

# tRNA array genomic survey unravels their presence and structure in Mycobacteria

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The tRNA arrays are genomic regions with highly density of tRNA found in eukaryotes and prokaryotes. Considering the importance of tRNAs in the translation machinery, these units influence the organism lifestyle. A previous *in silico* analysis showed their abundance in Firmicutes and conversely, rare among Actinomycetes. In the context of Mycobacterium genomic project, we sequenced several Mycobacteria genomes and analyzed them together with genomes from this genus. One of our focus was tRNA arrays identification. Currently, there is no tools to apply in the tRNA arrays identification. Therefore, we developed an *in house* perl script to identify such structures. The tRNA array units were defined as genomic regions containing at least 20 tRNA genes with a minimal tRNA gene density of 2 tRNA genes per kb. We identified tRNA arrays in several Actinomycetes genomes. These tRNA arrays contain from 21 to 62 tRNAs and are present in several *Mycobacterium* species, including *M. tuberculosis*. They were most abundant and diverse in *M. abscessus* complex. Same arrays in terms of composition and synteny were found intra and inter *Mycobacterium* species. However in *M. abscessus*, we identify the occurrence of diverse tRNA arrays, considering composition and synteny. The analysis based on the current script allowed the identification of distinct tRNA arrays in *Mycobacterium* genomes, raising questions about the impact of these structures in the biology of these organisms. The implementation of this script in genome pipelines would improve annotation as well as comparative genomic analyses of such structures.

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