MOLECULAR DISSECTION OF A CRIME SCENE - INTRODUCING STR SEQUENCING IN ROUTINE INVESTIGATION

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Progress is an integral part of science. That's why it is not surprising that also forensics is undergoing a change. With Massively Parallel Sequencing (MPS) we are able to perform a molecular dissection of DNA in order to shed more light into a criminal investigation. However with the new insights brought by forensic genomics, there also come new challenges concerning the data analysis and interpretation. In the past few years, due to significant number of validation studies, MPS has proven its potential to change our gold standards of STR analysis. Some of the issues still stopping MPS from becoming a standard tool among the forensic community will most likely solve themselves with time (e.g. nomenclature standards or population databases) but others can be worked out only with learning-by-doing. And for this to happen more laboratories have to decide to introduce MPS into their routine work so that its impact on the crime scene investigation can be presented to a broader range of the most crucial partners: the law enforcement.

In this study we investigated 57 challenging samples which represented the cross-section of the caseworks we face routinely in our institute. The samples were amplified and sequenced in duplicate using Precision ID GlobalFiler™ NGS STR Panel v2 and Ion GeneStudio S5 (ThermoFisher Scientific). For the data analysis we used the Converge™ Software v2.1. To evaluate the concordance with CE we used the kits we routinely work with: PowerPlex® ESX 17 System and PowerPlex® Fusion System. Among the samples selected for the study, there were complex mixtures (e.g.: up to 5 contributors; down to 5% of minor contributor), cold cases (e.g.: 40 years old stains; traces with DNA input of 15pg) and different biological material (e.g. muscle; bone; blood; semen). We present here the problems we faced when analyzing the most challenging forensic samples but also demonstrate the power of the results given by MPS when compared to the standard CE outcome.