Mini Review

Unusual spoligotypes among *Mycobacterium tuberculosis* isolates from Senegal: T5-RUS1 and central Asia (CAS1-Delhi)

Abstract

We aimed to determine the molecular profile of strains of Mycobacterium tuberculosis isolated in Senegal. From 2011 to 2014, 64 strains isolated at the National Reference Laboratory for Mycobacteria of the National Antituberculosis Program (NAP) were characterized by spoligotyping. T super family was the principal family identified with two unusual spoligotypes: T5-RUS1 and Central Asia (CAS1-Delhi).

Keywords: tuberculosis, spoligotypes, Senegal

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Introduction

Tuberculosis is a major public health problem in Senegal. Molecular epidemiology techniques could help us to understand the dynamics of tuberculosis transmission.[1] Several PCR-based methods have been developed to discriminate among strains, including spoligotyping.[2] Unfortunately, as in many African countries; few molecular typing data are available in Senegal for the strains involved. In this study, we determined the molecular profiles of mycobacterial strains isolated over a four-year period in Senegal.

Materials and methods

We worked on isolates obtained at the National Reference Laboratory for Mycobacteria of the National Antituberculosis Program (NAP) in Senegal and isolated between January 2011 and December 2014, mostly from patients experiencing treatment failure or relapse, from Dakar and other regions of Senegal. Culture and drug susceptibility tests (DSTs) were performed at the reference laboratory of the NAP in Senegal. Depending on the availability of reagents, the DSTs were performed by the proportion method[3] or by molecular methods. The molecular typing of the strains was carried out in the reference laboratory for mycobacteria in Cotonou, Benin. Spoligotyping was used for molecular characterization. We used the standardized method described by Kamerbeek et al.,[2] based on the detection of polymorphism of the direct repeat (DR) region. This retrospective study included data collected during routine diagnosis and treatment, so it did not require ethics committee approval.

Results

Among 64 strains, nine different spoligotypes were identified, three of which were unique, whereas the other six formed clusters of two to nine isolates (Table 1). The two principal families found were the T superfamily and Beijing. We found also two unusual spoligotypes: T5-RUS1 and Central Asia (CAS1-Delhi).

Table 1 Spoligo types of the strains circulating in Senegal

Familles	SIT	Total (%)
T	*53*	13 (20,3%)
T	*1580*	1 (1,56%)
T	*181*	1 (1,56%)
Beijing	*1*	9 (14,06%)
Cameroon	*61*	3 (4,69%)
Cameroon	*37*	3 (4,69%)
LAM	*42*	3 (4,69%)
LAM4	*60*	2 (3,13%)
CAS1-Delhi	*26*	3 (4,69%)
H3	*183*	2 (3,13%)
H2	*2*	2 (3,13%)
AFRI_1	*187*	1 (1,56%)
AFRI_1	*326*	1 (1,56%)
T5-RUS1	*765*	1 (1,56%)
Orphelins	/	19 (29,7%)
Total	/	64

SIT: shared-type number in the SITVIT database

Discussion

This study is one of the first to investigate the molecular profile of the mycobacterial strains circulating in Senegal. Data analysis and comparison with international databases, particularly the SITVIT2 and SpolDB3 databases identified two major spoligotypes: ST53

and ST1, corresponding to the T superfamily and the Beijing family, respectively.

We detected also two spoligotypes rarely found in West Africa: ST765 (2.27%) and ST26 (4.55%) corresponding to the T5-RUS1 and Central Asia (CAS1-Delhi) types. Type T5-RUS1 (ST765), previously known as "non-LAM families (T1 or T5-RUS)" and recently reclassified as belonging to the LAM family[4] originated in the European part of Russia.[5] The Central Asia type (CAS1-Delhi) may be geographically linked to North India or Pakistan, or to other countries or regions, such as Sudan, Libya or East Africa.[6] In a pediatric population in India, the CAS1-Delhi type was second in frequency only to the Beijing type among susceptible and MDR isolates.[7] Three of the four unusual strains were MDR strains (2 CAS1-Delhi and 1 T5-RUS1). The rapid propagation of these strains may be linked, as previously suggested,[6] for multiple reasons to immigrants originating from the Far East, demographic changes and globalization.

Conclusion

Spoligotypes of M. tuberculosis isolated in Senegal belong mostly to the T superfamily and Beijing. This study showed also that spoligotypes generally considered to be "European" or "Asian" are also circulating in Senegal. This work provided a snapshot of spoligotypes circulating in Senegal and need to be completed by another one which will combine two techniques: spoligotyping and MIRU-VNTR.[8]

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Conflicts of interest

We have no conflict of interest relating to this article to declare.

References

1. Affolabi D, Anyo G, Faïhun F, et al. First molecular epidemiological study of tuberculosis in Benin. *Int J Tuberc Lung Dis*. 2009;13:317–322.
2. Kamerbeek J, Schouls L, Kolk A, et al. Simultaneous detection and strain differentiation of *Mycobacterium tuberculosis* for diagnosis and epidemiology. *J Clin Microbiol*. 1997;35:907–914.
3. Canetti G, Rist N, Grosset J. Mesure de la sensibilité du bacille tuberculeux aux drogues antibacillaires par la méthode des proportions. *Rev Tuberc Pneumol*. 1963;27:217–272.
4. Abadia E, Zhang J, dos Vultos T, et al. Resolving lineage assignation on *Mycobacterium tuberculosis* clinical isolates classified by spoligotyping with a new high-throughput 3R SNPs based method. *Infect Genet Evol*. 2010;10:1066–1074.
5. Mokrousov I, Vyazovaya A, Narvskaya O. *Mycobacterium tuberculosis* Latin American-Mediterranean family and its sublineages in the light of robust evolutionary markers. *J Bacteriol*. 2014;196:1833–1841.
6. Bezanahary H, Baclet MC, Sola C, et al. Molecular strain typing contribution to epidemiology of tuberculosis in Limousin (1998 to 2006). *Med Mal Infect*. 2008;38:309–317.
7. Arora J, Sidiq Z, Sharma S, et al. Phylogenetic associations with drug-resistant Mycobacterium tuberculosis isolates in a paediatric population. *Int J Tuberc Lung Dis*. 2014;18:1172–1179.
8. Sola C, Filliol I, Legrand E, et al. Genotyping of the Mycobacterium tuberculosis complex using MIRUs: association with VNTR and spoligotyping for molecular epidemiology and evolutionary genetics. *Infect Genet Evol*. 2003;3:125–133.