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MLVA of *Dichelobacter nodosus*¹

Causes interdigital dermatitis and footrot in sheep, and approx. 90% of all cases of lameness in the UK flock

MLVA scheme developed based on four loci

77 global isolates characterised from GB and Australia (long history of footrot), India and Scandinavia (short history of footrot)

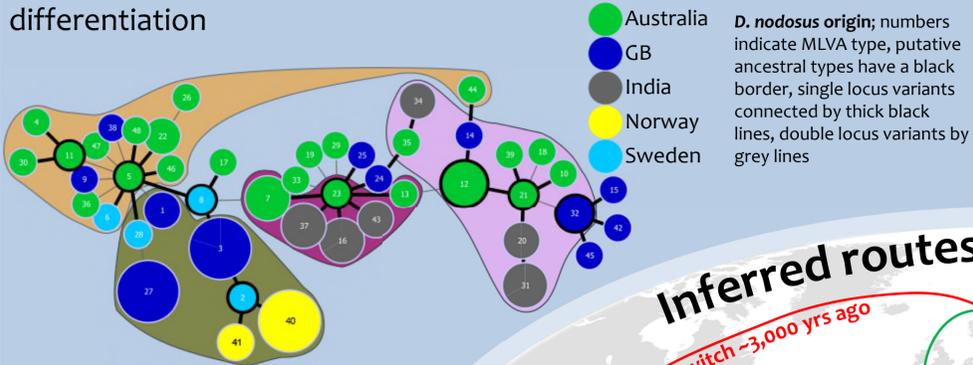
Four populations detected

Between locus variability suggests some regions evolve more rapidly than others, and allows capture of fast / slow evolution events

History of recombination within *D. nodosus*, short-term evolution driven by clonal expansion

International allelic distribution matches historical accounts of sheep movements

GB and Australian isolates cluster together with negligible differentiation



Indian and Scandinavian isolates are distinct from each other suggesting independent origins



MLST of *Staphylococcus aureus*²

Globally relevant and potentially zoonotic pathogen that is a major cause of clinical and subclinical mastitis in sheep (and other animals)

Diversity and spread of ovine *S. aureus* investigated using MLST

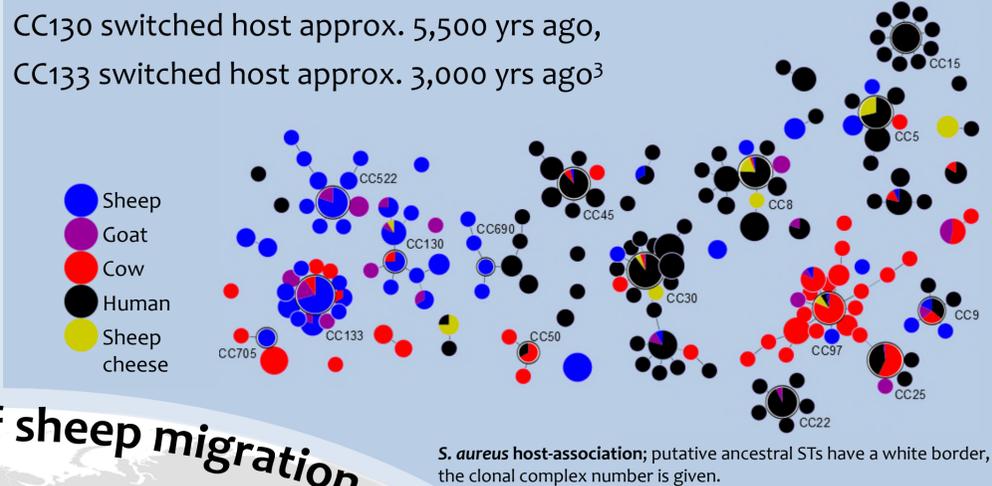
97 global isolates characterised from UK, Turkey, France, Norway, Australia, Canada and the USA

Compared with 196 sheep, 172 bovine, 68 caprine and 433 human *S. aureus* profiles

Majority of global ovine isolates belong to one of three clonal complexes (CC): CC522, CC130, CC133

CC522 detected in S. Europe and N. Africa; CC130 detected throughout Europe and in N. Africa; CC133 detected across the New World

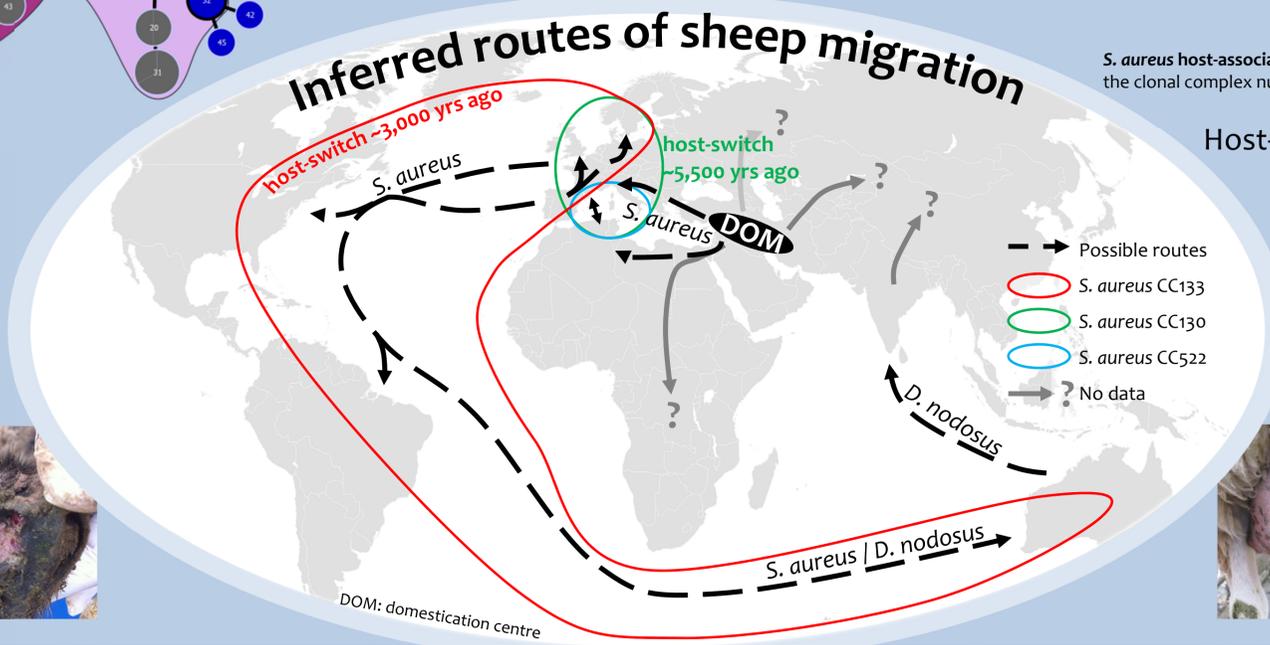
CC130 switched host approx. 5,500 yrs ago, CC133 switched host approx. 3,000 yrs ago³



Host-switching appears to match the location and timing of domestication [CC130] and selection for meat and wool production [CC133]



Inferred routes of sheep migration



Conclusions

Sheep migration has disseminated *S. aureus* and *D. nodosus* lineages globally

Livestock domestication and export appears to have been a driver of *D. nodosus* and *S. aureus* evolution as lineages have co-evolved and spread within sheep

The diversity of *D. nodosus* and *S. aureus* in Asia and Africa is largely unexplored and might reveal more about the domestication and spread of sheep populations.

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References

¹Russell et al, 2013. Infection, Genetics and Evolution: doi.org/10.1016/j.meegid.2013.05.026; ²Smith et al, 2013. Infection, Genetics and Evolution; Accepted; ³Weinert et al, 2012. Biology Letters: doi: 10.1098/rsbl.2012.0290.