Emerging clones of Mycobacterium tuberculosis in Russia and former Soviet Union countries: Beijing genotype and beyond

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Mycobacterium tuberculosis has a clonal population structure, but its different (sub)lineages are marked with different evolutionary pathways, with some of them having undergone a dramatic global dissemination. Furthermore, clinically/epidemiologically significant compact clusters have been identified by high-resolution genotyping. I will review some emerging M. tuberculosis clones from different genotype families (Beijing, Latin American–Mediterranean [LAM], and Ural) that started to attract attention in the recent decades and even years in Russia and other countries of the former Soviet Union.

The Beijing genotype includes two large clonal clusters: 94-32 and B0/W148. The B0/W148 cluster was previously defined as a successful Russian clone of M. tuberculosis [1]. Initially, it was designated as B0 [2] and W148 [3] based on IS6110-restriction fragment length polymorphism (RFLP) patterns. Results of 24-mycobacterial interspersed repetitive units-variable-number tandem repeat (MIRU-VNTR) typing revealed that this cluster greatly overlaps with type 100-32 (MIRU-VNTRplus.org). Beijing B0/W148 cluster is associated with multidrug-resistant tuberculosis (MDR-TB) and is a major driving force of the Russian TB epidemics. It is epidemiically spread across Russia (but not in the former Soviet Central Asia) and likely originated in Siberia. Recent studies independently rediscovered these strains and named them East European sublineage [4], resistant European clone ECDC0002 [5], East European cluster 2 [6], and CC2 clonal complex [7]. The Asian/Russian type Beijing 94-32 cluster is also termed Russian/Asian clone CC1 (defined by 24-MIRU-VNTR clustering) and corresponds to the IS6110-RFLP-defined A0 cluster [2,8]. It is highly prevalent in the former Soviet Central Asia and is one of the two largest and significant Beijing subtypes in Russia [6,7,9].

The LAM family in the former Soviet Union countries is dominated by the RD115/LAM-RUS branch. Two MDR-TB spoligotypes with partly overlapping areas of circulation have attracted attention in recent times. Spoligotype SIT252 is emerging in European Russia and Eastern Europe and has already been described in rare isolates in Ural and Kazakhstan. The M. tuberculosis SIT252 strains have highly conserved 24-MIRU-VNTR profiles, similar IS6110 fingerprints and mutations rpoB Asp516Ser, katG Ser315Thr, and inhA-15C/T [10]. Spoligotype SIT266 is still geographically limited to Belarus [11], and has been described in northwestern and central Russia and in Latvia. SIT266 is MDR (and perhaps extensively drug resistant) unlike its parental SIT264, which is more widespread but has very low prevalence and is not MDR ([12] and references therein).

The Ural family was traditionally considered to be low virulent, low transmissible, and not linked to MDR (reviewed in [13]). This may explain its low prevalence (~15%) and limited dispersal, still mainly in central Eurasia. However, recent reports described MDR Ural strains in some parts of Eastern Europe (Moldova and Lithuania) and northwestern Russia ([14] and references therein). Whole genome analysis of the Ural family genomes divided these strains into two large clusters: (a) ancestral, small, and diverse group and (b) modern, homogeneous, and more abundant group. A significant predominance of pansusceptible strains in the ancestral group (p < .05) was found [15].

Reasons of success of emerging clones may be different in each particular case and be related to TB control programs and strain properties. A strong association with MDR was shown for the Russian Beijing B0/W148 strain (compared with other Russian Beijing clones) and genetically, it was due to the
acquisition of particular resistance mutations, and likely due to certain compensatory mutations (although beyond rpoA/C). The mutation N51I in the regulatory gene relE was suggested to be a hallmark in the evolution of the modern Ural subgroup, and might promote development of drug resistance [15]. The different capacity of certain relatively homogeneous clonal groups to develop particular pathobiologically relevant properties may be a decisive factor for strain dissemination in the same human population where less hazardous parental strains have been circulating.

Conflicts of interest

The author has no conflict of interest to declare.

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