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Stenotrophomonas maltophilia from infected hospitalized patients: a focus on the most pathogenic genetic backgrounds

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Background: Stenotrophomonas maltophilia (Sm) is an archetypal opportunistic environmental bacteria responsible for healthcare-associated infections (HAIs). The aim of this study is to decipher the population structure of Sm from hospitalized infected patients, that is a key element to improve selectively the management of human or environmental reservoirs.

Material/methods: We characterized genotypically and phenotypically a willfully varied sample of 83 human strains from various clinical origins and from 18 geographically distant hospitals.

Results: Among the 80 MLST typeable strains, only 29% corresponded to described STs, mainly ST5 (n= 6) and ST4/26/31 (n=2). The ST distribution and the phylogenic tree based on the concatenated MLST housekeeping genes did not support a clusterization according to the geographical or clinical origin, or to the antimicrobial susceptibility. Noteworthy we detected a colistin heterogeneously resistant non-related subpopulation of strains. Beyond the MLST scheme, we confirmed (i) the previously reported genogroups organization, (ii) the predominance of the genogroups 6 and, unexpectedly, 2 that grouped 41% (33/80) and 16% (13/80) of the strains, respectively. These both genogroups represented 57% (20/35) of the respiratory and 75% (9/12) of the cystic fibrosis patient strains. Failing so far to identify predominant or emerging ST, we confirmed the over-representation of some genogroups among strains responsible for HAIs. The pathogenic potency of Sm environmental or human reservoirs should then be tested using this genogrouping affiliation rather than other molecular methods.

Conclusions: Our findings could facilitate the management of Sm reservoirs, focusing our efforts toward controlling environmental contamination or cross-transmission due to the human predominant and most pathogenic genogroups.