



B152 Small Unmanned Aerial System (sUAS) Attribution Phenomenology Via Plant/Fungal and Human DNA Sequencing

Josh Dettman, Lexington, MA; Tara Boettcher, BS, MIT Lincoln Laboratory, Lexington, MA 02421; Jim Comolli, PhD, MIT Lincoln Laboratory, Lexington, MA 02421; Martha Petrovick, PhD, MIT Lincoln Laboratory, Lexington, MA 02420*

Learning Overview: After attending this presentation, attendees will understand: (1) how signatures like trace/touch human DNA (hDNA) mixtures and plant/fungal environmental DNA (eDNA) may enable attribution of small unmanned aerial systems (sUAS) to people and places, (2) where successful signature collections occurred on sUAS as part of operationally-relevant experiments, and (3) how similar forensic phenomenology experiments conducted under realistic conditions can inform improvements in the practice of forensic science.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by presenting initial research findings related to exploitation of signatures to identify builders, pilots, or others who have handled the sUAS (human DNA sequencing) and testing locations (eDNA sequencing). Use of sUAS by the general public is continuing to increase, and law enforcement should expect an increasing number and variety of encounters with sUAS platforms and users with both benign and nefarious intentions.

Capabilities to attribute sUAS to builders/pilots and production/testing locations are important to deter and prevent their misuse. Attribution is enabled, in part, through understanding the production and operational networks that utilize these devices. To provide a supplement to exploitation of flight paths and other sUAS electronic data, attribution signature collection and analysis in this study was focused on.

Analysis of trace/touch human DNA mixture using single nucleotide polymorphism (SNP) sequencing to link unknown biometric identities (UBIs) of builders/pilots across different sUAS platforms (and by comparing profiles to those in a reference database where possible);

Analysis of plant and fungal eDNA found in dust collected from sUAS with metabarcoding and DNA sequencing to associate traces of species on the device with those found in previous testing locations.

Both naturally deposited and artificially added positive control DNA signatures were collected from nine different sUAS types under three potential law enforcement sUAS encounter scenarios: (1) pre-flight (prior to sUAS use), (2) post-flight (after successful flight and landing), and (3) post-crash (after unsuccessful landing). In all, 147 samples were collected at an initial test effort in Maryland, and 222 samples were collected during the main test event in Nevada.

The human DNA results from this data set indicate that recovery of DNA profiles from swabs of sUAS components post-flight (88% of samples yielded at least one DNA profile) and post-crash (92% of samples collected) is possible. Additional tests are needed to inform final recommendations regarding priority collection locations, but samples collected from commonly touched areas like circuit boards, internal component covers that require pressing down to secure, hand-launch points, and tape samples yielded sufficient quantity and quality of DNA for UBI detection and association in this study. Because the DNA naturally deposited on these sUAS was low-concentration touch samples with mixtures of contributors, current short tandem repeat (STR) analysis will be challenged to provide DNA profiles.

The initial results also indicate that there was sufficient recoverable eDNA from sUAS, both from post-flight and post-crash sampling, to assess the ability identify previous testing locations of the sUAS. DNA sequences corresponding to more than 10 different fungal and plant species were recovered from 94% of sUAS post-flight and post-crash samples. Recovery of eDNA and the number of identified fungal/plant species was similarly high across the samples from different exterior sites on the sUAS surfaces, so no preferred sampling site was obvious. An average of 17% of the identified species in samples from sUAS originally operated in Maryland, then in Nevada, were found in reference samples from the Maryland testing location. This demonstrated that plant and fungal species characteristic of previous locations could be used to identify previous testing locations of the sUAS. Results indicated that additional sampling from the sUAS and reference site to improve species coverage would increase the likelihood of definitive, statistically significant geographic attribution.

Small Unmanned Aerial System, Phenomenology, DNA Sequencing