Genetic analyses
of wildcat (*Felis silvestris silvestris*) samples from Luxembourg

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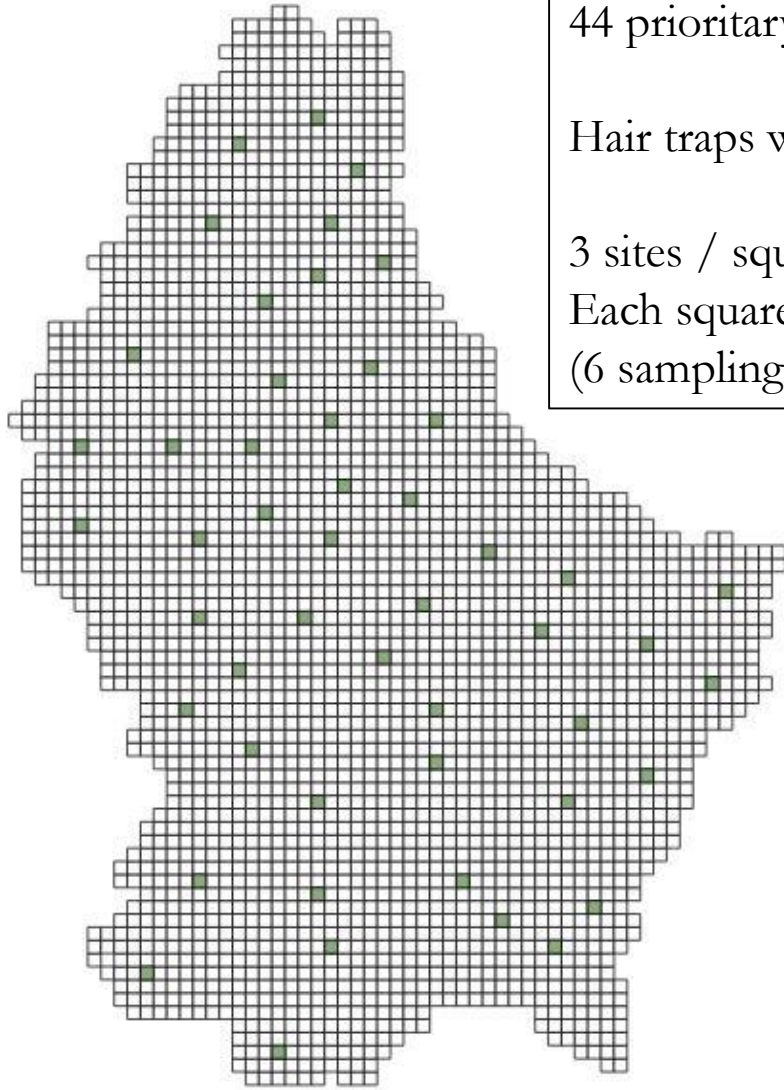
GeCoLAB

Conservation Genetics Lab

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www.gecolab.weebly.com

LUXEMBOURG INSTITUTE OF SCIENCE AND TECHNOLOGY

LIST

LE GOUVERNEMENT
DU GRAND-DUCHÉ DE LUXEMBOURG
Ministère du Développement durable
et des Infrastructures

Département de l'environnement

Non invasive field sampling

44 prioritary sampling squares

Hair traps with valerian

3 sites / square
Each square followed every 3 years
(6 samplings/site/square every 2 weeks)

Sample collection

2011- 2016 survey

- Field samples :

- hair (N=597)

- tissues (N=2)

- Veterinary samples (domestic cats) (N=23)

Main goals

Study of :

- Genetic structure
- Hybridization with domestic cat *(Felis silvestris catus)*
- Individual movements

Methods

- DNA isolation from hair or tissues
- Amplification of 15 microsatellite markers + 1 sex marker
- Genotyping (allele scoring) of each sample
- Bioinformatics / statistical analyses :

clustering analyses, multivariate analysis, …

Preliminary results

- 346 exploitable samples (min. 8 loci)
- < 50 samples : no amplification (hair from other species ?)
- Other samples : 1 to 7 amplified loci

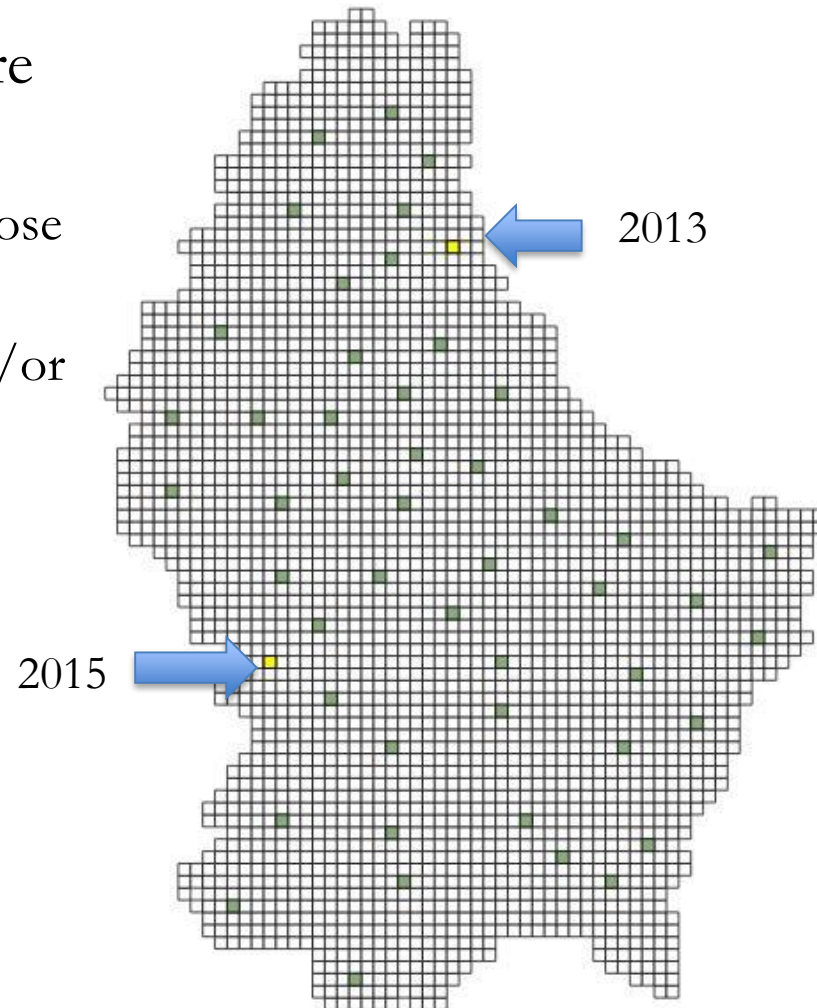=> typical of analyses based on non invasive samples

Individual identifications

GIMLET (Valière 2002)
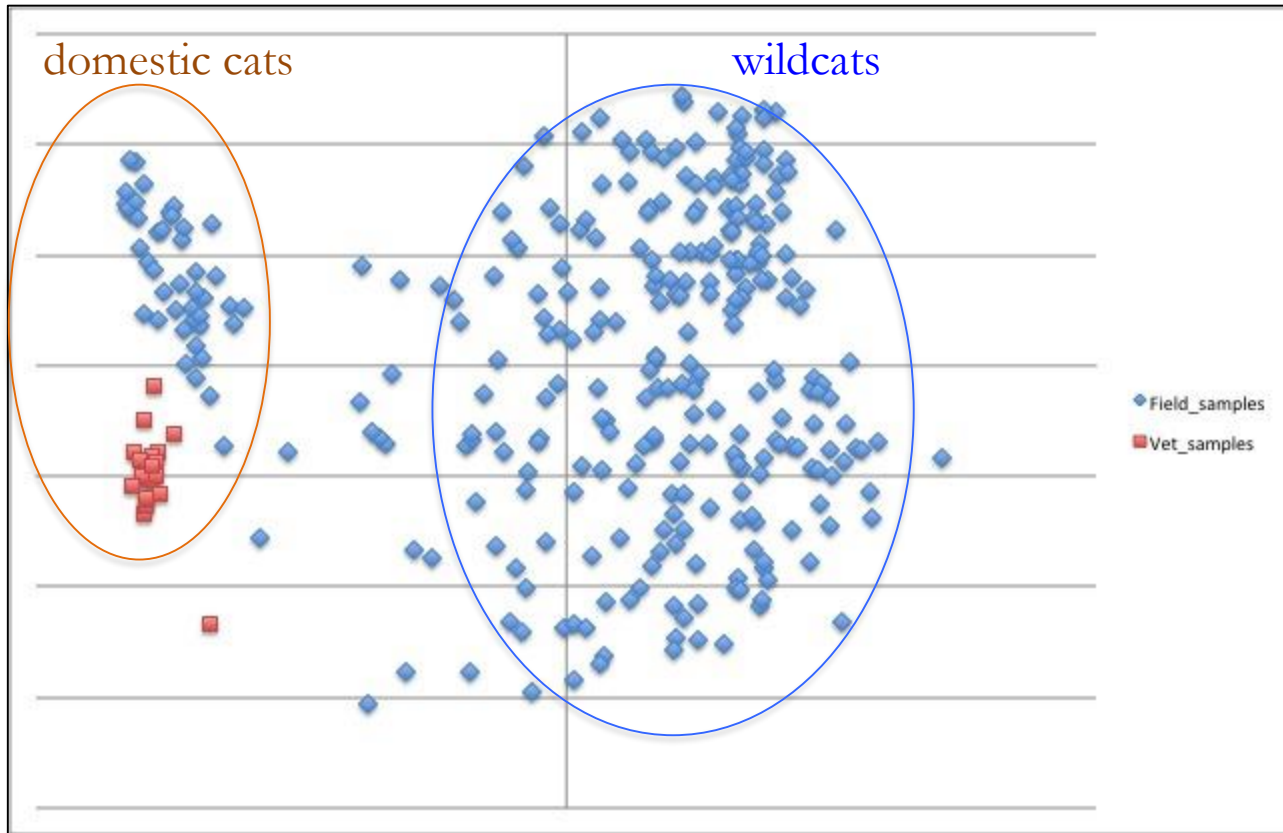
27 probable cases of recapture

(P_{sib} <1/10.000)

- most of the time : same year, close sites

- in some cases : distant sites and/or distinct years

2013

2015

Principal Correspondence Analysis (PCoA)

GenAlEX (Peakall & Smouse 2012)

Each dot = 1 sample (1 multilocus genotype)

Bayesian clustering

STRUCTURE (Pritchard et al. 2000)

2 main genetic clusters

Domestic cats (vet samples)

Domestic lineage : orange
Wild lineage : blue

Each line = membership coefficient for each cluster/1 sample

Presence of domestic cats in the field sampling
Presence of mixed patterns : putative hybrids (*F. s. silvestris x F. s. catus*)

Hybrids detection

NewHybrids (Anderson & Thompson 2002)

Program for computing the posterior probability that individuals in a sample fall into different hybrid categories

Field samples
2011-2016

- Wild
- Domestic
- F2
- Ambiguous
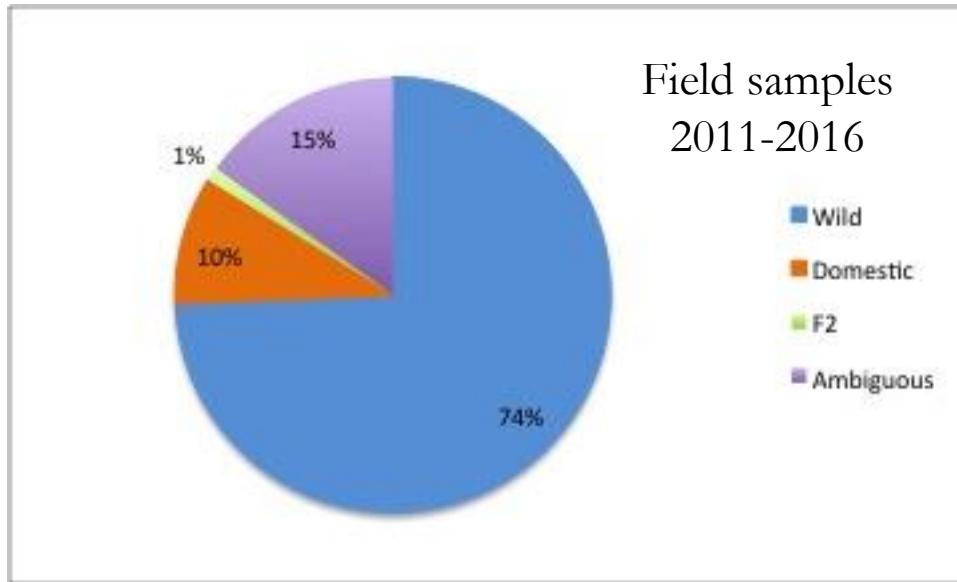
90% threshold

	Domestic	Wildcat	F1 hybr.	F2 hybr.	Bx dom.	Bx wild	Ambiguous
Field	10%	74%	0%	1%	0%	0%	15%
Vet	74%	0%	0%	0%	0%	0%	26%

Conclusion

- Presence of both subspecies (pure domestic and pure wild cats) in the sampling
- Presence of putative hybrids (F2, backcrosses)
- Ability of long distance movements in wildcat

- Perspective :
- analysis of genetic flows between the subspecies
- landscape genetics

Thank you for your attention

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