SCIENTIFIC POSTER

Automating HMW DNA extraction in clinical genetics: Evaluation of the chemagic 360 instrument in a hospital lab for routine genetic testing.

Authors

Alexadre Buffet
Karine Auribault

Département de Médecine Génomique des Tumeurs et Cancers,
Hôpital Européen Georges Pompidou,
Fédération de Génétique et de Médecine Génomique
AP-HP Centre Université Paris Cité

Catherine Goh
Janina Gerhards
Uwe Jaentges

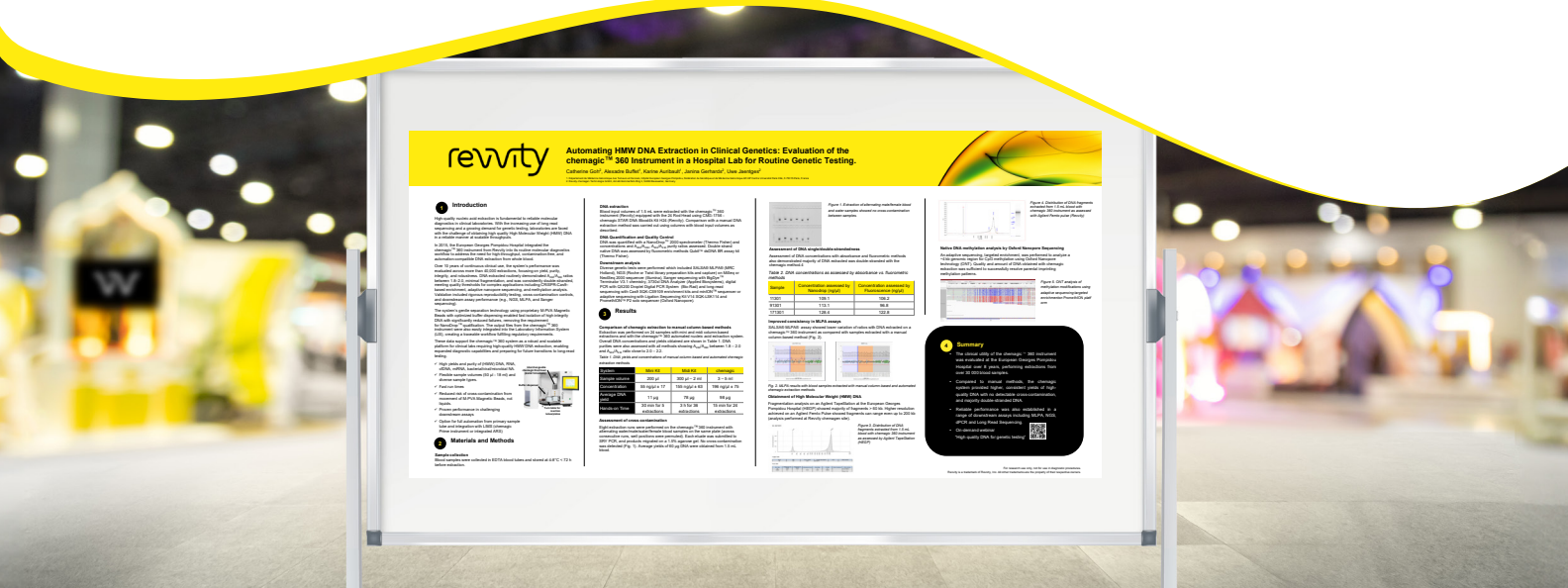
Revvity

Introduction

High-quality nucleic acid extraction is fundamental to reliable molecular diagnostics in clinical laboratories. With the increasing use of long read sequencing and a growing demand for genetic testing, laboratories are faced with the challenge of obtaining high quality High Molecular Weight (HMW) DNA in a reliable manner at scalable throughputs.

In 2015, the European Georges Pompidou Hospital integrated the chemagic™ 360 instrument from Revvity into its routine molecular diagnostics workflow to address the need for high-throughput, contamination-free, and automation-compatible DNA extraction from whole blood.

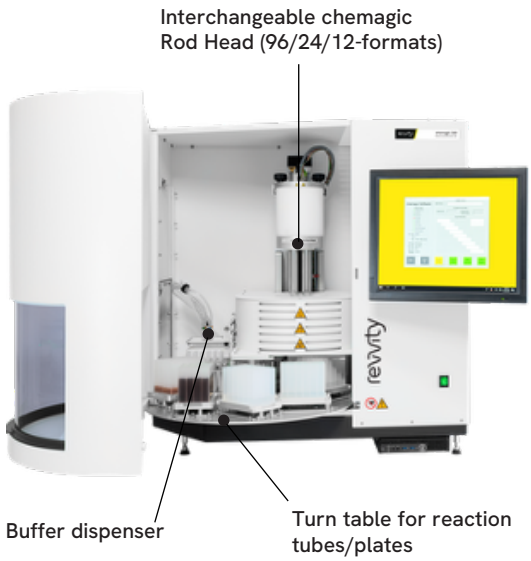
Over 10 years of continuous clinical use, the system's performance was evaluated across more than 40,000 extractions, focusing on yield, purity, integrity, and robustness. DNA extracted routinely demonstrated A_{260}/A_{280} ratios between 1.8–2.0, minimal fragmentation, and was consistently double-stranded, meeting quality thresholds for complex applications including CRISPR-Cas9–based enrichment, adaptive nanopore sequencing, and methylation analysis. Validation included rigorous reproducibility testing, cross-contamination controls, and downstream assay performance (e.g., NGS, MLPA, and Sanger sequencing).



The system's gentle separation technology using proprietary M-PVA Magnetic Beads with optimized buffer dispensing enabled fast isolation of high integrity DNA with significantly reduced failures, removing the requirement for NanoDrop™ qualification. The output files from the chemagic 360 instrument were also easily integrated into the Laboratory Information System (LIS), creating a traceable workflow fulfilling regulatory requirements.

These data support the chemagic 360 system as a robust and scalable platform for clinical labs requiring high-quality HMW DNA extraction, enabling expanded diagnostic capabilities and preparing for future transitions to long-read testing.

- High yields and purity of (HMW) DNA, RNA, cfDNA, miRNA, bacterial/viral/microbial NA.
- Flexible sample volumes (50 µl - 18 ml) and diverse sample types.
- Fast run times
- Reduced risk of cross-contamination from movement of M-PVA Magnetic Beads, not liquids.
- Proven performance in challenging downstream assays
- Option for full automation from primary sample tube and integration with LIMS (chemagic Prime instrument or integrated ARS)



Materials and methods

Sample collection

Blood samples were collected in EDTA blood tubes and stored at 4-8°C < 72 h before extraction.

DNA extraction

Blood input volumes of 1.5 mL were extracted with the chemagic 360 instrument (Revvity) equipped with the 24 Rod Head using CMG-1756 - chemagic STAR DNA Blood 4K Kit H24 (Revvity). Comparison with a manual DNA extraction method was carried out using columns with blood input volumes as described.

DNA quantification and quality control

DNA was quantified with a NanoDrop™ 2000 spectrometer (Thermo Fisher) and concentrations and A_{260}/A_{280}, A_{260}/A_{230} purity ratios assessed. Double strand native DNA was assessed by fluorometric methods Qubit™ dsDNA BR assay kit (Thermo Fisher).

Downstream analysis

Diverse genetic tests were performed which included SALSA® MLPA® (MRC Holland), NGS (Roche or Twist library preparation kits and capture) on MiSeq or NextSeq 2000 sequencer (Illumina), Sanger sequencing with BigDye™ Terminator V3.1 chemistry, 3730xl DNA Analyzer (Applied Biosystems), digital PCR with QX200 Droplet Digital PCR System (Bio-Rad) and long-read sequencing with Cas9 SQK-CS9109 enrichment kits and minION™ sequencer or adaptive sequencing with Ligation Sequencing Kit V14 SQK-LSK114 and PromethION™ P2 solo sequencer (Oxford Nanopore).

Results

Comparison of chemagic extraction to manual column-based methods

Extraction was performed on 24 samples with mini and midi column-based extractions and with the chemagic 360 automated nucleic acid extraction system. Overall DNA concentrations and yields obtained are shown in Table 1. DNA purities were also assessed with all methods showing A_{260}/A_{280} between 1.8 – 2.0 and A_{260}/A_{230} ratio close to 2.0 – 2.2.

Table 1: DNA yields and concentrations of manual column-based and automated chemagic extraction methods.

System	Mini Kit	Midi Kit	Chemagic
Sample volume	200 µl	300 µl – 2 ml	3 – 5 ml
Concentration	55 ng/µl ± 17	155 ng/µl ± 63	196 ng/µl ± 75
Average DNA yield	11 µg	78 µg	98 µg
Hands-on Time	30 min for 5 extractions	3 h for 36 extractions	15 min for 24 extractions

Assessment of cross-contamination

Eight extraction runs were performed on the chemagic 360 instrument with alternating water/male/water/female blood samples on the same plate (across consecutive runs, well positions were permuted). Each eluate was submitted to SRY PCR, and products migrated on a 1.5% agarose gel. No cross-contamination was detected (Fig. 1). Average yields of 60 µg DNA were obtained from 1.5 mL blood.

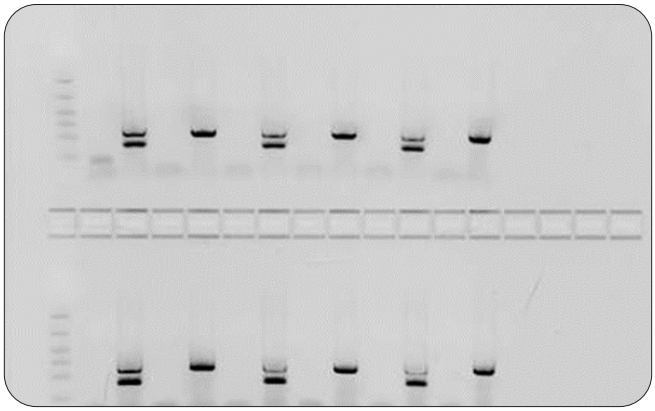


Figure 1: Extraction of alternating male/female blood and water samples showed no cross-contamination between samples.

Assessment of DNA single/double-strandedness

Assessment of DNA concentrations with absorbance and fluorometric methods also demonstrated majority of DNA extracted was double-stranded with the chemagic method.4

Table 2: DNA concentrations as assessed by absorbance vs. fluorometric methods

Sample	Concentration assessed by Nanodrop (ng/µl)	Concentration assessed by Fluoroscence (ng/µl)
11301	109.1	106.2
91301	113.1	96.8
171301	128.4	122.8

Improved consistency in MLPA assays

SALSA® MLPA® assay showed lower variation of ratios with DNA extracted on a chemagic 360 instrument as compared with samples extracted with a manual column-based method (Fig. 2).

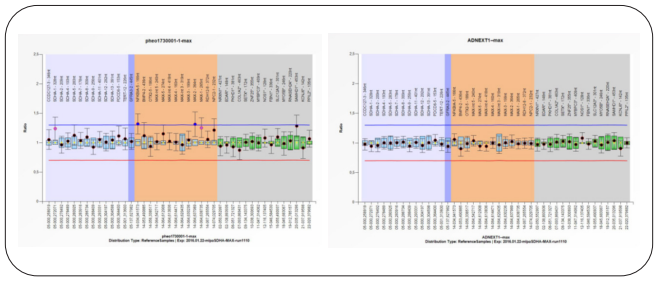


Figure 2: MLPA results with blood samples extracted with manual column-based and automated chemagic extraction methods.

Obtainment of high molecular weight (HMW) DNA

Fragmentation analysis on an Agilent TapeStation system at the European Georges Pompidou Hospital (HEGP) showed majority of fragments > 60 kb. Higher resolution achieved on an Agilent Femto Pulse system showed fragments can range even up to 200 kb (analysis performed at Revvity chemagen Technology GmbH).

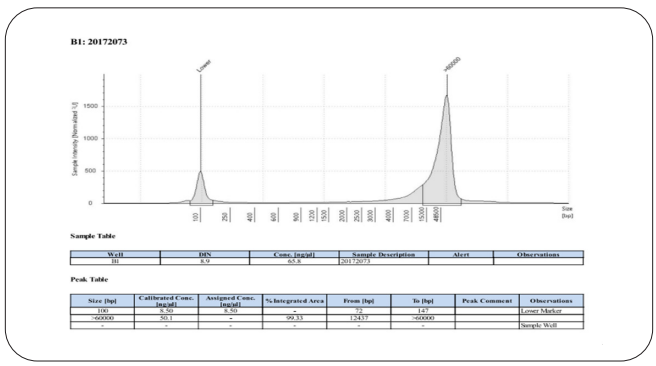


Figure 3: Distribution of DNA fragments extracted from 1.5 mL blood with chemagic 360 instrument as assessed by Agilent TapeStation system.

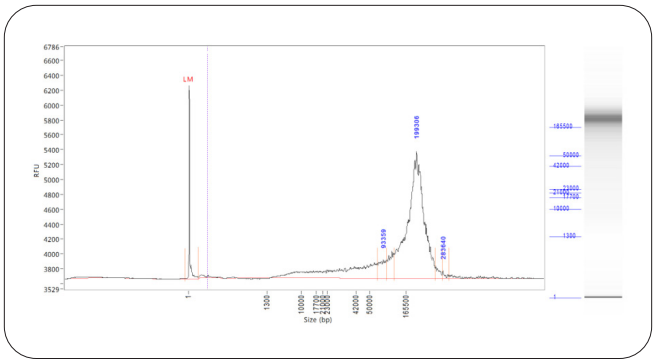


Figure 4: Distribution of DNA fragments extracted from 1.5 mL blood with chemagic 360 instrument as assessed with Agilent Femto pulse system.

Native DNA methylation analysis by Oxford Nanopore Sequencing

An adaptive sequencing, targeted enrichment, was performed to analyze a ~4 kb genomic region for CpG methylation using Oxford Nanopore technology (ONT). Quality and amount of DNA obtained with extraction was sufficient to successfully resolve parental imprinting methylation patterns.

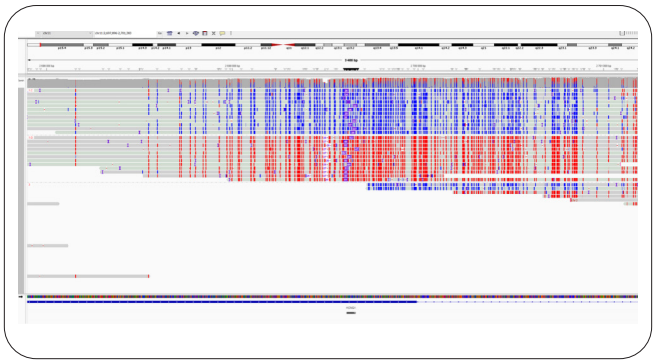


Figure 5: ONT analysis of methylation modifications using adaptive sequencing targeted enrichment on PromethION platform.

Summary

- The clinical utility of the chemagic 360 instrument was evaluated at the European Georges Pompidou Hospital over 8 years, performing extractions from over 30,000 blood samples.
- Compared to manual methods, the chemagic system provided higher, consistent yields of high-quality DNA with no detectable cross-contamination, and majority double-stranded DNA.
- Reliable performance was also established in a range of downstream assays including MLPA, NGS, dPCR and Long Read Sequencing.
- On-demand webinar “High quality DNA for genetic testing”

Register now

Scan or click to register today!