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Introduction of environmental DNA metabarcoding for forest ecosystem biodiversity assessment

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Introduction

Expert-based monitoring of species diversity is carried out to assess forest biodiversity. However, various disturbances from human surveys can lead to biased estimates of species.

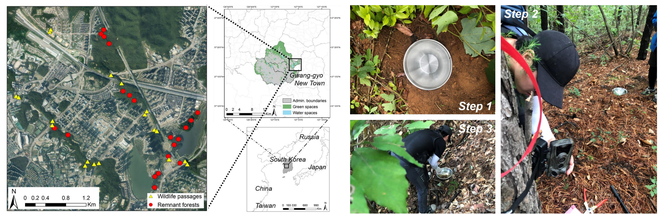
Environmental DNA (eDNA) has attracted attention as a rapid, non-invasive investigation method for aquatic species. eDNA has recently become an effective biodiversity evaluation alternative for terrestrial species, and comparative verification with species monitoring methods such as field investigations and camera traps is required.

Method

This study was conducted in Suwon-si, Gyeonggi-do, Korea. To lure wild animals and collect DNA, 40 artificial water tank(20 in forest ecosystems, 20 in ecological corridors) containing 2L of distilled water was installed in consideration of seasonal differences in July and November 2019.

The remaining water in the artificial water tank used by the terrestrial species (drinking water, bathing, swimming, etc.) was used as a DNA sample. In addition, a camera trap and field investigation were performed at the same locations.

The extracted DNA was amplified using the MiMammal 12S primer set, and data processing and taxonomic assignment were performed.



Result

We performed taxonomic assignment (85% query coverage and identity) in the identified molecular operational taxonomic units (MOTUs) to detect 13 terrestrial species in forest ecosystems and 12 terrestrial species in ecologicial corridors. There was no significant difference in the number of species detected between forest ecosystems and ecological corridors.

Family	Remnant forests	Ecological Corridors
Suidae		*Sus scrofa*(5)
Canidae	Canidae(1), *Nyctereutes procyonoides*(14)	Canidae(3), *Nyctereutes procyonoides*(20)
Felidae		Felis catus(11)
Muridae	*Mus musculus*(5)	*Apodemus agrarius*(2), *Apodemus chejuensis*(2), *Mus musculus*(8), *Rattus norvegicus* (1)
Sciuridae	*Sciurus vulgaris*(5)	
Columbidae	*Columba livia*(3), *Pica pica*(4)	*Streptopelia orientalis*(4)
Corvidae	*Garrulus glandarius*(1)	*Garrulus glandarius*(7)
Fringillidae	*Schoeniclus elegans*(1)	*Fringilla montifringilla**(2)
Paridae		*Parus major*(2)
Pycnonotidae	*Microscelis amaurotis*(1)	*Microscelis amaurotis*(1)
Coraciidae	*Eurystomus orientalis*(1)	
Phasianidae	Phasianidae(2)	
Muscicapidae	*Paradoxornis webbian*us(1)	

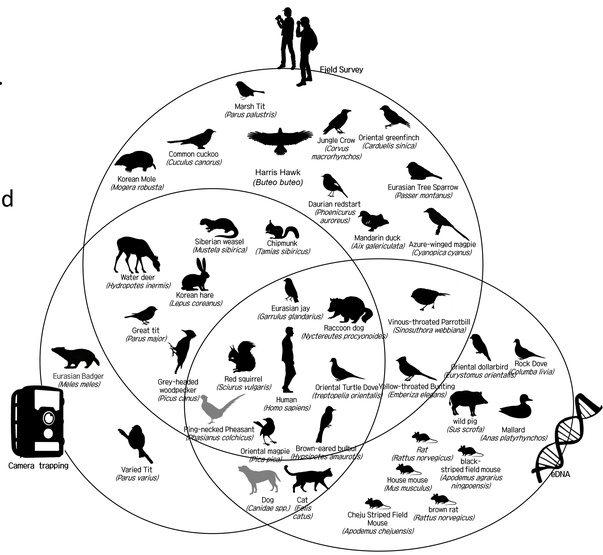
Camera Trap (CT) performed to verify the eDNA metabarcoding results was performed. A total of 18 terrestrial species were identified in CT, and 16 additional terrestrial species were identified in the field survey.

We detected a total of 51 terrestrial species through eDNA metabarcoding, camera trap, and field investigation. We identified significant inconsistencies between the species monitoring method results. Only seven species were detected by all three methods.

eDNA metabarcoding detected 22 species, among which, nine species (17.6%) were only detected using eDNA.

eDNA was the most useful for investigating small species, species with difficult morphological identification, and internal species vulnerable to disturbances.

Nevertheless, since most terrestrial bird species were not detected by either camera traps or eDNA, eDNA cannot replace field investigations in terrestrial ecosystems. Therefore, applying the technological advantages of eDNA to terrestrial ecosystems requires using both camera traps and field surveys.



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