



Young Forensic Scientists Forum—2020

Y14 Testing Kinship Via Mitochondrial DNA on Colony vs. Non-Colony Cats

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Learning Overview: The goal of this presentation is to draw attention to a portion of wildlife forensics and examine the social structure of colony and non-colony feral cats (*Felis catus*). Attendees will gain an understanding of Trap-Neuter-Return (TNR) and its role in this study via mitochondrial DNA (mtDNA), the mating structure of feral cat colonies showing degree of relatedness, and the impact of the *Felis catus* population on wildlife forensics.

Impact on the Forensic Science Community: This presentation will impact the forensics science community by examining the social structure of feral cats. In addition, *Felis catus* Short Tandem Repeats (STRs) were the first non-human STR evidence used in a court of law.

Populations of feral cats (*Felis catus*) have drawn public attention due to a variety of reasons, including the increasing population size, caterwauling, destruction of property, and decreasing rodent and bird populations. Although controversial, several communities have implemented the TNR method, developed in Rome, Italy.¹ TNR has been praised for population management, but cats are often demonized in wildlife forensics for their tendencies of property destruction and preying on rodent and bird populations. TNR clinics have provided the cat ear tips used in this study, which examined whether colony cats are more likely to be related than cats of the general population (non-colony cats). Colony feral cats are cats that were once domesticated and now returned to the wild, living in a specific environment with other cats. Non-colony feral cats are the same, but do not live in these groupings. Past research shows the importance of mtDNA in examining lineages. The degree of relatedness was to be determined separately for these two groups. The alternative hypothesis for this study is that colony cats are more related than non-colony cats.

Frankie's Friends, a non-profit spay and neuter clinic, was the ear tip provider for this research. The sample size is $n=40$ colony cat ear tips and $n=40$ non-colony cat ear tips. The method of extraction employed was the QIAGEN® QIAamp® DNA Mini Tissue Kit. This was followed by a quantitation step using the NanoDrop™ Lite Spectrophotometer by Thermo Scientific™. The average concentration for colony cats was about 11.7ng/uL after extraction. Two primer sequences, Lf15926 and Hf3, were used to amplify the HV1 region of mtDNA and followed up by sequencing with the ABI® BigDye® Kit, 3130 Genetic Analyzer, and Chromas software. The population statistics based on mtDNA testing will be presented.

Reference(s):

- ¹ Eckert I., Hartl G.B., Markov G., Suchentrunk F. Genetic diversity and integrity of German wildcat (*Felis silvestris*) populations as revealed by microsatellites, allozymes, and mitochondrial DNA sequences. *Science Direct*. 75 (2): 160-174. 2010.

Degree of Relatedness, MtDNA, TNR