

# Genetic structure in otter populations in the Czech & Slovak Republics

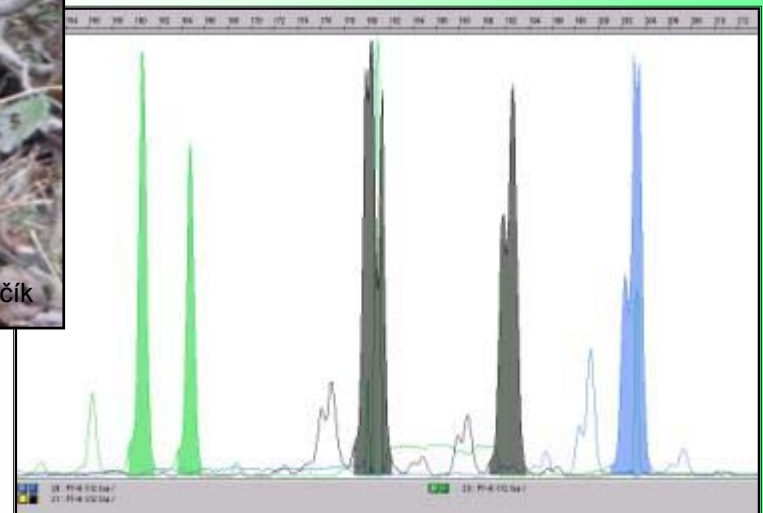


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Photo: J. Kormančík

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- until end of 19th century, distribution in all suitable habitats all over the Europe; strong hunting and persecution, but populations continuous and abundance high



- significant decline in 20th century: habitat destruction and changes in food availability, chemical pollution, persecution → local extinctions and fragmentation of populations
- **possible consequences:**
  - decrease in effective population size
  - decrease in genetic variability
  - increased genetic differentiation between populations

## **Czech Republic (CR)**

- legally protected from 1956, but decreasing – in 1980s only in South Bohemia, abundance estimate < 200 ind. in 1978
- recovery from second half of 1990s (29% squares positive in 1992 vs. 52% in 2003)

## **Slovak Republic (SR)**

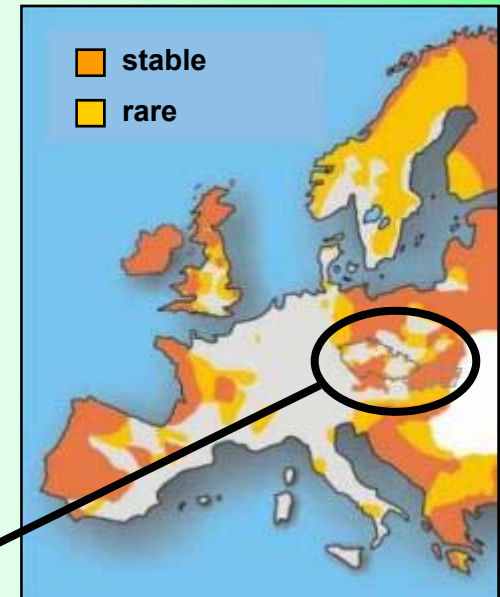
- legally protected from 1948, more moderate decrease – in 1980s mainly in Central and partly Eastern Slovakia, abundance estimate < 400 ind. in 1976
- recovery – moderate increase in distribution and numbers (80% squares positive in 2001)

# CR

- part of relatively strong but isolated Czech/Austrian/Bavarian population

# SR

- part of relatively continuous Central/Eastern European otter distribution range



- Czech and Slovak populations separated by narrow (50-80 km) region without otter presence
- populations recently reconnected



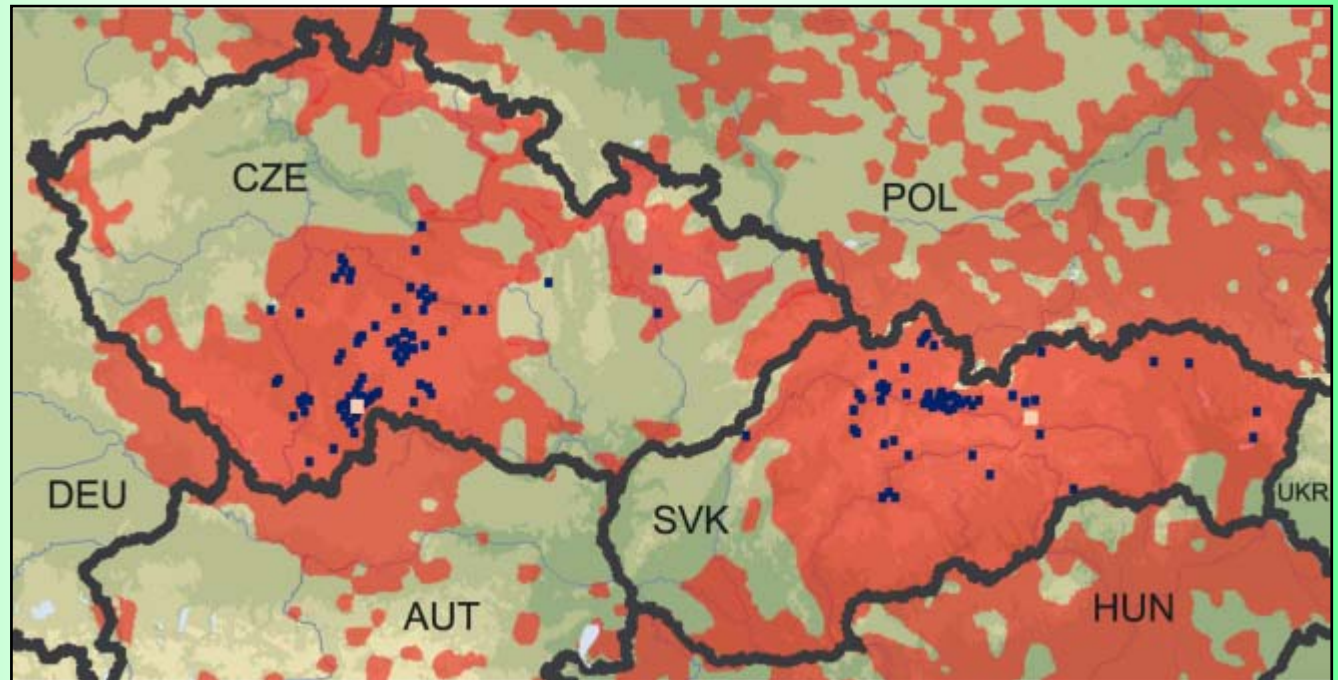
# Aims & Objectives

- (1) To estimate genetic variability and population genetic structure of otter populations in the Czech and Slovak Republics.
- (2) To infer past demographic history and possible occurrence of population bottleneck.



# Material & methods

- tissue samples from carcasses (mostly road-kills), n = 82 (CR) and n = 52 (SR)
- otter genotypes identified from spraints, n = 50 (Třeboňsko PLA & BR; CR), n = 13 (Slovenský Raj National Park; SR)
- 10 microsat. loci
- programmes  
FSTAT  
GENECLASS  
GENETIX  
STRUCTURE  
BOTTLENECK  
MSVAR



# Results: Genetic variability



- all analysed loci polymorphic, number of alleles 3-6

	ČR	SR
• number of alleles per locus	$n_a = 4.50$	$n_a = 4.70$
• allelic richness	$R_s = 4.12$	$R_s = 4.68$
• number of private alleles	$n_{pa} = 8$	$n_{pa} = 10$
• observed heterozygosity	$H_o = 0.51$	$H_o = 0.55$
• expected heterozygosity	$H_e = 0.53$	$H_e = 0.59$

⇒ **values similar and comparable with other European otter populations** (Dallas et al. 2002, Randi et al. 2003;  $n_a = 2.2 - 7.0$ ;  $H_o = 0.37 - 0.70$ ;  $H_e = 0.26 - 0.77$ )

# Results: F-indices



$F_{is}$  – „inbreeding coefficient“

CR:  $F_{is} = 0.023$ , N.S.

SR:  $F_{is} = 0.057$ ,  $P = 0.02$



Czech population in Hardy-Weinberg equilibrium, no evidence for inbreeding; Slovak population – sub-structure?

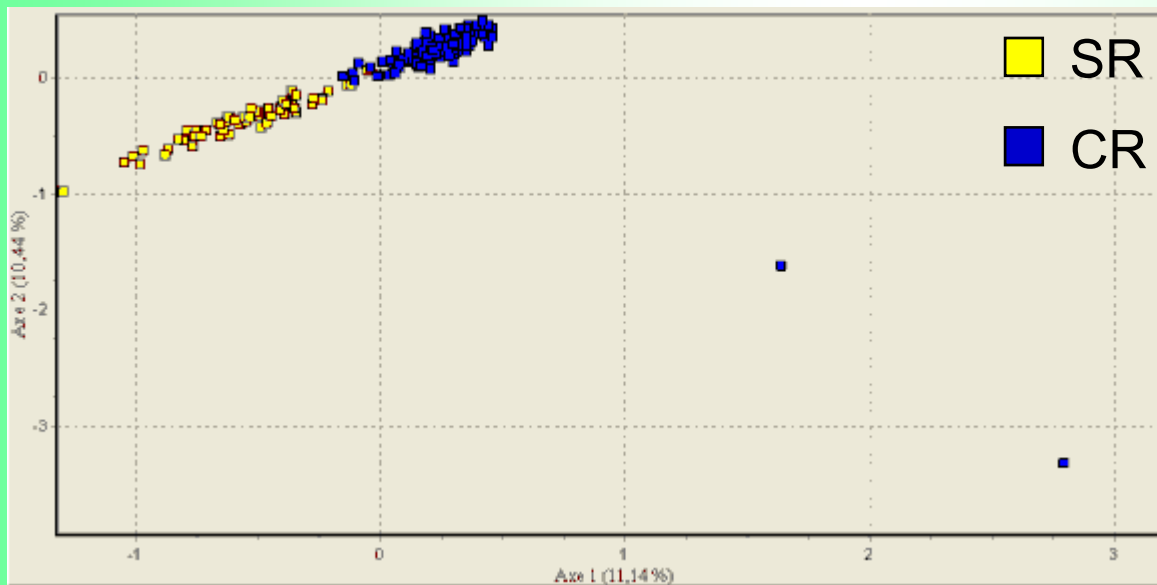
$F_{st}$  – „fixation index“

$F_{st} = 0.154$ ,  $P < 0.001$



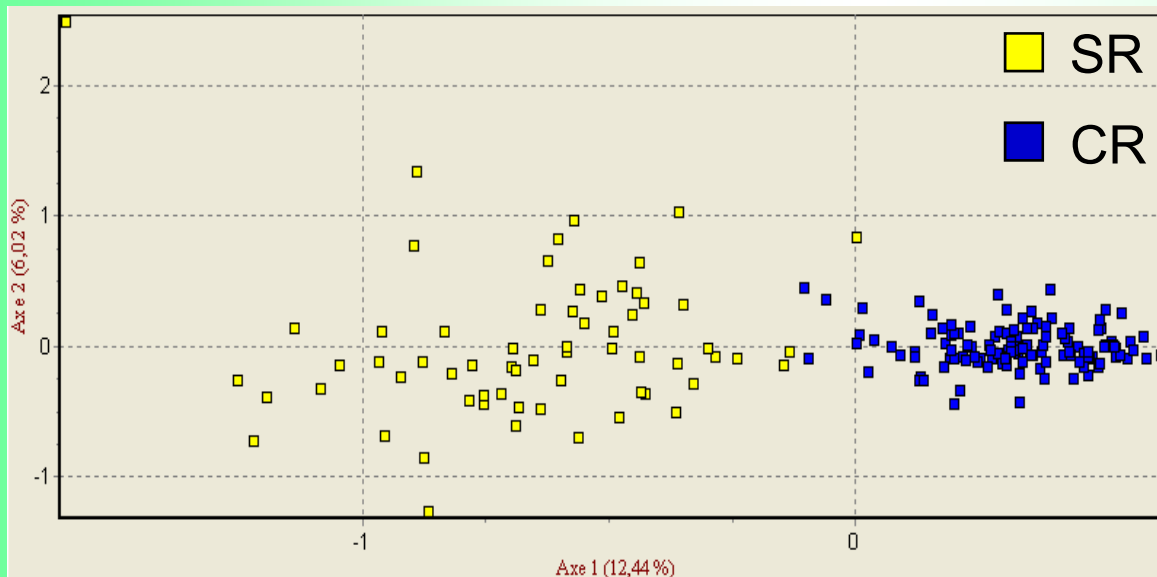
confirmed existence of gene flow barrier;  
relatively high genetic differentiation of populations





# FCA analysis (GENETIX)

## Bayesian clustering (STRUCTURE)



**$K = 3$  (clusters)**

**$\text{LnP(D)} = -3883.8$**

**cluster 1 = 129 (CR)**

**$q = 0.581$**

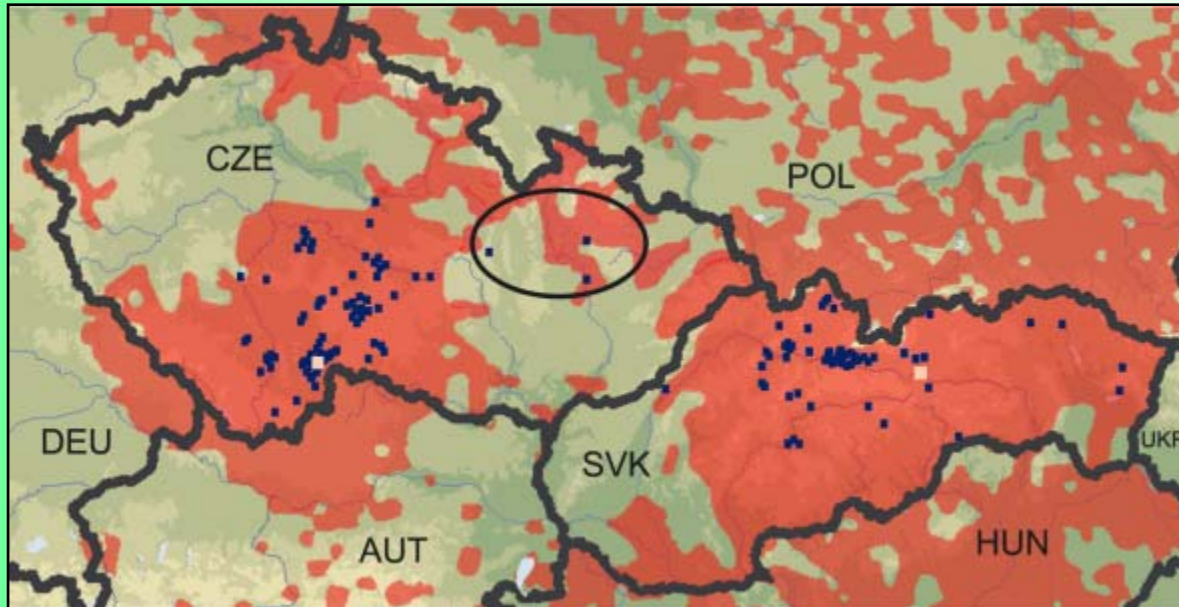
**cluster 2 = 65 (SR)**

**$q = 0.932$**

**cluster 3 = 3 (CR)**

**$q = 0.977$**

## „Outliers“ – 3 ind. from Czech population



- individuals from surrounding of reintroduction project
- unique allele 242 bp at locus Lut701 (+ other)

- collaborative European project – allele 242 bp found only in reintroduced otters in England and France, and in wild otters from Israel (Randi, Mucci et al. unpublished)
- reintroduction in NE Czechia (1997-2003) – 9 cubs from captive born ♀ Gesa released (fathers 2 ♂♂ from CR pop.)

## Locus Lut701

Gesa	<b>242/242</b>
C14	<b>202/242</b>
C21	<b>202/242</b>
C62	<b>206/242 (F2)</b>



- origin of ♀ Gesa (Otter Studbook) - B-line, Norfolk Wildlife Park (UK); origin of paternal line and part of maternal line in wild otters from England
- BUT: origin of 2 ancestors in maternal line unknown
- reintroduction evaluation: successful – reintroduced individuals reproducing (1 genotype of F2 generation); but individuals of unknown origin should not have been released

# Results: Demographic history

- BOTTLENECK (IAM): significant heterozygosity excess  
→ indication of recent bottleneck
- MSVAR: recent population decline (4-7 otter generations ago, e.g. 12-28 years ago)
- effective population size estimates (expon. model;  $N_e \approx 1/10 N$ ):

	CR	SR
past $N_e$ (before decline)	260 indiv.	590 indiv.
current $N_e$ (after decline)	70 indiv.	150 indiv.

⇒ lower  $N_e$  in Czech population; but rate of decline similar  
(decrease to  $\approx 25\%$  original  $N_e$ )



- population decline also well documented in literature (Hell & Cimbál 1978, Baruš & Zejda 1981)
- strongest decline probably between 1970s and mid-1990s
- **recent bottleneck for the first time genetically confirmed in otters**
- Pertoldi et al. 2001, Randi et al. 2003 – historical bottleneck (2000-4900 years ago)
- **Western Europe** – high anthropogenic pressure, population decline from first half of 20th century, strongest between 1950s-1970s (Erlinge 1972, Chanin & Jefferies 1978, Macdonald & Mason 1983), more moderate decline (?)
- **Central & Eastern Europe** – lower anthropogenic pressure, decline after stepwise accumulation of several negative factors (?) → bottleneck-like character

# Conclusions

- microsatellite DNA variability similar in Czech and Slovak otter populations, comparable to other populations in Europe
  - relatively high genetic differentiation between Czech and Slovak otter populations; no admixture revealed (yet)
  - recent population decline confirmed by genetic analysis
  - current effective population size low in both populations
- ➔ **populations vulnerable to rapid demographic change, retain status of legally protected species → reduction through legal culls not recommended → support of populations reconnection (by habitat conservation)**

**Thank you!**

