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Genetic diversity of Mycobacterium tuberculosis strains isolated in Algeria: Results of spoligotyping



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ABSTRACT

Objective/background: Molecular typing tools, including spoligotyping, are currently widely used in the monitoring and study of the dynamics of tuberculosis epidemics. *Methods:* A study of the molecular profile of a sample of 129 Myobacterium tuberculosis strains isolated during 2011 was carried out in the National Reference Laboratory for Tuberculosis and Mycobacteria at the Pasteur Institute of Algeria. This sample was selected at random from a set of 350 strains isolated from tuberculosis patients from central and eastern areas of the country.

Results: Genotypic analysis helped to clarify the frequencies of the different genotypes in the current study population: H family, 29%; LAM family, 26%; T family, 25%; S family, 5%, and other genomic families, including orphan strains, 15%.

Conclusion: The study of strains isolated between January and December 2011 has allowed insight into the frequency of different genomic families and the importance of existing clusters in the population of central and eastern Algeria.

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Introduction

Tuberculosis (TB) is an infectious and contagious disease that remains endemic in Algeria despite a long and welladministered national TB control program (NTBP). Algeria is classified by the World Health Organization into the group of countries having moderate TB prevalence, with an annual incidence of between 20 and 99 cases per 100,000 people [1,2]. In 2011, the incidence of microscopy-positive pulmonary TB cases was 19.4 out of 100,000 inhabitants, and the annual incidence of total TB was 57.7 out of 100,000 that same year. Molecular typing tools, including spoligotyping, are currently widely used in the monitoring and study of the dynamics of tuberculosis epidemics. Using these tools, a retrospective study of the strains isolated during the year 2011 was conducted, involving a sample of 129 strains of *Mycobacterium tuberculosis* isolated from TB patients diagnosed in the central and eastern regions of the country.

Materials and methods

The study was performed on 129 strains of M. tuberculosis identified from January 1st to December 31st, 2011. The study material was drawn from 14 departments of central and

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Fig. 1 – Distribution of individuals in the study population between the 14 departments from central and eastern Algeria.

eastern Algeria (Fig. 1). M. tuberculosis complex strains were confirmed by biochemical tests (nitratase, catalase) and by sensitivity to chemical substances, such as 2-thiophene carboxylic acid (TCH), Sodium 4-aminosalicylate (PAS), 4 nitrobenzoic acid (PNB). Each strain corresponds to a patient. The sensitivity tests for antituberculosis (isoniazid, streptomycin, rifampicin, ethambutol, kanamycin, and ofloxacin) were performed using the proportion method on Löwenstein-Jensen medium.

The strains included in the study were typed by spoligotyping [3,4]. The profiles obtained were analyzed by using the SPOLDB4 database [5]. A dendrogram was produced with the MIRU-VNTR software available on the website (http:// www.MIRU-VNTRplus.org, August 2008).

Results

Study population

The study was performed on 129 strains randomly selected from a sample of 350 strains isolated from TB patients between January and December 2011. Strains isolated from pulmonary localization represent 88% of cases, while 12% of cases represent extrapulmonary tuberculosis strains. The sex ratio was 1.43 and the average age of patients was 39 years. The proportion of previously treated patients was 41% (53 patients) of the sample. The demographic, clinical, and bacteriological characteristics of patients are reported in Table 1.

Antituberculosis drug resistance

The results of the sensitivity tests were available for 126 isolates (97.7%), of which 113 cases (89.7%) were sensitive to all of the first-line antituberculosis drugs. The majority of these strains (76.6%) were isolated from new TB patients and 53 strains were isolated from previously treated patients. Analysis of drug resistance profiles in patients previously treated or new patients shows that among 13 drug-resistant strains, nine were isolated from patients previously treated. Among these, six are multidrug resistant. Of the four strains isolated from new patients, one showed resistance to four major antibiotics tested. The results appear in Table 1.

Table 1 – Demographic, clinical, and bacteriological charac-

teristics of patients.			
Specifications	General data		
TB patients	129		
Male	76 (58%)		
Female	53 (42%)		
Sex ratio (M/F)	1.43		
Average age (y)	39		
Patients with unknown age	9		
Location of the TB			
Pulmonary	114 (88%)		
Extrapulmonary	15 (12%)		
History of the disease			
New cases	76 (59%)		
Previously treated cases	53 (41%)		
Results of susceptibility tests			
Total strains tested	129	76NC	53PC
Sensitive strains	113	72	44
Resistant strains	13	4	9
Н	1	0	1
S	2	1	1
HS	3	2	1
MDR (at least H+R))	7	1	6
Contaminated	3		
E = ethambutol; F = female;	H = isoniazid;		M = male;

MDR = multidrug resistant; NC = new cases; PC = previously treated cases; R = rifampicin; S = streptomycin; TB = tuberculosis.

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