



# 5th European Ground Squirrel Meeting

## Perspectives on an endangered species

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**EGSM 5**

**5th European Ground Squirrel Meeting**

# **Perspectives on an endangered species**

**ABSTRACTS**

**02-05 October 2014 • Rust • Burgenland • Austria**

## **5<sup>th</sup> European Ground Squirrel Meeting**

### **Perspectives on an endangered species**

**Published and edited by:**

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Revision of abstracts: Ilse E. Hoffmann, Werner Haberl  
Layout: Dagmar Rotter, Ilse E. Hoffmann, Michaela Brenner  
Cover: Ilse E. Hoffmann  
Photograph © Lukas Mroz / modified after [maps.iucnredlist.org](http://maps.iucnredlist.org)  
(<http://maps.iucnredlist.org/map.html?id=20472/>)  
Printed by: druck.at, Aredstraße 7, 2544 Leobersdorf, Austria

Printed with the support of: Amt der NÖ Landesregierung, Abteilung Naturschutz (RU5)

### Relations between genetic, geographic and acoustic distances in five populations of speckled ground squirrels *Spermophilus suslicus*

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Integrative study of genomic and acoustic variation helps to understand the relationship between the phenotypic traits that are important for survival of individuals and their underlying genomes. We compared alarm call structures and genetic polymorphism of a mitochondrial control region of five geographically isolated populations of the speckled ground squirrel *Spermophilus suslicus*. Alarm calls were recorded from individually marked adult animals sitting singly in live-traps. We analyzed 733 alarm calls from 75 individuals (15 ground squirrels per population, 5 to 10 calls per individual). We calculated acoustical distances between all populations based on Mahalanobis distances of discriminant functions using 10 acoustic variables of calls, averaged for each individual; their values varied from 0.99 to 7.32. Genetic distances between populations were calculated based on data of genetic polymorphism of the full-sized control region of mtDNA (999-1001 b.p.), obtained by sequencing of animals included into the acoustic analysis. Genetic distances ranged from 0% to 0.9% within populations and from 0.5% to 4.7% between populations. Ground squirrels from the Eastern part of the species distribution area displayed considerably lower genetic diversity compared to the Western populations of this species. Geographical distance between populations varied from 12 to 1274 km. Comparison of acoustic, genetic and geographic distances showed a significant positive correlation between genetic and geographical distances among populations ( $r=0.85$ ,  $p<0.005$ ). The acoustical distances were neither correlated with genetic ( $r=0.28$ ,  $p=0.44$ ) nor with the geographical distances ( $r=0.52$ ,  $p=0.12$ ). This study should be expanded, with adding more populations and by applying more variable genomic markers.

Supported by RFBR grants 12-04-00260, 12-04-31274 and the Research Program “Wildlife. Genofond conservation”