

Allegato 3a_4

Diet composition of Swiss National Park ungulates

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Introduction

Ibex are classed as mixed feeders on the borderline to grazers with their diet consisting mainly of grass, but also including forbs when available (Hofmann 1989; Pérez-Barbería et al. 2001). In Val Trupchun within the Swiss National Park, ibex share food resources with both chamois and red deer during the summer months. Here we investigate the dietary overlap between the three species.

Methods

Forty-two fresh fecal samples each of chamois and ibex, and 48 samples of red deer were collected in Val Trupchun between June 14th and September 18th 2013 and sent to PNGP to be processed along with chamois and ibex samples from PNGP.

Barcoding procedures followed the same methods as for samples from PNGP, using the universal gh plant primers (Taberlet et al. 2007). Unfortunately, only a small percentage of the collected samples from the Swiss National Park were processed (chamois: n=8, ibex: n=11, red deer: n=27).

The analysis was carried out at family level, as 100% of plant families can be identified by the universal primers, while the identification rate decreases at genus level (Ait Baamrane et al., 2012). Pianka's index of niche overlap (Pianka, 1973) was bootstrapped for each species pair using the pgirmess package (<http://cran.r-project.org/web/packages/pgirmess/pgirmess.pdf>) in R (R Development Core Team, 2006) in order to take account of the variation due to the small sample sizes particularly for chamois and ibex.

Results

Samples of all three species collected within Val Trupchun were both spatially and temporally heterogeneous. Amongst the samples which were processed, chamois samples represented altitudes between ca. 2200m and over 2800m and a temporal range from June 27th to September 17th, ibex samples between 2200m and 2800m from August 2nd to September 2nd, and red deer samples between 2000m and 2500m from June 14th to September 17th.

A total of 20 plant families could be detected overall in the diets of the three ungulate species in Val Trupchun. Each species fed on at least 9 plant families, although their identity differed between chamois, ibex and red deer. Only Asteraceae and Fabaceae were detected in samples of all three species, while 4 families (Boraginaceae, Geraniaceae, Polygonaceae and Primulaceae) could be detected only in red deer, 7 families (Campanulaceae, Caprifoliaceae, Caryophyllaceae, Cupressaceae, Gentianaceae, Saxifragaceae and Thesiaceae) only in ibex, and another 4 families (Orobanchaceae, Plantaginaceae, Polygalaceae, Salicaceae) only in chamois (Fig. 1).

If the relative importance of each plant family is measured as the proportion of individual animals which included it in their diet, Plantaginaceae were the most important diet item in chamois (present in 5 of 8 individuals), followed by Brassicaceae and Ericaceae (in 3 animals each). For ibex, the most important family was Fabaceae (in 8 of 11 individuals), and for red deer it was Rosaceae (in 15 of 27 individuals), followed by Geraniaceae (in 8 individuals; Fig. 1).

If only the point estimate for Pianka's index was considered, the dietary niche overlap was greatest between chamois and red deer, and smallest between ibex and red deer. However, due to the small sample sizes, the 95% CI's were very wide for all three pairwise comparisons, so that results for comparisons of dietary niche overlap from these data have to be interpreted with caution (Fig. 2).

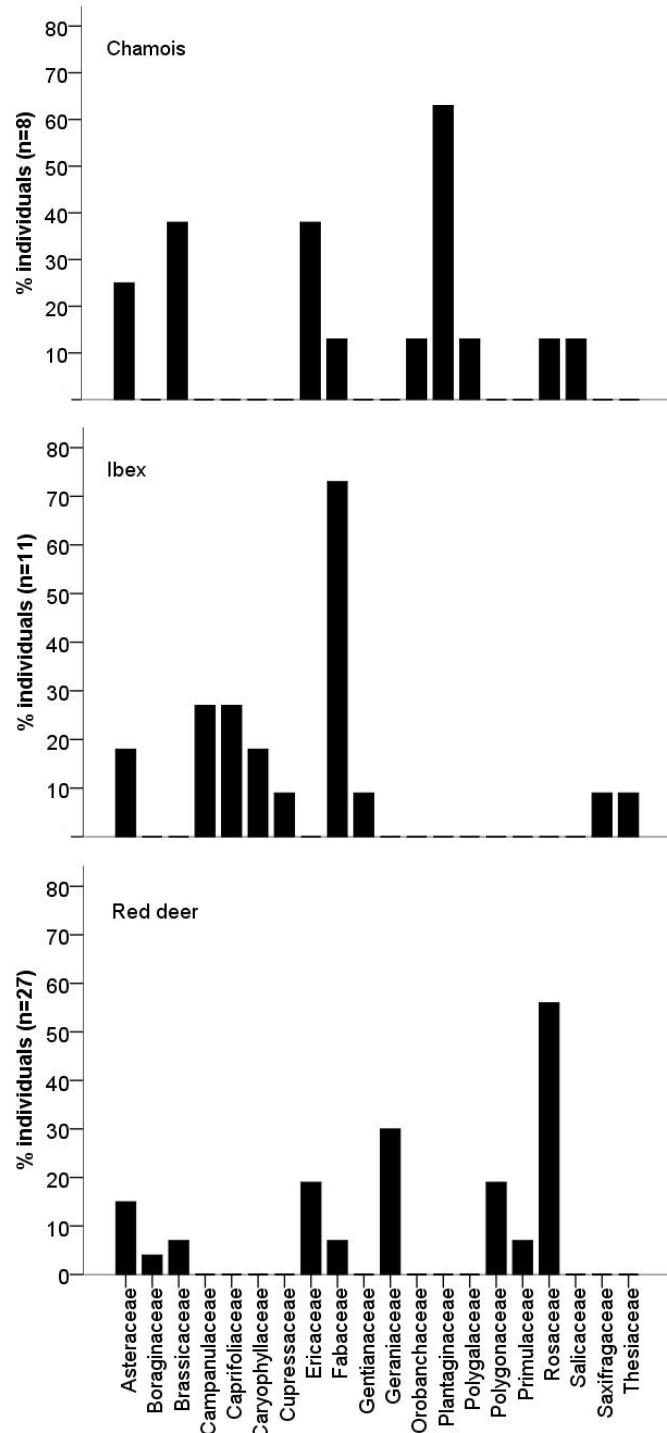


Fig. 1. Representation of the 10 plant families in the diets of chamois, ibex and red deer in percent of individuals in whose feces the family was found present.

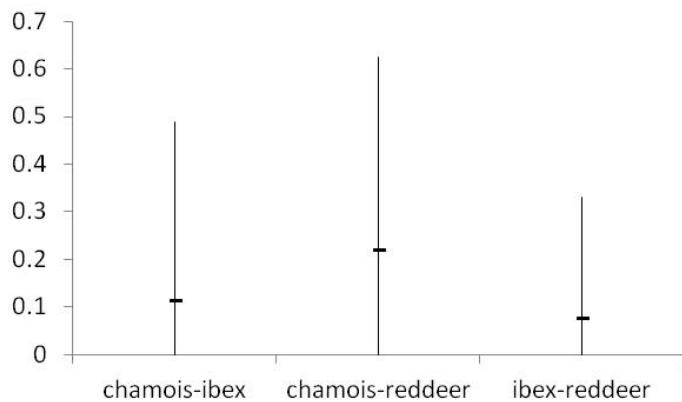


Fig. 2. Bootstrapped Pianka's index with 95% CI for each species pair based on presence/absence of plant families per individual fecal sample (chamois: n=8, ibex: n=11, red deer: n=27).

Discussion

As expected, all three species showed considerable variety in their diets, probably not only reflecting their relatively generalist dietary niches, but also the spatial and especially temporal heterogeneities in the small subset of samples which were analysed. Only a minimum estimate of the number and identity of plant families present in the diets of chamois, ibex and red deer within Val Trupchun is therefore possible based on the present data. For a quantitative analysis, detailed information about differences in the extent of degradation of different plant groups in the gut and thus their detectability in feces would additionally be necessary to obtain correction factors, along with substantially increased sample sizes.

References

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