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Bats as reservoirs of *Staphylococcus aureus* complex

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Background: The colonization of afro-tropical wildlife with *Staphylococcus aureus* and the derived clade *Staphylococcus schweitzeri* remains largely unknown. A reservoir in bats could be of importance since bats and humans share overlapping habitats. In addition, bats are food sources in some African regions and can be the cause of zoonotic diseases.

Material/methods: We carried out a cross-sectional survey employing pharyngeal swabs of captured and released bats (n=133) in a forest area of Gabon. Swabs were cultured on Columbia blood agar and *S. aureus* selective solid media. *S. aureus* and *S. schweitzeri* were subjected to genotyping (*spa* typing and multilocus sequence typing, MLST) and were screened for virulence factors (e.g. enterotoxins, exfoliative toxins, Panton-Valentine leukocidin). A phylogenetic tree was constructed with the concatenated sequences of the MLST typing scheme. In this phylogenetic analysis, we included

isolates of this study and all published sequence types (ST) of *S. schweitzeri* and a selection of the most common STs of *S. aureus* from Africa.

Results: We detected low colonization rates of *S. aureus* (4-6%) and *S. schweitzeri* (4%) in two out of four species of fruit bats, namely *Rousettus aegyptiacus* and *Micropteropus pusillus*, but not in insectivorous bats. MLST showed that *S. aureus* from Gabonese bats (ST2984, ST3259, ST3301, ST3302) were distinct from major African human associated clones (ST15, ST121, ST152). *S. schweitzeri* from bats (ST1697, ST1700) clustered with *S. schweitzeri* from other species (bats, monkeys) from Nigeria and Côte d'Ivoire. All isolates were negative for enterotoxins, exfoliative toxins, Panton-Valentine leukocidin.

Conclusions: In conclusion, colonization rates of bats with *S. aureus* and *S. schweitzeri* were low in our study. Phylogenetic analysis supports an intense geographical dispersal of *S. schweitzeri* among different mammalian wildlife hosts.