A144 Pollen DNA: A New Tool for Forensic Investigations

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After attending this presentation, attendees of this presentation will gain practical knowledge as it applies to the extraction and real-time quantification of Pinus echinata (yellow pine) pollen DNA, internal transcribed spacer (ITS) sequencing of extracted pollen DNA for verification of pollen grain origin as being from Pinus echinata, and the genetic analysis of existing *Pinus sp*. sequences for allele frequencies in the development of short tandem repeat (STR) markers used for STR analysis of the selected loci in yellow pine pollen.

This presentation will impact the forensic science community by providing forensic biology laboratories a novel point of view in the use of traditional forensic palynology practices combined with the recognition of species specific pollen DNA STR profiles from yellow pine as it relates in the use of pine pollen to link suspects or objects to specific locations.

Consequences resulting from the failure to undoubtedly associate suspects or objects to a crime and/or a crime scene through the use of traditional investigative techniques, including DNA profiling obtained from collected biological specimens as well as the identification of other crime related indicators, can be mitigated when pine pollen is present.

Yellow pine has the widest range of any pine in the southeastern United States. It grows in twenty two states with a dense population in eastern Texas. Additionally, yellow pine pollen is heavily shed at a time when other pollens are at relatively low numbers by comparison due to its wide distribution across the warmer regions of the Deep South. Yellow pine pollens predominate seasonally in the environment; collecting on clothing and other objects, in hair and even in nasal passages. The identification of yellow pine pollen in association with a specific crime by morphology alone may not provide any forensically defensible insight due to an inability to provide a sufficiently distinct region or subpopulation of taxa of pollen origin, therefore having low evidentiary value in a court of law. Yet, as a wind facilitated pollinator, *Pinus echinata* pollen is unlikely to travel long distances allowing for the evaluation and identification of genetically distinct subpopulations of yellow pine. Pollen grains can be linked to their male conifer donor through the use of population studies on existing pine DNA sequences and the genetic analysis of yellow pine strands using yellow pine pollen DNA.

The goal is to identify polymorphic microsatellite regions suitable for the development of STR markers. This goal will be achieved through the collection and extraction of DNA from yellow pine pollen and the evaluation of Pinus sp. DNA sequences already available through NCBI's Genbank. Once these markers have been developed, they can be used to amplify locus-specific regions in *Pinus echinata* pollen DNA to provide insight into the originating pine tree's associated geographical population substructure. Knowledge of this geographical distribution would allow for pollen grains to be traced back to their individual conifer donors. This presentation will also demonstrate that a system can be developed to enable this protocol to be used for any pollen for more extensive applications.

Pollen, DNA, Investigation

 ** Presenting Author*