Additional Y-STRs in Forensics: Why, Which, and When

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ABSTRACT: Male-specific DNA profiling using nonrecombining Y-chromosomal genetic markers is becoming ubiquitous in forensic genetics, with many laboratories and jurisdictions taking advantage of the benefits that Y chromosome short tandem repeat (Y-STR) profiling can bring. The current suite of 9–17 core Y-STRs, available as commercial kits, perform adequately for identifying male lineages in many populations, a feature highly suitable for excluding a male suspect from involvement in crimes such as sexual assaults where autosomal STR profiling is often troubled. However, there is a growing need to achieve higher resolution in paternal-lineage differentiation as adventitious matches between unrelated males are becoming increasingly common with the increasing size of Y-STR haplotype-frequency databases. Furthermore, with the currently used Y-STRs, male relatives (both close and distant) usually cannot be separated, marking a strong limitation in forensic applications as conclusions cannot be drawn on the individual level as desired. Performing Y-chromosome analysis in familial testing, which outperforms autosomal STR profiling in certain deficiency cases, with the current Y-STR sets can be troubled by mutations that complicate relationship-probability estimations. To overcome these limitations, considerable research has been performed over recent years to identify and characterize additional Y-STRs. This review summarizes the forensic performance of current sets of Y-STRs, points out their limitations in the three main areas of forensic Y-STR applications (male-lineage differentiation, male-relative differentiation, and paternity/familial testing), and discusses why and which additional Y-STRs are suitable to improve forensic Y-chromosome analysis in the future.

KEY WORDS: Deficiency cases, forensic, microsatellites, mutation rate, paternal lineage, paternity, RM Y-STR, sexual assault, SM Y-STRs, Y chromosome, Yfiler, Y-STR.