

P0367

Paper Poster Session

Fungal infection epidemiology

European study on *Pneumocystis jirovecii* short tandem repeats genotyping reveals wide population diversity with geographic specificities

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Background: *Pneumocystis jirovecii* is a human specific uncultivable ascomycetous fungus, for which the reservoir is immunocompetent human individuals. Immunocompromised patients are at risk of developing pneumocystis pneumonia (PCP) when exposed to *P. jirovecii* through their immediate environment. A recently described short tandem repeat (STR) typing strategy was applied to a population of patients from Paris and found a high diversity of genotypes (Gts) between the patients, but identical Gts reflecting putative interhuman nosocomial transmission (1). In contrast, another genotyping study using a different STR set described a limited global population of *P. jirovecii* testing isolates recovered from Africa (n=13), USA (n=49) and Europe (n=29) (2). Our objective is to determine the distribution of *P. jirovecii* STR genotypes across European hospitals.

Material/methods: We investigated a collection of 355 *P. jirovecii* microscopy or PCR positive respiratory samples recovered from 355 PCP patients in 12 European countries [France (n=5), Belgium, The Netherlands, Denmark, Germany, UK, Poland, Czech republic, Switzerland, Italy, Spain, and Portugal]. STR typing was performed as previously described (1). Amplification failure occurred in 32% of the samples, likely a result of insufficient *P. jirovecii* DNA. Therefore, 242 samples (median: 17 per center [8-24]) were further analyzed.

Results: Mixtures of STR markers (>1 allele for ≥ 1 locus) were detected in 66.7% [range : 36.4%-90.9%] of the samples, with a trend towards a lower proportion of mixtures in France-Centre 2 and Belgium. The distribution of alleles in all six markers was significantly different according to the countries in STRPj_138 ($p=0.0002$), STRPj_278 ($p=0.0085$), and STRPj_279 ($p=0.0069$). Genotyping was analyzed only in samples harboring one allele/locus (n=87) or several alleles for one locus only (n=56). This provided 200 analyzable combinations corresponding to 143 Gts. Of them, 123 were found only in one country, 16 in two, 2 in three and 1 in four and five countries. Nine Gts were found more than once per country. Gt123 was significantly associated with France (14/15, $p=0.0007$) and Gt132 with Belgium (5/5, $p<0.0001$). In details, Center 2 in France and Belgium were associated with a high proportion of one genotype (42.8% of Gt123 and 100% of Gt132, respectively), suggesting enrichment in one geographical area or increased interhuman transmission in the corresponding hospitals.

Conclusions: Our study of 16 European centers showed a wide population diversity across Europe. However, focusing on centers, our results evidenced clusters of patients harboring a given genotype suggesting nosocomial interhuman transmission and potential outbreak situations.

References

1. Gits-Muselli M et al. PLoS One. 2015;10(5):e0125763.
2. Parobek CM et al. J Clin Microbiol. 2014 May;52(5):1391–9.