

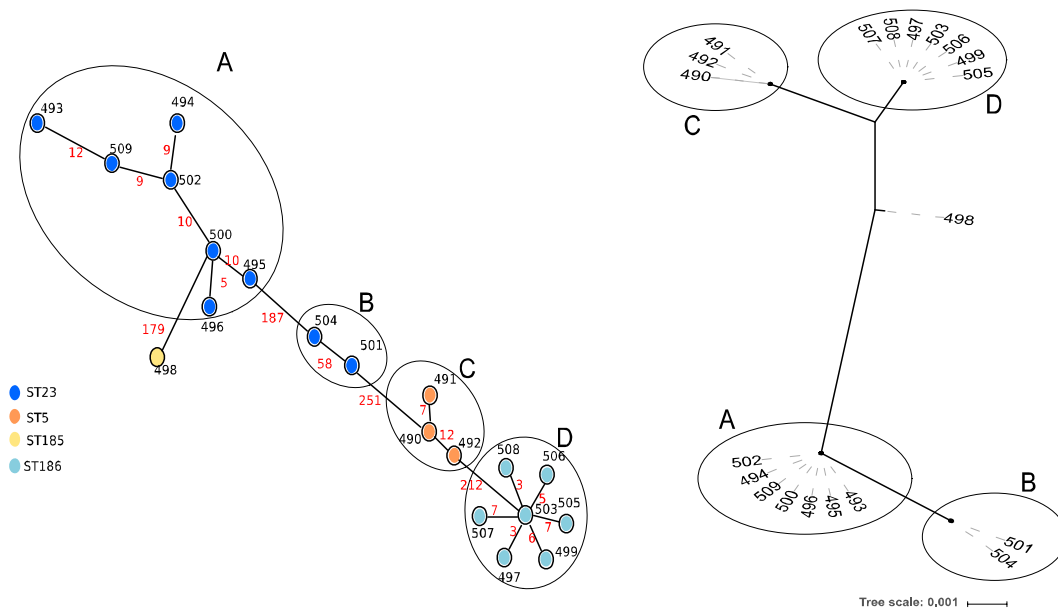
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554 **Figure 1. Distribution of gene presence and absence for *mecA*, *ccrAB*, *ica* and *fdh* loci**
 555 **among 252 infection isolates and 194 commensal isolates from the BIGSdb database.**

556 *mecA* encodes penicillin-binding protein 2 (PBP2); *ccrA* and *ccrB* encode cassette
 557 chromosome recombinase A and B respectively; *icaA* and *icaD* genes are involved in
 558 polysaccharide intercellular adhesin (PIA) production; *fdh* encodes a formate dehydrogenase.
 559 There was a positive association between infection isolates and *mecA*, *ccrA* and *ccrB* loci
 560 compared to commensal isolates (** Fisher<0.001) and there was a positive association
 561 between commensal isolates and *fdh* locus compared to infection isolates (* Fisher <0.005).

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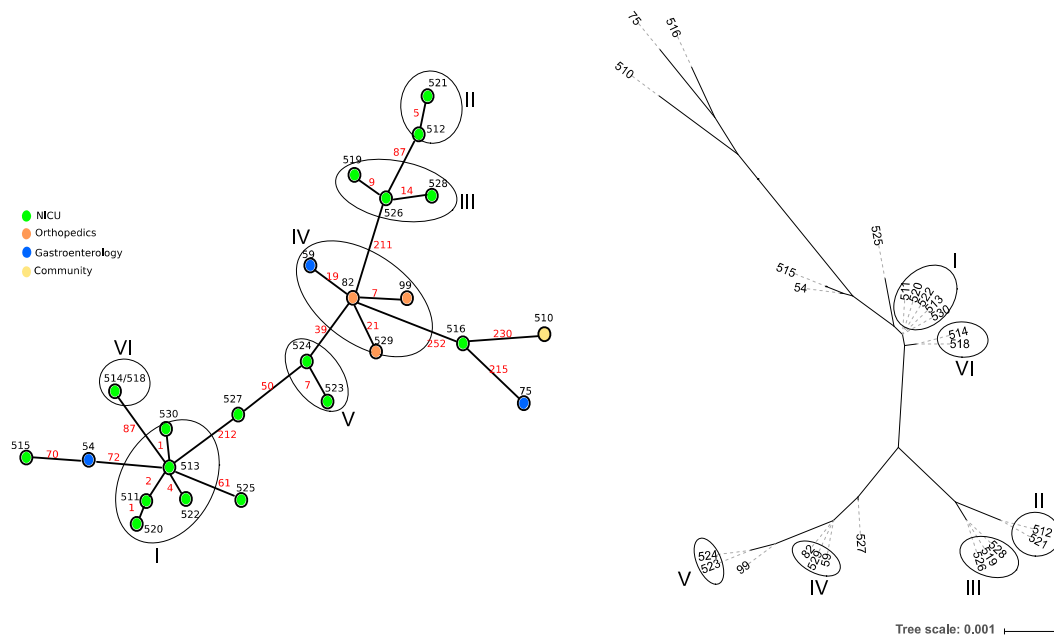
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Figure 2. Comparison of cluster analysis based on cgMLST allelic profiles with phylogenetic analysis based on core genes alignments for 20 linezolid-resistant isolates.

The minimum-spanning tree based on cgMLST allelic profiles is shown on the left side. The tree was generated from allelic profiles of 699 core genes and visualised with PHYLOViZ. Each node represents an isolate and is coloured according to the 7-loci ST. *In silico* MLST performed on the *de novo* assemblies revealed that isolates UCLA-Sa-LR-14 (497) and UCLA-Sa-LR-21 (503) had been erroneously assigned to ST24 and ST186-like respectively in the original publication [6]. We found that in fact both strains belonged to ST186. Black numbers next to the nodes indicate the BIGSdb identifiers of each isolate. Red numbers on the connecting lines indicate the number of core gene allele differences between adjacent nodes. Link lengths are loosely related to the number of allelic differences.

The tree based on 699 core gene sequences alignments is shown on the right side. The tip labels indicate the BIGSdb identifiers of each isolate.

Clusters reported by Tewhey *et al.* based on the alignments of 2,093 core genes [6] are indicated by circles and letters (A, B, C and D).

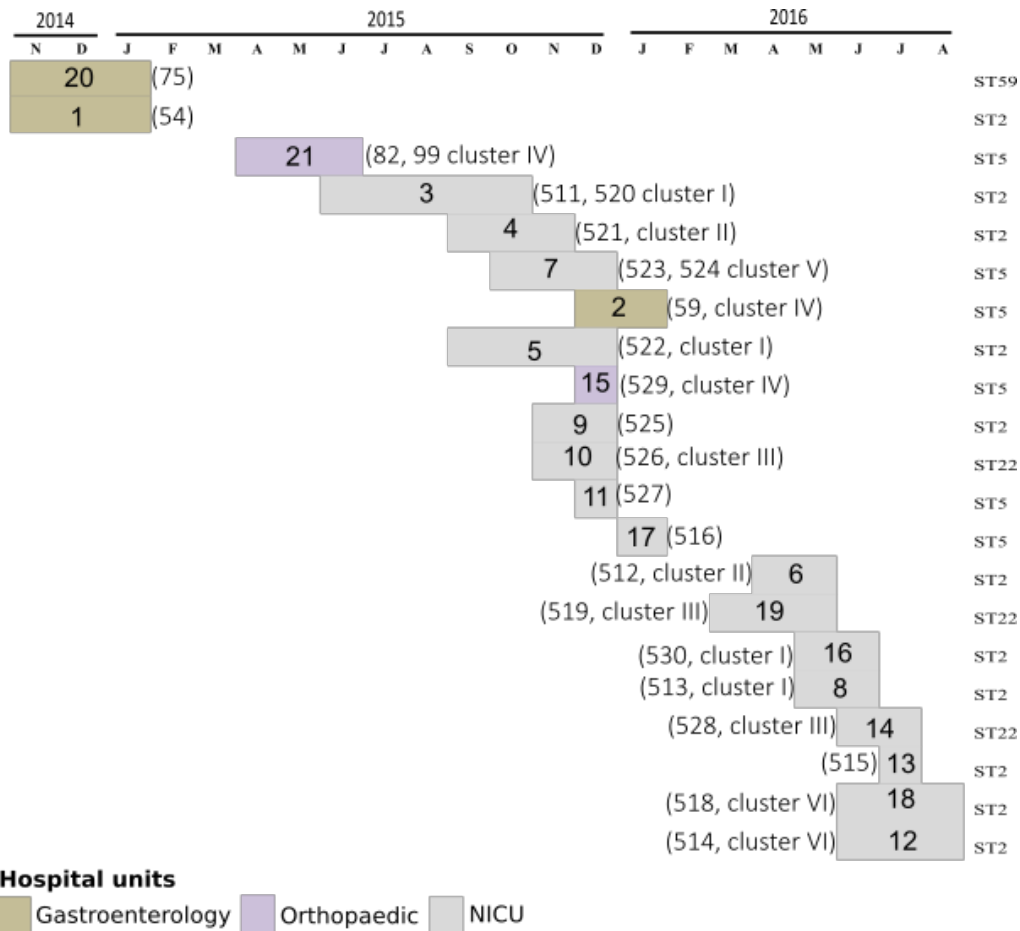


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583 **Figure 3. Comparison of clustering analyses based on cgMLST allelic profiles and on**
 584 **core gene sequences alignment, for 25 *S. epidermidis* isolates sequenced in this study.**

585 The minimum-spanning tree based on cgMLST allelic profiles is shown on the left side. The
 586 tree was generated from allelic profiles of 699 core genes. Each node represents an allelic
 587 profile and corresponds to a single isolate except the node corresponding to cluster VI where
 588 2 isolates have the same profile. Nodes are coloured according to the ward where patients
 589 were hospitalised. Black numbers next to the nodes indicate the BIGSdb identifiers of each
 590 isolate. Red numbers on the connecting lines indicate the number of core gene alleles
 591 differences between adjacent nodes. Link lengths are not proportional to the number of allelic
 592 differences. Clusters of closely related genotypes (≤ 21 allele differences) are surrounded by
 593 circles and are numbered (I to VI).

594 The tree based on 699 core genes alignment is shown on the right side. The tip labels indicate
 595 the BIGSdb identifiers and names of each isolate. Clusters are indicated by circles and are
 596 numbered (I to VI) as in the minimum-spanning tree.



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599 **Figure 4. Timeline of the 21 hospitalized patients from which 24 *S. epidermidis* isolates**
 600 **were sequenced.**

601 The patient numbers indicated in the coloured boxes and the patient isolate numbers indicated
 602 between brackets correspond to those in **Table 1**. The clusters to which isolates belong
 603 correspond to those in Figure 3. The isolate sequence type (ST) is indicated on the right side
 604 of the graph.

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