

**Fig 1.** Geographical distribution of *M. tuberculosis* isolates from the 16 Egyptian governorates used in the present study.



**Figure 2.** UPGMA-tree dendrograms. **(A)** Phylogenetic analysis based on Multi-Locus Sequence Typing (MLST), 12 MIRU-VNTR loci and spoligotyping patterns of *Mycobacterium tuberculosis* isolates representing the largest spoligotype-defined cluster SIT53/T1. **(B)** Strains diversity based on combined results of 12 MIRU-VNTR loci, SNP typing, and spoligotyping analysis of isolates representing the spoligotype-defined clusters included (SIT34/S and SIT4/unknown clade). The categorical-based UPGMA tree was generated by an MIRU-VNTR*plus* database application available online (http://www.miru-vntrplus.org/).