A COMPARISON OF TREPONEMA PALLIDUM MOLECULAR TYPING SYSTEMS: MLST VS. ECDCT

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Background Several syphilis typing systems have been proposed. Recent work suggests that multilocus sequence typing (MLST) may be superior to enhanced CDC typing (ECDCT), particularly because ECDCT type may differ among organisms amplified from different anatomical sites in the same person. The goal of this study was to compare the two systems.

Methods DNA was extracted from 20 Treponema pallidum isolates propagated in rabbits, 10 oral and 10 genital or non-genital lesion swabs, and 10 blood samples from patients with syphilis. MLST type for tp0136, tp0548 and tp0705 and ECDCT type were determined according to published methods. Samples were chosen because they were completely type-able by ECDCT. ECDCT types were also determined for samples from different anatomical sites in 7 patients, and from blood and blood isolates (rabbit propagated) in 8 patients.

Results MLST type could be fully determined for 19 (95%) of 20 bacterial isolates, 8 (80%) of 10 bloods, 7 (70%) of 10 lesion swabs, and 5 (50%) of 10 oral swabs. 13 subtypes were identified by ECDCT, and 12 by MLST. While MLST was able to subdivide two common ECDCT types (1.1.1, 1.1.2, 1.1.9, and 1.1.71 within 14d/f; and 1.3.1, 1.38.1, and 6.3.1 within 14d/g) it failed to distinguish among less common ECDCT types. ECDCT type was identical in 5 paired lesion and oral swabs, 1 paired blood and oral swab, and 1 paired blood, lesion and oral swabs. In addition, ECDCT type was identical in 8 paired blood and blood isolates.

Conclusion Compared to ECDCT, determination of MLST was less often successful from isolates and from clinical samples, and it was not uniformly more discriminating. ECDCT was stable among anatomical sites and between direct patient-derived samples compared to rabbit propagated organisms.

Disclosure No significant relationships.