



Poster #447

Session : Nosocomial infection surveillance & epidemiology

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

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Background

- *Stenotrophomonas maltophilia* (Sm) is an opportunistic multi-drug resistant bacteria responsible for healthcare-associated infections (HAI) (1)
- In-hospital infection control management of carriers and environmental reservoirs is unclear.

Aim of the study

- to decipher the population structure of Sm from hospitalized infected patients,
- to identify some putative highly pathogenic subpopulations requiring upgraded infection control measures.

Methods

- We characterized phenotypically and genotypically a sample of 83 diverse human strains from various clinical origins from 18 geographically distant hospitals (Fig. 1):
- Antimicrobial susceptibility (disc diffusion / MIC determination - Etest®)
 - MLST typing using the scheme of Kaiser et al. (2)
 - Construction of a phylogenetic tree based on the concatenated MLST housekeeping genes (3,591 bp) including all the 173 MLST profiles available at the PubMLST website at the first October, 2016, and the 64 strains of the original work of Kaiser et al. (2)

Results and Discussion

- Neither predominant nor emerging ST was identified.
- Among the 80 MLST typeable strains, only 29% corresponded to described STs, mainly ST5 (n= 6) and ST4/26/31 (n=2).
- No clusterization according to the geographical or the clinical origin or to the antimicrobial susceptibility was identified from ST distribution and from the phylogenetic tree based on the concatenated MLST genes
- The phylogenetic tree including the 173 ST profiles of the MLST database and our 80 typeable clinical strains (Fig. 2):
 - confirmed the **high genetic diversity** of Sm,
 - confirmed the previously reported **genogroups organization** (2),
 - confirmed the predominance of the **genogroup 6** (33/80, 41% of the strains),
 - pointed out the unexpectedly importance of the **genogroup 2**, the second most prevalent genogroup including 16% (13/80) of the strains.
 - These both genogroups represented 57% (20/35) of the respiratory and 75% (9/12) of the cystic fibrosis patient strains.

Conclusion

- Beyond MLST typing, we confirmed the over-representation of some genogroups among strains responsible for HAIs
- We supported this genogrouping affiliation to selectively implement infection control measures

References

- (1) Brooke JS. Clin Microbiol Rev 2012;25:2-41.
- (2) Kaiser S et al. J Bacteriol 2009;191:2934-2943.



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Figure 2. Maximum-likelihood tree based on the concatenated sequences of the seven housekeeping gene fragments (3,591 bp). The tree was rooted with a sequence from *S. rhizophila*. The genogroup affiliation according to MLST in the original study is indicated by colored frames (2).

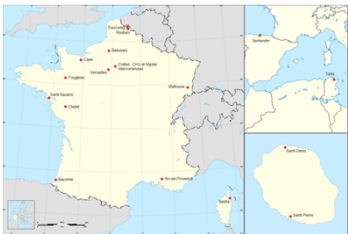
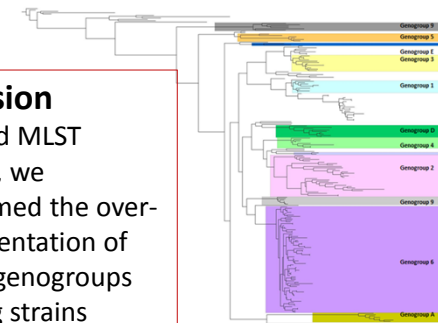


Figure 1. Geographical distribution of the 18 hospitals, including the two non-metropolitan (Reunion Island) and two extra-national centres (Spain, Tunisia).

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