Clinical and strain associations with recent *M. tuberculosis* infection among HIV-positive patients in the DARDAR TB vaccine trial

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Introduction. Molecular strain typing can be used to identify clustering and recent infection with *M. tuberculosis* (MTB).
Objectives. To identify clustered isolates of MTB and clinical and genetic correlates of clustering among HIV-positive patients in a TB vaccine trial in Tanzania.
Methods. IS*6110* typing and spoligotyping were performed on MTB isolates. Isolates with the same IS*6110* patterns were defined as "clustered" (recent infection); isolates with related IS*6110* patterns were defined as a "family"
Results. 98 isolates were analyzed, including 36 from HIV-positive study patients and 62 concurrent community isolates (HIV-status unknown). Among study patients 10/36 (28%) isolates were clustered as were 15/62 (24%) of community isolates (p=0.8). Clustering was present in 6/18 (33%) with CD4>200 and 4/18 (22%) with CD4 <200 (p=0.7). Clustering was not associated with baseline tuberculin reactivity or prior tuberculosis. The most common family (designated GD) of isolates comprised 33 isolates representing a genetic lineage previously identified in East Asia; 15 (45%) were clustered versus 10 (15%) of the remaining 65 isolates (p=.003). Spoligotyping demonstrated 10 strain families. Additional strain data will be presented.
Conclusion: Recent MTB infection in Tanzania is associated with East Asian strain MTB, but not with prior tuberculosis, tuberculin reactivity or CD4 count.