## B68 A Comparison of the Statistical Significance in the Loci of the Promega Powerplex® 16 System From Identified Remains

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After attending this presentation, attendees will get a idea of the statistical significance of each of the Promega PowerPlex® 16 loci when used for identification of missing persons from the former Yugoslavia.

This presentation will impact the forensic community and/or humanity by providing useful information for people using STR systems for large scale identification work.

The ICMP has developed a DNA-led identification effort to assist in the identification of the estimated 30,000 – 40,000 missing persons who remain missing as a result of the breakup of the former Yugoslavia. Due to the conditions of the recovered bodies, coupled with a relative lack of medical and dental records, the vast majority of bodies currently being recovered cannot be identified without the use of DNA testing. Currently more than 10,000 bone samples and 43,000 blood samples have been successfully tested with the Promega PowerPlex® 16 system. The process of matching STR profiles from the reference database to profiles in the missing person database is challenging, especially considering the large number of samples in these databases.

The vast majority of the missing has either a parent or a child as a blood donor. Because of this fact, the ICMP has developed software that performs an initial search based upon half-band sharing patterns. Due to the large size of the database, random half-band sharing matches are relatively common for any given bone sample. In order to determine a random match from a true match, additional factors are addressed. First, blood samples are taken from multiple donors for each missing person, and the DNA profiles from all blood donors must correspond to the potential match with the bone sample. On average the ICMP collects three blood references for each missing person. Once a match is found to exist between a bone sample and multiple donors from the same family, the statistical significance of the match is determined using DNAview software. The DNAview software gives a likelihood ratio (LR) for the significance of the match at each locus. Following the LR analysis, matches that produce a posterior probability of 0.9995 or larger are considered strong enough to generate a matching report. For the matches where the posterior probability is less than 0.9995, additional family reference samples are sought, which can strengthen or exclude the match. When there are no additional family relatives available to donate a blood sample, additional loci can be tested. It should be noted that the DNA report does not stand alone in the identification process. After the pathologist in charge of the case receives the DNA report, they combine all other forensic evidence together in order to make the identification.

To examine the effectiveness of the alleles in the Promega PowerPlex® 16 system the LR produced by each locus in the matching reports generated by ICMP have been examined. Initial results show that Penta E produces, on average, the strongest LR. Other loci such as TPOX and CSF1PO produce much lower likely hood ratios in matching reports. The substitution of the loci that produce relatively low LR ratios for ones that produce greater discriminating potential could simplify the identification process by reducing the number of random half-band sharing matches that occur upon initial screening.

**DNA, DNAview, Statistics**

 ** Presenting Author*