

**PREVENTION AND DETECTION OF DNA CONTAMINATION EVENTS IN A FORENSIC LABORATORY.**

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Multiplex STR analysis with fluorescence-based detection is a remarkably sensitive method for DNA profiling and has been in use for over a decade in many forensic laboratories. As a consequence of this sensitivity, exhibits and samples are vulnerable to contamination from exogenous DNA. Thus, forensic DNA laboratories must implement procedures that minimize the risk of contamination and carry out extensive verification of DNA analysis results. In our laboratory, in addition to well-known prevention measures and extensive use of robotics, we have developed an integrated, computer-based approach for the detection of DNA contamination events, using a specific, profile verification module of our LIMS system (*DNAProfiles*, a FileMaker database developed by Synchrone Infosystèmes). Following amplification of DNA samples using both Profiler+® and Cofiler® multiplexes (Applied Biosystems), distinct profiles (single-source or mixtures) from a case are included temporarily (approx. 12 months) in a verification database that also contains lab personnel and visitor profiles (others may be included on a case by case basis). Profiles detected within reagent blanks (extraction and amplification) are included permanently. Upon inclusion, single-source profiles are checked against all profiles present in the database. Mixture profiles present a particular challenge. Unless a potential perpetrator profile can be deduced and treated as a single-source profile, a mixture profile will be used as a target against personnel/visitor profiles. Verifications for case profiles are carried out by the analyst responsible for the case and are documented on a standardized form produced by the *DNAProfiles* system. Presence of the relevant forms within the case file is a required element during the case review by a peer. Only uninformative profiles are excluded from the verification process. Matches with personnel profiles are reported directly to designated individuals responsible for QA/QC and documented. Matches between case samples are checked via *DNAProfiles* for co-processing at any step. Any suspicious match is reported to the same designated individuals. All necessary additional analyses are then carried out to establish either the validity of the match (repeat sampling) or the step at which the contamination event occurred. Corrective measures may be implemented as required following result review.

Results and conclusion: We have reviewed DNA contamination events in our laboratory over an 18-month period. Exogenous DNA profiles detected on either case samples or extraction/amplification blanks were considered. A large proportion of events (>40%) were attributed to transfer of laboratory personnel DNA while handling exhibits or DNA samples. In general, total DNA was very low in samples where personnel contamination was detected with either weak or no relevant profiles present. Approximately 20% of events involved DNA transfer between cases or from case sample to blank (direct or indirect). Transfer events were detected at all steps of the analytical process and often involved a sample with an unusually high DNA concentration. A number of profiles of unknown origin were detected only through the use of two multiplexes and appear to be

due to DNA present on disposable material prior to use. Overall, contamination events are rare relative to the number of samples processed and are not very likely to compromise a case as 1) they often involve samples where little or no relevant DNA is present 2) repeat experiments can be performed when contamination occurred in the later stages of the analytical process and 3) the perpetrator profile may be present on other samples.