

Fine-scale population genetic structure and short-range sex-biased dispersal in a solitary carnivore, *Lutra lutra*

LORENZO QUAGLIETTA,* VANIA C. FONSECA, PETRA HÁJKOVÁ, ANTÓNIO MIRA, AND LUIGI BOITANI

University of Rome 'La Sapienza,' Viale dell'Università 32–00185, Roma, Italy (LQ, LB)

Present address of LQ: Rua Barão do Rio Branco 112A, 69470-000, Tefé, Amazonas, Brazil

Unidade de Biologia da Conservação (UBC), Universidade de Évora, Núcleo da Mitra, Valverde 7002-554, Évora, Portugal (LQ, VCF, AM)

Present address of VCF: Instituto de Desenvolvimento Sustentável Mamirauá–Estrada do Bexiga 2584, Fonte Boa 69470-000, Tefé, Amazonas, Brazil

Mediterranean Agricultural and Environmental Sciences Institute (ICAAM), University of Évora 7002-554, Évora, Portugal (AM)

Present address of AM: Biodiversity and Genetic Resources Research Center (CIBIO), Pólo de Évora, University of Évora, Núcleo da Mitra 7002-554, Évora, Portugal

Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, v.v.i., Květná 8, 603 65, Brno, Czech Republic (PH)

* Correspondent: lorenzo.quaglietta@gmail.com

The genetic structure of animal populations is influenced by, among other factors, dispersal and relatedness. Limited dispersal may cause local spatial restrictions in gene flow, which can have important management and conservation implications. We used radiotracking and genetic data to verify the existence of a spatial structure in relatedness within a resident native Eurasian otter (*Lutra lutra*) population at a fine spatio-temporal scale, and to better understand dispersal in this species. We obtained 51 individual genotypes from 65 biological samples collected from 2007 to 2010 in an area of southern Portugal of 1,125 km². In addition, we radiotracked 7 (2 female, 5 male) young otters. Relatedness estimates and geographic distances were inversely related in females, whereas the relationship was not significant in males. Among the tracked subadult animals, only males dispersed, covering on average a distance of 21 km ($SD = 6$ km; range: 11–25 km). Both genetic and field data therefore revealed male-biased dispersal and suggested female philopatry. The observed overall pattern of genetic structuring was up to a scale of 21 km, although no putative landscape barriers were present. These findings concur with the few others previously available, indicating how restricted contemporary gene flow may occur at fine spatiotemporal scales within continuous carnivore populations, and can therefore constitute a cryptic cause of risk (being driven by mechanisms not necessarily related to the movement capabilities of the species), adding complexity to the conservation and management of these animals.

Key words: conservation genetics, dispersal distances, Eurasian otter, isolation by distance, radiotracking, restricted gene flow, spatial relatedness structure, spatiotemporal scale

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The study of population genetic structure and gene flow patterns is crucial, allowing, among other things, the identification of conservation or management units (Manel et al. 2003) and the assessment of the effects of local losses, the potential for natural recolonization, and the need for reintroductions (Blundell et al. 2002). Since dispersal has a major influence on genetic structure and gene flow in animal populations (Cushman and Lewis 2010), especially among solitary and territorial species (Støen et al. 2006), knowledge of this ecological process is equally important in such contexts (Slatkin 1985; Manel et al. 2003). Nonetheless, investigations on dispersal have been severely limited by technical difficulties

(Kokko and López-Sepulcre 2006), with empirical studies being very rare compared with simulations (Ronce 2007). In particular, the effects of sex-biased dispersal on fine-scale genetic structure (Banks and Peakall 2012) and on dispersal distances (Ronce 2007) have been poorly studied, especially in unbounded natural populations.

Factors driving ecological processes are scale dependent, both in space and time. Thus, the choice of the sampling scale

