Intrasexual home range overlap and dispersal in the European wildcat

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1. Introduction

In carnivores many species lead a solitary life[1,2]. Solitary means that their home ranges overlap to some extent but that they have only limited contact with conspecifics and show no cooperative behaviour[3]. Home range overlap indicates at least some resource sharing with conspecifics. The European wildcat (*Felis silvestris silvestris*, SCHREBER 1777) is often described as being solitary living [4–6] but is also expected to show social interactions under certain conditions and during specific times[7]. Besides environmental factors, such as habitat quality, intrasexual home range overlap is also assumed to be influenced by the degree of relatedness[8,9]. An increase in home range overlap among related individuals is common in female solitary carnivores[10,11]. Home range overlap in males on the other hand is not expected to correlate with relatedness[12]. Prerequisites for the influence of relatedness on female home range overlap are male-biased dispersal and female philopatry[8,13]. The sex that remains philopatric in the natal area is more likely to form associations between relatives and should therefore exhibit increased home range overlap[12–16].

Hypothesis 1: It is predicted that dispersal in the European wildcat is male-biased, leading to higher relatedness values in females than in males at a site.

Hypothesis 2: Given female philopatry, it is further assumed that female home range overlap rises with increasing relatedness, while home range overlap is independent from relatedness in males.

2. Methods

Telemetry and genetic data were available for 29 male and 36 female intrasexual wildcat dyads from five study areas in Rhineland-Palatinate (Germany) and the North-Vosges (France) (Figure 1). Data collection took place from 2001-2013 during several research projects carried out by OEKO-LOG field research (Parlow, Germany). Home range overlap was calculated with the utilisation distribution overlap index (UDOI). The UDOI accounts for the intensity of use in the overlapping area and gives an approximation for contact rates [17,18]. Relatedness was based on genetic analysis of 14 microsatellite markers and calculated with COANCESTRY 1.0.1.5 [19].

Hypothesis 1: We conducted a permutational analysis of variance in R 3.1.3[20] to test whether at each site relatedness was higher in females than in males. Additionally, a genetic spatial autocorrelation analysis, which tests for correlations between genetic and geographic distances, was carried out with GenAlex 6.5[21] to investigate differences in spatial genetic structure between sexes.

Hypothesis 2: In order to test for correlations between home range overlap and relatedness we applied a Mantel test[22] in R 3.1.3[20].
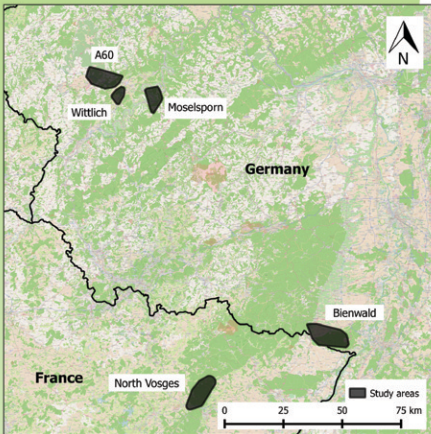

Figure 1 The five study areas in the Eifel region (A60 and Wittlich), the Hunsrück (Moselsporn) and North Vosges and Bienwald in the South-East of Rhineland palatinate (Germany) and France. Basis cartography by ©OpenStreetMap-contributers under CC BY-SA licence.

3. Results

Hypothesis 1: Intrasexual relatedness did not significantly differ between the sexes in the study areas. Even so, spatial autocorrelation analysis revealed significant spatial genetic structures in both sexes ($Omega_{female}= 39.586$, $p\text{-value}_{female}= 0.001$; $Omega_{male}= 28.168$, $p\text{-value}_{male}= 0.005$), with non-significant differences between the sexes ($Omega= 4.93$, $p\text{-value}= 0.64$). However, the correlogram shows the highest correlation (r) between genetic and geographic distance at the lowest distance class (500 m) for females, while for males the highest r was detected at the distance class of 7500 m (Figure 2).

Hypothesis 2: In males, no correlation between home range overlap and relatedness could be detected in any study area. In females on the other hand, positive correlations were found in two study areas (Moselsporn: r= 0.62, p-value= 0.0448; North Vosges: r= 0.48, p-value= 0.06).

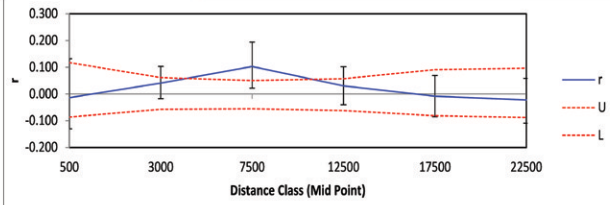### Females
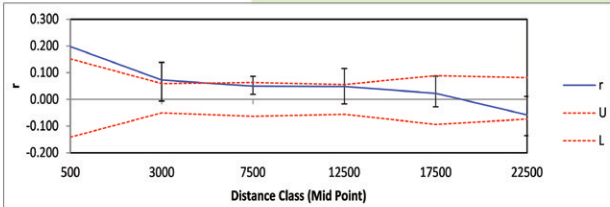
Males

Figure 2 Results for female (A) and male (B) wildcat spatial autocorrelation, where the correlation coefficient (r) indicates correlation between genetic and spatial distance plotted at the mid point of each distance class. Upper and lower error bars bound the 95% confidence interval about r as determined by bootstrap resampling (no. of bootstraps= 1,000). Upper (U) and lower (L) confidence limits bound the 95% confidence interval about the null hypothesis of no spatial structure for the combined data set.

4. Discussion and Prospects

Hypothesis 1: Male-biased dispersal could not be supported in this study. From telemetry studies, examples of both sexes dispersing over c. 25 km are known[24,25]. The genetic structure of males (Figure 2) could result from male mating excursions or short distance dispersal, where they do not leave the broader natal range. Such behaviour would likewise be supported by the selection pressures favouring male-biased dispersal, such as spatio-temporal variability in resource availability, avoiding kin competition and inbreeding avoidance[26].

Hypothesis 2: In two study areas, female UDOI rose with increasing relatedness. In these areas mother–daughter dyads were present and the habitat quality for the European wildcat was high[24]. This supports the kin selection theory[27]. However, UDOI values in these areas were still similar to UDOI values of other solitary living carnivores, like cougars (*Puma concolor*)[28]. In the other areas, unrelated individuals also showed a similar amount of UDOI. This could be because of higher mortality due to fragmentation by roads. High mortality has been shown to increase range overlap and reduce relatedness[28].

Further research is needed to refine the results and to allow more detailed inferences. A sufficient sample size is crucial, especially for spatial autocorrelation analysis[29]. A road-kill approach could be used to improve the sample size. In addition, the number of microsatellite markers should be enhanced because the assignment of second degree relatives is inaccurate with only 14 markers, c. 50 markers are recommended for such analysis[30].

5. References

1. Gittleman, J. in Carnivore Behavior, Ecology, and Evolution (ed. Gittleman, J.) 183–207 (Springer US, 1989). doi:10.1007/978-1-4757-4716-4_8
2. Sandell, M. in Carnivore Behaviour, Ecology, and Evolution (ed. Gittleman, J. L.) 164–182 (Springer US, 1989). doi:10.1007/978-1-4757-4716-4_7
3. Leyhausen, P. The communal organization of solitary mammals. Anim. Behav. 12, 379–393 (1964).
4. Corbett, L. K. Feeding Ecology and social organization of wildcat (Felis silvestris) and domestic cat (Felis catus) in Scotland. (University of Aberdeen, Scotland, 1979).
5. Piechocki, R. Die Wildkatze: Felis silvestris. (Ziemsen, 1990).
6. Biró, Z., Szemethy, L & Heltai, M. Home range sizes of wildcats (Felis silvestris) and feral domestic cats (Felis silvestris f . catus) in a hilly region of Hungary. Wild-life Biol. 69, 302–310 (2004).
7. Herrmann, M. Symposium Biology and Conservation of the European Wildcat (Felis silvestris silvestris). in Biology and Conservation of the European Wildcat (Felis silvestris silvestris) (ed. Herrmann, M.) 44 (ÖKO-LOG field research, 2005).
8. Ratnayeke, S., Tuskan, G. a & Pelton, M. R. Genetic relatedness and female spatial organization in a solitary carnivore, the raccoon, Procyon lotor. Mol. Ecol. 11, 1115–1124 (2002).
9. Moyer, M. A., McCown, J. W., Eason, T. H. & Oli, M. K. Does genetic relatedness influence space use pattern? A test on Florida black bears. J. Mammal. 87, 255–261 (2006).
10. Lührs, M. L. & Kappeler, P. M. Simultaneous GPS tracking reveals male associations in a solitary carnivore. Behav. Ecol. Sociobiol. 67, 1731–1743 (2013).
11. Balkenhol, N., Michler, F.-U., Köhnemann, B. & Gramlich, S. Genetic structure of a raccoon population (Procyon lotor) in Müritz National Park – a result of landscape resistance or space-use behaviour? Beiträge zur Jagd und Wildforsch. 36, 531–537 (2011).
12. Støen, O.-G., Bellemain, E., Sæbø, S. & Swenson, J. E. Kin-related spatial structure in brown bears Ursus arctos. Behav. Ecol. Sociobiol. 59, 191–197 (2005).
13. Greenwood, P. J. Mating system, philopatry and dispersal in birds and mammals. Anim. Behav. 28, 1140–1162 (1980).
14. Janečka, J. E. et al. Kinship and social structure of bobcats (Lynx rufus) inferred from microsatellite and radio-telemetry data. J. Zool. 269, 494–501 (2006).
15. Støen, O.-G. Natal dispersal and social organization in brown bears. (Norwegian University of Life Sciences, 2006). at <http://www.bearproject.info/uploads/publications/PhD thesis Stoen.pdf>
16. Macdonald, D. W., Mosser, A. & Gittleman, J. L. in Biology and Conservation of Wild Felids (eds. Macdonald, D. W. & Loveridge, A. J.) 125–160 (Oxford University Press, 2010).
17. Fieberg, J. & Kochanny, C. O. Quantifying home-range overlap: the importance of the utilization distribution. J. Wildl. Manage. 69, 1346–1359 (2005).
18. Robert, K., Garant, D. & Pelletier, F. Keep in touch : Does spatial overlap correlate with contact rate frequency? J. Wildl. Manage. 76, 1670–1675 (2012).
19. Wang, J. COANCESTRY: a program for simulating, estimating and analysing relatedness and inbreeding coefficients. Mol. Ecol. Resour. 11, 141–145 (2011).
20. R Core Team. R: A language and environment for statistical computing. (2015). at <http://www.r-project.org/>
21. Peakall, R. & Smouse, P. E. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research–an update. Bioinformatics 28, 2537–2539 (2012).
22. Mantel, N. The detection of disease clustering and a generalised regression approach. Cancer Res. 27, 209–220 (1967).
23. CC-by-SA. Creative Commons Attribution-ShareAlike 2.0 license at <http://www.openstreetmap.org/copyright/en, [05/06/2014]>
24. Severon, A. Wildcats in space: spacing and kinship analysis in the European wildcat (Felis silvestris silvestris, SCHREBER 1777). (University of Natural Resources and Life Sciences, Vienna, 2015).
25. Götz, M. & Roth, M. Reproduktion und Jungenentwicklung von Wildkatzen im Südharz - eine Projektvorstellung. Natur-schutz im L. Sachsen-Anhalt 43, 3–10 (2006).
26. Lawson Handley, L. J. & Perrin, N. Advances in our understanding of mammalian sex-biased dispersal. Mol. Ecol. 16, 1559–1578 (2007).
27. Hamilton, W. D. The genetical evolution of social behaviour I. J. Theor. Biol. 7, 1–16 (1964).
28. Maletzke, B. T. et al. Effects of hunting on cougar spatial organization. Ecol. Evol. 1–8 (2014). doi:10.1002/ece3.1089
29. Banks, S. C. & Peakall, R. Genetic spatial autocorrelation can readily detect sex-biased dispersal. Mol. Ecol. 21, 2092–2105 (2012).
30. Blouin, M. S. DNA-based methods for pedigree reconstruction and kinship analysis in natural populations. Trends Ecol. Evol. 18, 503–511 (2003).