

Rapid DNA extraction from buccal swab samples: enhancing efficiency and performance

Willing, Lydia¹; Seip, Nicole²; Salazar-Rondon, Maria²; Torres-Benito, Laura² ¹ BioEcho Life Sciences, Inc. 400 Tradecenter Drive, Suite 6900, Woburn, MA 01801, US. ² BioEcho Life Sciences GmbH, BioCampus Cologne, Main Building, Nattermannallee 1, 50829 Cologne, Germany.

Key Take Aways

• Novel and efficient method for buccal cells DNA extraction from buccal swab samples, significantly reducing processing time

• High-quality DNA, resulting in reproducible qPCR

• Short tandem repeat (STR) and microarray analysis prove suitability for genetic analysis



Introduction

The extraction of high-quality DNA from buccal cells is of utmost importance in various fields of genetic research, forensic science, and medical diagnostics. However, conventional DNA extraction methods often involve time-consuming protocols that might reduce the overall efficiency. We introduce a novel method for buccal cells DNA extraction from buccal swabs, designed to improve convenience and prove compatibility with downstream applications such as qPCR testing, short tandem repeat (STR), and microarray analysis: the EchoLUTION technology.

Materials and Methods

qPCR: We collected buccal cells with swabs (Herenz DS-Swab) from seven individuals and extracted DNA with the EchoLUTION™ Buccal Swab DNA Kit. We determined concentration and yield using Qubit™ (ThermoFisher® Scientific), and performed qPCR with these samples.

STR analysis: We extracted DNA from buccal cells from six individuals to test aneuploidy in chromosomes 13, 18, 21, X and Y. Eluates were diluted to 1 ng/µL, amplified via Quantitative Fluorescence PCR (QF-PCR), and data were analyzed with Gene®Marker V2.6.7 (SoftGenetics®).

Microarray analysis: We isolated DNA from blood (EDTA precipitation) and buccal cells from the same individual (three biological replicates each). To concentrate the buccal swab eluates, we dried them (Speedvac™, ThermoFisher®Scientific) and resuspended in 4 µL. We performed genome-wide genotyping using the Infinium® Global Screening Array-24 v3.0 (Illumina®). Genotypes were called using GenomeStudio® 2 (Illumina®).

Results

DNA extraction



Figure 1. Buccal cells DNA extracted from buccal swabs. DNA concentration (A) and yield (B) measured with fluorometry . N = 3individuals, n = 6 replicates. Error bars represent standard deviation.

qPCR



Figure 2. *CFTR* gene qPCR curves from DNA extracted from buccal cells. N = 3individuals, n = 6 replicates. Orange curves from 2 µL of sample input; blue ones represents a 1:10 dilution; grey curves are the negative controls.

STR analysis





Microarray analysis

Sample	Call rate	Calls	No calls
Blood 1	0.9949402	726365	3694
Blood 2	0.9952867	726618	3441
Blood 3	0.9954812	726760	3299
Buccal swab 1	0.9863504	720094	9965
Buccal swab 2	0.9887584	721852	8207
Buccal swab 3	0.9723694	709887	20172

Table 1. Quality metrics of array genotyping from DNA isolated from EDTA blood and buccal swab samples from the same individual. The call rate reflects the percentage of successfully called SNPs. In this data set, all arrays achieve a call rate of > 0.97. Data demonstrate that DNA extracted from buccal cells results in



Figure 3. STR analysis with DNA extracted from buccal cells. A. Ratio plot derived from the QF-PCR. Y-axis represents the peak value for each locus in chromosomes X, Y, 13, 18, and 21. **B.** The figure depicts a trisomy analysis based on the allele peak ratio from the analyzed loci. Each symbol represents the mean of two replicates. Ratios lying between 0.7 to 1.5 indicates that there are two copies of the allele. No trisomy was observed in this patient (ratio < 0.70 or > 1.50).

Β



reliable genotype data.

Figure 4. Heatmap of concordance rate between arrays. The concordance rate corresponds to the rate of

matched genotype calls between the replicates. The concordance rate is slightly lower for buccal DNA samples, however, the rate was > 0.998 for all samples. E: EDTA- blood, B: buccal swab.

Further information:

www.bioecho.com/buccal-swab



Conclusion

The EchoLUTION technology exhibits a significant advancement in the extraction of DNA from dry buccal swab samples. The reduction in processing time, coupled with the competent efficiency, ensures increased sample throughput and enables accurate and reliable downstream applications such as qPCR, STR, and microarray analysis.