A STUDY OF DEGRADED BONE SAMPLES USING CE AND NGS METHODS

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DNA analysis from human remains is of immense relevance in missing persons identification and disaster victim identification (DVI). DNA degrades gradually in hard tissues, such as bones and teeth under a high temperature, humidity, pH, geochemical properties of the soil, the presence of microorganisms and all other factors that affect the preservation of DNA in skeletal remains. Recent advances in massively parallel sequencing (MPS, provides some advantages over previously used technologies to analyse DNA from human remains, particularly ancient. The aim of this study was to investigate if we could use the Illumina ForenSeq DNA signature kit to genotype autosomalSTRs, X and Y STRs as well as SNPs in bone samples for use in disaster victim identification. The beta-version of the ForenSeq kit was used to genotype 32 bone samples from Serbia lab that previously profiled using GlobalFiler amplification kit using 3500 capillary electrophoresis (CE). A total number of 86 samples were typed on 3500 CE and 32 were selected for NGS work. Results of Run on FGx-MiSeq sequencing showed a cluster density of 866 K/mm2. A total 95% of clusters generated run passed filters. The results of the samples will be shown between the CE and NGS results. The beta-test worked rather well for a beta-test using one independent run. Ancestry, Identity and phenotypic SNPs had been typed in the degraded samples. The CE GlobalFiler data -STR markers and the Illumina ForenSeq DNA signature kit showed remarkable results for concordance.