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Research Progress in Forensic Body Fluids Identification Based on Nucleic Acid Molecules

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Introduction

Identifying the type and origin of body fluids left at a crime scene is helpful to crime scene reconstruction for it can link the sample donors and actual criminal acts [1]. As Hanson et al. [2] pointed out, the identification of the biological material might be crucial to the prosecution of the case. The appearance of a person's DNA only suggests that he once has been to the crime scene, but his acts were unknown for us. If we can identify origin of the biological material, for example semen stains, we can get more information from the crime scene. Numerous types of body fluid identification methods have been developed since last century, such as chemical tests [3-5], immunological tests [6,7], protein catalytic activity tests [8,9], spectroscopic methods [10-15] and microscopy [16]. However, these conventional body fluid identification methods are prone to various limitations such as sample consumption, intensive labor, time consumption, varying degrees of sensitivity and specificity [17,18]. Recent developments in nucleic acids detection methods have expanded the available molecules for forensic body fluid identification. Detection of DNA methylation [19-24], body fluid-specific microbial DNA [25-28], mRNA profiling [29-34] and expression profiling of miRNA [2,35-40] are the typically new methods of body fluid identification based on nucleic acids. DNA methylation is one of the most important epigenome makers [41]. Recent studies indicated that DNA possessed tissue-specific methylation patterns and there are several chromosone segments called tissue-specific differently methylated regions (tDMRs) which show varying methylation patterns according to tissue or cell type [41]. Comparing with other makers, simple extraction and purification methods, high sensivity and specificity make DNA methylation a more favourable detection method [19,21,24,42]. According to previous studies, only semen had specific DNA methylation loci that USP49 and DACT1 is unmethylated in 90 percent semen samples but high methylated in all blood, saliva, vaginal secretion and menstrual blood samples [43]. The degree of DNA methylation is affected by many various exogenous and endogenous factors such as ageing [44-46], nutrition and diets [47,48], early life experience [49,50], exposure to pollutants as well as social environments [51], which restrict the use of DNA methylation in body fluids identification.

Various bacteria reside in human body. Different body regions contain different kinds of bacteria. The use of bacteria for the identification of body fluids has been widely investigated, with Streptococcus species being used for the identification of saliva. Lactobacilli species have been found to be the predominant bacteria in the vagina of women. Only these two body fluids possessed relatively stable microflora. Similar to DNA methylation, several factors influenced the specificity and sensitivity of the bacteria [52-54]. Different age groups may have different bacteria in saliva and vaginal secretion, for instance, the diversity of bacteria of saliva in children and old man was more abundant than adults. Besides, antibiotics may change major species of bacteria in body fluids [55]. MRNA (message RNA) showed best performance in body fluid identification among the new markers. European DNA profiling group (EDNAP) has intensively studied and evaluated mRNA profiling of different body fluids and obtained satisfactory results in

their collaborative exercises [56-60]. MiRNAs are one of small, non-coding RNA molecules with a length of 18-25 nucleotides [61-64]. The intrinsically small size and tissue-specific expression pattern make it less prone to aggressive environmental factors comparing against mRNA [17,18]. Another advantage of miRNA is in mixture stains, while mRNA profiling identifies origin of the sample, miRNA profiling is helpful to further distinguish the major donor and minor donor. Quantitative detection of mRNAs and miRNAs were performed in tissues with different RIN values (3-10) simultaneously in a study [65]. The expression of miRNAs was quite stable while the Ct values of mRNAs rose gradually as the RIN values decreased, which suggest miRNAs were indeed more stable comparing with mRNAs. The expression of some miRNA was more abundant than other body fluids which can differentiate target body fluid from others. Several studies have screened miRNA for body fluid identification [2,35-40], however the overlap in body fluid-identification miRNA markers between studies is low. The agreement on miRNAs for body fluid identification should be reached. Combination of mRNAs and miRNAs may achieve better results.

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