

Hybridisation Between Wolves and Dogs in Europe

Introduction

Hybridisation between different members of the family *Canidae* is a common occurrence. This study analysed the extent to which European populations of the domestic dog (*Canis lupus familiaris*) and the gray wolf (*Canis lupus*) had interbred in the wild.

Mitochondrial DNA sequences from wolves, dogs and 'wolfdogs' - dogs with very recent wolf ancestry- were compared in order to identify the presence of polymorphisms to infer if wolves had exclusive haplotypes- that is unique DNA sequences compared to domesticated dogs.

No haplotypes were identified that were exclusive to wolves, and so hybridisation appears to be a widespread phenomenon.



Above: *Canis lupus*. Wolves are regionally extinct in many European countries and populations continue to dwindle in others.

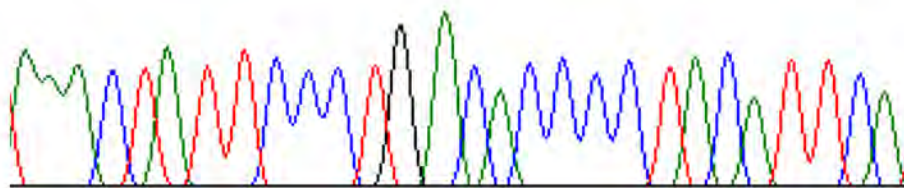
Method

Mitochondrial DNA, which is maternally inherited, was extracted from 57 saliva and tissue samples. This was then quantified, and those samples which had sufficient DNA concentration were purified and replicated using a process known as polymerase chain reaction.

This process also happens to trim the DNA to a known size (750 base pairs), and so to check that the DNA was this length, a process known as gel electrophoresis was used. This was followed by mitochondrial DNA sequencing.

The following sequences were aligned using computer software and any sequencing mistakes were manually corrected. Only one copy of each haplotype was retained for incorporation into a median joining network- a type of family tree. The sequences were then compared to an online database to check whether they were found in wolves, dogs or both.

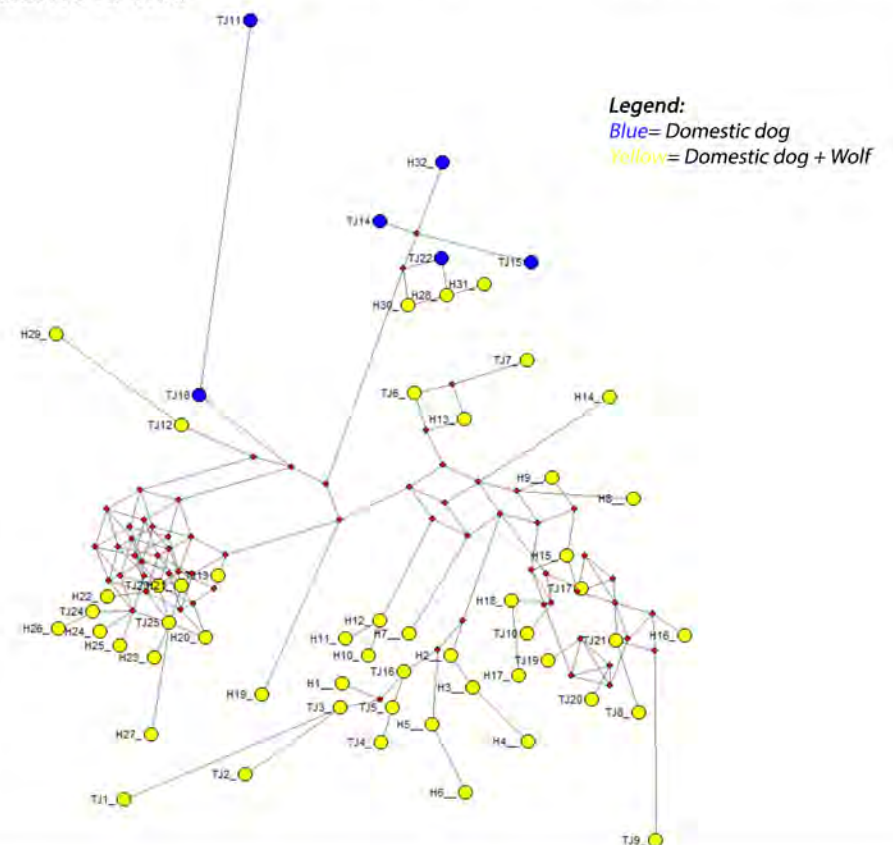
AAAC TA T TCCC TG ACACCCC TACA T TCA



Above: Mitochondrial DNA chromatogram. Each base (A,T,C or G) has a different light absorbance peak and this is how the computer distinguishes each different base apart.

Results

The median joining network is coloured to show haplotypes that occurred exclusively in domestic dogs and those haplotypes that occurred in both wolves and dogs. Wolves and dogs from across Europe were included in this study and it was found that most of the haplotypes that were identified were found in both of the subspecies rather than being exclusive to one.



Conclusion

The study has found that none of the haplotypes that were identified were exclusive to wolves, indicating that hybridisation may be occurring to a great extent, though whether introgression is occurring from wolf to dog or the opposite is unknown. It is also possible that most of the haplotypes were found in both wolves and dogs as they share recent ancestry. Bi-parental markers may be needed in order to confirm that shared haplotypes are actually due to hybridisation.

Hybridisation could potentially lead to the absence of pure wolf genomes as new genomic elements are introduced into the grey wolf gene pool, potentially resulting in the production of maladapted hybrids that are not genetically fit- potentially causing further reduction in the number of grey wolves. It may be necessary to evaluate current conservation practices in order to prevent further introgression of hybrids into wolf populations, either by removing hybrids from the wild or reducing the number of free-ranging domesticated dogs in Europe. Also, wolf-dog hybrids present a potential legal loophole as they are not afforded the same protection from hunting as pure-bred wolves, meaning that some pure-bred wolves may be mistaken for hybrids and killed, as it is quite difficult to distinguish a wolf morphology from a hybrid wolf-dog. It may be necessary to protect hybrids in order to prevent wolves from being killed by mistake, as this would have a detrimental impact on the size of the European wolf population.

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