

***Staphylococcus ursi* sp. nov., a new member of the ‘*Staphylococcus intermedius Group*’ isolated from healthy black bears**

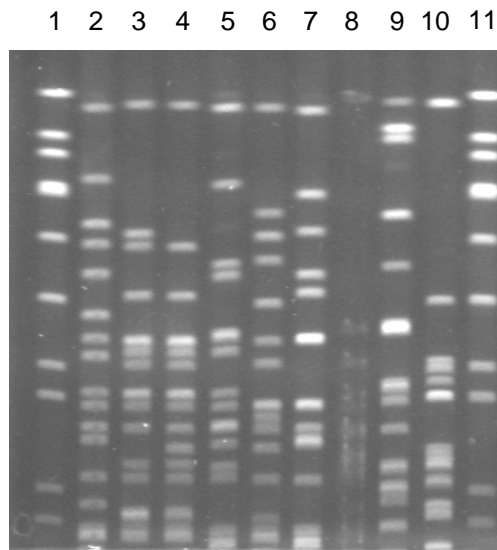
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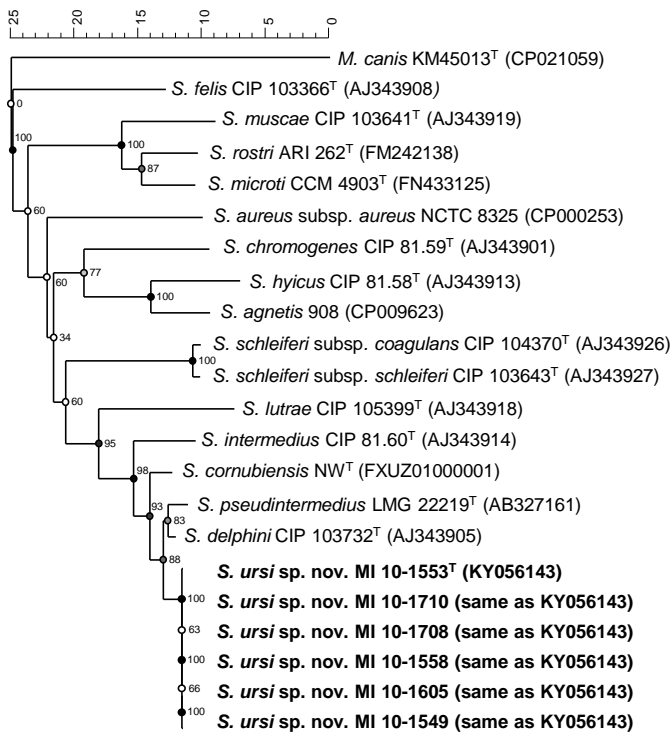
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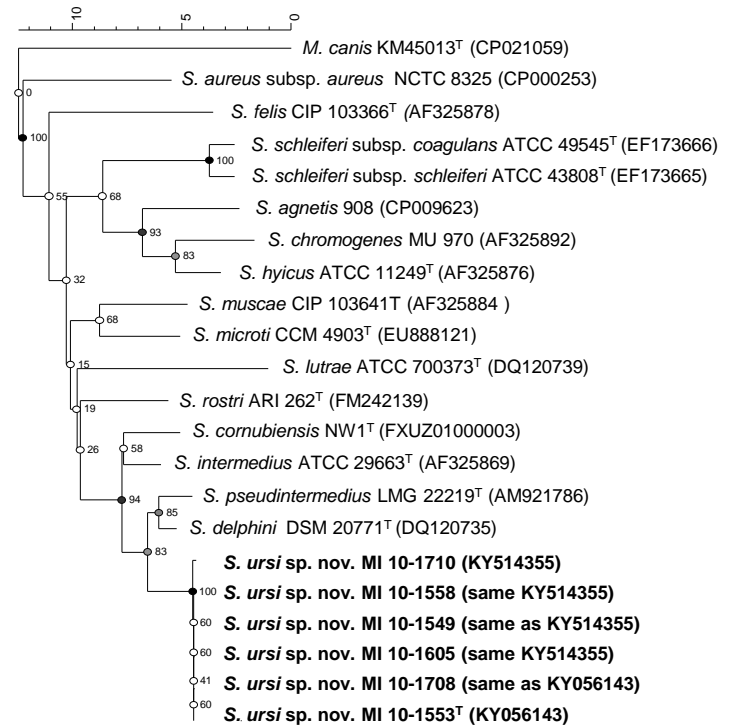


Supplementary Figure S1. Pulsed-field gel electrophoresis (PFGE) of Cfr9I-digested DNA from *Staphylococcus ursi* sp. nov. (lanes 2 to 7) and other type strains of the *Staphylococcus intermedius* group, namely *Staphylococcus delphini* (lane 8), *Staphylococcus intermedius* (lane 9) and *Staphylococcus pseudintermedius* (lane 10). 1 and 11, *Staphylococcus aureus* NCTC 8325 as marker; 2, MI 10-1549; 3, MI 10-1553^T; 4, MI 10-1558; 5, MI 10-1605; 6, MI 10-1708; 7, MI 10-1710; 8, DSM 20771^T; 9, DSM 20373^T; 10, CCUG 49543^T. PFGE was run in 1% agarose gel in 0.5X TBE on a Bio-Rad CHEF-DR III system for 18h with pulse from 0.5 to 15s and for 5h with pulse from 20 to 25s and at 14°C and 5.6 V/cm.

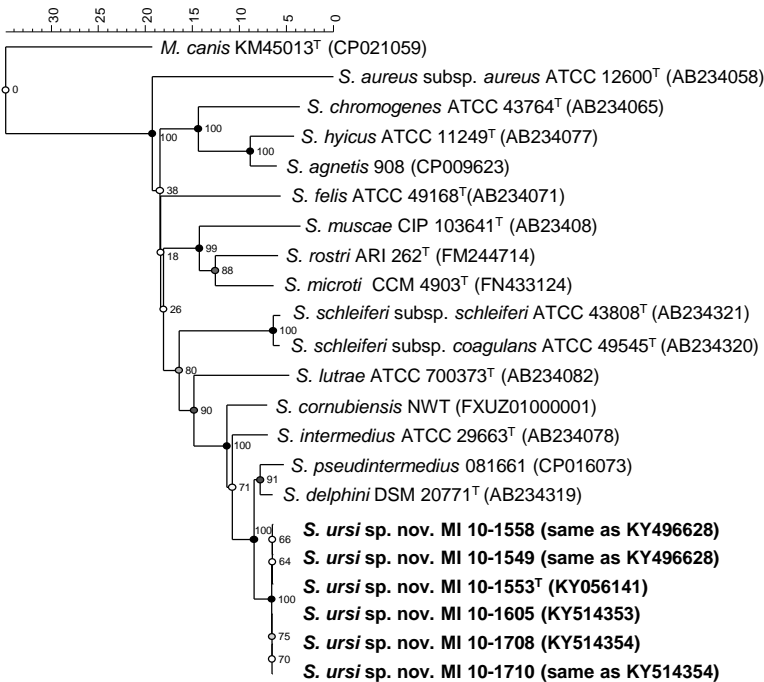
A) *sodA*



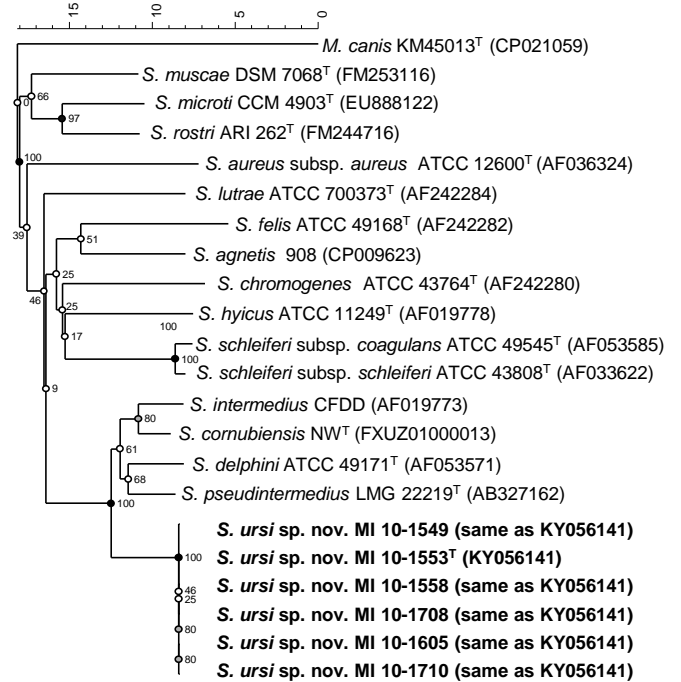
B) *rpoB*



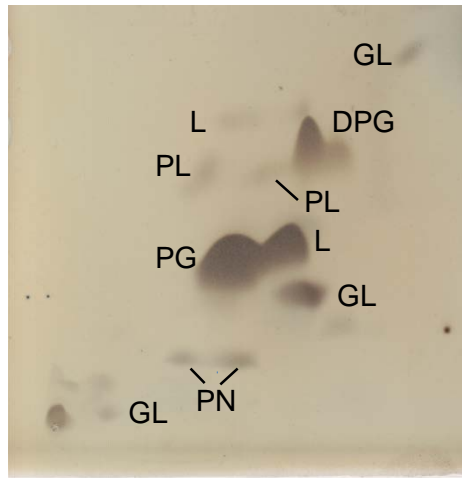
C) *dnaJ*



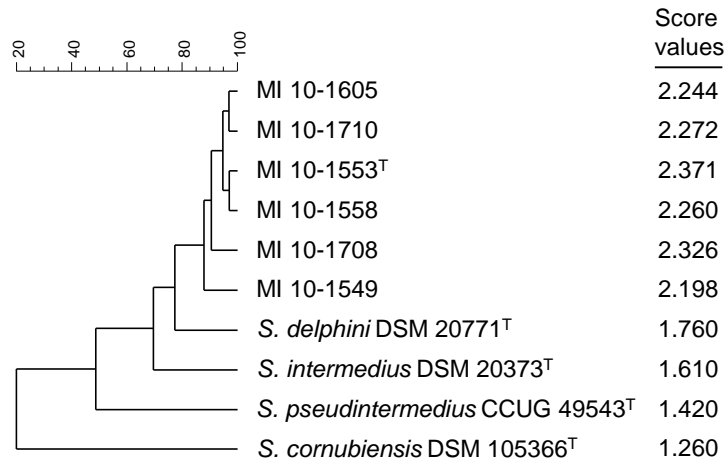
D) *hsp60*



Supplementary Figure S2: Phylogenetic tree constructed from partial gene sequences of *sodA* (416 bp) (A), *rpoB* (476 bp) (B), *dnaJ* (883 bp) (C), and *hsp60* (552 bp) (D) of *Staphylococcus ursi* sp. nov. and the *Staphylococcus* species of the *Staphylococcus hyicus-intermedius* group, as well as *S. aureus*. The trees were generated by Neighbor Joining analysis [Multiple alignment (OG: 100%, UG: 0%), discard unknown bases, use active zones only] and Jukes-Cantor correction using BioNumerics 7.5 (Applied Maths, Sint-Martens-Latem, Belgium). Bootstrap values are shown at each node as percentage of 1500 replicates. The sequences of the *Macrococcus canis* type strain KM45013^T were used as outgroup to root the trees. The GenBank/EMBL/DDBJ accession numbers are provided in the parentheses.



Supplementary Figure S3. Polar lipid profiles of *Staphylococcus ursi* MI 10-1553^T as determined by two-dimensional thin-layer chromatography. L, lipid; PL, phospholipid; PG, phosphatidylglycerol; PN, aminophospholipid; GL, glycolipid; DPG, diphosphatidylglycerol.



Supplementary Figure S4. Dendrogram obtained by cluster analysis of MALDI-TOF MS (Bruker Biotyper version 3.1) spectrum profiles (SP) of 6 strains of *Staphylococcus ursi* sp. nov. including type strain *S. ursi* MI 10-1553^T and of the other type strains of the *Staphylococcus intermedius* group (SIG), namely *S. intermedius*, *S. pseudintermedius* and *S. delphini*. Each SP was obtained from 3 different measurements. The score values were obtained using the MSP of *S. ursi* MI 10-1553^T as reference. The tree was constructed using Pearson's correlation with UPGMA clustering using Bionumerics 7.6 (Applied Maths, Sint-Martens-Latem, Belgium).