



Contents lists available at ScienceDirect

Forensic Science International: Genetics Supplement Series

journal homepage: www.elsevier.com/locate/fsigss

Detection of human DNA in the air

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ARTICLE INFO

Keywords:
DNA
Aerosol
Transfer
Forensic

ABSTRACT

Large quantities of human cells and DNA fragments are continually released into the air and this constitutes a significant proportion of indoor dust. This study explored the feasibility of aerosol DNA as a source of information to aid human identification in criminal cases. Air samples were collected using the AirPrep™ ACD220 electret filter air sampler from indoor environments. Dust samples were collected in parallel from surfaces in the same areas. A new method to extract human DNA from the air filters was developed. DNA profiles were evaluated in relation to the use and time of occupancy of the room from where samples were collected. This study showed that human DNA can be collected from air in sufficient amounts to yield full STR genotypes, suggesting the potential use of aerosol DNA as a novel investigative tool for forensic applications.

1. Introduction

Humans continually shed skin cells and DNA into the air. DNA was previously recovered from dust in sufficient amounts to yield STR genotypes [1,2]. The collection and isolation of human DNA from the air could help to identify suspects in criminal cases where no contact traces have been left on the crime scene. In this study we investigated methods to collect, isolate and analyze human DNA from the air. We further compared DNA profiles obtained from air samples to DNA profiles obtained from dust samples collected in parallel from the same room. We finally explored if the results are related to the type of room and time since human occupancy.

2. Methods

This study was approved by the data protection officer (DPO) at Oslo University Hospital (reference: 20/20155). All participants delivered informed consent before participation in the study.

Thirty air samples and 104 dust samples were collected from indoor premises at the Forensic Genetics Unit of Oslo University Hospital. Air samples were collected using the AirPrep™ ACD220 electret filter air sampler (Innovaprep®). Seventeen air samples were collected from offices 0 h after occupancy, while seven samples were collected from offices one day after occupancy; six air samples were collected from meeting rooms 0 h after occupancy. The air sampler was run continuously for 2 h at maximum flow rate (200 LPM), while standing in a

standard off-camera tripod located in the middle of the room. The sampler was cleaned after each sample collection, using 70% ethanol and subsequently UV irradiated for 15 min. The external sampler surface and the tripod were further cleaned with 0.1% hypochlorite solution to avoid contaminations. Dust samples were collected in parallel to air samples from the same rooms, using moistened cotton swabs, from dusty undisturbed surfaces (e.g. ledge above doors). Participants of the study were asked to fill in a questionnaire to gather information about the activity in their room during the sampling day. A control study was conducted to select a DNA extraction method to isolate DNA from the air filters. The first method tested involved the use of Innovaprep® Elution kit to recover the biological material captured in the filter, followed by DNA extraction with a standard QIAamp® DNA mini kit (Qiagen); however, this method provided no DNA profiles or low quality results. A direct DNA extraction from the air filters was then tested, using a modified QIAamp® DNA mini kit (Qiagen) procedure and QIAshredder columns (30 µl elution volume) and was adopted as ultimate extraction method. Dust samples were extracted following the same protocol as air samples. All samples were quantified with PowerQuant® System (Promega) on the 7500 RealTime PCR System (Applied Biosystems) and amplified using PowerPlex® Fusion 6 C System (Promega) on Applied Biosystem® Veriti 96-Well Thermal Cycler (ThermoFisher). Amplification products were run on the Applied Biosystem® 3500xL Genetic Analyzer (ThermoFisher). The data were analyzed on GeneMapper ID-X v.1.6 (Life Technologies) with an analytical threshold (AT) set to 50 RFU for air samples and to 100 RFU for dust samples. EuroForMix v.3.2.0

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<https://doi.org/10.1016/j.fsigss.2022.10.063>

Received 14 September 2022; Received in revised form 19 October 2022; Accepted 24 October 2022

Available online 25 October 2022

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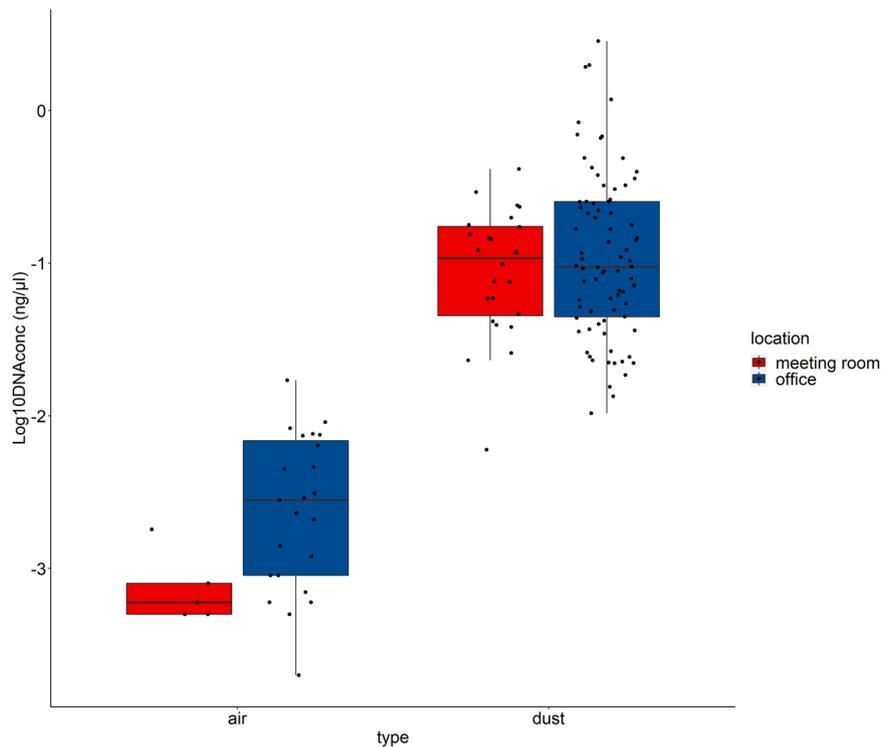


Fig. 1. Log_{10} of DNA concentration ($\text{ng}/\mu\text{l}$) for air and dust samples collected from meeting rooms vs offices.

(EFM) was used for LR calculations. One example is illustrated which was best interpreted as a minimum three-person mixture: the prosecution (H_p) and defense (H_d) propositions were set as described by (Eq. (1)). The numerator was conditioned upon the POI and two unknown individuals while the denominator was conditioned upon three unknown individuals (Un).

$$LR = \frac{\Pr(E|H_p : POI + U_1 + U_2)}{\Pr(E|H_d : U_1 + U_2 + U_3)} \quad (1)$$

3. Results and discussion

Air samples displayed an average DNA concentration of $0.003 \text{ ng}/\mu\text{l}$ and resulted in the DNA profiles of the individuals that occupied the rooms from where samples were collected. A full DNA profile of at least one of the room occupants was obtained from 13.3% of the air samples. Dust samples showed higher DNA concentration values (mean= $0.2 \text{ ng}/\mu\text{l}$) in comparison to air samples and resulted in complex DNA mixtures. Air samples collected from offices displayed higher DNA concentration values (mean= $0.004 \text{ ng}/\mu\text{l}$) in contrast to samples collected from meeting rooms (mean= $0.0008 \text{ ng}/\mu\text{l}$), (Fig. 1). This may be a result of the fact that employees spend more time in their office than in the meeting rooms; hence, they are likely to shed more DNA into the office environment. Moreover, the higher DNA quantities observed in offices may be related to the presence of personal items (e.g. garments), on which some DNA may be deposited and further transferred to the air through normal daily activities. Room dimensions may also have an influence on the amount of DNA that can be collected from the air; offices are smaller than meeting rooms and DNA may result more diluted in larger spaces [3]. A longer sampling time may be required to collect a similar amount of DNA from the meeting rooms as the one collected from offices. Dust samples showed instead comparable DNA concentration values regardless of the type of room from where they were recovered, (Fig. 1). Air samples, displayed slightly higher DNA concentration values when collected from offices 0 h after occupancy than when collected one day after occupancy. This suggests that DNA may not

persist in the air for long time and that human presence and activity in a room may influence the levels of DNA present in the air.

As an example, we calculated two different LRs for an air sample collected from an office of two employees (hereafter named P1 and P2) 0 h after occupancy; LRs were calculated following (Eq. (1)). In LR_1 , P1 was conditioned as POI , in LR_2 , P2 was conditioned as POI . Both P1 and P2 declared to have spent 4–7 h in their office during the sampling day, with P1 who was the last person to leave the office. The two employees stated to have had a short visit in the office (5–10 min) from another individual during the day. The sample resulted in a minimum three-person mixture where a full P1 profile and a partial P2 profile could be detected. Alleles from unknown contributor(s) were also present. The LR_1 value was 5.6×10^{26} , while LR_2 value was only 21.4. In addition to P1 and P2, an unknown individual could have contributed to the DNA mixture. This could be someone who had been in the office beforehand or someone who had been in contact with the two employees, and there was subsequent secondary transfer from clothes, skin or personal items to the air.

4. Conclusion

This study shows that human DNA can be collected from the air and provide STR genotypes of the individuals that have recently spent time in a room. Dust samples could instead be useful to identify individuals who occupied a room over longer time periods. The method developed could help to identify suspects when no contact traces have been left on the crime scene. The method could further be applied to monitor bio aerosol contaminations in a forensic laboratory. The results of this study will also help to establish the propensity of detectable aerosolized human material, from innocent individuals, to spread at the crime scene.

Acknowledgments

We would like to acknowledge the volunteers that participated in this study.

Conflict of interest statement

The authors declare no conflict of interest.

References

[1] L.M. Milstone, Epidermal desquamation, *J. Dermatol. Sci.* 36 (3) (2004) 131–140.

- [2] M.H. Toothman, K.M. Kester, J. Champagne, et al., Characterization of human DNA in environmental samples, *Forensic Sci. Int.* 178 (1) (2008) 7–15.
- [3] E.L. Clare, C.K. Economou, C.G. Faulkes, et al., eDNAir: proof of concept that animal DNA can be collected from air sampling, *PeerJ* 9 (2021), e11030.