



Clustering trees. A. Trees obtained using MLVA-based genotyping for strains harboring clinically important toxins. For each strain, year of isolation, *SCCmec* type, toxin content, MLST and *agr* types are also indicated (Year/*SCCmec*/ST/*agr*). Major clusters appear in grey. ND. Not determined. NT: non-typable.

* Clonal strains isolated from the familial cluster of ST80-MRSA-IV harboring the PVL gene. ** The first ST80-MRSA-IV harboring the PVL gene isolated in 1994. *** atypical ST149 strain clustering with other ST149 isolates, showing two different important toxins, ^A single locus variant of ST395, ^B small familial clusters of clonal strains isolated in 2 pairs of relatives, ^C and ^D are 2 pairs of clonal strains from a neonatology cluster previously described (7), ^E patients returning from New York infected with USA300, ^F clusters of isolates from 2 prison inmates, ^G the only patient of the collection (IV drug user) with a strain highly related to USA400, ^H isolate showing molecular content of the ST59 pacific clone. **B.** Trees obtained using MLVA-based genotyping for strains devoid of clinically important toxins. For each strain, year of isolation, *SCCmec* type, toxin content, MLST and *agr* types are also indicated (Year/*SCCmec*/ST/*agr*). ^A familial cluster of ST1-MRSA-V composed of a mother and her 2 children, ^B control strain MW2 (USA400), ^C control strain ST228-MRSA-I representing the common nosocomial strain in our area.