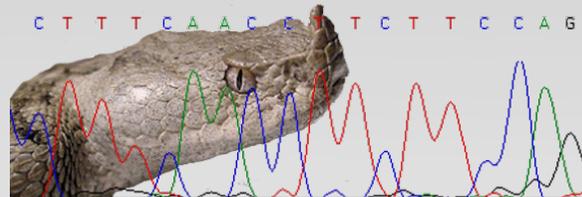
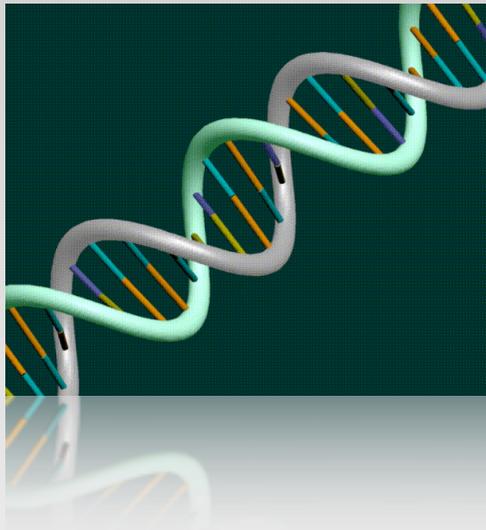


Conservation genetics

from theory to practice:

Management of wild populations



Sylvain Ursenbacher
NLU, room 36



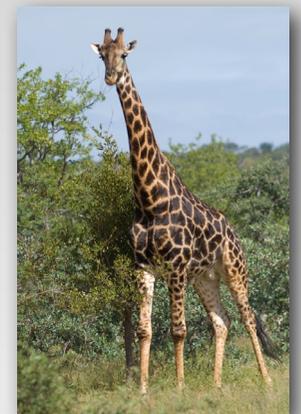
Management of wild populations: *genetic can be used for...*

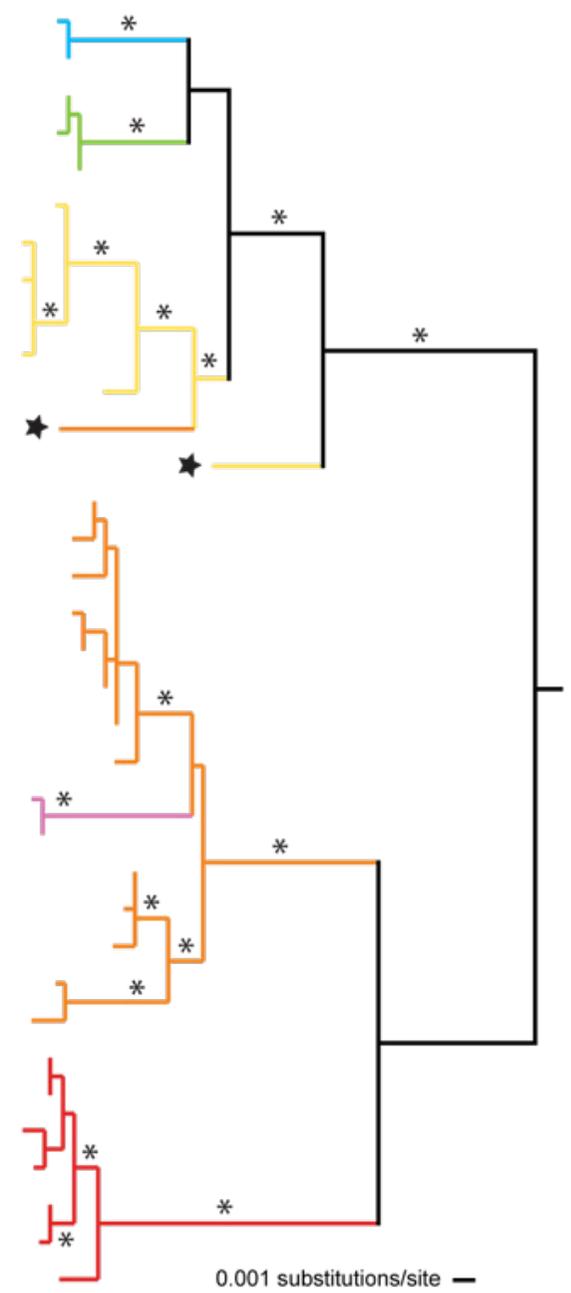
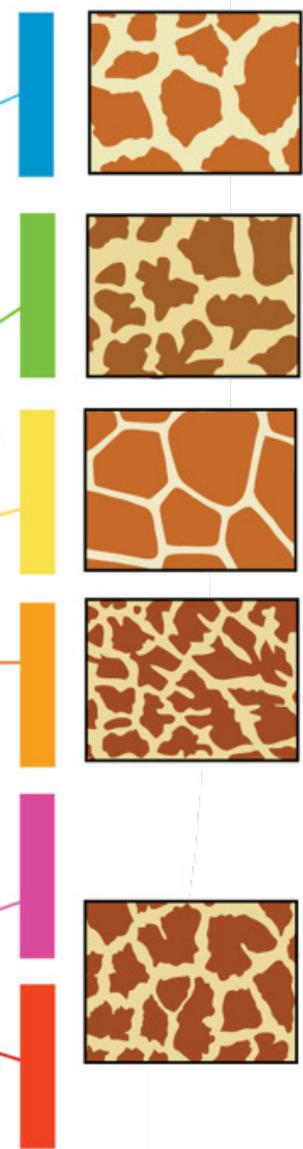
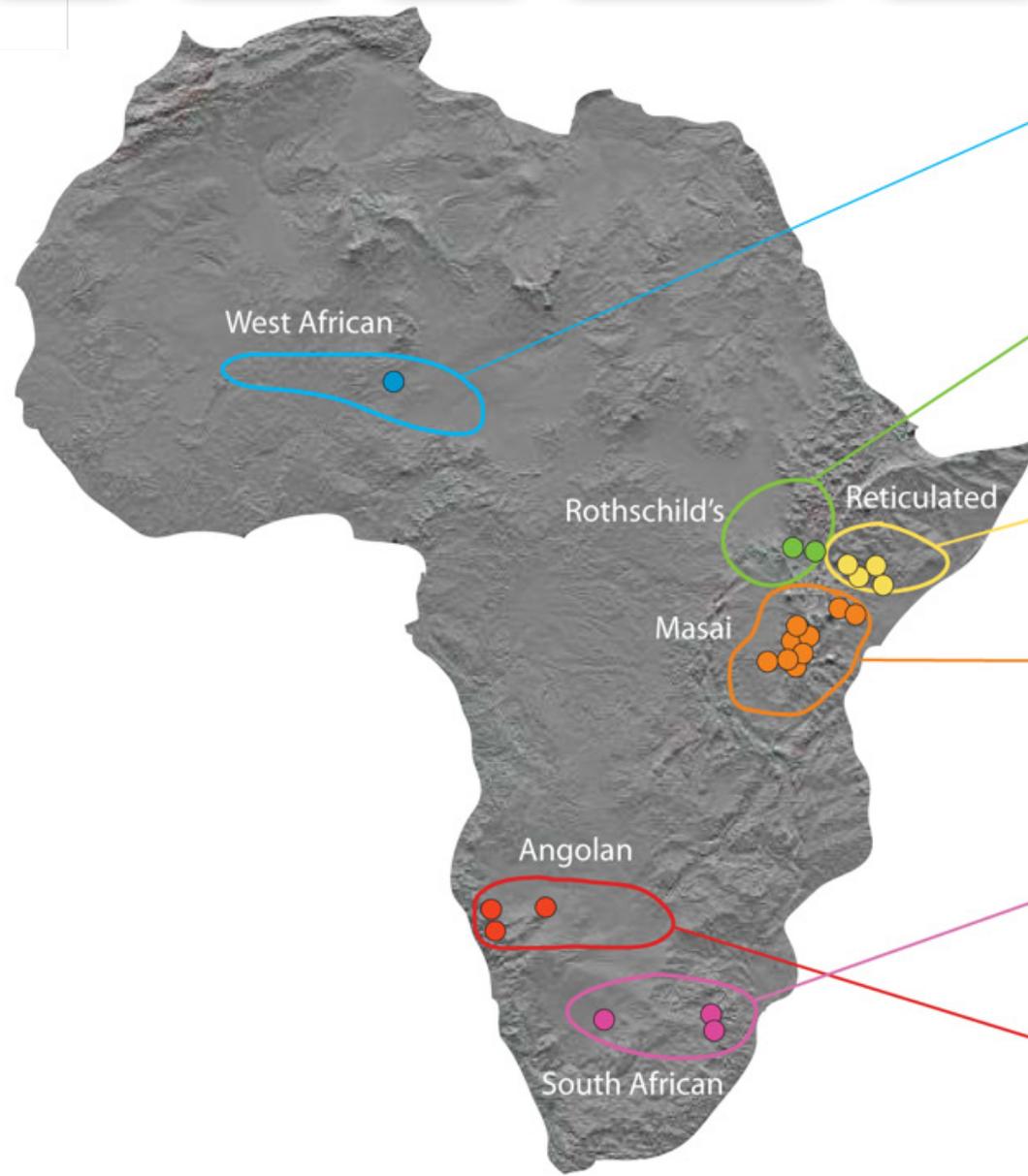
- resolving taxonomic uncertainties, defining management units
- genetically viable populations
- habitat fragmentation
- management of wild populations
- management of captive populations
- reintroduction
- forensic

Management of wild populations: *resolving taxonomic uncertainties, defining management units*

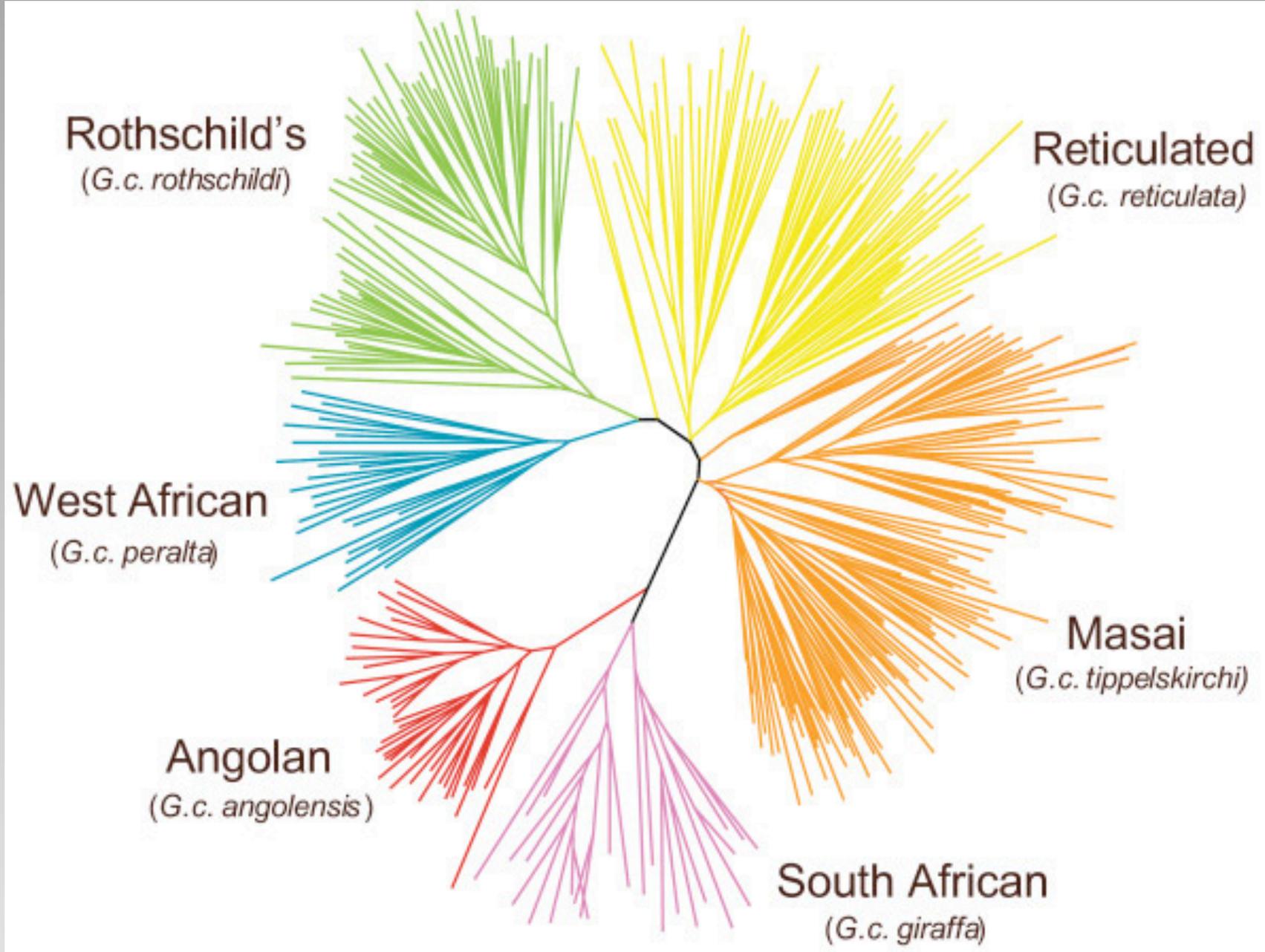
- large scale genetic structure

e.g. : Giraffe (*Giraffa camelopardalis*)





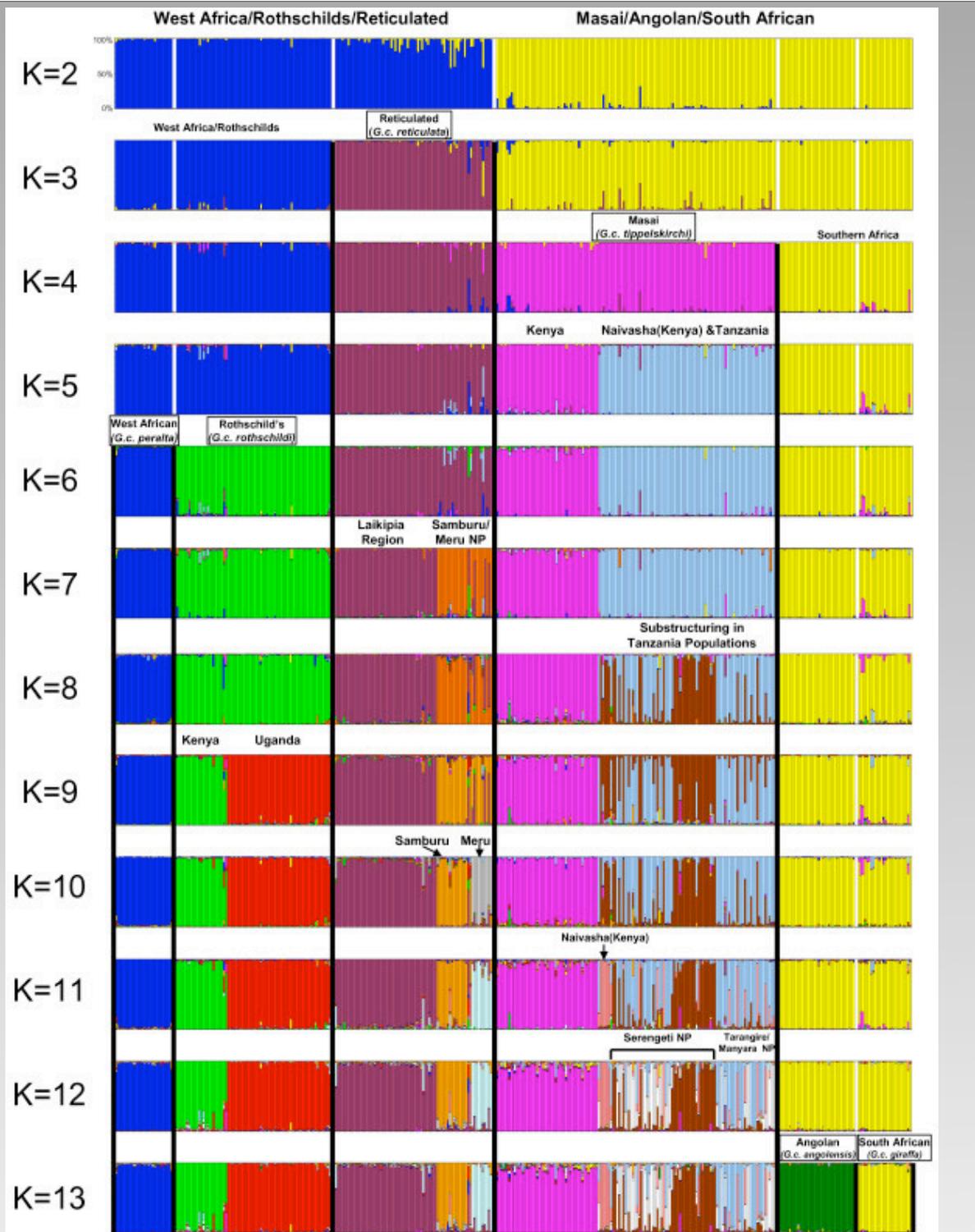
Brown et al. (2007) Extensive population genetic structure in the giraffe, BMC Biology 5:57



Genetic subdivision in the giraffe based on microsatellites alleles. Neighbor-joining network of allele-sharing distances (D_s) based on 14 microsatellite loci typed in 381 giraffes. Colors are coded as in Figure 1A.

Genetic subdivision among giraffe groups and populations based on Bayesian cluster analysis [23] of 14 microsatellite loci from 381 individuals. Shown are the proportions of individual multilocus genotypes attributable to clusters (K) indicated by different colors. Sample group designations and sampling locations are denoted. We varied K from 2–16 and at least six groups corresponding to currently defined subspecies and 11 geographic clusters are resolved as indicated.

Brown et al. BMC Biology 2007 5:57

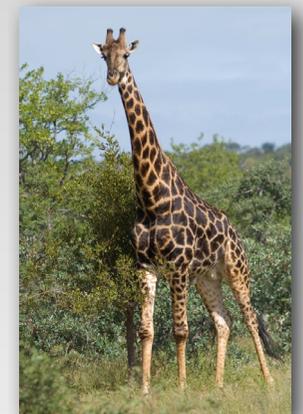


Management of wild populations: *resolving taxonomic uncertainties, defining management units*

- large scale genetic structure

e.g. : Giraffe (*Giraffa camelopardalis*)

- ▶ previously considered as one unique Evolutionary Significant Unit
- ▶ after this work: 6 genetically distinct lineages, with limited interbreeding between them.
6 ESU
- ▶ possible presence of different species (parapatric subspecies, e.g. among Masai, reticulated and Rothschild's giraffes)
- ▶ previous conservation status: Low Risk for the UICN Red List
- ▶ some genetically isolates groups: highly endangered



Management of wild populations: *genetically viable populations*

- how large do populations need to be to ensure their genetic “health”?
 - ▶ avoid inbreeding depression
 - ▶ ability to evolve in response to environmental changes
 - ▶ avoid accumulation of deleterious mutations
- based on different simulations: variable results...

goal	N_e	Recovery time (in generation)
retain reproductive fitness	50	
retain evolutionary potential	500	100-1000
	5000	
	570-1250	
retain single locus genetic diversity	100'000 - 1'000'000	100'000-10'000'000
avoid accumulating deleterious mutations	1000	
	100	
	12	

Franklin (1980), Soulé (1980), Lande & Barrowclough (1987), Lande (1995), Franklin & Frankham (1998), Lynch et al. (1995), Charlesworth et al (1993)

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Management of wild populations: *examples*

- adder (*Vipera berus*)
 - ▶ small venomous snake
 - ▶ limited dispersal
 - ▶ Madsen and collaborators (Sweden)



Inbreeding depression in snakes

115

Table 1. Effective population sizes of reproducing adults in an isolated population of adders, *Vipera berus*, at Smygehuk in southern Sweden

Year	No. of adult females	No. of reproductive females	No. of adult males	No. of males that mated	Total no. of adults	No. of reproductive adults	Effective population size ^a
1984	13	9	25	13	38	22	21.27
1985	17	1	23	2	40	3	2.67
1986	11	5	23	13	34	18	14.44
1987	22	14	20	16	42	30	29.87
1988	17	6	20	12	37	18	16.00
1989	22	15	19	18	41	33	32.73
1990	17	4	17	10	34	14	11.43
Mean values	17.0	7.71	21.0	12.0	38.0	19.71	Arithmetic = 18.34 Harmonic = 9.9

^aEffective population size is calculated from Wright's (1940) equation to compensate for skewed sex ratios: $4N_mN_f/(N_m + N_f)$ where N_m = number of males, N_f = number of females.

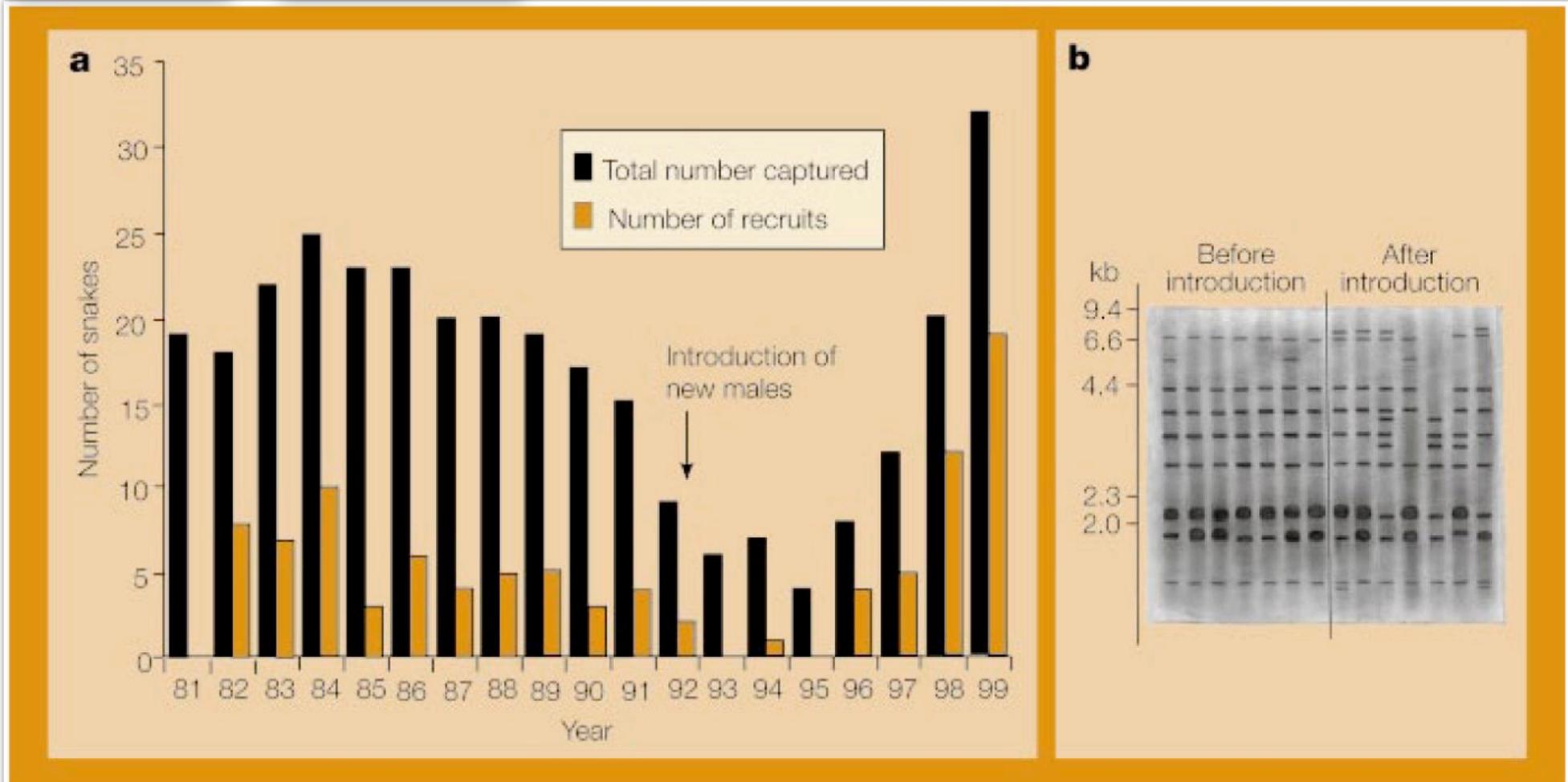


Figure 1 Introducing new males increases the genetic diversity and enables the adder population to recover. **a**, Total number and number of recruited male adders captured in Smygehuk from 1981 to 1999. **b**, Southern-blot analysis of major histocompatibility complex (MHC) class I genes in seven males sampled before the introduction of new males (left) and in seven recruited males sampled in 1999 (right).

Management of wild populations: *examples*



Madsen et al., 1996

	Smygehuk	Genarp	Captivity
population	isolated ($N_e < 20$)	not close	
body condition	similar ($p = 0.34$)		
Pesticides	no significantly differences		
genetic variation (2 enzymes and with DNA fingerprinting)	significant lower genetic diversity ($p > 0.001$) higher band-sharing (similar bands) in Smygehuk ($p < 0.001$)		
neonate mortality rate	0.31	0.09	0.05
	significantly higher in Smygehuk ($p = 0.0001$)		
offspring mass	similar ($p = 0.73$)		
brood size	significantly smaller for Smygehuk		

- 3 females from Smygehuk cross with males from Genarp:
neonate mortality rate = 0

Management of wild populations: *examples*

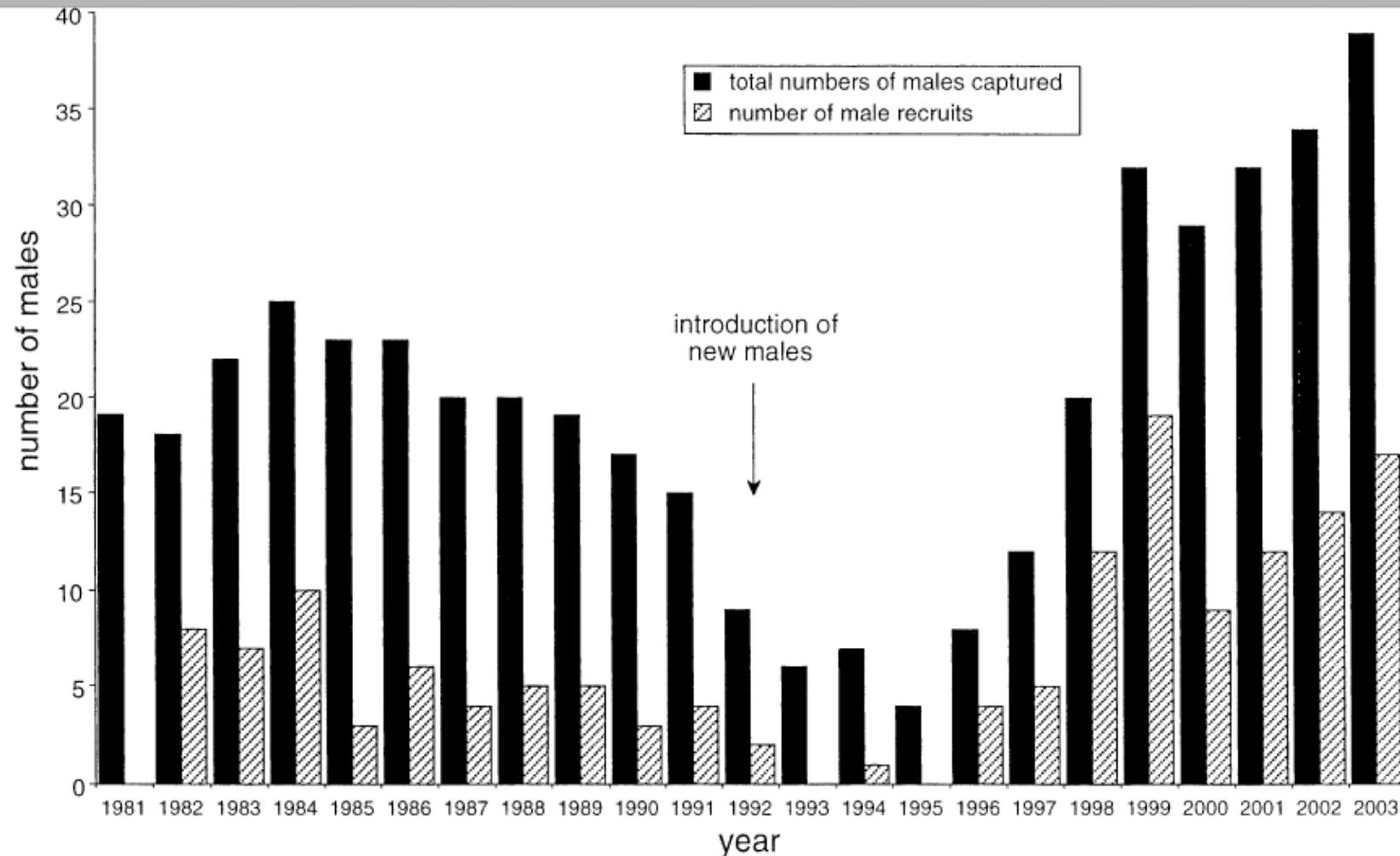


Fig. 1. Total number and number of recruiting males captured in Smygehuk from 1981 to 2003. The introduced males are not included in the figure.

Madsen et al., (2004) Novel genes continue to enhance population growth in adders (*Vipera berus*), Biological Conservation

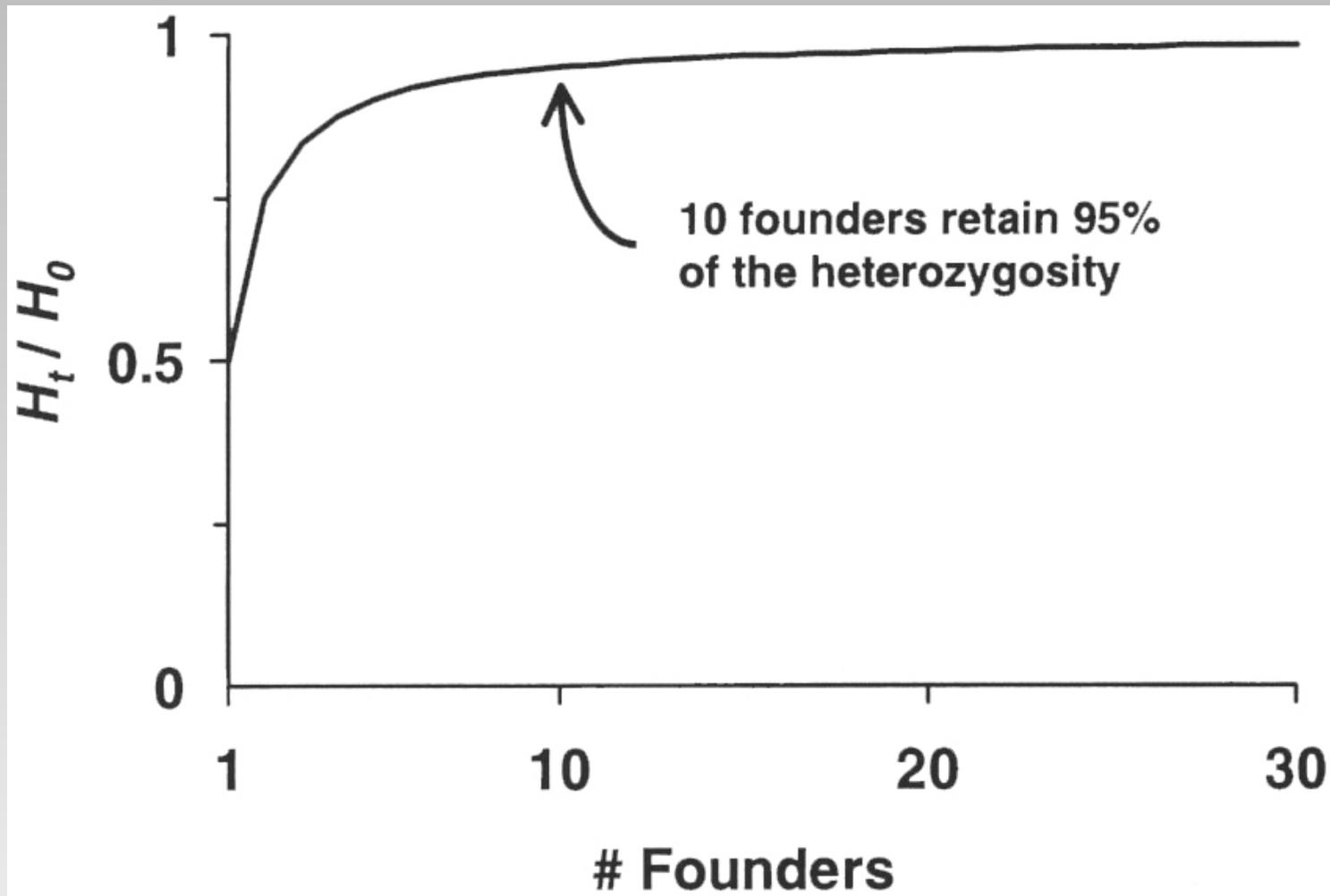
Management of captive populations

- the aims
 - ▶ maintain high level of genetic diversity over long period of time
 - ▶ minimise the kinship
- examples
 - ▶ Arabian oryx (*Oryx leucoryx*) 9
 - ▶ Przewalski's horse (*Equus caballus przewalskii*) 12
 - ▶ European bison (*Bison bonasus*) 18
 - ▶ Californian condor (*Gymnogyps californianus*) 14 (3 clans)



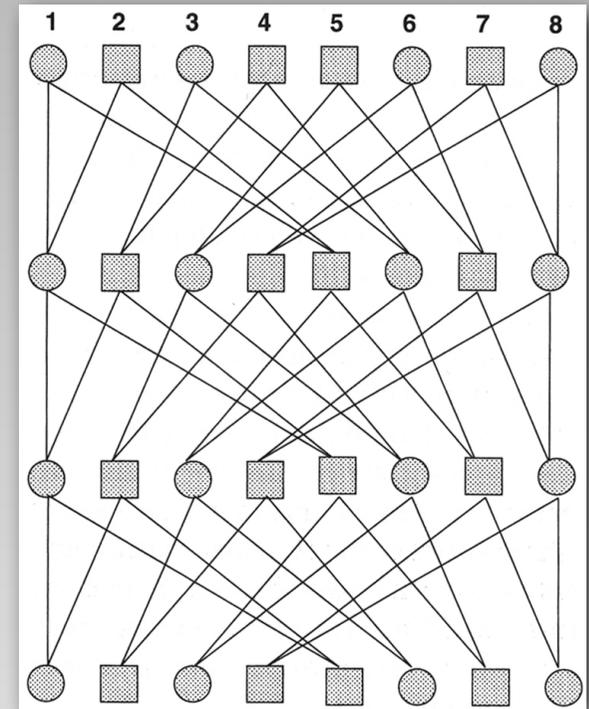
Management of captive populations

- impact of the number of founders



Management of captive populations

- maximising N_e/N
- maximum avoidance of inbreeding
 - ▶ knowledge of the pedigree
- minimising kinship
 - ▶ choose the couple with the lowest relationship



Genetic management for reintroduction

- avoid genetic changes in captivity that affect reintroduction success
- avoid genetic adaptation to captivity
- choosing individuals to reintroduce
 - ▶ genetically not too closely related to the wild/reintroduced animals
- supportive breeding (regular addition of individuals from captive populations)
 - ▶ deleterious impacts in the long term on the genetic composition
 - ▶ deleterious impacts in the long term on the reproductive fitness mixing with genetical adaptation to captivity
 - ▶ Hindar et al. (1991): lower fitness of captive populations compare to wild populations in 9 studied cases
 - ▶ drift can be limited by maintaining continuous gene flow between captive and wild populations

Forensic

- can help to determine illegal hunting
- estimation of bottlenecks
- estimation of effective size
- parentage analyses
- determination of sex
- hybridisation
- ...

Forensic: *illegal hunting*

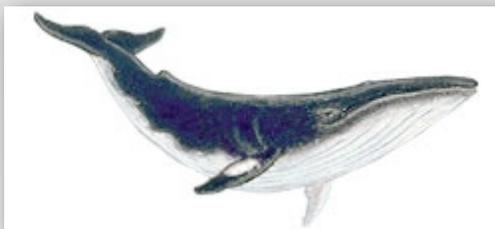
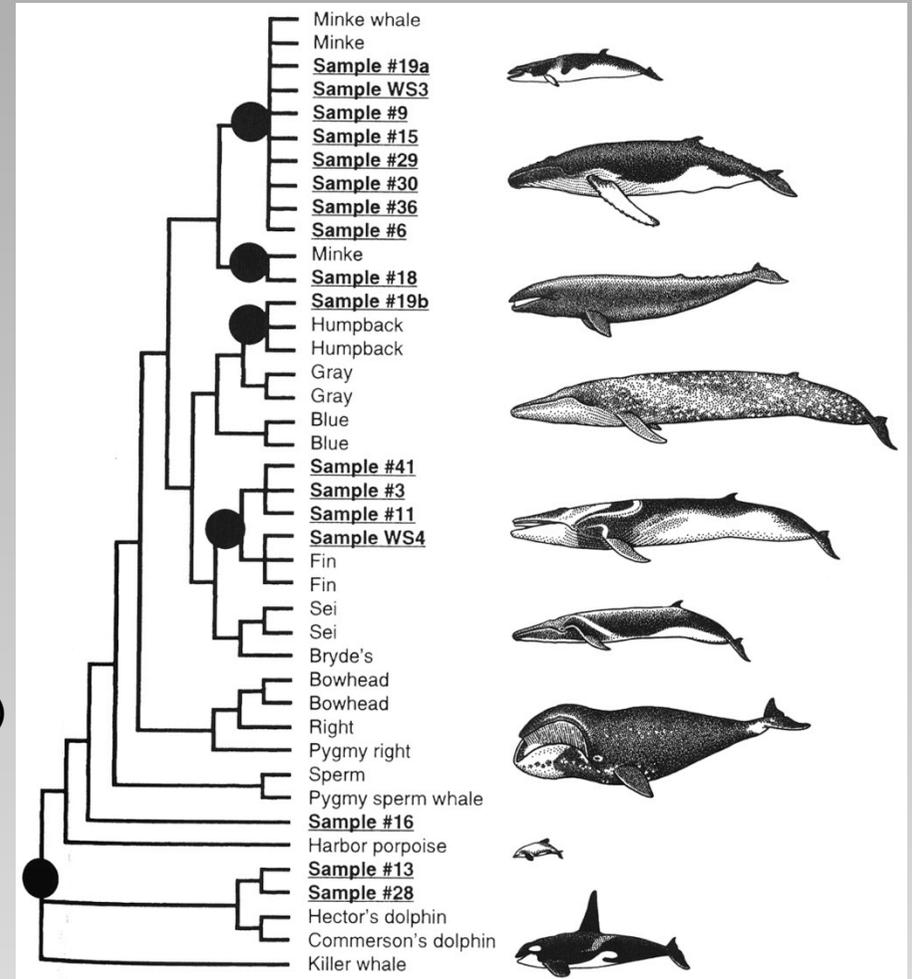
- e. g.: meat of whales

▶ Baker & Palumbi (1996)

- using portable PCR laboratory, installed in an hotel room
- amplification of the control region (mtDNA), sequencing in their lab.
- 16 samples taken
- 9 = mink whale (legal “scientific” whaling)
- 1 = humpback whale, 4 = fin whales
- 3 = dolphins

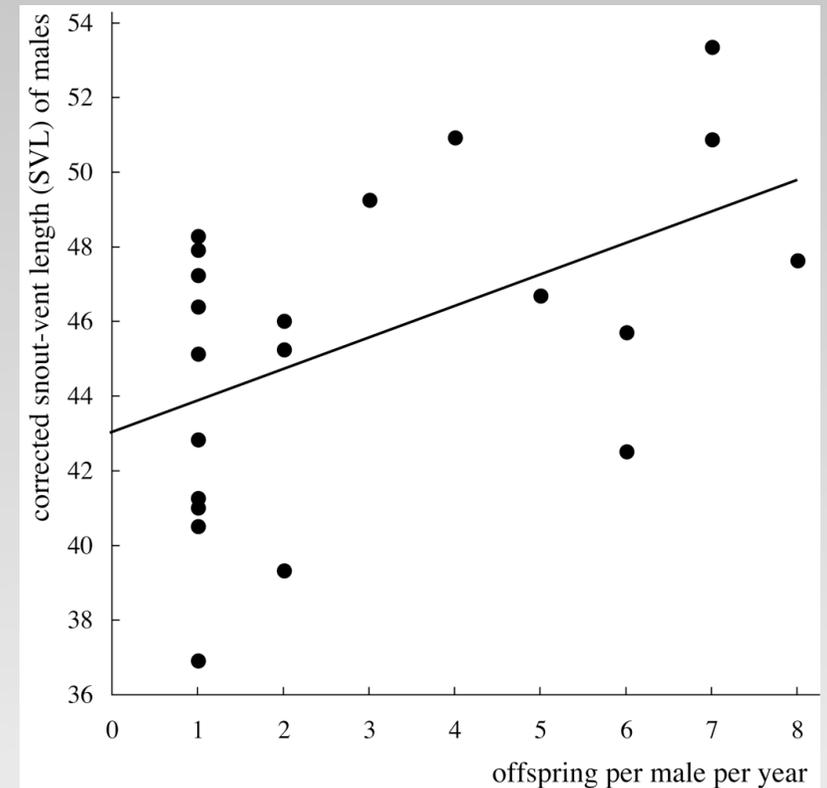
▶ Dizon et al (2000)

- 954 samples
- 773 = whales, 9% coming from protected species
- rest: dolphins, porpoises, sheep and horses



Forensic: *parentage analyses*

- used for pedigree determination
- better knowledge of the biology of the species
 - ▶ e.g.: multiple paternity in adder
 - ▶ microsatellite analyses to assign the paternity
 - ▶ high level of multipaternity: 69%
 - ▶ clutch with only one father: bigger males ($p < 0.001$)
 - ▶ relationship between length and number of offspring sired



Forensic: *hybridisation*

- e. g. hybridisation between introduced and native species
 - ▶ domestic cat and wild cats (Randi, 2008)

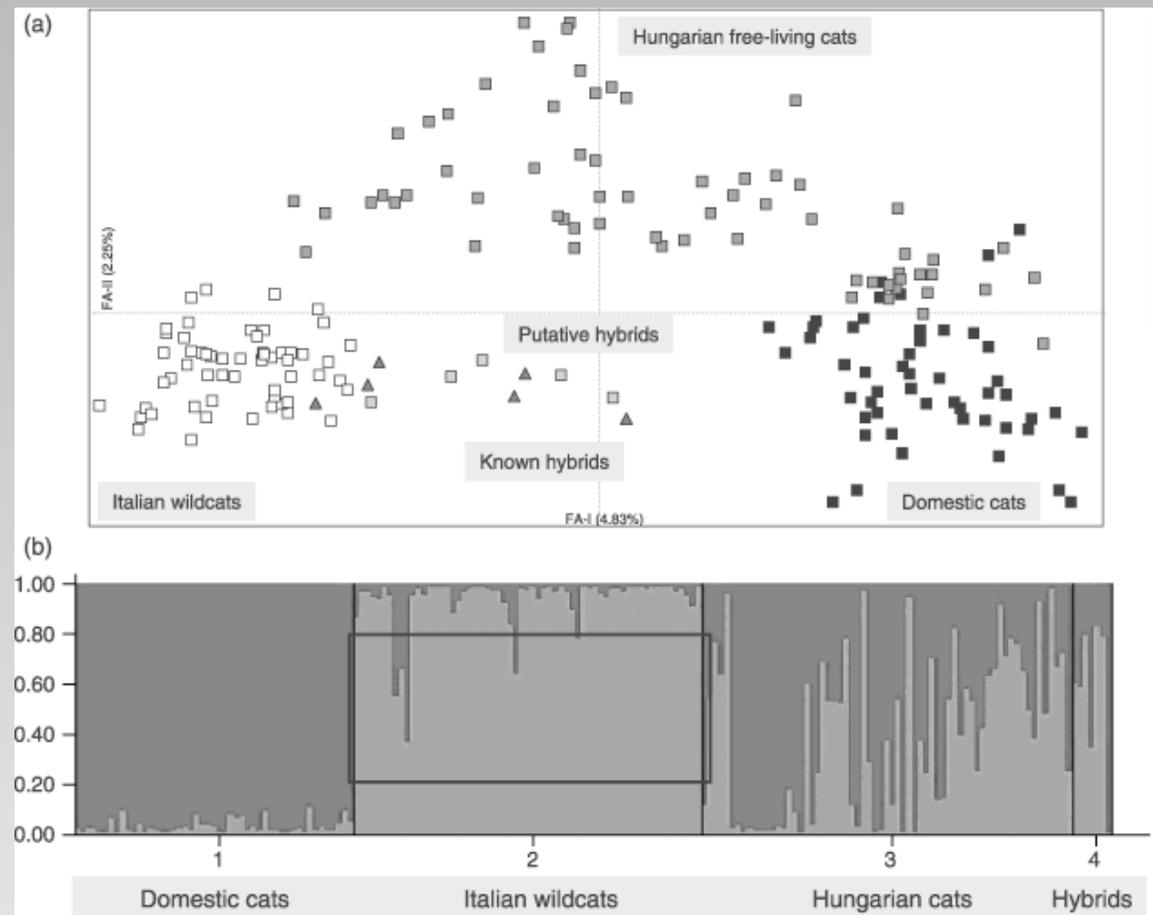
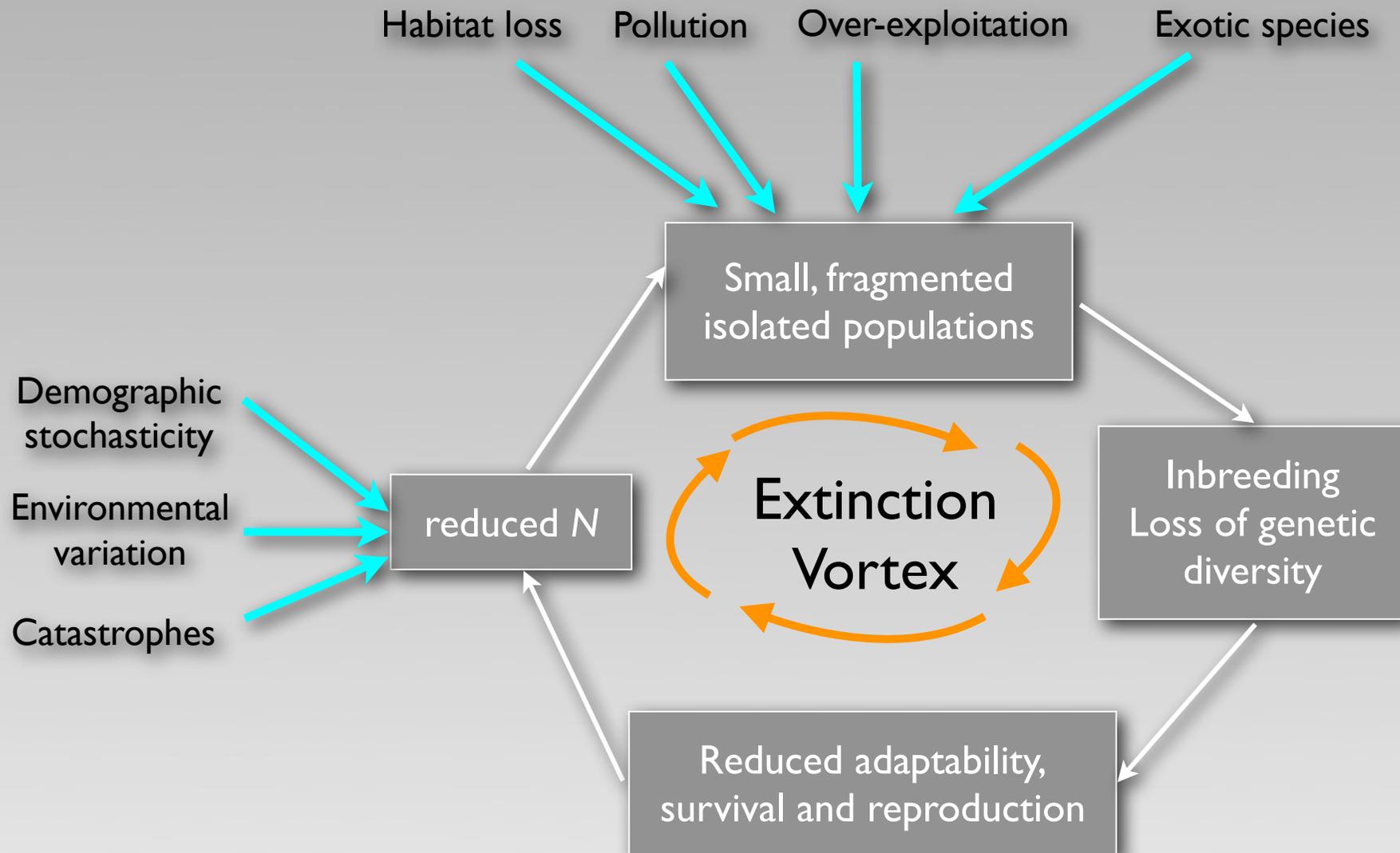


Fig. 2 (a) Factorial correspondence analysis showing relationships among the multilocus genotypes of individual Italian wildcats, freeranging Hungarian cats, domestic cats and putative or known hybrids. FA-I and FA-II are the first and second principal factors of variability. (b) structure analyses (performed assuming $k = 2$ distinct genetic clusters) of multilocus microsatellite genotypes of domestic cats, Italian wildcats, Hungarian free-ranging cats and captive-reproduced hybrids. Admixed genotypes, at threshold $q_i = 0.80$, are evidenced.

General conclusions: *Extinction vortex*



General conclusions

- reduction of genetic diversity inevitable in small closed populations
- to maintain genetic diversity
 - ▶ populations must be big enough
 - $N_e > 50$ to avoid inbreeding depression
 - $N_e = 500-5000$ to retain evolutionary potential
 - ▶ gene flow must be maintain between population
 - with about 1 migrant between pop. per generation, genetic drift is limited
 - ▶ manage to reduce genetic drift in fragmented populations and the lost of genetic diversity within them
- why?
 - ▶ genetic factors generally contribute to extinction risk
 - ▶ inbreeding has deleterious effect on reproduction and survival
 - ▶ loss of genetic diversity reduce the ability to adapt in response to environmental changes
- resulting mainly from fragmentation and population size reduction

General conclusions

- genetics: interesting tools to answer several questions
 - ▶ global genetic structure
 - species
 - ESU
 - ▶ population history
 - phylogeny / phylogeography
 - bottleneck detection
 - ▶ population structure
 - population differentiation / migration
 - inbreeding, inbreeding depression
 - ▶ forensic
 - e.g. illegal hunting
 - ▶ better understanding of the biology of the species
 - pedigree, paternity assignment
 -

General conclusions

- genetics: interesting tools to answer several questions

BUT

- must be combined with other approaches
 - ▶ biology of the studied species
 - ▶ history
 - ▶ Population viability analysis (PVAs)
 - as well as combining with e. g. genetic impacts of inbreeding
 - ▶ ...

for conservation, genetic is just a tool