

**Turkey Meat as Source of CC9/CC398 Methicillin-Resistant *Staphylococcus aureus* in Humans?**

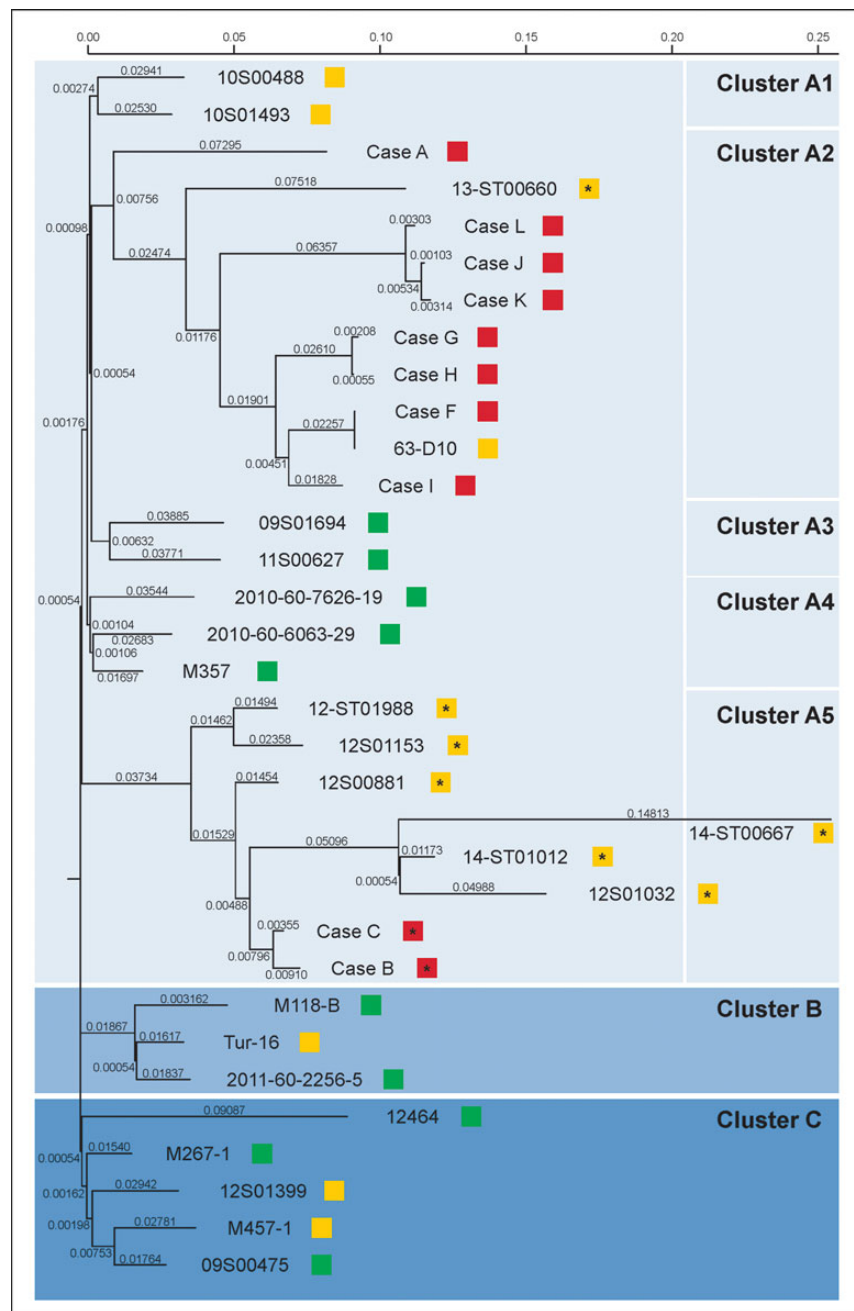
TO THE EDITOR—Livestock-associated methicillin-resistant *Staphylococcus aureus* (MRSA) of clonal complex (CC) 398 were first reported to cause severe infections in humans in 2005 [1]. Direct animal exposure is considered the most effective means of MRSA CC398 transmission from livestock to humans. However, about 20%–38% of MRSA CC398 cases among humans cannot be epidemiologically linked to direct livestock contact, indicating other transmission pathways [2]. As recently reported in this journal by Larsen et al [3], poultry meat may serve as a vehicle for livestock-to-human transmission. Here, we present similar findings for CC9/CC398 MRSA (displaying *spa* type t899 and related), which shares unique characteristics with human clinical isolates in Denmark as shown by Larsen et al [3], strongly supporting the implication of poultry, especially turkey meat, as the source of CC9/CC398.

Of a collection of >14 000 compromising strains, mainly of food and livestock origin, we identified 37 CC9/CC398 MRSA strains in addition to those described by Larsen et al [3]. Among these, 31 strains (all of poultry origin) were positive for *sak/scn/chp* (indicative genes carried by the  $\phi$ Sa3 prophage) by DNA microarray (see [4] for details), and 8 of 31 (7 from turkey meat, 1 from broiler meat) also carried the  $\phi$ Av $\beta$  prophage (SAAV\_2008/2009 genetic markers, respectively), as tested by a polymerase chain reaction assay [5]. The nucleotide sequence of the 4 turkey meat isolates—12S01032, 13-ST00660, 14-ST01012, and 14-ST00667—was determined using a PacBio RSII sequencer (Pacific Biosciences).

De novo assembling of the readings by HGAP3 resulted in a closed draft genome for each isolate. In general, all 4 isolates

exhibit similar genome features, chromosomal resistance genes, and virulence

factors (Supplemental Material Table S1). However, distinct differences were



**Figure 1.** Phylogenetic relationship of clonal complex (CC) 9/CC398 methicillin-resistant *Staphylococcus aureus* (*spa* types t899 and related) of our own study and selected isolates of the collection of Larsen et al [3]. Single-nucleotide polymorphism tree analysis was conducted using the services of the Center for Genomic Epidemiology. Phylogenetic clusters (A–C) were highlighted by different background colors; subdivisions represent subclusters. Isolates of human, turkey, and broiler chicken origin are indicated in red, yellow, and green, respectively. Genomes comprising the  $\phi$ Av $\beta$  prophage are marked by asterisks.

observed in the content of mobile genetic elements (ie, plasmids, and phages). Further phylogenetic single-nucleotide polymorphism tree analysis against selected human cases and poultry isolates of the collection of Larsen et al [3] confirm that 3 of our 4 CC9/CC398 isolates (12S02032, 14-ST01012, and 14-ST00067) cluster together with whole-genome sequences of the Danish human cases B and C (subcluster A5), whereas 13-ST00660 is more related to the human cases A, F–K, and the turkey isolate 63-D10 (subcluster A2); obviously, strains originating from broiler chickens were present only in other (sub) clusters (A3, A4, B, and C) (Figure 1).

Trace-back investigations of turkey meat along the food chain revealed an epidemiological link to Poland in 4 of 7  $\phi$ Av $\beta$ -carrying CC9/CC398 strains; that is, animals either originated from or were slaughtered or processed in Poland. The 3  $\phi$ Av $\beta$  prophage-carrying turkey cluster strains (12S00881, 12-ST01988, and 12S01153) that formed a separate group within the poultry-associated subclade, as shown by Larsen et al [3], are also linked to Poland. Moreover, the majority of the turkey meat was traced back to a narrow area in the North of Poland, implicating a point source of origin for the  $\phi$ Av $\beta$ -positive CC9/CC398 clones. These findings strongly show the high demand on comprehensive monitoring and intervention strategies from farm to fork to prevent further distribution of pathogenic MRSA of livestock origin via the global food chain, together with in-depth comparisons between MRSA strains of human and turkey origin.

### Supplementary Data

Supplementary materials are available at <http://academic.oup.com/cid>. Consisting of data provided by the author to benefit the reader, the posted materials are not copyedited and are the sole responsibility of the author, so questions or comments should be addressed to the author.

### Notes

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