Background: Among HIV-positive individuals with CD4 ≤100 cells/mm3, *M. tuberculosis* (MTB) bacteremia is associated with a positive tuberculosis Urine Lipoarabinomannan (LAM) test. We conducted a retrospective study, to determine the effect of MTB lineage on the performance of the Determine TB LAM lateral flow (LF-LAM) assay.

Methods: This was nested in a prospective TB diagnostics accuracy study among HIV-positive presumptive TB patients from Mulago National Referral Hospital, Kampala, Uganda including both inpatients and outpatients. We considered data of 51 HIV-positive individuals with both pulmonary and MTB bacteremia. We also evaluated the effect of having mixed MTB strains using both spoligotyping and MIRU-VNTR 24 loci methods.

Results: LF-LAM was; negative among 4 (7.8%; 95% CI, 2.17%-18.8%), positive among 39 (76.5%; 95% CI, 62.5%-87.2%) and indeterminate among 8 (15.7%; 95% CI, 7.0%-28.5%) participants. MTB lineages from blood samples were; Central Asian Strain (CAS; L3) 10/51 (19.6%) and Euro-American lineage (L4) 41/51 (80.4%). MTB lineages from sputum samples were 7/51(13.7%) L3 and 44/51 (86.3%) were L4. Among participants with L3 in blood, LFLAM was positive in 9 (90%; 95% CI, 55.4%-99.7%) whereas those with L4, LF-LAM was positive among 30 (73.2% 95% CI, 57.0%-85.7%). For those with L3 in sputum, LF-LAM was positive among 7 (100%) and those with L4 was 32 (72.7%; 95% CI 57.2 %-85.0%). Two participants had mixed MTB strains (all L4) and all LF-LAM positive (2+ and ≥4+).

Conclusions: Our study shows that *M. tuberculosis* lineage 3 may have more sensitivity for LF-LAM assay than lineage 4. The high number of indeterminate results with L4 require more investigations. Our findings suggest that LF-LAM performance may differ by geographical regions depending on the dominant *M. tuberculosis* lineage.