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Abstract

Background: The process of extracting DNA from whole blood is critical for numerous downstream applications including diagnostics, forensics, pharmacogenomics, and long-term biobanking. Over time, extraction methodologies have evolved substantially, reflecting changing demands for purity, speed, automation, and sample preservation.

Scope of Review: This review synthesizes the history, current practices, and emerging technologies in blood-based DNA extraction. We begin with the development of traditional methods such as phenol–chloroform and salting-out, proceed to automated and bead-based systems, and highlighted cutting-edge innovations like lab-on-chip and magnetic nanoparticle-based methods. Key challenges including sample degradation, inhibitors, and contamination are discussed, along with strategies to maximize yield and quality. We also analyzed application-specific requirements across clinical diagnostics, forensic science, pharmacogenomics, NGS, and biobanking.

Findings and Implications: Our analysis underscores that no single method universally outperforms other. The optimal choice depends on balancing trade-offs: cost, time, purity, throughput, and sample condition. Emerging methods promise faster, greener, and more field-adaptable extraction, but they must be validated carefully for each use-case.

Conclusion: Effective DNA extraction from blood remains a dynamic field where technological innovation and practical constraints must converge. Our review offers a comprehensive guide to select and customize extraction workflows in light of application-driven demands, while forecasting future directions for method development.

Keywords: Biobanking, forensics, pharmacogenomics, field-adaptable extraction

1. Introduction

Deoxyribonucleic acid (DNA) extraction from blood remains a foundational step in molecular biology, underpinning diverse applications from clinical diagnostics to forensic analysis [1]. Since the discovery of DNA in the 19th century, methodologies for isolating genomic DNA have evolved dramatically progressing from labour-intensive organic solvent techniques to rapid, high-throughput automated systems [2]. Whole blood is among the most widely used sources of DNA owing to its accessibility, rich cellular content, and broad

applicability [3]. However, no single extraction method is universally optimal. Each approach involves trade-offs in terms of cost, purity, yield, throughput, and sample compatibility.

In recent years, continuous innovation has produced a spectrum of techniques from classical phenol–chloroform protocols to modern magnetic bead, solid-phase, and microfluidic platforms [3]. These advances have allowed laboratories to tailor extraction workflows according to their requirements, whether aiming for maximal purity, minimal hands-on time, or scalability. Despite these developments, selecting the "best" protocol is not easy, the decision depends on multiple factors, including downstream application, available resources, and sample quality.

This review explores the evolution of blood-based DNA extraction methods, examining traditional and modern approaches, sample-specific challenges, quality considerations, contamination risks, and future trends. By mapping this methodological journey, we aim to provide a practical and scientific framework to help researchers and clinicians choose the most suitable DNA extraction strategy for their specific needs.

2. Historical Overview of DNA Extraction Techniques

The process of DNA extraction has evolved through many decades of scientific discovery. It began in 1869, when Friedrich Miescher first isolated a new substance from white blood cells while studying their chemical composition [4]. He collected leukocytes from surgical bandages and discovered a material in the nuclei that was different from proteins, which he named "nuclein."[4] With guidance from his mentor Felix Hoppe-Seyler, Miescher published his methods in 1871, marking the first known isolation of what we now recognize as DNA [4]. In 1958, Meselson and Stahl used salt-density gradient centrifugation in Escherichia coli to demonstrate semiconservative DNA replication [5]. This landmark experiment also highlighted reproducible approaches for DNA isolation and separation, reinforcing DNA extraction as a standard molecular biology technique [5]. Over time, these early discoveries have been refined into numerous laboratory protocols, adapted for different biological materials such as whole blood, tissues and cell cultures.

DNA extraction protocols, whether manual or automated, generally follow a conserved workflow involving cell lysis, protein disruption, nuclease inactivation, contaminant removal, and DNA precipitation for recovery and storage [6]. Lysis is typically achieved with detergents such as SDS or Triton™ X-100, often supplemented with Proteinase K to degrade proteins and inactivate DNases and RNases; denaturants like urea or guanidinium salts may be used to enhance lysis, though they can compromise yield or quality [7]. DNA is subsequently precipitated by salts such as sodium chloride or ammonium acetate, which neutralize the phosphate backbone and promote aggregation in the presence of ethanol (95–100%) or isopropanol (40–50%) [8]. The resulting pellet is washed with 70% ethanol to remove residual salts and impurities, then resuspended in TE buffer (10 mM Tris, 1 mM EDTA), where Tris maintains pH stability and EDTA chelates divalent cations to protect against enzymatic and oxidative damage [9]. These chemical principles underpin both traditional approaches, including phenol–chloroform extraction, and modern kit-based systems, underscoring the importance of understanding the underlying chemistry to optimize DNA yield, purity, and integrity from whole blood and other biological materials.

3. Strategies for Efficient DNA Isolation

A range of strategies have been developed to isolate genomic DNA with high yield and purity, each employing distinct chemical principles and reagents. The Phenol–Chloroform–Isoamyl alcohol (PCI) method is a classical organic solvent–based technique in which proteins and lipids partition into the organic phase, leaving DNA in the aqueous layer [10]. Despite its labor-intensive nature, PCI remains a benchmark for purity and yield and is widely used for teaching, validation, and high-quality genomic DNA isolation [10] (**Table 1).**

The salting-out method offers a simpler alternative, relying on high salt concentrations to precipitate proteins, followed by DNA precipitation with isopropanol and ethanol washing [11]. Buffers and detergents facilitate selective cell lysis, while NaCl removes proteins, producing DNA of sufficient purity (A260/A280 ~1.7–1.8) and yield for downstream applications [6] **(Table 1).**

More recently, automated extraction systems represent advanced, high-throughput platforms designed to streamline nucleic acid isolation [12]. Initially adopted in medium to large laboratories, they are now increasingly common as automation improves workflow consistency and reduces manual effort. These systems lower hands-on time, reduce labour costs, enhance operator safety, and improve reproducibility by minimizing human error, thereby strengthening laboratory efficiency and output quality [13].

3.1 Solid-Phase Nucleic Acid Purification

Solid-phase extraction, widely incorporated into commercial kits, offers faster and more reliable purification than traditional liquid–liquid methods [6]. Nucleic acids bind to solid supports depending on buffer pH and salt concentration, primarily through hydrophilic, ionic, or affinity-based interactions. Spin-column formats, which use centrifugal force to facilitate binding, washing, and elution, yield high-purity DNA within short timeframes [14]. Common supports include silica matrices, glass particles, diatomaceous earth, and anion-exchange resins, with workflows generally comprising lysis, adsorption, washing, and elution [15]. (**Table 1).**

3.2 Silica Matrices

Silica-based materials are widely used due to their strong and selective affinity for DNA [16]. Binding occurs under high-salt and alkaline conditions, where sodium ions bridge the negatively charged DNA backbone to the silica surface [17]. After contaminants are removed through wash steps, DNA is eluted under low ionic strength conditions using TE buffer or sterile water [18]. Commercial kits such as Wizard® (Promega), NucleoSpin™ (Clontech), UltraClean® BloodSpin® (MO BIO), and QIAamp® (QIAGEN) employ this principle, typically yielding high-quality DNA within 40–60 minutes [18]. (**Table 1).**

3.3 Diatomaceous Earth

Diatomaceous earth, composed largely of silica, has long been used in filtration and chromatography and serves as a solid-phase support for DNA binding in the presence of chaotropic salts [19]. Bound DNA is washed with

alcohol-based buffers and eluted with low-salt solutions [19]. Products such as Quantum Prep® (Bio-Rad) utilize this method, while semi- and fully automated platforms (e.g., BioRobot EZ1® Advanced, Biomek® 4000) integrate silica- or diatomaceous-earth–based kits into automated workflows. These systems reduce pipetting errors and sample transfers, though their high cost remains a limitation. (**Table 1).**

3.4 Anion-Exchange Resins

Anion-exchange resins, such as DEAE-functionalized silica beads, selectively bind negatively charged nucleic acids through electrostatic interactions with the DNA phosphate backbone [20]. Binding efficiency depends on buffer pH and salt concentration, with medium-salt buffers removing proteins and RNA while DNA remains attached until eluted with high-salt solutions [21]. Chelex® 100, a chelating ion-exchange resin, is widely used in forensic applications to protect DNA from nuclease cofactors [22]. Chelex-based protocols, first described by Walsh et al. (1991), employ proteinase K or heat for lysis, followed by resin treatment to remove impurities, yielding DNA suitable for downstream analysis [22]. (**Table 1).**

3.5 Magnetic Bead–Based Extraction

Magnetic bead based DNA extraction has emerged as a widely adopted modern technique due to its speed, simplicity, and compatibility with automation [23]. Magnetic particles, typically magnetite (Fe_3O_4) or maghemite (γ-Fe_2O_3) cores coated with silica, polymers, or hydroxyapatite bind DNA through functional surface chemistries [24]. Application of an external magnet enables rapid separation of DNA-bound particles from the sample, facilitating efficient washing and elution with minimal manual handling [25]. Originally introduced for plasmid DNA isolation [26] and later adapted for genomic DNA from whole blood [25], this approach combines SDS lysis, nanoparticle binding in high-salt/PEG buffer, magnetic separation, ethanol washing, and elution in TE buffer [25]. Magnetic bead systems offer significant advantages over conventional methods, including reduced contamination risk, high reproducibility, low hands-on time, and seamless integration with automated and high-throughput platforms. (**Table 1).**

3.6 Lab-on-Chip (LOC) Techniques

Lab-on-chip systems are microfluidic devices that integrate sample preparation, lysis, nucleic-acid capture, purification, and often detection within a single miniaturized platform [27]. They enable rapid DNA extraction from very small blood volumes (1–50 µL), making them particularly valuable for point-of-care diagnostics [27]. Most LOC devices employ solid-phase extraction zones, nanoporous membranes, or paper-based discs to selectively bind DNA, while automated microvalves, pumps, and flow channels manage reagent handling, washing, and elution [28]. Applications include one-step DNA extraction with real-time PCR chips for pathogen detection, silica bead-packed microchip chambers for rapid purification, electrophoresis-based microchips for downstream qPCR or LAMP analysis, acoustic microchips for sepsis diagnostics, and low-cost paper-based platforms for direct PCR [29]. These systems reduce reagent use, minimize user intervention, and accelerate workflows, while also supporting multiplex biomarker detection, blood-group antigen typing, and nanoscale FET-based pathogen sensing [29]. (**Table 1).**

4. Sample-Specific Challenges in Blood DNA Extraction

Blood samples encountered in research, diagnostics, or forensic investigations vary widely in their condition. Factors such as age, storage environment, and degradation strongly influence DNA integrity and extraction efficiency[30]**.** DNA contamination can arise from residual proteins, RNA, reagents, or environmental sources such as skin cells and airborne particulates, ultimately compromising yield and downstream applications (**Figure 1**). Understanding these sample-specific challenges is essential for selecting the appropriate workflow and ensuring reliable downstream analysis.

4.1 Fresh vs. Aged Blood Samples

Blood samples differ significantly in quality depending on whether they are fresh or stored. Freezing and long-term storage often introduce DNA fragmentation, with frozen blood showing higher baseline damage compared to fresh samples [31]. Nevertheless, proper cryopreservation protocols allow archived samples to remain usable for genetic analysis. Clotted or archived blood presents another challenge, as clots hinder efficient lysis and reduce yield [11]. Mechanical dispersion using sterile ball bearings, combined with modified salting-out methods, has proven effective in recovering high-quality DNA from such samples, making them valuable for molecular studies [11].

4.2 Degraded or Compromised Samples (Forensic Applications)

Forensic blood samples are frequently degraded due to environmental exposure. Dry storage conditions preserve DNA far better than moist environments, where microbial growth accelerates degradation [32]. Direct PCR can be applied to low-DNA trace samples, but inhibitors from substrates or contaminants often interfere with amplification, and stochastic effects such as allele drop-out complicate interpretation [33]. Highly degraded DNA from old stains or skeletal remains is often fragmented and chemically damaged, requiring specialized extraction strategies and amplification of shorter loci to improve recovery [34].

4.3 Inhibitor removal

Blood contains natural inhibitors such as hemoglobin, salts, and environmental contaminants that interfere with DNA extraction and PCR [35]. Rapid detergent-based methods using NP-40 or Triton X-100 can recover DNA quickly, though magnesium levels must be carefully controlled to prevent degradation [36]. Forensic samples exposed to heat or repeated freeze–thaw cycles are particularly prone to inhibitor accumulation, necessitating additional pre-processing[37]. Even RNA-based assays for blood detection are vulnerable, as inhibitors like hematin or humic acid can block amplification [38]. Furthermore, extraction methods themselves introduce challenges like phenol–chloroform yields high purity but involves hazardous chemicals, while commercial kits are safer but may leave residual contaminants [2].

4.4 Low-Volume Samples

Working with pediatric or limited-volume samples requires careful handling, as only small amounts of DNA are available and preanalytical errors can significantly reduce quality. Umbilical cord tissue offers a reliable alternative source, yielding DNA of high quality and showing complete genotyping concordance with blood samples [39]. Pediatric blood is particularly prone to hemolysis and clotting due to collection difficulties, which compromise DNA integrity [40]. Integrating DNA sequencing into newborn screening adds further complexity, with challenges including high costs, variant interpretation, bioinformatics requirements, and ethical considerations such as parental consent and privacy [41].

4.5 Storage Conditions and Their Impact

Storage conditions strongly influence DNA integrity. DNA remains stable for months at room temperature but degrades rapidly above 45°C, while frozen storage at −70°C or −80°C preserves quality long-term[42]. Anticoagulants such as ACD solution B help maintain DNA stability during shipping at ambient temperatures, reducing costs. RNA is more fragile than DNA and requires stricter storage conditions to prevent degradation [43]. Large biobanking studies confirm that DNA stored at −80°C for decades remains suitable for genetic analysis, while newer dry-storage media such as SampleMatrix™ provide room-temperature stability without inhibiting PCR, offering practical alternatives for forensic and clinical applications [44].

5 Emerging Technologies and Innovations in DNA Extraction

Rapid advances in biotechnology, microfluidics, nanomaterials, and computational sciences are reshaping how DNA is isolated, processed, and interpreted in both forensic and diagnostic contexts [45]. These innovations aim to make nucleic acid extraction faster, safer, environmentally sustainable, and adaptable for field use, particularly in settings with limited laboratory infrastructure.

5.1 Rapid DNA Extraction and Analysis Techniques

Rapid DNA systems are automated, portable platforms capable of generating complete STR profiles within 60–120 minutes [46]. They integrate lysis, purification, amplification, electrophoretic separation, and data interpretation into a single closed cartridge, eliminating the need for skilled operators or specialized laboratory equipment [47]. Applications range from crime scene investigation and border security to disaster victim identification, military use, and arrestee processing. However, challenges include high instrument costs, limited performance with degraded or mixed samples, and varying legal acceptance across jurisdictions. Future developments focus on improved mixture handling, portable next-generation sequencing (NGS), and harmonized global standards [47].

5.2 Point-of-Care (POC) DNA Extraction

POC platforms aim to deliver rapid, reliable nucleic acid extraction outside conventional laboratories by miniaturizing the fundamental steps of lysis, contaminant removal, binding, and concentration into compact devices[48]. Chemically driven methods such as CsCl–EtBr, guanidinium thiocyanate–phenol–chloroform,

CTAB, Chelex®, and alkaline extraction offer varying levels of purity and safety, while solid-phase strategies including silica matrices, magnetic beads, anion-exchange resins, cellulose cards, and diatomaceous earth enable efficient binding and recovery [49]. Devices range from spin columns and magnetic bead systems to automated liquid-handling robots and microfluidic lab-on-chip cartridges. Despite their promise, portable integration faces limitations such as polymer incompatibility with solvents, reduced sensitivity due to small sample volumes, and challenges in homogenization [50]. Implementation is further constrained by the WHO ASSURED criteria (Affordable, Sensitive, Specific, User-friendly, Rapid/Robust, Equipment-free, Deliverable), which few nucleic acid tests fully meet due to complex sample preparation, training requirements, infrastructure gaps, and high manufacturing costs [51].

5.3 AI and Machine Learning in Forensic DNA Analysis

Artificial intelligence (AI) and machine learning (ML) are increasingly integrated into forensic genomics to accelerate interpretation, reduce human bias, and optimize complex workflows [52]. Key applications include automated mixture deconvolution, where algorithms estimate contributor numbers and allele probabilities; pattern recognition and data mining for large DNA databases; phenotype and ancestry prediction from genetic markers; and bioinformatics automation for sequence alignment, variant calling, and reporting [53]. Despite their promise, challenges remain: biased or insufficient training data can compromise reliability, "black-box" models face scrutiny in legal contexts, and ethical concerns arise around privacy and potential reinforcement of racial bias. Standardization and validation are essential before courtroom adoption. Looking ahead, AI has the potential to enable fully automated forensic workflows, environmental DNA profiling, and specialized training programs for forensic practitioners [53].

5.4 Environmentally Friendly "Green Extraction"

Sustainable extraction approaches aim to eliminate hazardous chemicals while maximizing DNA recovery under diverse environmental conditions. Studies show that low temperatures (–13 °C) preserve DNA integrity best, while sunlight and UV exposure rapidly degrade DNA through structural damage such as thymine dimers [54]. Moist soil yields intermediate recovery due to microbial and chemical interactions, whereas poor storage practices lead to contamination and unreliable profiles [9]. These findings highlight the importance of freezing for long-term preservation, minimizing UV exposure, and maintaining proper packaging and storage [9]. In forensic contexts, understanding environmental impacts on DNA yield is critical for accurate crime-scene interpretation and reducing inconclusive results [55].

5.5 Nanotechnology Applications: Magnetic Nanoparticle–Based DNA Extraction

Magnetic nanoparticles (MNPs) provide a rapid, equipment-free alternative to traditional chemical or column-based extraction methods. Their superparamagnetic properties allow DNA-bound particles to be separated using a simple magnet, eliminating the need for centrifugation or hazardous solvents [56]. Manufacturing approaches typically involve coprecipitation of iron precursors (e.g., $FeCl_2/FeCl_3$), with silica coatings applied to enhance DNA binding efficiency [56]. Extraction workflows commonly use PEG + NaCl for binding, ethanol for

washing, and Tris-EDTA buffer for elution [57]. Reported yields range from 0.03 to 116 µg with purity ratios (A260/A280) between 1.09 and 1.99, suitable for human, animal, plant, and microbial samples [57]. Advantages include speed, scalability, compatibility with automation, and environmental sustainability. MNP-based extraction is emerging as a versatile tool across diagnostics, food safety, environmental testing, and forensic applications [58].

6. Application-Driven Requirements for DNA Extraction

The choice of DNA extraction method is determined by the downstream application, as clinical diagnostics, forensic investigation, pharmacogenomics, next-generation sequencing (NGS), and long-term biobanking each demand specific standards of yield, purity, and fragment integrity. Ensuring these application-driven requirements is essential for reproducibility, accuracy, and meaningful biological interpretation.

6.1 Clinical Diagnostics

Clinical workflows require rapid, reliable, and contamination-free DNA extraction to support PCR, qPCR, and sequencing assays. Rapid extraction methods can deliver high-quality DNA in under one hour, enabling timely pathogen detection [6]. Commercial kits such as QIAamp DNA Blood Mini consistently yield high-purity DNA from small volumes, while solid-phase and magnetic bead systems provide automation-friendly performance for high-throughput laboratories [14]. Salting-out remains a cost-effective option in resource-limited settings. Pre-analytical factors, including anticoagulant choice and protease treatment, strongly influence yield, and immediate processing or freezing at –20 °C is recommended to maintain integrity [59].

6.2 Forensic Analysis

Forensic applications often involve small, degraded, or contaminated samples, requiring methods that recover short DNA fragments while removing inhibitors. Chelex-100 resin provides rapid extraction from low-volume samples suitable for STR profiling, while silica-based protocols such as the Dabney method enhance recovery of damaged DNA from compromised evidence [22]. Pre-library purification improves success in STR and NGS workflows, and enzyme-free extraction of frozen blood offers cost-effective recovery. Ethical concerns surrounding NGS in forensic genomics highlight the need for privacy safeguards and standardized protocols [60].

6.3 Pharmacogenomics

Pharmacogenomic testing demands high-purity DNA (A260/280 ~1.8) and sufficient yields (>1 µg) to genotype drug-response genes accurately [61]. Validated platforms such as QIAamp and Maxwell 16 ensure reproducibility under ISO standards, while rapid kits like SwiftX enable centrifuge-free extraction in under 15 minutes for point-of-care testing. Fresh blood treated with deionized water has been shown to yield exceptionally pure DNA, supporting sensitive applications such as adverse drug event research [62].

6.4 Next-Generation Sequencing (NGS) Compatibility

NGS requires intact, high-molecular-weight DNA (30,000–150,000 bp) to ensure uniform coverage. Automated capillary-based systems preserve fragment length better than conventional methods, while Chelex extraction from dried blood spots supports ultra-low input for long-read sequencing [63]. Mechanical lysis improves metagenomic representation, and specialized protocols from PacBio and BioEcho provide consistent extraction for advanced sequencing platforms [64].

6.5 Long-Term Biobanking

Biobanking emphasizes DNA stability over decades. Frozen storage at –20 °C or –80 °C maintains integrity, with studies confirming usability even after 21 years [65]. Emerging technologies such as cryosilicification enable room-temperature preservation, reducing reliance on cold chains. Commercial systems like Oragene tubes provide stable DNA for transport and multi-year storage, while quality control frameworks ensure concentration, purity, and structural integrity [66]. Ethical guidelines reinforce the importance of secure sample management and standardized assessment.

7. Conclusion

Blood-based DNA extraction has evolved remarkably from the early, labor-intensive phenol–chloroform protocols to today's highly automated, sensitive, and rapid platforms. Despite this progress, the central challenges remain: maximizing yield and purity while minimizing time, cost, and degradation.

This review underscores that the optimal extraction method is application-dependent. Clinical diagnostics prioritize speed and purity; forensic workflows demand sensitivity and inhibitor removal; NGS requires intact, high-molecular-weight fragments; pharmacogenomics emphasizes reproducibility and yield; and biobanking focuses on long-term stability. Recognizing these distinct requirements enables researchers to select workflows tailored to their specific context.

Emerging technologies including microfluidic systems, lab-on-chip devices, and magnetic nanoparticles offer promising avenues for democratizing DNA extraction. These innovations may enable field-deployable workflows, environmentally sustainable chemistries, and unprecedented throughput. However, rigorous validation and standardization remain essential to ensure that novel protocols deliver consistent downstream performance and reproducibility.

In essence, the trajectory of DNA extraction reflects the broader dynamics of molecular biology: a continual balance between precision, practicality, and innovation. By understanding the strengths and limitations of each technique, practitioners can design workflows that meet current demands while anticipating future challenges.

Table 1: Different types of DNA extraction methods

Method	Principle	Advantages	Limitations	Applications	Typical Yield/Purity
Phenol–Chloroform (PCI)	Organic solvents partition proteins into organic phase, DNA remains aqueous	High purity, benchmark method	Toxic reagents, labor-intensive	Teaching, validation, genomic studies	10–20 µg DNA / A260/A280 ~1.8–2.0
Salting-out	High salt precipitates proteins, DNA recovered by alcohol precipitation	Safe, inexpensive, avoids organic solvents	Lower purity than PCI	Routine genomic DNA isolation	6–10 µg DNA / A260/A280 ~1.7–1.8
Automated Systems	Robotics and kits streamline extraction	High throughput, reproducible, minimal hands-on time	Expensive equipment, consumable dependency	Clinical diagnostics, large-scale studies	5–15 µg DNA / A260/A280 ~1.8–2.0
Solid-phase purification	DNA binds to solid matrices under specific conditions	Efficient, scalable, compatible with automation	Requires specialized kits	Molecular biology workflows	5–12 µg DNA / A260/A280 ~1.8–2.0
Silica matrices	DNA binds silica in presence of chaotropic salts	High yield, purity, widely adopted	Cost of kits, requires chaotropic agents	PCR, sequencing, forensic analysis	8–15 µg DNA / A260/A280 ~1.8–2.0
Diatomaceous earth	DNA adsorption onto silica-rich particles	Inexpensive, effective	Less standardized, variable efficiency	Research, teaching labs	5–10 µg DNA / A260/A280 ~1.7–1.9

Anion-exchange resins	DNA binds to positively charged resins, eluted with salt gradient	Scalable, good purity	Requires optimization, longer protocols	Large-scale plasmid/genomic DNA prep	10–20 µg DNA / A260/A280 ~1.8–2.0
Magnetic beads	DNA binds to coated beads, separated magnetically	Rapid, automation-ready, minimal manual handling	Cost of beads, requires specialized equipment	Clinical labs, point-of-care testing	5–12 µg DNA / A260/A280 ~1.8–2.0
Lab-on-chip microfluidics	Miniaturized channels integrate lysis, binding, washing, elution	Ultra-fast, portable, low sample requirement	Emerging technology, limited availability	Point-of-care diagnostics, field research	1–5 µg DNA / A260/A280 ~1.7–1.9

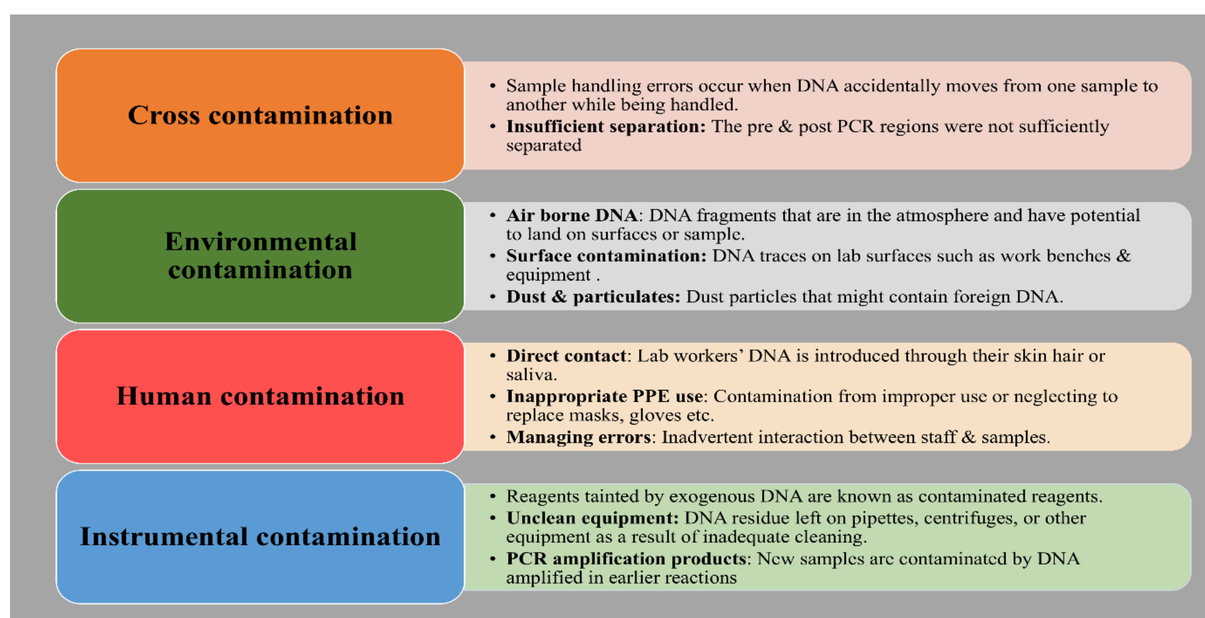

Figure 1: Sources of DNA contamination in laboratory workflows. This schematic categorizes contamination into four major types: cross contamination (sample handling errors, insufficient separation of pre- and post-PCR areas), environmental contamination (airborne DNA, surface residues, dust/particulates), human contamination (direct contact, improper PPE use, staff handling errors), and instrumental contamination (tainted reagents, unclean equipment, carryover of PCR products). Each category highlights typical causes that can compromise DNA integrity and downstream analyses.

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