

## ASSESSMENT OF DNA YIELDS FROM SWABBING DIFFERENT AREAS OF THE HUMAN BODY IN A PERUVIAN POPULATION

Maher Nouredine PhD<sup>1</sup>, James A. Bailey PhD<sup>2</sup>, Gian Carlo Iannacone<sup>3</sup>, Martha Palma Málaga<sup>4</sup>  
Michele Rosso<sup>5</sup>, and Santina Castriciano<sup>5</sup>

<sup>1</sup> ForensiGen, LLC

<sup>2</sup> Minnesota State University Mankato

<sup>3</sup> National Prosecutors Office

<sup>4</sup> Ministry of Justice

<sup>5</sup> COPAN Italia Spa

**Background:** Buccal samples are currently viewed as the most reliable and least invasive source for high quality DNA from living subjects. In instances where a buccal sample cannot be obtained from the subject, an alternate, minimally invasive, and reliable source of biological sample should be available to the collector. The objective of this study was to evaluate the DNA quantity and quality obtained from swabs collected from various superficial areas of the human body and to identify whether one area can serve as a reliable alternative to the buccal swab.

**Experimental Design:** A cohort of 23 volunteers from the village of Rosaspata in the Huamanga province of Peru were enrolled in this study. Area residents traveled to a nurse's station in the village to donate the samples. After signing an informed consent form, each volunteer was swabbed using a 4N6FLOQSwabs<sup>®</sup> Genetics (Copan Italia). Six swabs were collected from each volunteer (n=138). In addition to obtaining a buccal swab from each donor, the additional areas sampled were 1) nose sill and alar rim, 2) alar flare, 3) temporal scalp, 4) back of auricle lobule, and 5) axillary fossa.

**Results:** DNA samples and full profile data were obtained from all 23 buccal swabs (mean = 15.49 ng/μl; SD +/- 32.73 ng/μl). DNA samples were obtained from all 23 swabs collected from the nose sill and alar rim (mean = 1.78 ng/μl; SD +/- 2.47 ng/μl). Of those, 21 samples (91%) revealed full, single source DNA profiles. Significantly lower quantitation values were obtained from swabbing the alar flare (mean = 0.035 ng/μl; SD +/- 0.041 ng/μl). The swabs collected from the temporal scalp region showed similar DNA yields to those obtained from the alar flare. However, three samples yielded less than 0.001 ng/μl. Similarly, the swabs collected from the back of the auricle lobule revealed low yields. Interestingly, the swabs from the axillary fossa revealed low yields (seven samples < 0.0005 ng/μl). Full, single source DNA profiles were obtained from approximately 25 % of each of the three groups: the alar flare, the temporal scalp region, and the auricle lobule. Full, single source DNA profiles were obtained from approximately 8% of the axillary fossa samples. Mixed DNA profiles were observed in one sample from the alar flare and in one sample from the temporal scalp. Those areas might not be suitable as collection sites for reference DNA samples due to possible exposure to exogenous DNA in the donor's environment. The results from this study suggest that the nose sill and alar rim is a viable alternate site for the collection of reference human DNA samples.