



Letter to the Editor

Is Africa the origin of major Haitian *Staphylococcus aureus* lineages?



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 Dear Editor,

We read with interest the article by Rosenthal et al. on the microbiological characterization of *Staphylococcus aureus* isolates ($n = 16$) from carriers in Haiti.¹ They reported a high prevalence of Panton–Valentine leukocidin (PVL) gene-positive ($n = 3$) and tetracycline-resistant ($n = 6$) isolates associated with multilocus sequence type (MLST) clonal complexes CC5 ($n = 4$) and CC152 ($n = 2$). PVL can be associated with skin and soft tissue infections, but its definitive role in the pathogenesis of disease remains controversial.^{2,3} CC152 is the major PVL-positive clonal complex in Sub-Saharan Africa.⁴

On the grounds of the findings of Rosenthal et al., we performed an ad hoc analysis of 10 *S. aureus* isolates from infections (i.e., skin and soft tissue infections, empyema; [Table 1](#)), which were collected

consecutively at the Albert Schweitzer Hospital in Deschapelles, Haiti in 2014. These isolates harboured PVL genes ($n = 9$), were resistant to tetracycline ($n = 3$), and belonged to CC152 ($n = 3$), CC5 ($n = 3$), CC30, CC88, CC121, and CC672 ($n = 1$ each; [Table 1](#)).

The high prevalence of PVL gene possession and tetracycline resistance in association with CC5, CC121, and CC152 are typical of *S. aureus* from Sub-Saharan Africa.^{4,5} Descendants of black African slaves form the majority (95%) of the Haitian population.⁶ Due to our molecular-epidemiological findings and the origin of the Haitian population, we hypothesize that the Haitian *S. aureus* isolates that are closely related to African clones might have originated from Africa during the slave trade or later in the African Diaspora. This has already been suggested for hepatitis B subgenotype A5, which most likely emerged from the Bight of Benin, West and Central Africa, to Haiti.⁷ This further supports the ‘out of Africa’ hypothesis of certain pandemic *S. aureus* clones, which have been found in remote African Pygmy populations.^{8,9} Indeed, the major European community-acquired PVL-positive methicillin-resistant *S. aureus* (ST80 CA-MRSA) most likely originated from Sub-Saharan Africa, as revealed by whole genome sequencing analyses.¹⁰

In conclusion, the study by Rosenthal et al. and our report point towards the significance of migration in the spread of certain pathogens such as *S. aureus*. Haiti, as a former target country of the slave trade, may play a central role when assessing the global spread of certain *S. aureus* lineages in the future.

Table 1*Staphylococcus aureus* isolates from infections, Haiti, 2014

ID	Infection	<i>spa</i> type	ST	CC	<i>mecA</i>	PVL	Penicillin	Tetracycline	Co-trimoxazole
267	Empyema	t14132	ST25	CC5	No	Yes	R	R	S
283	SSTI	t355	ST2164	CC152	No	Yes	R	R	S
303	SSTI	t4701	ST88	CC88	No	Yes	S	S	S
312	Osteomyelitis	t1096	ST152	CC152	No	Yes	R	S	S
339	Abscesses	t4198	ST3144	CC121	No	Yes	R	S	R
340	Empyema	t548	ST3074	CC5	No	No	R	R	S
342	Empyema	t665	ST3143	CC30	Yes	Yes	R	S	R
366	SSTI	t14132	ST25	CC5	No	Yes	R	S	S
368	SSTI	t355	ST2164	CC152	Yes	Yes	R	S	S
381	SSTI	t422	ST672	CC672	No	Yes	S	S	S

ST, sequence type; CC, clonal complex; PVL, Panton–Valentine leukocidin; R, resistant; S, sensitive; SSTI, skin and soft tissue infection.

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Conflict of interest: The authors have no conflicts of interest to declare.

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