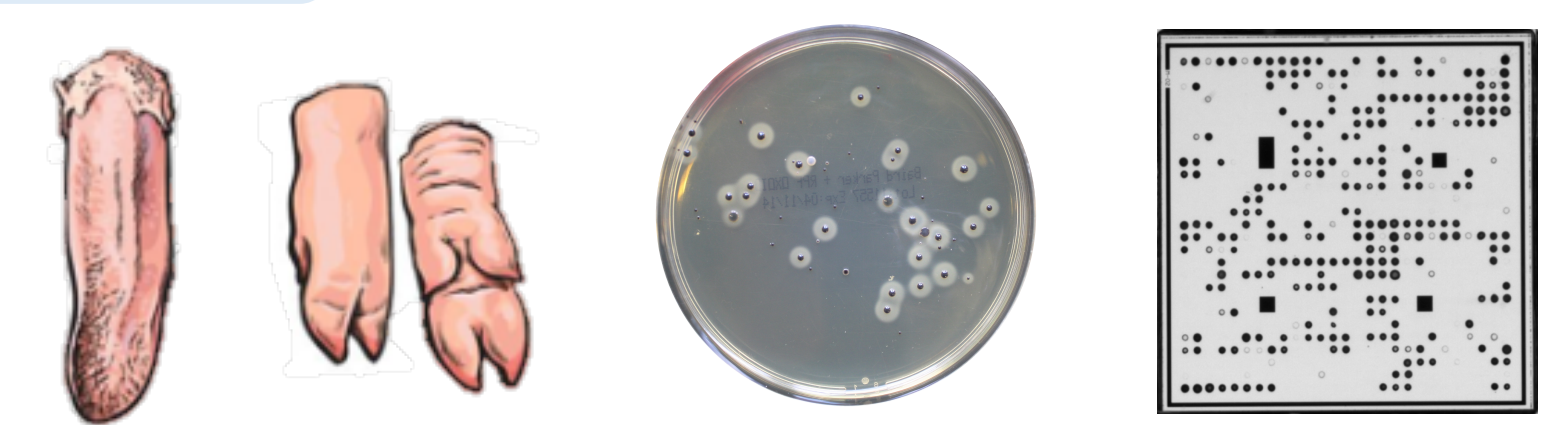
Objective

We screened 524 pork byproducts for *S. aureus* and genetically typed the obtained isolates.



Materials & methods

- Plating samples on RPF
- spa* typing
- DNA microarray



S. aureus prevalence

Prevalence of *S. aureus* on sampled byproducts

Organ	Positive samples ^a /total samples	Prevalence [%]
Sternum	5/56	9
Rib bone	7/56	13
Hind foot	0/56	0
Forefoot	1/56	2
Intestine	1/20	5
Heart	3/42	7
Liver	1/42	2
Stomach	0/56	0
Ear	10/42	24
Bladder	0/56	0
Tongue	12/42	29
Total	40/524	8

^a>100 CFU/g

8% of the 524 sampled byproducts positive

highest prevalence: tongue (29%) and ear (24%)

No *S. aureus* detected in hind foot, stomach and bladder

S. aureus detected in four of the six sampled abattoirs

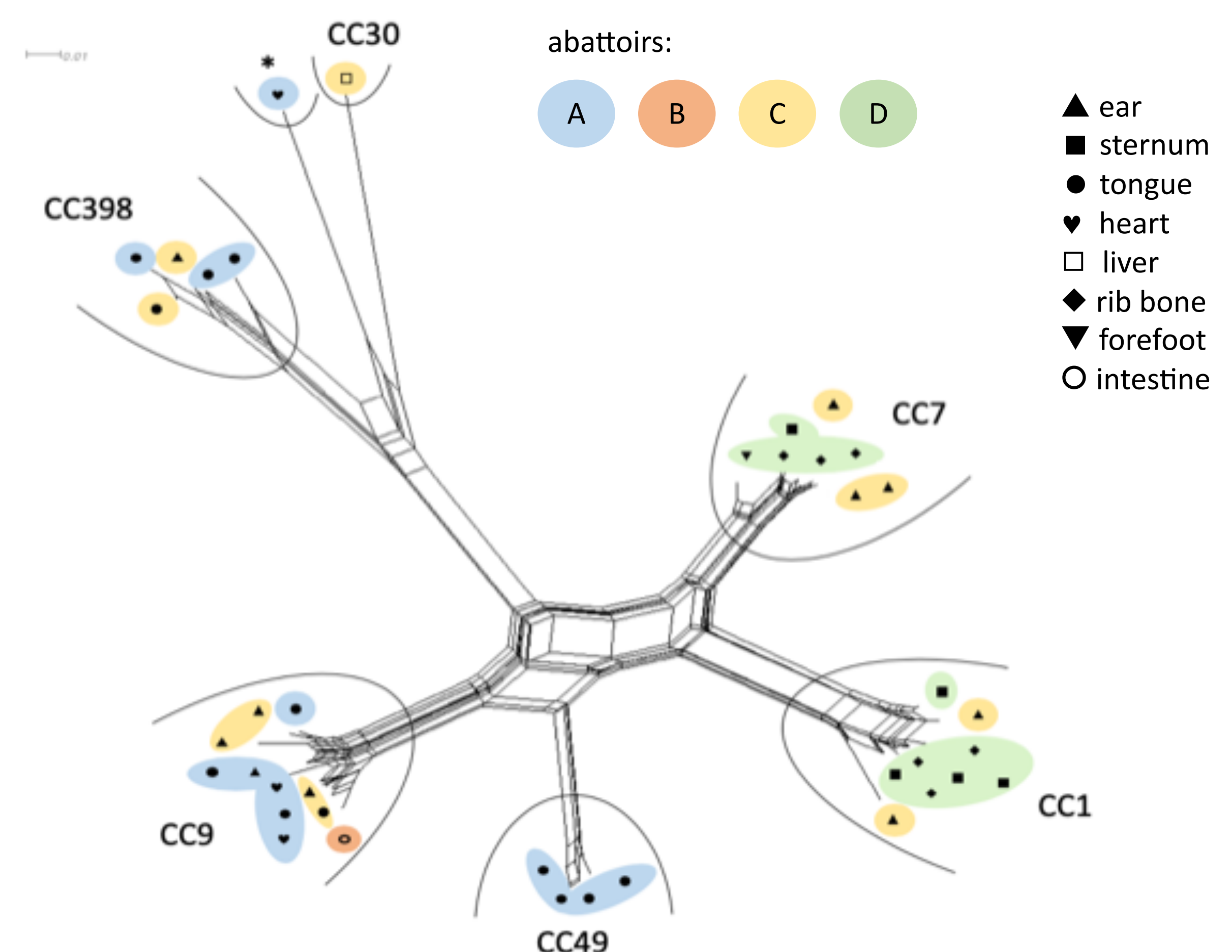
Clonal complexes and *spa* types

The 40 *S. aureus* were assigned to seven clonal complexes (CC) and 12 *spa* types.

Most prevalent CCs: **CC9** (27.5%), CC1 and **CC7** (22.5%).

Most frequent *spa* types: **t091** (n = 9), **t1491** (n = 8), **t899** (n = 6) and **t034** (n = 5).

Similarity of genomic profiles



Association of certain CCs and abattoirs

No association of CCs with particular body parts or outer/inner organs

Resistance and enterotoxin genes

Characteristics of 40 *S. aureus* isolates obtained from pork abattoir byproducts.

Clonal complex	<i>spa</i> type	n isolates	Resistance genes ^a	Enterotoxin genes ^a
CC1	t1491	8	<i>blaZ</i> /I/R (7)	<i>sea</i> ^d (2), <i>seb</i> (3), <i>sec</i> (1), <i>seh</i> (3), <i>sei</i> (1), <i>egc</i> ^d (2)
	t1778	1	<i>qacC</i>	<i>sea</i> ^d
CC7	t091	9	<i>aacA-aphD</i> (1)	<i>sea</i> ^d (2), <i>seh</i> (1), <i>egc</i> (5)
CC9	t337	3	<i>blaZ</i> /I/R, <i>fosB</i>	<i>seb</i> (1), <i>seh</i> (1), <i>egc</i> (1)
	t899	6	<i>blaZ</i> /I/R (1), <i>fosB</i>	<i>seb</i> (2), <i>seh</i> (2), <i>egc</i> (2)
CC30	t2922	1	<i>blaZ</i> /I/R, <i>fosB</i>	<i>egc</i>
	t7439	1	<i>blaZ</i> /I/R, <i>fosB</i>	ND
	t1333	1	<i>fosB</i>	<i>seb</i> , <i>seh</i>
CC49	t208	2	<i>blaZ</i> /I/R	<i>sea</i> ^d (1)
	t4049	2	<i>blaZ</i> /I/R	<i>sea</i> ^d (1), <i>egc</i> (1)
CC398	t034	5	<i>blaZ</i> /I/R (2), <i>vgaA</i> (2), <i>tetK</i> (1), <i>tetM</i>	<i>sea</i> ^d (2), <i>seb</i> (1), <i>seh</i> (1), <i>egc</i> (1)

^aIf not all isolates assigned to the respective *spa* type harbored a gene, the number of positive isolates is indicated in brackets.

^bAllelic variant *sea* N315

^cEnterotoxin gene cluster (*egc*) containing genes: *seg*, *sei*, *sem*, *sen*, *seo*, *seu*

Conclusions

Sampling of pork byproducts in Switzerland demonstrated low prevalence of *S. aureus*. Microarray based genetic profiling of 40 *S. aureus* isolates revealed a diverse population structure. No MRSA were detected. A variety of enterotoxin genes was found distributed over almost all clonal complexes. The isolates did not differ considerably from those found in previous studies in conventional pork meat cuts. Our findings suggest that occurrence of *S. aureus* on byproducts was linked to contamination during the slaughtering process in some abattoirs. Adequate handling of these processing sidestreams should ensure proper quality and therefore minimize product loss.

This study has already been published and is available online:

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