

OTTER *LUTRA LUTRA* MOVEMENTS ASSESSED BY GENOTYPED SPRINTS IN SOUTHERN ITALY

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ABSTRACT - This paper analyses some otter (*Lutra lutra*) spatial data, obtained by the location of genetically typed spraints in the Pollino national park and surrounding areas (southern Italy). A sample of 214 otter spraints was collected (27 faeces in 2001-02 and 187 in 2004) along 10 streams of the park, and their location was digitalized by a Geographic Information System (Arcview 3.1) for spatial analysis. DNA was extracted using the GuSCN/silica method and each faecal sample was genotyped by PCR amplification of twelve microsatellite loci. Finally, 103 (48.1%) spraints yielded a reliable genotype, providing the identification of 31 otters.

The maximum distance, measured along watercourses between the genotyped faecal samples of each individual identified by at least two faeces, varied from 0.02 to 34.8 km. On the whole, our results outlined a ranging pattern based on the occupation by one otter of a long stretch of watercourse (21.6 and 34.8 km), including 4-6 partially overlapped short stretches (from 0.02 to 14.1 km) occupied by as many animals.

Key words: *Lutra lutra*, movements, spraint genetic analysis, southern Italy

RIASSUNTO – *Spostamenti della Lontra Lutra lutra valutati mediante analisi genetica delle feci in Italia meridionale.* Tramite l'estrazione del DNA da feci "fresche" e la successiva amplificazione di 12 loci microsatellite, da un campione di 214 feci di Lontra raccolto lungo 10 corsi idrici del Parco Nazionale del Pollino e aree limitrofe (27 feci nel 2001-02 e 187 nel 2004) sono stati ottenuti 103 genotipi affidabili (48,1%), consentendo l'identificazione di 31 individui. La localizzazione delle feci genotipizzate è stata stabilita mediante GPS (Global Positioning System) e trasferita su una mappa digitalizzata (scala 1:10000) tramite GIS (Geographic Information System). La distanza massima, misurata lungo i corsi idrici investigati, tra i campioni fecali tipizzati di ciascun individuo è variata da 0,02 a 34,8 km. Nel complesso, i risultati ottenuti hanno evidenziato un modello di ripartizione spaziale delle lontre consistente nell'occupazione da parte di un individuo di un lungo tratto di corso idrico (21,6 e 34,8 km), comprendente 6-9 tratti più brevi (da 0,02 a 14,1 km), in parte sovrapposti e occupati da altrettanti individui.

Parole chiave: *Lutra lutra*, spostamenti, analisi genetiche delle feci, Italia meridionale

INTRODUCTION

The recent development of DNA molecular methods, allowing to extract

and genotype DNA from faeces collected in the field, has provided a new powerful technique for sampling animals without trapping or observing them

(Kohn *et al.*, 1999; Pearse *et al.*, 2001; Creel *et al.*, 2003; Wilson *et al.*, 2003). Recently this technique has been applied to estimate the otter (*Lutra lutra*) population size (0.18-0.20 otters/km of watercourse; Prigioni *et al.*, in press) in the Pollino National park and surrounding areas (southern Italy), where the species is widely distributed and seems to be rather stable and abundant in some rivers (Prigioni *et al.*, 2005a). The Pollino national park covers a wide part of the residual national otter range and plays a strategic role for the conservation of the species in Italy (Prigioni *et al.*, 2005b). In this paper we report about otter spatial data, obtained by the location of genetically typed spraints. In detail, we estimated the longest ranging movements of otters along two main watercourses and their tributaries and the overlapping rate among individual stretches, suggesting some considerations about otter spatial organisation.

STUDY AREA

The Pollino National Park is located in southern Italy between Calabria and Basilicata regions (Fig. 1). It is about 1930 km² in size, with altitudes ranging from the 200 m a.s.l. of the lower Sinni river valley, to the over 2000 m a.s.l. of the Pollino massif. The hydrographic system is dominated by the River Sinni, which forms a wide east-west oriented valley in the north portion of the protected area and flows into the Ionian Sea, and by the River Mercure-Lao, that originates from the Pollino massif and runs south-westwards toward the Tyrrhenian Sea. The main water system of the park consists of 408 km of rivers and streams, of which about 212 km forming the Sinni catchment and 73.5 km the

Mercure-Lao catchment. The estimated watercourse density is 0.21 km of streams per km². Discharge peaks in winter, while it is lower in late summer. Riparian woods are formed mainly by poplar (*Populus alba*, *P.nigra*), alder (*Alnus glutinosa*) and willow trees (*Salix* spp.).

METHODS

A sample of 214 otter spraints of fresh appearance was collected (27 in 2001-02 and 187 from March to September 2004) along 10 watercourses of the park and surrounding areas. The search was carried out in the early morning to prevent daytime parching and DNA degradation, walking into the water on both river sides and along small islands, and paying attention to survey uniformly the monitored catchments. The location of each faecal sample was established by Global Positioning System and transferred on a digitalized map (scale 1:10.000) by a Geographic Information System (Arcview 3.1) for spatial analysis. DNA was extracted using the GuSCN/silica method (Gerloff *et al.*, 1995), and twelve microsatellite loci were amplified by PCR to genotype each faecal sample, following a standard laboratory procedure (Prigioni *et al.*, in press). Some 103 (48.1%) of the 214 collected spraints were successfully typed, and 31 different genotypes, corresponding to as many otters, were identified. Otter movements were assessed as the distance between the two farthest genetically typed spraints found during the study period.

RESULTS AND DISCUSSION

The longest distance, covered by an otter (genotype OT2; Tab. 1), was 34.8 km, measured along both the River Sinni and one of its tributaries, the River Cogliandrino. The 14 faecal samples belonging to this otter were spread

Movements of otters



Figure 1 - Study area

on about four years, but the two farthest faeces were gathered over a short time period (7 April and 27 April 2004). Along the watercourse occupied by OT2, the contemporaneous presence of almost other six otters, identified by a total of 27 faecal samples gathered from April to August 2004, was recorded (Fig. 2). Four of these otters showed stretches of watercourse overlapped (from 6.3% to 24.1%) with that of OT2. Two faeces gathered in 2002 along the same watercourses pointed out the presence, not confirmed in 2004, of two other individuals (OT28 and OT24).

A similar distribution pattern was outlined for the Mercure-Lao catchment. One otter (OT10) steadily occupied at least 21.6 km of watercourse, shared between the rivers Mercure and Battendiero. The 12 faecal samples assigned to this otter were gathered between January 2001 and September

2004, and the two farthest ones were collected in summer 2004 (27 May and 8 September). Along the stretch occupied by OT10 the contemporaneous presence of other four otters was recorded (Fig. 2), by means of a total of 21 faecal samples gathered from May to September 2004. Three otters (OT11, OT20 and OT31) shared wide stretches (from 49.5% to 63.0%) with that of OT10. Three further individuals (OT29, OT25 and OT26) were identified by 4 faeces gathered in 2001 and 2002.

The “shape” of water-bodies affects otter home range size (Chanin, 1985). River otter home ranges extend predominantly in length, so that they are usually described as linear development of watercourse (e.g. kilometres) rather than as surface (Erlinge, 1967; Melquist and Hornocker, 1983; Green *et al.*, 1984). The maximum length of

Table 1 - Maximum distance, measured along watercourses, between the faecal samples of each genotype identified by at least two faeces.

Genotypes	Number of faecal samples	Time of collection of faecal samples	Maximum distance measured along watercourses (km)
OT2	14	January 2001 - August 2004	34.8
OT10	12	October 2001 - September 2004	21.6
OT31	2	May - September 2004	14.1
OT20	13	February 2002 - September 2004	12.7
OT11	2	September 2002 - May 2004	11.1
OT3	5	February 2002 - May 2004	10.2
OT9	4	May - August 2004	8.4
OT12	10	June - August 2004	5.0
OT14	9	July 2004	3.8
OT15	4	August 2004	2.2
OT5	3	April 2004	2.0
OT17	2	January 2001 - August 2004	0.5
OT26	2	January 2001 - February 2002	0.2
OT1	3	March 2004	0.2
OT21	2	September 2004	0.02

watercourse used by an otter in the two monitored catchments (OT2 and OT10) was close to those found for male otters

in fresh water habitats of Scotland (18-39 km: Green *et al.*, 1984; 34.6 km: Kruuk *et al.*, 1993).

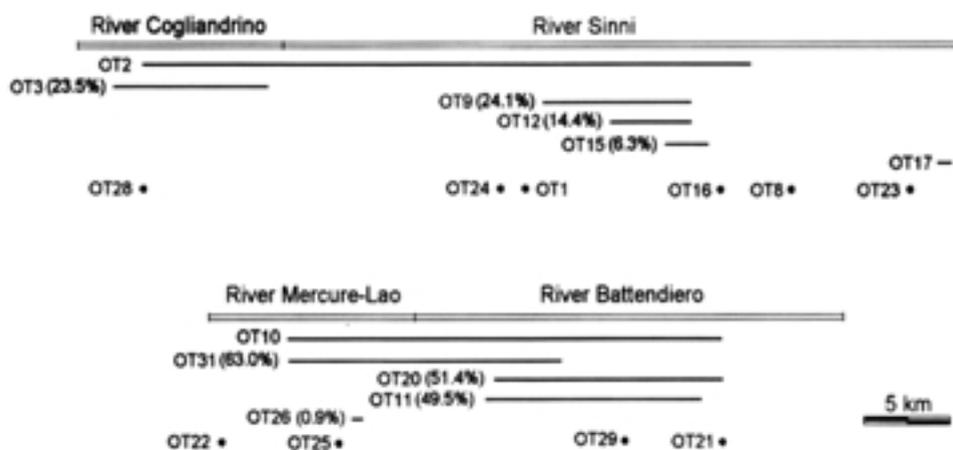


Figure 2 - Distribution of identified otters (OT) along Cogliandrino and Sinni rivers and along the upper course of the River Mercure-Lao and the River Battendiero. Otters identified by only one spraint are displayed as points. For OT3, OT9, OT12, OT15, and OT31, OT20, OT11, OT26, the percentage of overlap of shared stretches with OT2 and OT10 respectively is indicated.

Our data should be interpreted prudently, both because they are not comparable with those obtained by radiotelemetry with an adequate number of independent locations, and because our genetic analysis did not ascertain the sex of identified otters.

Nevertheless a spacing pattern consisting in a long stretch of watercourse occupied by a single otter sharing shorter stretches with other 4-6 animals seems to emerge, reflecting a typical social organisation of mustelids (Powell, 1979), with males maintaining wide territories which include those of adult females with their cubs and/or juveniles (Erlinge, 1968; Erlinge, 1981; Green *et al.*, 1984).

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