

The *mecC* story

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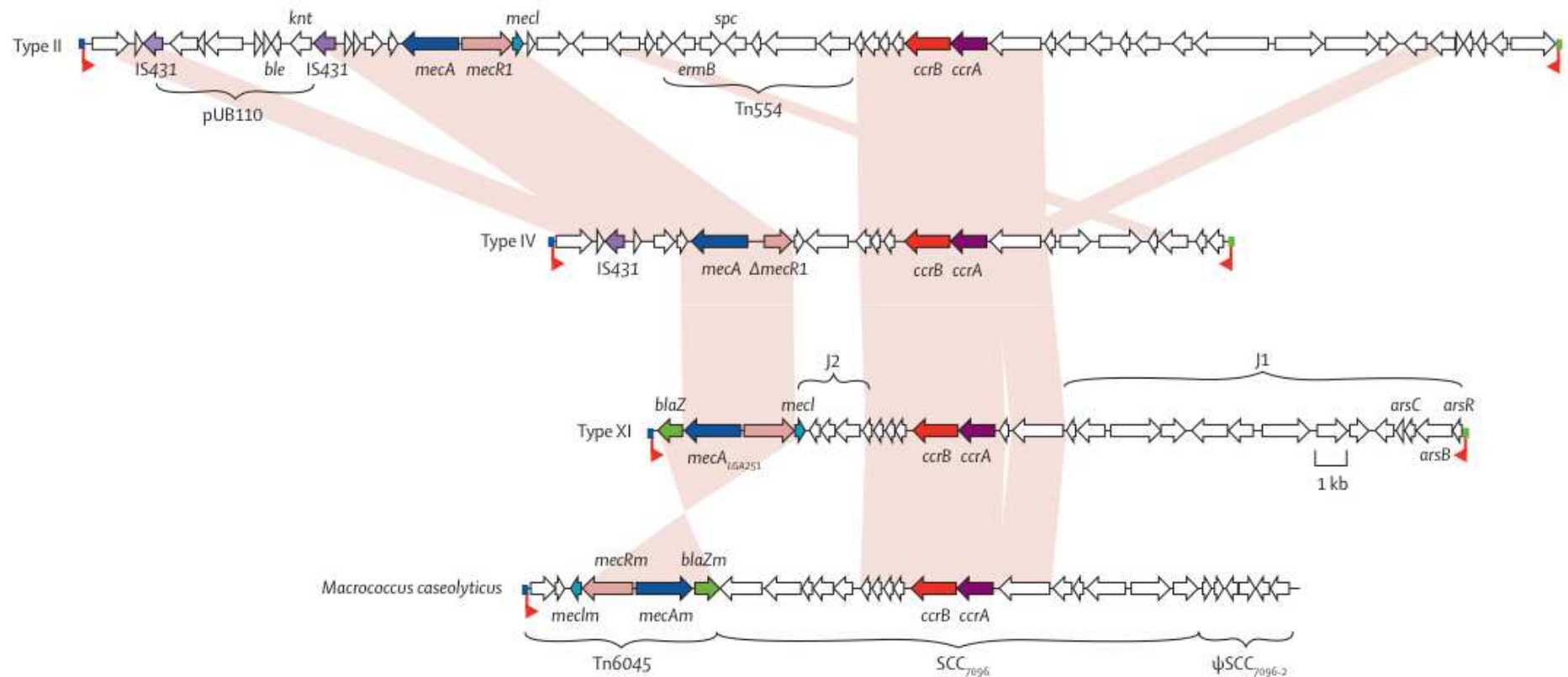


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Discovery of the new MRSA strain (LGA251)

- We found *S. aureus* that were highly resistant on one farm (ST425)
- Looked for *mecA* gene – negative results
- Sequenced whole genome to look for the reason
- Found a divergent *mecA* gene inside a mobile genetic element
 - (and nothing else to account for the resistance)
 - Surprisingly different (only 60% the same, but accounted for the previous negative results)
 - Designed a new *mecA* test

SCC*mec*_{LGA251} – Type XI SCC*mec*



new mec nomenclature

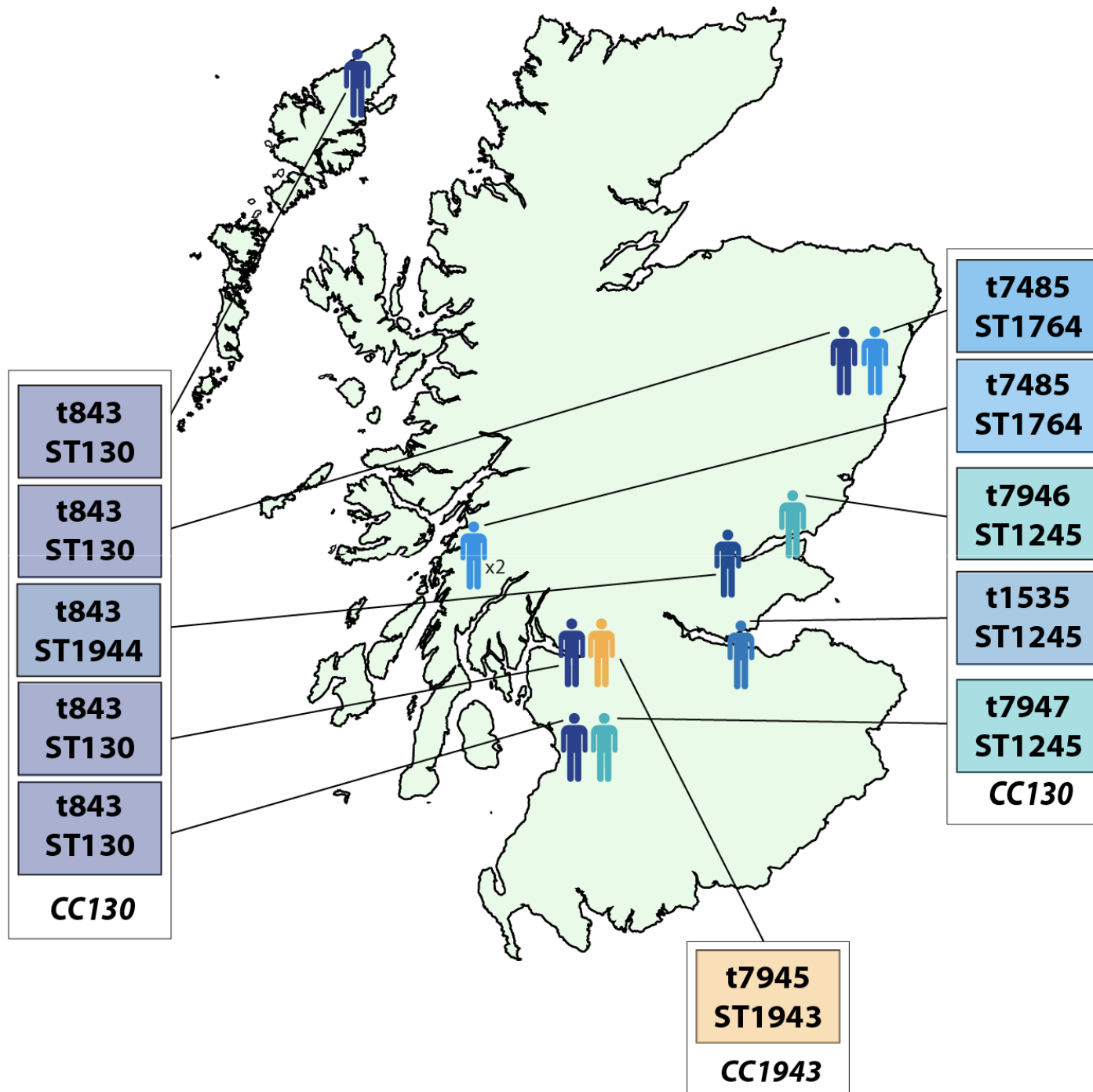
- Teryo Ito et al (IWG-SCC)
- *mecA* – conventional MRSA
- *mecB* – *Micrococcus caseolyticus*
- ***mecC*** – *mecA*_{LGA251}

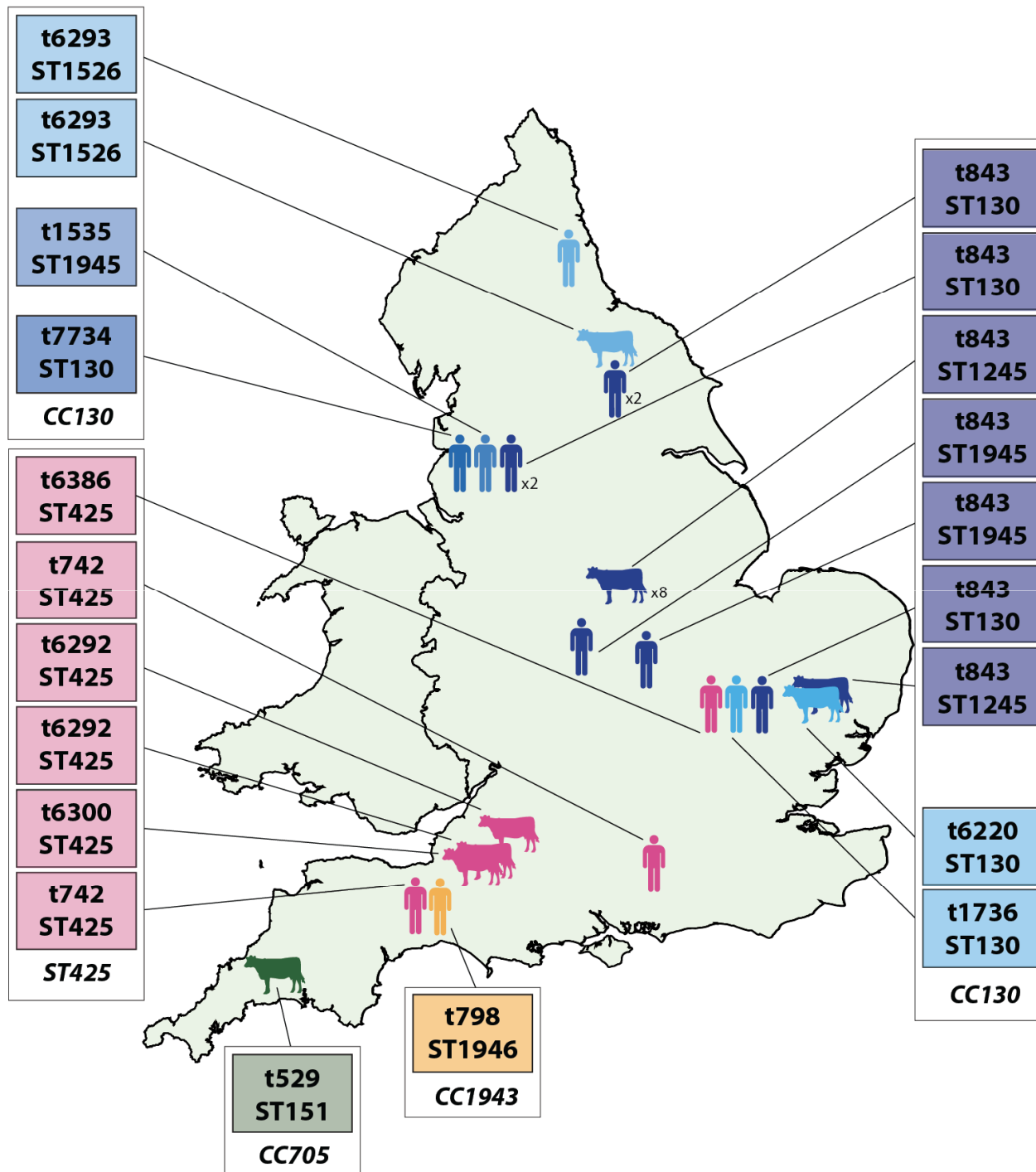
Further searching in cows

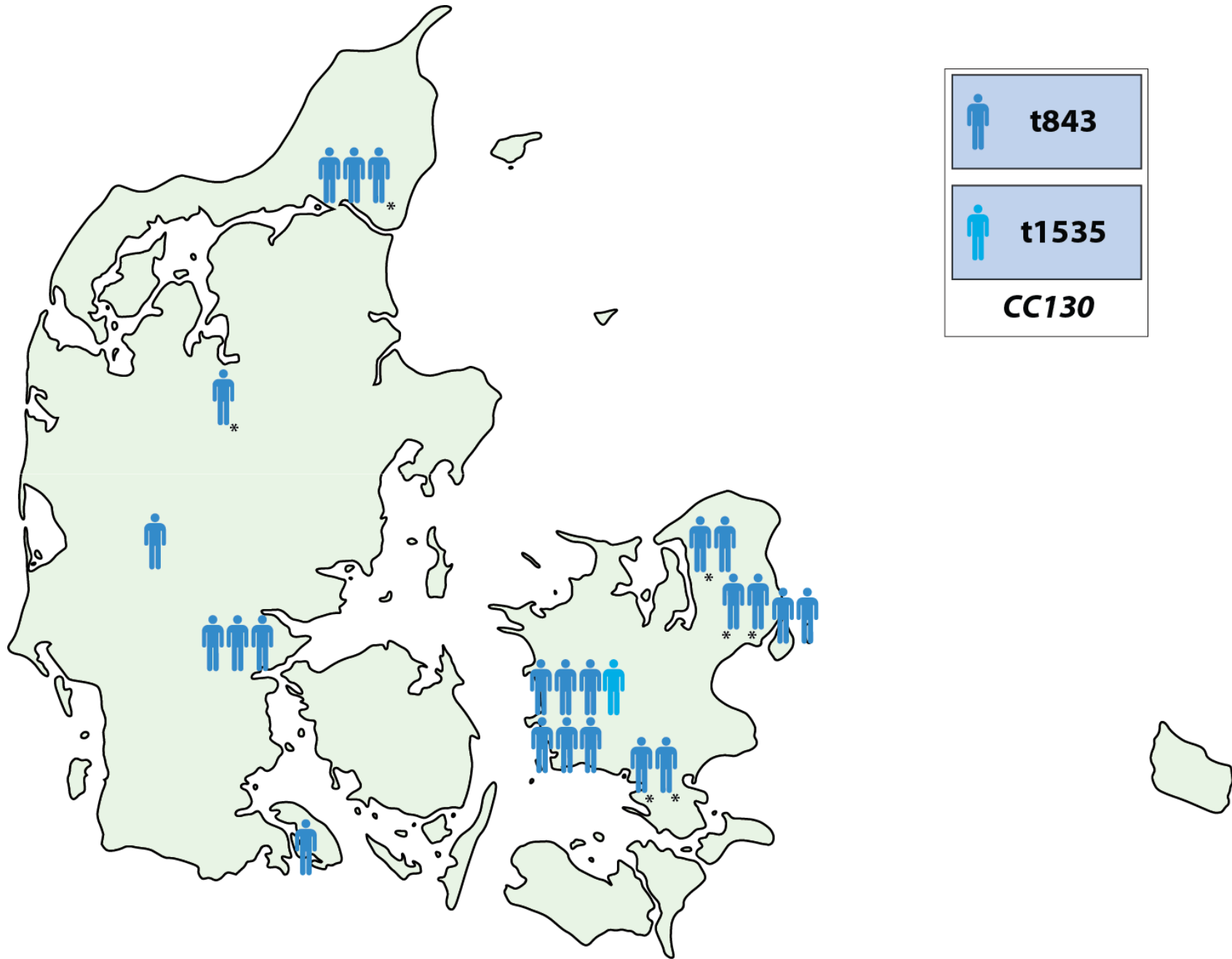
- Found that AHVLA had performed a survey and not found MRSA
 - But they had found 24 resistant *S. aureus* (above BSAC breakpoints for MRSA)
 - Negative for *mecA* using PCR
 - Reported as 'atypical MSSA'
- We obtained & tested these with new primers
 - 13 had *mecC* gene
 - remaining 11 have no *mec* gene

Searching in human samples

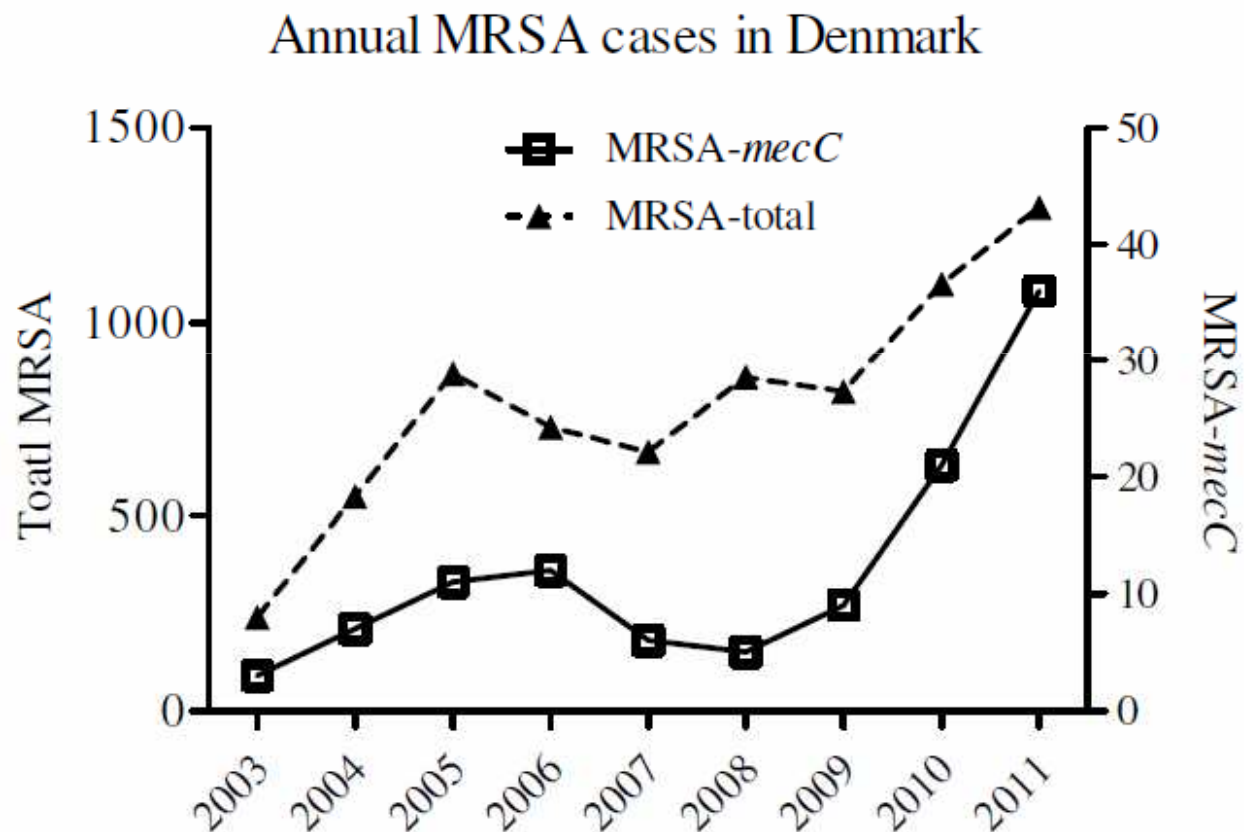
- First found in a sample from Cambridge (2009)
- We distributed details of the new test in 2010, first results obtained December 2010
- Tests on samples from Scotland, England, and Denmark
 - 12 from Scotland
 - 14 from England
 - 24 from Denmark
- We then used MLST (sequencing 7 housekeeping genes) and *spa* typing (protein A repeats) to see how related they were







New human MRSA isolates by year



Petersen A. et al. : Clin Microbiol Infect. 30. Aug 2012

Meticillin-resistant *Staphylococcus aureus* with a novel *mecA* homologue in human and bovine populations in the UK and Denmark: a descriptive study



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Summary

Background Animals can act as a reservoir and source for the emergence of novel meticillin-resistant *Staphylococcus aureus* (MRSA) clones in human beings. Here, we report the discovery of a strain of *S aureus* (LGA251) isolated from bulk milk that was phenotypically resistant to meticillin but tested negative for the *mecA* gene and a preliminary investigation of the extent to which such strains are present in bovine and human populations.

Methods Isolates of bovine MRSA were obtained from the Veterinary Laboratories Agency in the UK, and isolates of human MRSA were obtained from diagnostic or reference laboratories (two in the UK and one in Denmark). From these collections, we searched for *mecA* PCR-negative bovine and human *S aureus* isolates showing phenotypic meticillin resistance. We used whole-genome sequencing to establish the genetic basis for the observed antibiotic resistance.

Findings A divergent *mecA* homologue (*mecA*_{LGA251}) was discovered in the LGA251 genome located in a novel staphylococcal cassette chromosome *mec* element, designated type-XI SCC*mec*. The *mecA*_{LGA251} was 70% identical to *S aureus* *mecA* homologues and was initially detected in 15 *S aureus* isolates from dairy cattle in England. These isolates were from three different multilocus sequence type lineages (CC130, CC705, and ST425); *spa* type t843 (associated with CC130) was identified in 60% of bovine isolates. When human *mecA*-negative MRSA isolates were tested, the *mecA*_{LGA251} homologue was identified in 12 of 16 isolates from Scotland, 15 of 26 from England, and 24 of 32 from Denmark. As in cows, t843 was the most common *spa* type detected in human beings.

Interpretation Although routine culture and antimicrobial susceptibility testing will identify *S aureus* isolates with this novel *mecA* homologue as meticillin resistant, present confirmatory methods will not identify them as MRSA. New diagnostic guidelines for the detection of MRSA should consider the inclusion of tests for *mecA*_{LGA251}.

Funding Department for Environment, Food and Rural Affairs, Higher Education Funding Council for England, Isaac Newton Trust (University of Cambridge), and the Wellcome Trust.

Published Online

June 3, 2011

DOI:10.1016/S1473-

3099(11)70126-8

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Human – CC130, ST425, CC1943

Cattle – CC130, ST425

Dog – CC130

Chaffinch – CC130

Harbour seal – CC130



Denmark

Human – CC130, CC1943

Cattle – CC130

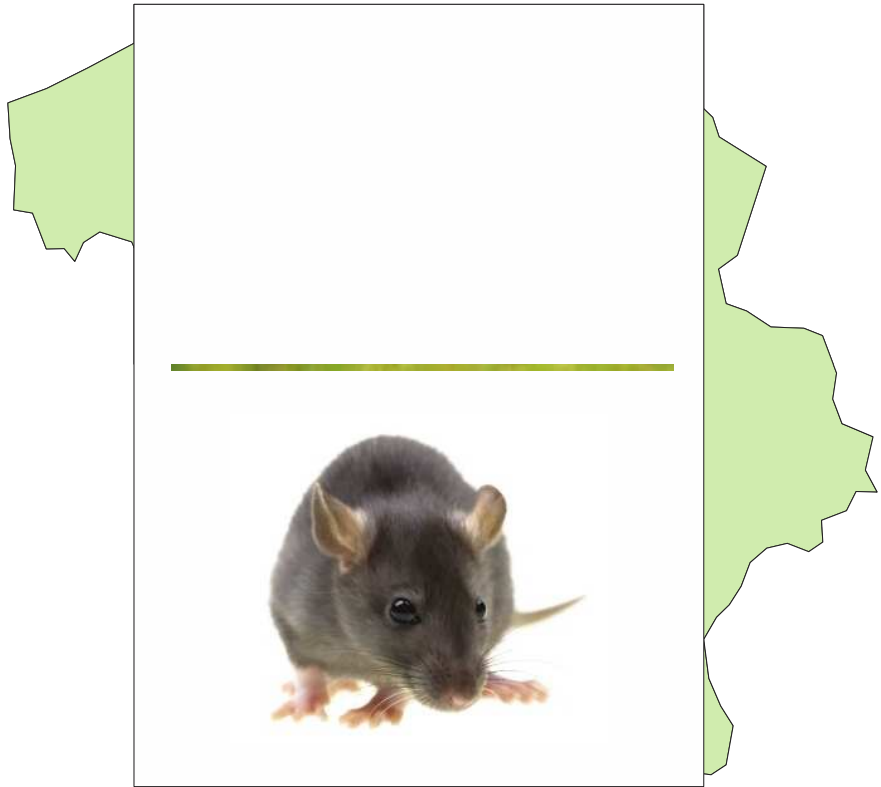
Sheep – CC130



Belgium

Rabbits – ST425

Rats – CC49



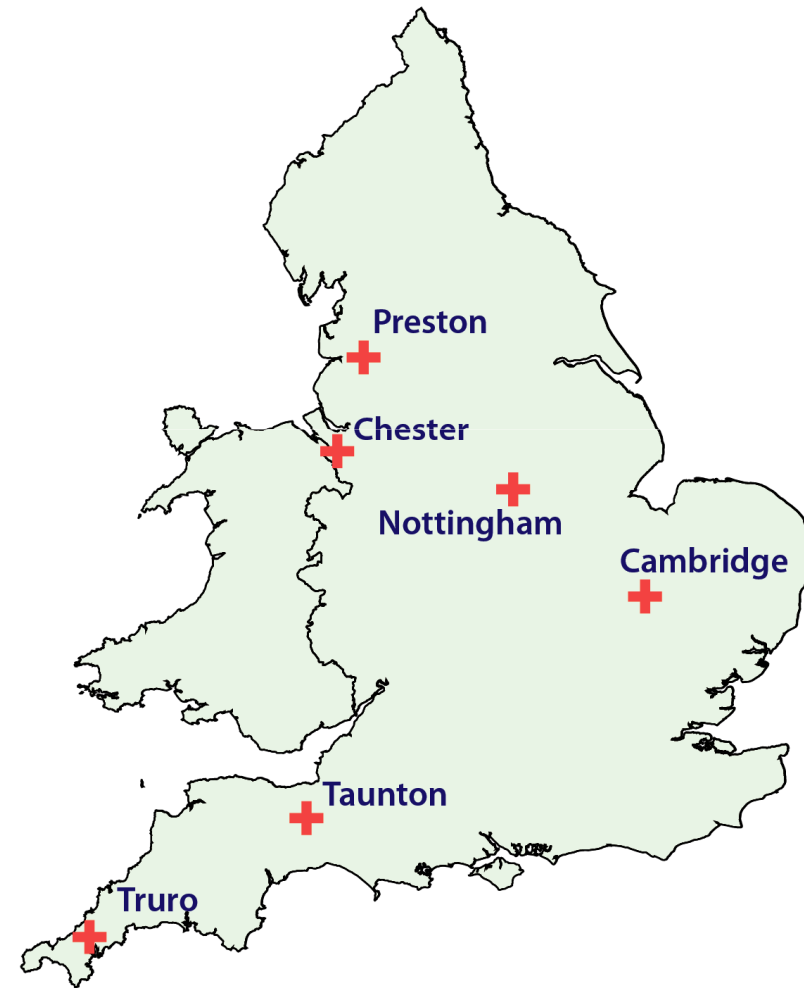
Germany

Humans – CC130
Cows – CC130
Sheep – CC130
Rats – CC130
Cats – CC130, CC599
Dogs – CC599
Guinea Pig – CC130
Roe Deer – CC130
Horse – CC130



Human prevalence in England

- 6 hospitals
- 6 x 350 MRSA isolates
(2100, all unique isolations,
up to 1 yr)
- MRSA mostly identified by
chromogenic ID agar
- **Interim result:**
Currently 0.45% (9/2,000)
- Cambridge 0.9% (3/350)

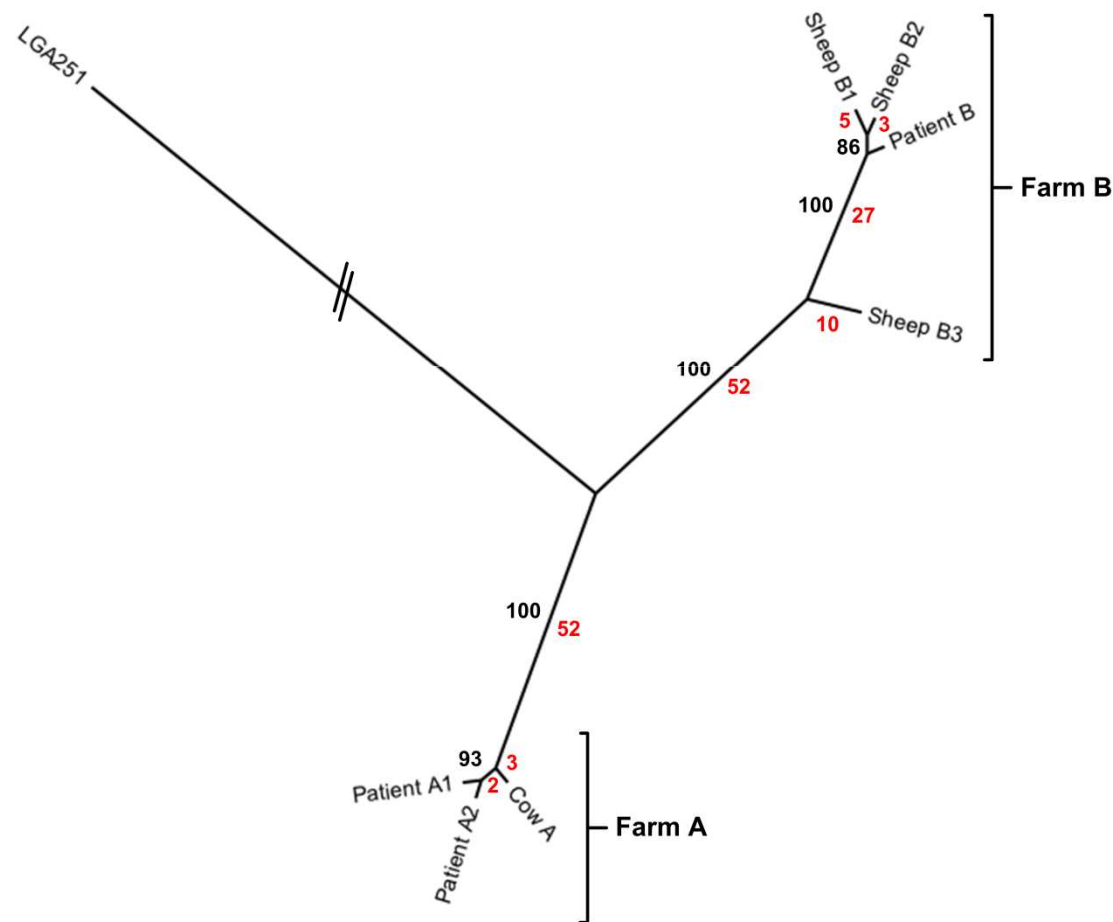


Bovine prevalence study

- 600 farms in England & Wales, 600 farms in Scotland (NMR samples)
- About 30% of samples +ve MRSA id agar
- **Interim results PCR:**
 - **2.5% (10/403) in England & Wales**
 - **0% (0/600) in Scotland**
- Almost 100% have MR-CoNS



Evidence of likely transmission between livestock and humans



Conclusions (risks and hazards)

- Anecdotally we have no evidence that *mecC* MRSA are more pathogenic than other *S.aureus* in man or animals
- The prevalence is low in man and in dairy farms (reliably quantified)
- We don't know the role of other animals in *mecC* MRSA epidemiology
- *We need to monitor the situation and collect more evidence to support these suppositions*

Acknowledgements



Cambridge

Derek Brown, Martin Curran, Sharon Peacock



VLA

Chris Teale



HPA Staphylococcal reference lab

Angela Kearns, Bruno Pichon



Scottish MRSA reference lab

Giles Edwards



Denmark

Robert Skov, Anders Rhod Larsen

Jesper Larsen, Marc Stegger



More Acknowledgements

Katleen Hermans
Birgit Walther
Hannah Jørgensen
Geoff Foster
Nick Davison
Olga Sakwinska
Sarne De Vlieghe
Gerard Wellenberg
Mariella Vitale
Sabine Leroy
Xander Huijsdens
Christiane Cuny & Wolfgang Witte
Frederic Laurent
Vic Simpson
Vincent Perreten

Robin Köck & Karsten Becker
Frank M. Aarestrup
Andrew Robb & Geoff Foster
Sara Hæggman

Gavin Paterson
Ewan Harrison
Fiona Morgan

Julian Parkhill
Sharon Peacock
Ruth Zadoks

National Milk Laboratories

Funding

- HEFCE
- DeFRA
- Isaac Newton Trust, Cambridge University
- Wellcome Trust
- This work is currently funded by an MRC Partnership Grant

