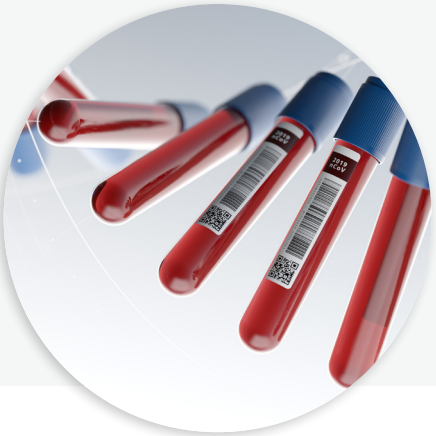
Customer Spotlight

Innovation Under Pressure: DNA Extraction in Harsh Environments





Marie-Claude Gingras, PhD
Director, Nucleic Acids Laboratory
Human Genome Sequencing Center,
Baylor College of Medicine

Photo credit: Baylor College of Medicine

The study of wild mammals in their natural ecosystems poses unique challenges. Morphological and physiological analyses require humane capture, biological sampling and safe release—often under harsh environmental conditions with limited access to laboratory infrastructure.

For Dr. Marie-Claude Gingras—Director of the Nucleic Acids Laboratory at the Human Genome Sequencing Center, Baylor College of Medicine—these challenges are familiar territory, as she routinely supports a diverse network of collaborators who rely on her expertise to advance their research.

Pushing the Boundaries of Field-Based DNA Extraction

In a recent collaboration, Dr. Gingras was entrusted with a critical task: extracting high-quality DNA from blood samples collected from wild mammals in Africa. The study aimed to generate detailed morphological and genetic insights into a unique mammalian population.

The challenge? These samples were collected from regions with extremely limited access to laboratory equipment and minimal storage or preservation capabilities. All were stored for weeks at ambient temperatures reaching 95°F (35°C) in RNAlater preservative before arriving at her laboratory. Despite these logistical difficulties, Dr. Gingras and her team successfully isolated high-quality DNA for downstream genetic analysis.

Their success underscores a powerful message: with minimal handling and a robust isolation protocol, DNA integrity can be preserved even under harsh field conditions. Dr. Gingras' work not only supports vital genetic biodiversity research—it also shows how innovation and expertise can overcome logistical barriers in remote, resource-limited environments.

"Our goal is to ensure that DNA integrity is preserved, no matter the starting point," says Dr. Gingras.

Innovation in the Face of Adversity

Isolation of DNA from the samples was initially attempted using salt-out precipitation and phenol/chloroform extraction, both of which failed. Since no DNA could be obtained using the first two methods, it was concluded that the DNA was likely already in solution and that only a direct DNA capture could be performed on the samples. Dr. Gingras and her team pivoted to bead-based capture using the GenFind V3 Genomic DNA Extraction Kit—a method that proved successful.

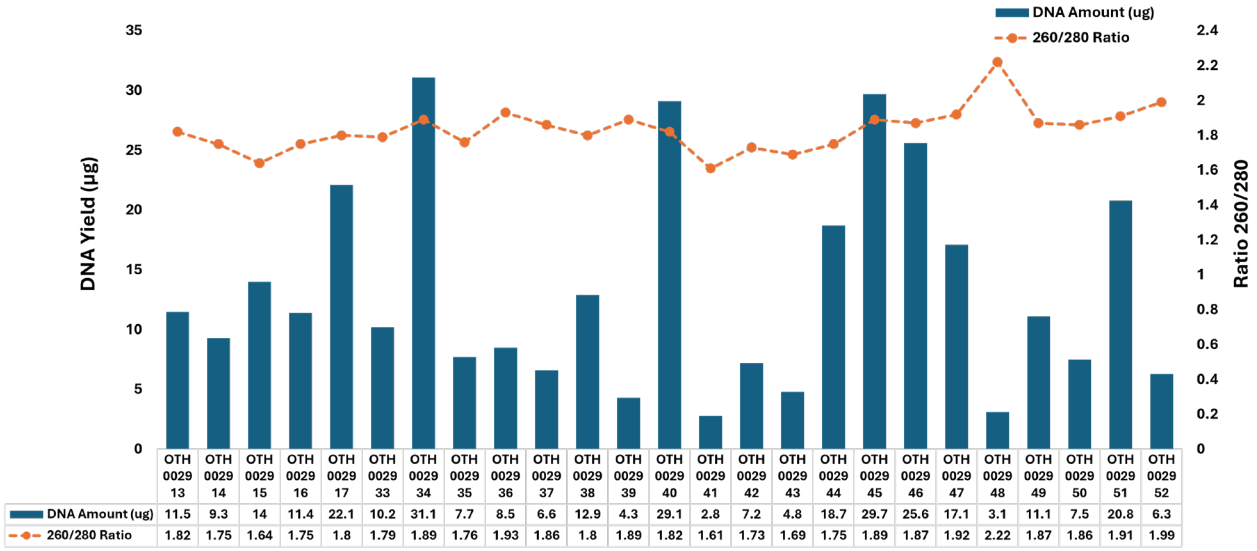
Despite significant sample instability and blood visual flakiness, Dr. Gingras and her team used a fully manual extraction protocol to optimize yield and protect DNA integrity. The isolation of 400 µL blood samples delivered DNA yield ranging from 2.8-31.1 µg and a consistent 260/280 ratio above 1.8—indicating high purity and no contamination (**Figure 1**). All DNA samples show no sign of degradation and exceeded 10 kb as indicated by the 1 kb ladder (**Figure 2**), meeting stringent quality standards. The Sample IDs and their corresponding gel wells are detailed in Table 1.

This high-quality DNA enabled robust library preparation and whole genome sequencing. Sequencing quality was exceptionally high across the entire batch of samples, with an on-target (or genome-wide) mean coverage controlled at 30x (**Figure 3A**), with duplicate reads below 15% (**Figure 3A**), a 98.5% of reads properly aligned to the reference genome, and over 94% of bases with at least 20× coverage (**Figure 3B**). These outcomes highlight the effectiveness of the extraction reagents and demonstrate that reliable sequencing results can be achieved even under challenging sample conditions.

"This project was a testament to the importance of choosing the right protocol to salvage these samples," Dr. Gingras explains.

The resulting data enabled researchers to characterize genetic variation within the studied population and compare it to other conspecific populations and related species. This achievement not only deepened understanding of mammalian genetic diversity but also demonstrated the feasibility of conducting high-quality genomic research in remote, resource-limited settings.

For information about the GenFind V3 Genomic DNA Extraction Kit and our other genomic solutions, beckman.com/reagents/genomic



	OTH 0029 13	OTH 0029 14	OTH 0029 15	OTH 0029 16	OTH 0029 17	OTH 0029 33	OTH 0029 34	OTH 0029 35	OTH 0029 36	OTH 0029 37	OTH 0029 38	OTH 0029 39	OTH 0029 40	OTH 0029 41	OTH 0029 42	OTH 0029 43	OTH 0029 44	OTH 0029 45	OTH 0029 46	OTH 0029 47	OTH 0029 48	OTH 0029 49	OTH 0029 50	OTH 0029 51	OTH 0029 52
DNA Amount (ug)	11.5	9.3	14	11.4	22.1	10.2	31.1	7.7	8.5	6.6	12.9	4.3	29.1	2.8	7.2	4.8	18.7	29.7	25.6	17.1	3.1	11.1	7.5	20.8	6.3
260/280 Ratio	1.82	1.75	1.64	1.75	1.8	1.79	1.89	1.76	1.93	1.86	1.8	1.89	1.82	1.61	1.73	1.69	1.75	1.89	1.87	1.92	2.22	1.87	1.86	1.91	1.99

Figure 1. DNA yield and purity.

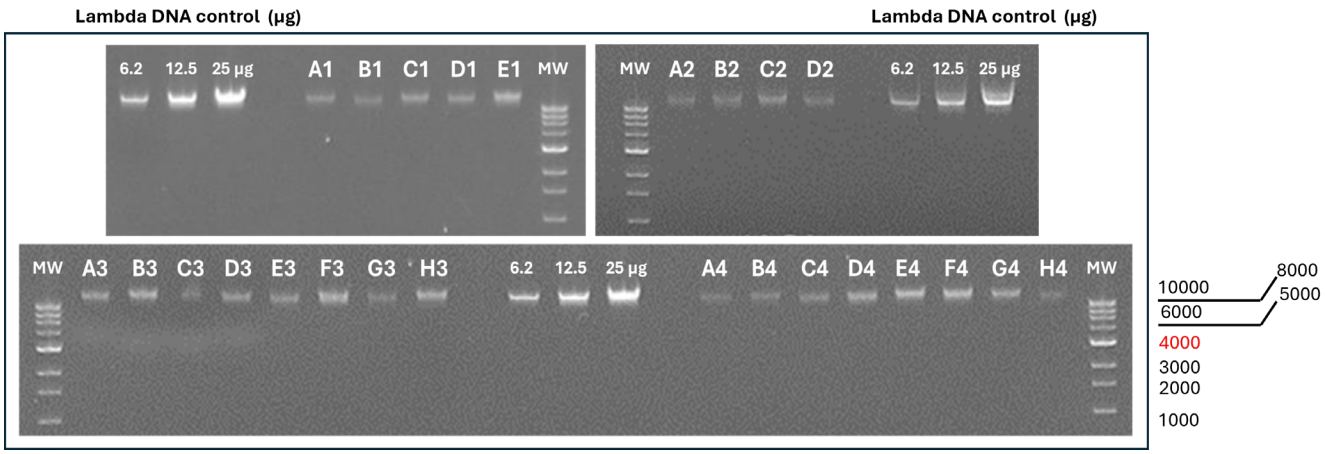


Figure 2. Gel image shows the extracted DNA size.

Location on Gel	Sample ID
A1	OTH002913
B1	OTH002914
C1	OTH002915
D1	OTH002916
E1	OTH002917
A3	OTH002933
B3	OTH002934
C3	OTH002935
D3	OTH002936
E3	OTH002937
F3	OTH002938
G3	OTH002939
H3	OTH002940
A4	OTH002941
B4	OTH002942
C4	OTH002943
D4	OTH002944
E4	OTH002945
F4	OTH002946
G4	OTH002947
H4	OTH002948
A2	OTH002949
B2	OTH002950
C2	OTH002951
D2	OTH002952

Table 1. Gel well positions and sample IDs

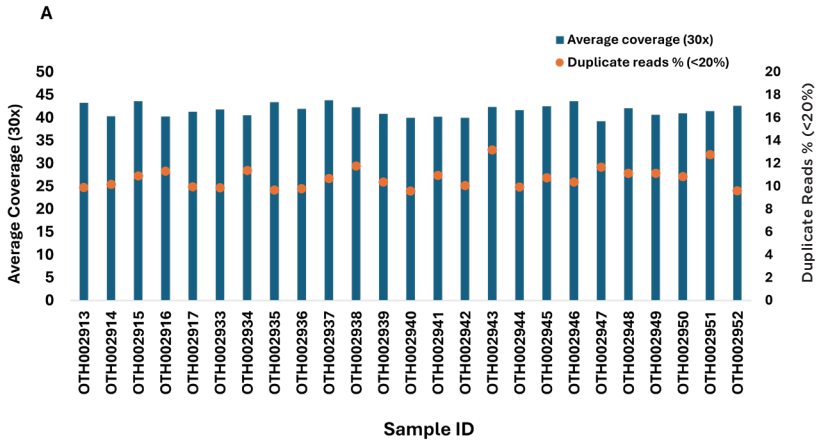
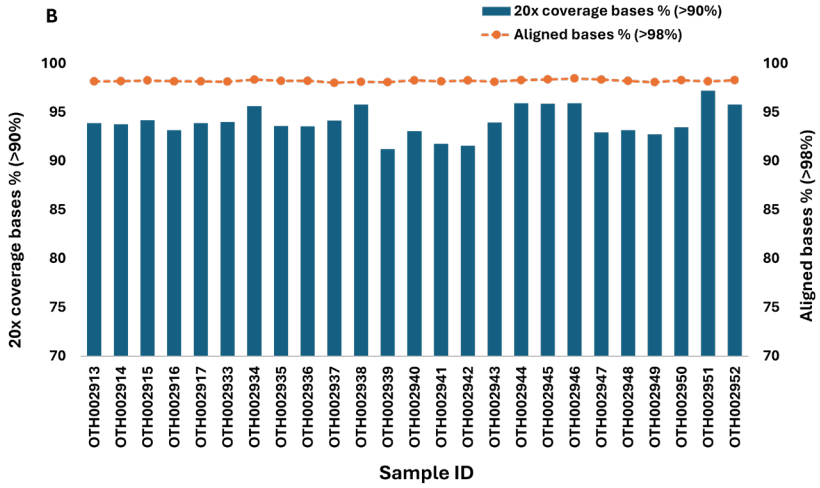


Figure 3: Sequencing quality metrics. (A) Mean coverage at 30× and proportion of duplicate reads (<20%). (B) Percentage of aligned bases (>98%) and proportion of bases with ≥20× coverage (>90%).



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