

IDENTIFICATION OF HIGHLY SPECIFIC RNA BIOMARKERS FOR THE IDENTIFICATION OF VAGINAL SECRETIONS IN FORENSIC CASEWORK

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The inability to definitively determine the tissue source of origin of forensically relevant biological fluids could result in a failure to provide crucial information necessary to the investigation and prosecution of the case. For example, in instances of sexual assault with a foreign object or digital penetration, the identification of vaginal secretions (VS) transferred to such objects or possibly the perpetrators would be critical in establishing the circumstances of the assault. Conventional serological and immunological methods for body fluid identification can confirm the presence of human blood and semen. However, currently none of the routinely used biochemical tests can definitively identify the presence of human saliva or VS. However, it has been demonstrated that mRNA (or miRNA) profiling of body fluid stains can provide a degree of identification specificity of tissue and body fluids heretofore unattainable by conventional means. Early promising VS candidate RNA biomarkers failed to exhibit the required degree of specificity or sensitivity and thus, at present, it is not possible for the forensic scientist to positively identify VS using molecular genetics techniques.

The aim of this work was to find novel highly specific RNA biomarkers for the identification of VS. Whole transcriptome profiling (*RNAseq*) of vaginal swab samples from different donors resulted in the identification of a number of putative VS-specific mRNA candidates. After detailed evaluation of >200 RNA candidates from the tens of thousands of RNA species found in VS, two mRNA transcripts consistently demonstrated high specificity and sensitivity for VS. Importantly they are able to differentiate between VS and other body fluids enriched in epithelia, particularly saliva and skin. We believe they represent excellent VS biomarkers that, upon further validation by others, would be suitable for incorporation into assays for routine forensic casework use.

In addition to the VS mRNA biomarkers, we screened >1,100 miRNAs (current through miRBase v.16) and identified several novel miRNAs that demonstrate a high level of specificity for VS.

This presentation will describe the RNA candidates in detail and summarize the specificity and sensitivity validation data to date.

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