Streamlining Forensic Workflows: Field Test Results of Forensic Samples using the HID NIMBUS® Presto QNA System

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INTRODUCTION

Integrating automation into forensic laboratories is essential for increasing sample throughput while minimizing human error. The HID NIMBUS® Presto QNA System (HIDNP QNA), initially validated for purification, has now been scripted and validated for use with Applied Biosystems quantification and STR amplification kits. The HIDNP QNA System combines the KingFisher Presto Purification System with a liquid handler to purify DNA from lysed samples (Figure 1) (1).

The performance of the HIDNP QNA System must be evaluated and compared against manual methods for processing challenging sample types. DNA from skeletal remains is often degraded and/or is of low quantity (2). Similarly, nails, hair, blood, and gum contain inhibitors that can comprise STR profile quality (3-5).

A field test conducted at Sam Houston State University assessed the HIDNP QNA scripts for DNA quantification and amplification using a variety of mock forensic casework samples. These included burned, buried, surface decomposed bones, gum, hair, nails, blood on a cotton swab, and a dilution series. The samples were processed manually and on the HIDNP QNA system for comparison.

Figure 1: HIDNP QNA System

MATERIALS & METHODS

Sample Selection

Various forensic casework samples (Figure 2) were selected to evaluate the HIDNP QNA workflow, as shown in Figure 3.

Figure 2: Sample types chosen for the SHSU field testing. A) Surface decomposed remains (N=4), B) Burned remains (N=4), C) Buried remains (N=4). D) Nail clippings (N = 3). E) Chewing gum (N = 5). F) Hair (N=4), G) Dried blood on a cotton swab (N=1), H) Dilution series using control 007 DNA including 0.0625ng, 5ng, 10ng, and 20ng (N=4).

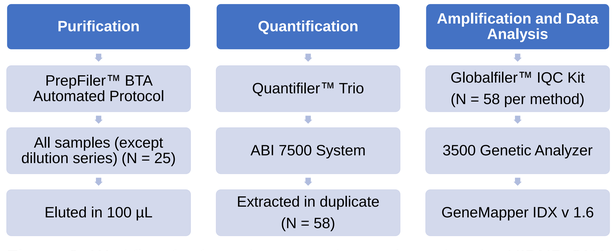

Figure 3: Workflow for forensic casework samples using the HIDNP QNA System

RESULTS & DISCUSSION

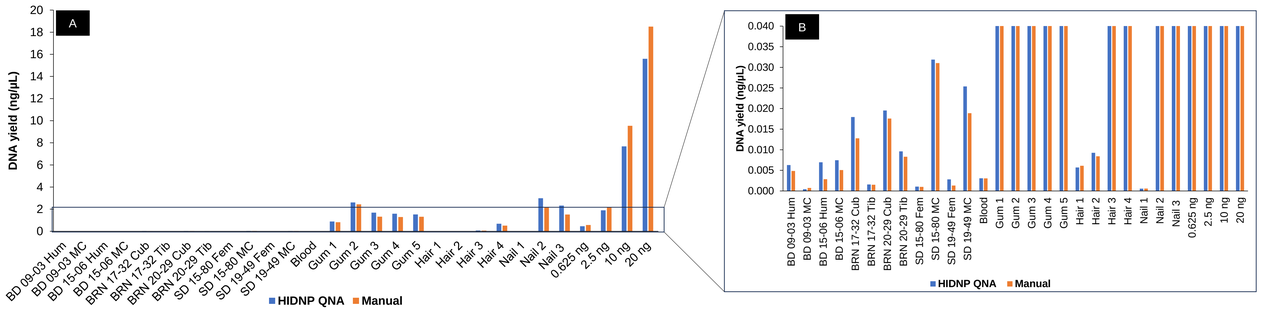

Figure 4: A) Average DNA quantity between the HID NIMBUS Presto QNA System and manual workflows B) Low concentration samples (<0.040 ng/µL)

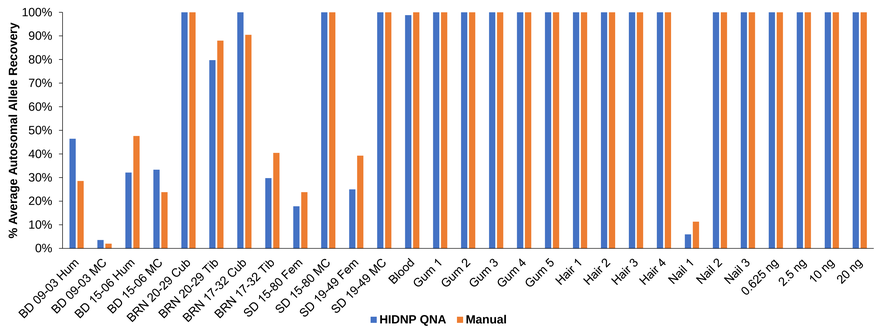

Figure 5: The percent average autosomal allele recovery between the HIDNP QNA System and manual workflow for all sample types (N = 58).

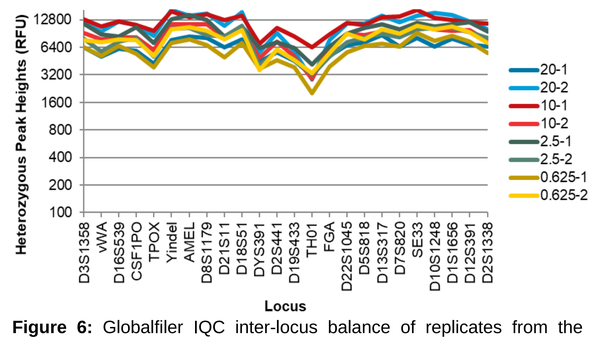

Figure 6: Globalfiler IQC inter-locus balance of replicates from the sensitivity series.

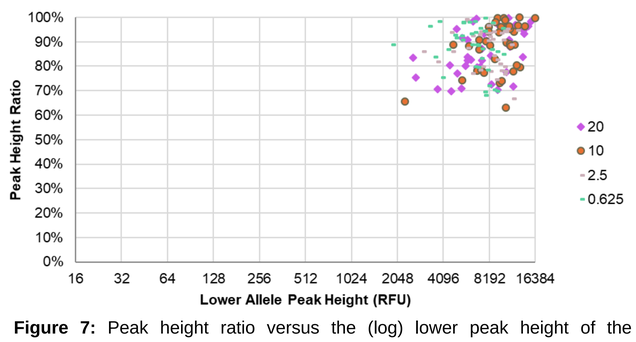

Figure 7: Peak height ratio versus the (log) lower peak height of the sensitivity series prepared by the HIDNP QNA System.

- All samples yielded quantifiable amounts of DNA ranging from 0.0004 – 18.5 ng/µL. Skeletal remains, blood from a cotton swab, Hair 1, Hair 2, and Nail 1 produced DNA amounts less than 0.035 ng/µL. In contrast, gum, most nail samples, Hair 3, Hair 4, and the dilution series exhibited DNA quantities higher than 0.89 ng/µL (Figure 4). Replicates processed using the HIDNP QNA and manual methods demonstrated reproducible results with expected sample variation (data not shown). All IPC C_T were within 1 C_T difference for all replicates (data not shown).
- Standard curves prepared using automation yielded expected metrics with an R^2 value >0.99 and slope of -3.314, consistent with manual set up (data not shown).
- Both methods showed comparable performance for average STR recovery. Among the skeletal types, buried remains were the least successful, with less than 50% allele recovery. Burned and surface-decomposed remains exhibited variable recovery rates, ranging from 20% - 100%. All gum, Nail 2, Nail 3, and dilution series yielded 100% recovery. For the blood sample, automation produced an average of 99% allele recovery, with one allele dropping out in one replicate while both profiles for manual methods yielded a full profile (Figure 5). Notably, the blood sample profile was slightly degraded, with a degradation index (DI) of 1.
- The inter-locus balance of the replicates from the sensitivity series produced heterozygous peak heights above 1600 RFUs (Figure 6). Additionally, the minimum peak height ratio for all samples within the sensitivity series was above 60% (Figure 7).

CONCLUSIONS

- The HIDNP QNA System can provide a streamlined, automated workflow from purification, quantification, normalization, and amplification setup for forensic samples.
- Samples processed with the HIDNP QNA System yielded similar quantification and STR results to manual methods.
- The time saving capabilities of the HIDNP QNA System was evident for quantification and normalization and amplification setup as seen in Figure 8.

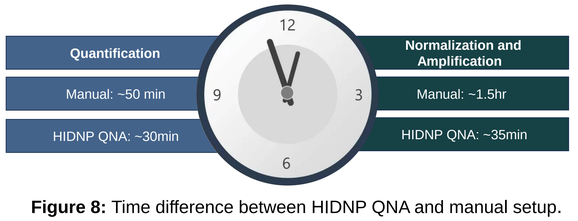

Figure 8: Time difference between HIDNP QNA and manual setup.

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