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# MOLECULAR ECOLOGY

# A diet rich in C3 plants reveals the sensitivity of an alpine mammal to climate change

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Keywords:	Alpine mammal, C3 Photosysthetic pathway, Climate Change, diet, metabarcoding, Himalaya



1	Running head Title: Sensitivity of an alpine mammal to climate change
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4	A diet rich in $C_3$ plants reveals the sensitivity of an alpine mammal to climate
5	change
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#### 20 Abstract

21 Plant-herbivore interactions provide critical insights into the mechanisms that govern the 22 spatiotemporal distributions of organisms. These interactions are crucial to understanding 23 the impacts of climate change, which are likely to have an effect on the population dynamics 24 of alpine herbivores. The Royle's pika (Ochotona roylei, hereafter pika) is a lagomorph found 25 in the western Himalaya, and is dependent on alpine plants that are at risk from climate 26 change. As the main prey of many carnivores in the region, the pika plays a crucial role in 27 trophic interactions. We examined topographical features, plant genera presence, and 28 seasonal dynamics as drivers of the plant richness in the pika's diet across an elevational 29 gradient (2600–4450 m). We identified 79 plant genera in the faecal pellets of pikas, of 30 which 89% were forbs, > 60% were endemic to the Himalaya and 97.5% of the plant genera 31 identified followed the C<sub>3</sub> photosynthetic pathway. We found that during the pre-monsoon 32 season, the plant richness of the pika's diet decreased with increasing elevation. We 33 demonstrate that a large area of talus supports greater plant diversity and, not surprisingly, 34 results in higher species richness in the pika's diet. However, in talus habitat with deep 35 crevices, pikas consumed fewer plant genera suggesting they may be foraging sub-optimally 36 due to predation risk. The continued increase in global temperature is expected to have an 37 effect on the distribution dynamics of C<sub>3</sub> plants and consequently influence pika diet and 38 distribution, resulting in a significant negative cascading effect on the Himalayan ecosystem. 39 40 Keywords: Alpine mammal, C<sub>3</sub> photosynthetic pathway, climate change, diet,

41 metabarcoding, Himalaya, herbivore

43 44	Introduction
45	Plant-herbivore interactions provide critical insights into diverse ecological processes
46	shaping community dynamics across an array of fields linking co-evolution (Ehrlich et al.
47	1964; Johnson et al. 2015), chemical ecology (Hay & Fenical 1988; Rasher et al. 2015),
48	foraging and nutritional ecology (Raubenheimer et al. 2009; Wetzel et al. 2016). These
49	interactions are key determinants of the mechanisms which govern a species' spatial
50	distribution, abundance, community dynamics, primary productivity and function in the food
51	web (Oerke 2006; Lurgi et al. 2012) and the impact of changing climate on landscape level
52	patterns in a terrestrial ecosystem (Mulder <i>et al.</i> 1999). Determining the diet of a herbivore
53	is fundamental to understanding trophic interactions and assessing dietary plasticity to
54	climate change, and for developing effective monitoring, management and conservation
55	strategies (Bernstein <i>et al.</i> 2007).
55 56	strategies (Bernstein <i>et al.</i> 2007). In alpine ecosystems, pikas ( <i>Ochotona</i> spp.), small-bodied lagomorphs, are good examples of
55 56 57	strategies (Bernstein <i>et al.</i> 2007). In alpine ecosystems, pikas ( <i>Ochotona</i> spp.), small-bodied lagomorphs, are good examples of how a changing climate impacts plant-herbivore interactions. The American pika ( <i>Ochotona</i>
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65 The Royle's pika (*Ochotona roylei*) is a widely distributed alpine mammal found in rocky

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66	areas at elevations ranging from 2,400–5,000 m in the Himalayan region. It is found on rock
67	talus and is an obligate herbivore species with limited dispersal ability due to its small body
68	size and fairly narrow ecological niches (Bhattacharyya et al. 2009, 2013, 2014a, 2014b,
69	2015; Bhattacharyya & Smith 2018). The Royle's pika is a diurnal species and produces
70	distinct piles of faecal droppings (Bhattacharyya et al. 2014a, 2014b). Similar to other
71	lagomorphs in the Himalayan region, the Royle's pika does not hibernate and forage on
72	alpine plants along the talus-vegetation interface throughout the year (Bhattacharyya et al.
73	2009, 2013, 2014a, 2014b, 2015; Bhattacharyya & Smith 2018). Hence unlike other
74	Ochotona species, the Royle's pika does not store hay for winter survival (Bhattacharyya &
75	Smith 2018). Previous dietary analysis using visual observations indicated that forbs and
76	grasses were preferred diet plants (Shrestha et al. 1999; Awan et al. 2004; Bhattacharyya et
77	al. 2013), which have a significantly higher protein, lipid and moisture content (Ge et al.
78	2012; Bhattacharyya et al. 2013). Pikas are able to consume plants with high toxic
79	components including secondary metabolites (Bhattacharyya et al. 2013), which are usually
80	avoided by large herbivorous mammals (Sorensen et al. 2005). In addition, the Royle's pika is
81	the main prey for a range of carnivore species ( <i>e.g.,</i> yellow-throated marten ( <i>Martes</i>
82	flavigula), Himalayan weasel (Mustela sibirica), snow leopard (Panthera uncia), red fox
83	(Vulpes vulpes) in alpine and subalpine ecosystems in the Himalayan region (Robert 1977; Oli
84	et al. 1994). Thus, pikas play a crucial role in plant-herbivore trophic interactions, and their
85	extinction or range contraction is likely to have a significant negative cascading effect on the
86	functioning of the whole ecosystem.

B7 DNA metabarcoding using high-throughput sequencing enables the identification of dietary
 species using DNA extracted from faecal samples more accurately than visual observations

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89	or conventional faecal analysis (Kartzinel et al. 2015). This technique has helped to identify
90	herbivore gut contents, revealing cryptic functional diversity and niche partitioning (Kress et
91	al. 2015). Plastid genes such as <i>rbc</i> L (CBOL Plant Working Group 2009) and nuclear ribosomal
92	internal transcribed spacer (ITS; Hollingsworth 2011) are commonly used for plant
93	metabarcoding (Hollingsworth 2011). Using these techniques, we aimed to identify the diet
94	plants using faecal pellets of Royle's pikas and examine the effects of talus characteristics,
95	topography, and plant richness, abundance and seasonal dynamics (pre and post-monsoon)
96	on diet, across five sites in the western Himalaya, India. Food availability (plant species'
97	presence and abundance; Huntly et al. 1986; Dearing 1995, 1996; Wilkening et al. 2011;
98	Bhattacharyya et al. 2013, Bhattacharyya et al. 2014a; Bhattacharyya and Ray 2015), habitat
99	topography (elevation, slope, aspect; Walker et al. 1993; Deems et al. 2002; Wilkening et al.
100	2011; Rodhouse et al. 2010; Gurung et al. 2017) and predation risk (rock cover, crevice
101	depth, nearest talus distance; Calkin et al. 2012; Bhattacharyya et al. 2014 a, b; Castillo et al.
102	2014; Bhattacharyya et al. 2015) significantly impact the foraging ecology of the Royle's pika
103	and potentially influence access to nutritive plants, and thereby affect individual fitness
104	(Bhattacharyya 2013). For talus dwelling Ochotona spp., talus size (area) and connectivity
105	between talus are known to influence the habitat occupancy (Franken and Hik 2004). In
106	Royle's pikas, high proportion of rock cover in talus habitat provides refuge from predation
107	risk, which in turn increases their habitat occupancy and abundance (Bhattacharyya et al.
108	2014a; Bhattacharyya et al. 2015). Topographical features determine the distribution and
109	abundance of alpine plants (Bruun et al. 2009). The pre-historic distribution of small
110	mammals (Ochotonidae), highly adapted to arctic or alpine environment was closely
111	associated with preferred $C_3$ food plant diet which is high in protein and moisture content

112	(Ge et al. 2012). Whilst the interplay between plants and herbivores is a key determinant of
113	community structure (see Wisz et al. 2013; Dolezal et al. 2016), climate induced expansion
114	of C <sub>4</sub> plants is believed to have resulted in extinction and range contraction in pikas (Ge et al.
115	2012). Furthermore, in highly seasonal montane habitats, dietary constraints in herbivores
116	tend to be strongly linked to quality of forage available. In the Himalayan region, both plant
117	quality and available biomass may act as constraints for pikas. Seasonal dynamics in diet
118	selection can reflect dietary adaptations (plasticity) in a seasonal alpine habitat. Our Royle's
119	pika diet analysis will provide insights into the plant genera selected during foraging and test
120	the following hypotheses:
121	i) Seasonal difference in diet (pre-monsoon versus post-monsoon) will demonstrate dietary
122	flexibility and the pikas will select plants with the highest nutrient gain possible from the
123	feeding habitats available.
124	ii) Larger areas of talus habitat will result in more plant availability and will increase species
125	richness of the diet.
126	iii) Talus characteristics such as rock cover, depth of crevices etc. would increase species
127	richness in the diet by providing refuge from predators and allowing pikas to access larger
128	foraging ground.
129	iv) Forbs and grasses constitute the largest proportion of their diet.
130	v) Pikas prefer diets rich in $C_3$ plants, which signify potential threat due to climate change as
131	$C_3$ plants are dependent on high rainfall and low temperature.
132	

133	Materials and Methods
134	Study area, collection of faecal pellets and habitat data
135	The Royle's pika inhabits rock crevices in talus fields with a home range of approximately
136	50m <sup>2</sup> (Kawamichi 1968; Bhattacharyya <i>et al.</i> 2015). During 2014–15, 104 rock talus habitats
137	were surveyed and faecal pellets collected from five sites at elevations ranging between
138	2,600 to 4,450 m above sea level (a.s.l): Chopta–Tungnath (TUN), Rudranath (RUD),
139	Madmaheshwar (MAD: Kedarnath Wildlife Sanctuary), Har ki Doon (HAR: Govind Wildlife
140	Sanctuary), Bedni-Roopkund (NAN: Nandadevi Biosphere Reserve; Figure 1) in Garhwal,
141	Uttarakhand, India. The sampling was conducted in two seasons: post-monsoon (October to
142	November 2014) in TUN, RUD, HAK and pre-monsoon (May to June 2015) in TUN, MAD and
143	NAN.
144	
145	Following Bhattacharyya <i>et al.</i> (2015), we selected 50m <sup>2</sup> survey plots in each talus habitat,
145 146	Following Bhattacharyya <i>et al.</i> (2015), we selected 50m <sup>2</sup> survey plots in each talus habitat, and these were searched for fresh piles of faecal pellets (moist, dark brown/black). One site
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156	campanulatum and/or Vivernum sp.) and trees (e.g., Abies pindrow, A. spectabilis, Quercus
157	semecarpifolia, Rhododendron arboretum; Van Hees & Mead 2000; Bhattacharyya et al.
158	2015).
159	
160	DNA metabarcoding of faecal pellets
161	The Royle's pika's diet is rich in secondary metabolites (Bhattacharyya et al. 2013), which
162	often inhibit downstream enzymatic reactions in Polymerase Chain Reaction (PCR; Weishing
163	et al. 1995). Therefore, we homogenized 20–30 mg of the faecal samples and extracted DNA
164	using QiaAmp DNA stool kit (Qiagen Inc., Germany) following minor modifications in the
165	manufacturer's protocol (e.g. overnight incubation at 56°C with ASL stool lysis buffer; Qiagen
166	Inc., Germany). As Royle's pika were the only lagomorph species present in the study area
167	(Green 1985, Bhattacharyya 2013) with very distinct faecal pellets, the chances of
168	misidentification of the faecal samples was ruled out.
169	
170	We amplified the ITS2 region of plant nuclear DNA using primer pair UniPlantF (5'-
171	TGTGAATTGCARRATYCMG-3') and UniPlantR (5'-CCCGHYTGAYYTGRGGTCDC-3';
172	187–380 bp; Moorhouse-Gann et al. 2018) and the rbcL region of chloroplast DNA using
173	primer pair <i>rbcLa-F</i> (5' ATGTCACCACAAACAGAGACTAAAGC-3' and <i>rbcLa-R</i> (5'-
174	GTAAAATCAAGTCCACCRCG-3'; 553 bp; Levin et al. 2003, Kress et al. 2009, Yoccoz et al.
175	2012). Primers had overhang adapter sequences added to the 5' end for the initial PCR
176	amplification, following Campbell et al. (2015). This allows unique 6 bp dual index sequences
177	to be added along with Illumina capture sequences to each sample in a subsequent PCR step
178	prior to pooling samples for sequencing. Initial PCR amplifications were performed in 10 $\mu$ L

179	reaction volumes including 5 $\mu$ L of Qiagen Multiplex PCR Master Mix (Qiagen, Manchester,
180	UK), 1 $\mu L$ of each primer (1 $\mu M$ ), 2 $\mu L$ nuclease free water (ThermoFisher Scientific, Inc.) and
181	1 $\mu L$ of DNA template. Reaction conditions were as follows: initial denaturation at 95°C for
182	15 minutes; 44 cycles of 94°C for 90 seconds, 55°C for 30 seconds, 72°C for 60 seconds; final
183	extension of 72°C for 10 minutes. We used DNA from Quaking grass (Briza media) as positive
184	control and a negative control for each PCR run (Zarzoso et al. 2013). The PCR products
185	amplified by each primer pair were separated on a 1% agarose gel stained with SYBR®Safe
186	and amplicon size compared to a 100 bp ladder (Thermo Fisher Scientific, Paisley, UK) and
187	amplification success assessed. In addition, each PCR product was quantified in BioAnalyzer
188	(Agilent Technologies, Santa Clara, CA) to accurately estimate the amplicon size and DNA
189	concentration. Only amplicons with clear visible band following electrophoresis were
190	processed further. The ITS2 and <i>rbcL</i> PCR products were pooled in equal amounts and
191	quantified using a Qubit (Thermo Fisher Scientific, Waltham, MA) to ensure approximately
192	equal amounts of amplicon DNA was used in the second amplification step to attach the
193	Illumina tags. This PCR amplification was performed in a 10 $\mu$ L reaction volume including 5
194	$\mu L$ of Qiagen Multiplex PCR Master Mix (Qiagen, Manchester, UK), 0.5 $\mu L$ of forward and
195	reverse Illumina Multiplex Identifier (MID) tagged or indexed primers (1 $\mu$ M), 2 $\mu$ L DNase
196	and nuclease free water (Thermo Fisher Scientific, Inc.) and 4 $\mu L$ of DNA template (pooled
197	product from previous ITS2 and <i>rbcL</i> PCR). Reaction conditions were: initial denaturation at
198	95°C for 15 minutes; 10 cycles of 98°C for 10 seconds, 65°C for 30 seconds, 72°C for 30
199	seconds; final extension of 72°C for 5 minutes. The concentrations of these PCR products (2
200	$\mu$ L) were measured using a fluorimeter (Thermo Fisher Scientific, Paisley, UK) and pooled
201	together in batches of 8 samples with similar concentrations. Each batch of pooled samples

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202	was then purified following the Agencourt AMPure XP PCR Purification Kit protocol
203	(Beckman Coulter Genomics, Aus.) to remove non-target DNA fragments and primer dimer,
204	and eluted in 40 $\mu$ L of ultrapure water (Murray <i>et al.</i> 2015). Each cleaned pool was then
205	analysed on a Tape Station (Agilent Technologies, US) to check for successful removal of
206	primer dimer. Each pool was then serially diluted and quantified using quantitative PCR
207	(Applied Biosystems, CA, USA) where a diluted custom synthetic oligonucleotide of known
208	molarity was used as standard to determine the final volume of library to use for
209	sequencing. The qPCR amplification was performed in a 25 $\mu$ L volume containing KAPPA
210	library quantification kit (Kappa Biosystem, Inc.), 0.4 $\mu M$ of specific forward and reverse
211	primer and 2 $\mu L$ of pooled amplicon library and using these reaction conditions: 95°C for 5
212	minutes, followed by 35 cycles of 95°C for 30 seconds and 60°C for 45 seconds. Based on the
213	Cycle Threshold (CT) values observed, each pool of 8 samples were combined in equimolar
214	proportions (4 nM) to make a single library with unique Illumina tagged PCR product for all
215	124 samples to run using the 500 cycle v2 (2 x 250bp paired-end reads) sequencing kit on
216	the MiSeq Desktop Sequencer (Illumina, San Diego, CA).
217	
218	Identification of plant diet from sequencing data
219	The bioinformatic analyses were performed using Iceberg, the High Performance Computing

220 Cluster at the University of Sheffield, UK. The paired-end reads were filtered for quality

221 (minimum quality score 20 over a 4 bp sliding window) and any Illumina adapter sequences

- removed using Trimmomatic v 0.32 (Bolger et al. 2014), retaining only reads of at least 90 bp
- in length. For ITS2, filtered sequences were then aligned using FLASH (Magoč & Salzberg
- 224 2011) and aligned sequences with matches to the ITS2 primer sequences only were

225	extracted and primer sequences removed using the "trim_seqs" command in Mothur
226	(Schloss et al. 2009). The ITS2 region was extracted from the whole amplicon sequence
227	(which includes ~73 bp of 5.8S sequence, Moorhouse-Gann <i>et al.</i> 2018) using ITSx
228	(Bengtsson et al. 2013). The "derep_fulllength" and "uchime2_denovo" commands were
229	used in usearch software v 9.2.64 (Edgar 2010) to eliminate all sequences which had less
230	than 10 copies per sample and any chimeric sequences. Each unique ITS2 sequence found in
231	the dataset was then compared against the NCBI GenBank nucleotide database using the
232	BLAST algorithm (Altschul <i>et al.</i> 1997) to assign a taxonomic unit for each plant sequenced
233	identified. Only matches with at least a 97% identity to the reference sequence were
234	retained for downstream analysis. The software MetaGenome Analyzer v 4 (MEGAN, Huson
235	et al. 2016) was used against NCBI taxonomic framework for mapping and visualization of
236	the BLAST results, keeping all default parameters for the LCA assignment algorithm except
237	the bit score minimum support threshold, which was set at 1%. For <i>rbcL</i> the analysis pipeline
238	differed slightly as we did not expect a region of overlap between the paired sequencing
239	reads with these ~550 bp long amplicons. Instead, we used a custom script to reverse
240	complement read 2 and combine with read 1 to form an <i>rbcL</i> sequence starting and ending
241	with the primer sequences but having at least a 50 bp gap in the middle. Prior to performing
242	the BLAST search we also clustered the dereplicated and non-chimeric at 97% sequence
243	similarity using the "cluster_fast" commands in usearch. Owing to limited reference plant
244	database from the Himalayan region, we were able to identify plants only at genus level. The
245	reliability of each molecular operational taxonomic unit (mOTU) corresponding to a specific
246	plant genus was further evaluated against a published list of plants reported from the study
247	area (Bhattacharya et al. 2007; Rai et al. 2012), and online plant [e.g. flora Himalaya

248	database (http://www.leca.univ-savoie.fr/db/florhy/infos.html), Dobremez et al. 2009] and
249	biodiversity databases [e.g. The Global Biodiversity Information Facility
250	(https://www.gbif.org/)], which provided information on elevation and geographic range of
251	the plant genus. Plant genera not reported from the Himalayan region were not considered
252	for further analysis.
253	
254	Information of ecological and evolutionary linkages of plants in Royle's pika diet
255	The adaptation ability, ecological requirements, physiology, and nutritional quality of plants
256	often depend on their photosynthetic pathways ( $C_3$ , $C_4$ or Crassulacean acid metabolism
257	[CAM]; Ehleringer & Monson 1993). The photosynthethic pathway of plants belonging to the
258	same genus is often considered to be the same (Osborne et al. 2014; Sage 2016). Therefore,
259	we obtained information on photosynthetic pathways of pika food plants from published
260	sources (Ge et al. 2012; Osborne et al. 2014; Bhattacharyya et al. 2016; Sage 2016), and
261	information on evolutionary origin (e.g., endemic to Himalaya, Tropical, Holarctic) average
262	upper and lower elevation distribution range of each diet plant genus was obtained from
263	flora of Himalaya database (http://www.leca.univ-savoie.fr/db/florhy/infos.html ; Dobremez
264	et al. 2009), Global Biodiversity Information Facility (https://www.gbif.org/search) and IUCN
265	red list of threatened species online portal (http://www.iucnredlist.org/).
266	

267 Statistical analysis

268 Plant composition and seasonal dynamics in diet

269 We compared the plant diet composition at family and genera level. We used Multiple

270 Response Permutation Procedure (MRPP; Mielke *et al.* 1976; Zimmerman *et al.* 1985) to

271	understand seasonal variation in diet composition at plant genera level across multiple sites.
272	We used contingency table analysis to test for heterogeneity in plant family in diet across
273	sites, which was assessed by G-tests followed by partitioned analyses (Rohlf & Sokal 1995).
274	In addition, we have used generalized linear models (GLMs) to understand the effect of
275	elevation on plant diet richness (number of genera) across seasons and comparison of plant
276	families across sites sampled in the same season. The significance of fixed effects was
277	evaluated with Wald's $\chi^2$ tests (Bolker <i>et al.</i> 2009). To understand if relative contribution of
278	vegetation type (forbs, grass, shrub, tree) in pika diet is proportional to their availability in
279	the environment, we conducted compositional analysis (Aebischer et al. 1993) using
280	Adehabitat v 1.8.20 package in R (Calenge 2006). We restricted our analysis to the
281	vegetation types which qualified within the criteria of a minimum of two data points greater
282	than zero per vegetation category in the environment dataset (Calenge 2006). In addition,
283	the contribution of each plant genus to overall pika diet with their corresponding
284	evolutionary origin and distribution range was visually explored using boxplots.
285	
286	Modelling effect of talus habitat on diet richness
287	We investigated the effect of food availability (tree, shrub, grass and forbs cover), predation
288	risk (talus area, distance between talus, depth of crevices) and talus topography (elevation,
289	aspect, slope) on plant diet richness. We fitted 32 GLM models and used AIC-based multi-
290	model inference to identify well-supported statistical models that describe the relationships
291	between plant diet richness and biological parameters relevant to foraging ecology of
292	Royle's pika (Table S1). Season was not incorporated as an explanatory variable in the model

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294	MuMin v 1.40.4 package in R (Barton & Barton 2018) on the model set generated from the
295	global model, applying a threshold-corrected Akaike's information criterion ( $\Delta$ AICc; Burnham
296	and Anderson 2002) to select the best candidate model based on the lowest (AIC) values
297	corrected for sample size bias, or AICc values ( $\Delta$ AICc) > 2 units than the quality of other
298	competing models. Alternatively, when two or more models had difference in AICc < 2, we
299	used multimodel averaged estimates to check the validity of the top ranking model in each
300	case, only including models with $\Delta$ AICc < 2 (Burnham & Anderson 2002). The relative
301	importance (RI) of each parameter after model-averaging was calculated by summing
302	Akaike's weight (wi) across all models in which the parameter was present. All data was
303	checked for normality and corrected for over-dispersion if required. We tested for possible
304	collinearity of the explanatory variables using Pearson's correlation analysis in the global
305	model; the mean correlation was 0.14 and strongest was 0.64. All the correlated variables
306	were used only in interactive models but not in additive models. All analyses were
307	conducted in R v 3.3.3 (The R Foundation for Statistical Computing, http://www.r-
308	project.org/).
309	
310	Results
311	The Illumina run produced a total of 3,685,142 paired-end reads (2 x 250 bp), with an
312	average of 29,719 reads per sample (range 172–113,816 reads, n=124).

313 Plant composition and seasonal dynamics in pika diet

314 We successfully obtained information from 110 fecal pellets (after controlling for data

315 quality) representing 66 out of 104 sampled rocky talus plots. A total of 79 plant genera

316	(ITS2= 66, <i>rbcL</i> =13, 12 were common to both) were identified. We retrieved 62 genera and
317	28 families of forbs, ten genera and one family of grass, three genera and three families of
318	shrubs, three genera and three families of trees (Table S2).
319	
320	Of the 32 plant families recorded in the pikas diet, Asteraceae, Poaceae, Primulaceae,
321	Ranunculaceae, Rosaceae and Scrophulariaceae showed significant differences across sites
322	in the mean proportion of occurrence within diet (Table 1). We found no significant
323	difference in proportion of plant families in the pre-monsoon (GLM: $F_{12}$ =111.42, P< 0.25) and
324	post-monsoon season (GLM: $F_6$ =49.74, P< 0.08). In the pre-monsoon season, we found
325	significant differences between sites in the proportion of plant family per faecal sample
326	(GLM: $F_2$ =126.92, <i>P</i> < 0.0001; proportions listed in Table 1) with NAN having significantly low
327	number of plant families (t=-4.18, P< 0.001), whereas TUN showed no difference (t=-1.5, P<
328	0.110). In the post-monsoon season, the proportion of plants in the diet varied significantly
329	across sites (GLM: $F_2$ =37.61, P< 0.011) with RUD showing more plant families (t=2.84,
330	<i>P</i> <0.001) than TUN (t=2.18, <i>P</i> < 0.03). However, high proportion of certain family (e.g.
331	Asteraceae in RUD) in a site is possibly driven by low sample size.
332	
333	Forbs constituted 89% of richness, which was significantly higher than both shrubs (7%) and
334	grasses (3%) (GLM: $F_2$ =48.91, <i>P</i> < 0.03). We found pre-monsoon composition of plant genera
335	in diet varied significantly (delta obs. = 2.54, delta exp. = 2.56, A=0.006, P< 0.05, Figure S1)
336	across sites, whereas there was no variation in plant genera composition in the post-
337	monsoon season. Across seasons within site, Tungnath (TUN) showed significant variation in

338	proportion of plant richness in diet (GLM: $F_1$ =18.68, P< 0.0001) with the pre-monsoon
339	season having lower plant richness (t=-4.38, P<0.0001) than post-monsoon.
340	Plant genus richness during pre-monsoon varied across elevation, where it increased with a
341	decrease in elevation (Wald's $\chi^2$ =9.51, d.f. = 1, <i>P</i> < 0.001); Figure 2). Comparing food
342	availability in the environment with dietary results revealed that the Royle's pika prefers
343	forbs (e.g. Potentila) over shrubs (e.g. Vibernum) in talus habitat during the pre-monsoon
344	season in TUN (lambda=0.019, P< 0.01) and NAN (lambda=0.46, P< 0.01 Figure S2), and
345	during the post-monsoon season in TUN (lambda=0.11, P<0.01) and HAK (lambda=0.007, P<
346	0.05, Figure S2). No prominent preference for forbs or grasses was observed in MAD
347	(lambda=0.20, <i>P</i> > 0.05). Overall, composition analysis of vegetation types in the
348	environment and faecal samples across sites during pre- and post-monsoon indicated high
349	preference towards forbs (pre-monsoon: lambda=0.008, P> 0.01; post-monsoon:
350	lambda=0.10, P> 0.001). Due low sample size in RUD, no site-wise vegetation comparison
351	was conducted.
352	
353	A high proportion (> 50%) of the plant genera (e.g., Anaphalis, Berberis) detected in both the
354	pre-monsoon (TUN=52.02%, MAD=56.25%, NAN=56.67%) and post-monsoon (TUN=53.48%,
355	RUD=64.28%, HAK=56.66%) seasons were endemic to the Himalayan region, followed by
356	plants of Holarctic origin (e.g., <i>Deschampsia, Festuca;</i> pre-monsoon: TUN=22.97%,
357	MAD=28.12%, NAN=25.0%, post-monsoon: TUN=26.35%, RUD=21.42%, HAK=26.66%) origin
358	(Figure 3A & B; Table S2). The upper distribution limit of more than 90% of all pre and post-
359	monsoon dietary plants was 3,500 m and above (Figure 4). A significant proportions of pre-
360	monsoon (TUN=77.70%, MAD=75.32%, NAN=72.8%) and post-monsoon (TUN=74.49%,

- 361 RUD=80.00%, HAK=97.14%) dietary plants were found to have a lower altitudinal range of
- 362 2,000 m to 1,000 m (Figure 5). C<sub>3</sub> plants constituted 97.5% of the pikas' diet with much
- 363 smaller proportions being C<sub>4</sub> (1.25%) and CAM (1.25%; Table S2).
- 364
- 365 Effect of talus habitat on plant diet richness
- 366 Model-averaged estimates derived from the 90% model set agreed with the best-
- 367 approximating model with two variables: talus area cover and crevice depth, which were
- 368 detected as significant predictors for diet richness; each having RI values of 1.0. Talus area
- 369 has significant positive influence on plant diet richness. However, crevice depth showed a
- 370 negative influence on plant richness (Table 2).
- 371
- 372

#### 373 Discussion

- 374 This is the first study of the diet for any Himalayan pika species that uses non-invasive
- 375 sampling and metabarcoding. It allowed us to quantify genus richness and revealed cryptic
- 376 aspects of functional diversity and useful insights into niche partitioning across an
- 377 elevational gradient. Our study provides an excellent example of how DNA metabarcoding
- 378 can be used in understanding diet and feeding preferences of an elusive herbivore species
- 379 found in fragmented alpine terrain and is applicable for other herbivores dependent on C<sub>3</sub>
- 380 and  $C_4$  plants. We found DNA metabarcoding outperformed traditional methods by revealing
- 381 the huge diversity of plant genera consumed by pikas and their reliance on species endemic
- 382 to the Himalayas. Earlier studies based on traditional visual and microscopic observation

383	reported only 22 food plant genera for Royle's pika (Bhattacharyya et al. 2013), whereas our
384	DNA metabarcoding results indicated more than 70 plant genera in the diet, which includes
385	all of the 22 plant genera reported earlier. Forbs constituted the highest proportion of the
386	diet. We demonstrate quantitative estimates of relative consumption of plant genera and
387	capture fine-scale distribution across an elevational gradient, which has been difficult to
388	detect using traditional methods of diet analysis. In addition, diet plant richness in the pre-
389	monsoon season varied significantly across sites and decreased in higher elevation sites. We
390	also demonstrate the effects of habitat characteristics, such as talus area and depth of
391	crevices between rocks, on the genus richness in the Royle's pika's diet.
392	Plant composition and seasonal variation in Royle's pika diet
393	Our study revealed that pikas exhibit dietary flexibility with high genus richness in their pre-
394	monsoon diet at lower elevation, possibly due to a longer growing period in this habitat.
395	Thick snow cover delays the beginning of the growing period of alpine plants in higher
396	elevation areas (Inouye 2008). Therefore, plants experience comparatively longer growing
397	periods at lower elevations. However, the lack of precipitation and low temperature during
398	the post-monsoon period leads to the end of the growing period for alpine plants. This may
399	explain why no variation in diet plant richness with elevation was observed during the post-
400	monsoon season. Compared to other Asian pika species such as Northern pika (Ochotona
401	hyperborean; Khlebnikova 1976; Revin & Boeskorov 1990), Royle's pikas show a preference
402	for plants such as forbs (e.g., Potentila spp., Primula spp. and Anaphalis spp.). The
403	contribution of forbs in the pika's diet was found to be proportionately higher than its
404	availability in the environment possibly due to the high nutrient value of forbs compared to

405	other vegetation ty	pes, such as grasses.	shrubs and trees (	(Bhattacharv	va et al. 2013).
100					,

406 Talus dwelling Ochotona species usually exhibit prominent hay building activity in the 407 summer to cache food for survival during the winter (Hudson et al. 2008; Bhattacharyya & 408 Ray 2015). This food caching helps in lowering the quantity of secondary metabolites during 409 winter consumption (Dearing 1997). However, Royle's pikas do not collect or store plants as 410 haypiles, but instead feed on dry leaves of shrub and tree species which have low plant 411 secondary metabolites only during the resource-limited post-monsoon season. Himalaya 412 experiences a relatively short snow covered period compared to other mountain regions, 413 and food plants (mosses, lichens, dry leaves from trees and shrubs) are available during the 414 post-monsoon and winter, which probably led to the weak hoarding behaviour observed in 415 the Royle's pika. Its pre-monsoon diet is rich in nitrogen, moisture, low in secondary 416 metabolites and probably more suitable for spring litter. Although, one of the caveats in this 417 study was the inconsistent seasonal sampling across sites, which would have allowed us to 418 explore seasonal differences within the sites more effectively.

419 Effect of habitat structure on plant diet richness

In western Himalayan Royle's pika populations, plant diet richness increased with large talus area, whereas depth of crevices between rocks had a negative effect on plant diet richness. Plant richness in pika diet increased with talus area as larger areas have higher plant diversity (area-richness relationship). Large talus areas provide good cover and habitat both in terms of food availability and refuge from predators. Large talus provide pikas with many escape routes from predators, allowing pikas to forage on surrounding meadows and reduce the dependence on the availability of local vegetation. This may explain the higher plant diet

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richness that was observed, as predation risk plays an important role in determining the
food selection in Royle's pika (Bhattacharyya *et al.* 2013).

429 Predation risk has significant impacts on prey populations, either by direct predation-430 mediated mortality, or indirectly by altering their physiology and behaviour (Lima & Dill 431 1990; Sinclair & Arcese 1995; Schmitz et al. 1997; Lima 1998). Large talus areas with high 432 rock cover and vegetation help in forage selection by reducing other constraints such as 433 energy demands (Stephens & Krebs 1986). Pikas balance predation risk associated with 434 foraging activity against nutritional quality and availability of diet plants, a typical strategy 435 found in central place foragers by exploiting nearby talus habitats (Huntly et al. 1986; Smith 436 et al. 1990; Morrison et al. 2004; Bhattacharyya et al. 2013). Large rock talus fields with 437 crevices possibly act as escape cover from predators and allow pikas to access extended 438 foraging grounds and diverse array of food plants, and hence have a positive influence on 439 diet richness. Furthermore, Royle's pikas are sensitive to high temperature, and stable 440 microclimate talus habitat serves as a refuge from harsh climate as well as predators 441 (Bhattacharyya et al. 2014b). Royle's pika utilises crevices in their talus habitat to build their 442 nests (Bhattacharyya et al. 2015). The structure of rock talus and availability of small crevices 443 (< 15 cm) appear to govern occupancy of Royle's pika habitat as it reduces predation risk; 444 wide crevices probably make it easier for predators such as weasels and red foxes to catch 445 pikas (Bhattacharyya et al. 2015). We found deep crevices had a negative effect on plant diet 446 richness. The negative effect of deep crevices probably indicates foraging under fear 447 response. The deep crevices often also have wider openings that increase predation risk 448 from small size predators such as weasels and red foxes (Bhattacharyya et al. 2015). Hence, 449 pikas inhabiting talus with deep crevices probably utilise the foraging ground less extensively

and have a narrow choice of plants. This could be a mechanism behind the avoidance of

451	such taluses as restricted diet can further reduce individual fitness. These findings are in line
452	with previous studies on the Royle's pika and other talus dwelling pikas, which tend to
453	forage close to the talus habitat where predation risk is the least, and venture out to open
454	meadows to forage only when talus patches are well connected (Holmes 1991; Roach et al.
455	2001; Morrison et al. 2004; Bhattacharyya et al. 2013).
456	Ecological and Evolutionary linkages in the Royle's pika diet
457	The majority (97.5%) of diet plants in this study were $C_3$ food plants, followed by $C_4$ (1.25%)
458	and CAM (1.25%) plants. Previous research has shown that expansion of $C_4$ plants with low
459	nutrient quality might have led to the distributional range contraction as well as extinction
460	of herbivorous mammals dependent on $C_3$ plants during the late Miocene (MacFadden &
461	Ceding 1994; Cerling et al. 1998; Ehleringer et al. 2002; Osborne & Beerling 2006; Osborne
462	2008, Ge et al. 2012). The pre-historic distribution of pikas was closely associated with
463	distribution of their preferred $C_3$ food plants, such as those with high protein and moisture
464	content (Ge et al. 2012). Climate change has also been found to alter the distribution and
465	abundance of alpine plants based on their temperature sensitivity (Scherrer & Körner 2011).
466	Replacement of $C_3$ plants by $C_4$ plants across large landscapes during the late Miocene
467	resulted in the extinction of a high number of pika species (Ge et al. 2012). Gottfried et al.
468	(2012) suggested that the thermophylisation process could lead to the replacement of cold
469	and moist environment plant species (e.g. $C_3$ plants) with an abundance of warm and dry
470	environment plant species, (e.g. $C_4$ , CAM plants). Given that the Royle's pika diet consists of
471	$C_3$ plant species (e.g., <i>Potentila</i> , <i>Anaphalis</i> ), the increase in temperature and rainfall patterns

472 are bound to influence the distribution range of plant species as well as pikas. In the past 25

473	years (1982–2006), the Himalayan arc has experienced significant decreases in winter
474	precipitation (17mm), which has resulted in an increase in mean annual (0.04–0.08°C per
475	year), spring (0.02–0.08°C per year) and winter temperatures (0.03–0.04°C per year;
476	Shrestha et al. 2012). This continued increase in temperature could have a significant effect
477	on the distribution dynamics of $C_3$ species and potentially influence plant-herbivore
478	interactions at a microhabitat level.
479	Alpine species adapted to cold climatic conditions are more vulnerable to global warming
480	(Hughes 2000). Moritz et al. (2008) indicated significant changes in distributions and range
481	contraction in mountain-dwelling small mammals. Walther et al. (2002) predicted upslope
482	range shifts in animals to cope with changing (warming) environmental conditions. However,
483	habitat fragmentation might not allow small mammals such as pikas to move their ranges
484	fast enough to track shifts in suitable microclimates (Scholss et al. 2012; Ray et al. 2012).
485	Given that the Royle's pika can cope with physiological stress (e.g., hypoxia) in high elevation
486	environments, the upper limit of the distribution of diet plants (> 4,500 m) could still pose a
487	threat to their survival and fitness. Isolated high altitude mountain habitats, also known as
488	"Sky-islands", differ significantly in environmental conditions from intervening valleys
489	(Shepard & Burbrink 2008). These intervening valleys were found to have significant impacts
490	on the dispersal of cold-adapted mountain dwelling species, such as pikas, across sky-islands
491	(Galbreath et al. 2010). Hence, the Royle's pika would potentially need to travel across the
492	lowland valleys to find favourable habitat to cope with the changing environment. Apart
493	from high sensitivity to warm environments (Bhattacharyya et al. 2014b) and predation risk
494	(Bhattacharyya et al. 2015), absence of diet plants below 1,500 m elevation might hamper

495	such contemporary migration through lowland valleys. Furthermore, loss of distribution
496	range and connectivity between habitat patches along with nutritional stress might also
497	make small pika populations more vulnerable to both climatic changes as well as other
498	threats, such as the susceptibility to infectious diseases (Hanski & Gilpin 1991; Harvell et al.
499	2000; Epstein 2001; Biebach & Keller 2009).
500	India holds 28% of the flora which is endemic to the Himalayan region (Chitale <i>et al.</i> 2014).
501	We found a high dependency of the Royle's pika on endemic plants, and 53–64% of dietary
502	plant genera (e.g. <i>Geum, Fragaria</i> ) are endemic to the Himalayan region. Increases in
503	summer temperature and precipitation and the frequency of freeze-thaw cycles are
504	predicted to have detrimental, multi-dimensional, and spatially variable impact on these
505	endemic alpine plants (Dolezal et al. 2016). Recent research has suggested around 23.9% to
506	41.34% reduction in the distribution of endemic plants in various biodiversity hotspots in
507	Himalaya by 2080 (Chitale et al. 2014). Therefore, changes in the distribution and abundance
508	of Himalayan endemic plants might have significant negative impacts on the overall
509	nutritional ecology of the Royle's pika. Lack of a plant genetic reference library from the
510	Himalayan region, especially from our study site, did not allow us to achieve species level
511	identification of pika diet. Future research is needed to build a plant genetic resource
512	reference library for insights to be gained at the plant species level.

513 Conclusions

514 This is the first study of the Royle's pika diet using DNA metabarcoding which provides an

515 excellent example of genetic barcode use to understand feeding preferences in climate-

516 sensitive herbivore. We were able to quantify the genus richness in the pika's diet in various

517	habitats and at different elevations. We revealed the high dependency of the pika on $C_3$
518	plants and plants endemic to the Himalayan region. We showed that seasonal differences in
519	the diet are associated with elevation and that diet varies at different sites due to
520	differences in topography and climate. A significant amount (> 89%) of the pika's diet
521	consisted of forbs. The genus richness in the diet is strongly predicted by the size of the talus
522	available to the pika for foraging, with large areas resulting in the highest levels of diversity
523	observed in the diet. Crevice depth negatively influences plant diet richness due to increase
524	predation risk. The continued increase in temperature could have a significant effect on the
525	distribution of $C_3$ plants and reduce the amount of plant species available on which the pika
526	can feed, which would be likely to impact both pika numbers and their distribution,
527	especially in lower elevation habitats.
528	
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973	Data Accessibility Statement
974 075	CPS locations of all sample collection points. P code and data for generalized linear modeling
975	GPS locations of all sample collection points, R code and data for generalized linear modeling,
976	DNA sequences generated during the study can be accessed in the Dryad database (
977	doi:10.5061/dryad.nt40m53).
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981	Authors' contribution
982	SB collected the samples and performed the laboratory work; DAD and FI supervised the
983	project; SB, HH and FI analysed the data; SB, DAD, HH and FI wrote the manuscript. All authors
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1000	<b>Table 1:</b> Presence of plant families in the Royle's pika's diet across each sampled site (TUN:
1001	Tungnath; MAD: Madmaheswar; NAN: Bedni- Roopkund; RUD: Rudranath; HAK: Har ki
1002	Doon), with results from G-test (G statistics and p values), to estimate differences in the
1003	mean proportion of plant families within diet. Proportion of plant family is presented for
1004	each site; those highlighted in bold differ across sites at P<0.05. * Plant family not
1005	considered for comparison across sites as they were found only in one study site.
1006	

	Pre-monsoon Post-monsoon		on						
	Total	TUN	MAD	NAN	TUN	RUD	HAK		
Family	genus	(n=27)	(n=13)	(n=32)	(n=26)	(n=4)	(n=8)	G	Р
Apiaceae	5	3.70	0.00	6.25	11.54	25.00	0.00	1.74	0.41
Asteraceae	7	55.50	23.07	15.60	61.50	100.00	12.50	76.41	<0.0001
Balsaminaceae*	1	0.00	7.69	0.00	0.00	0.00	0.00	*	
Berberidaceae*	1	0.00	0.00	6.25	0.00	25.00	0.00	*	
Betulaceae*	1	3.70	0.00	0.00	0.00	0.00	0.00	*	
Boraginaceae*	2	0.00	7.69	0.00	0.00	0.00	0.00	*	
Brassicaceae*	2	0.00	0.00	3.13	0.00	0.00	0.00	*	
Campanulaceae*	1	0.00	7.69	0.00	3.85	0.00	0.00	*	
Caprifoliaceae	2	11.11	0.00	3.13	7.69	25.00	0.00	2.69	0.26
Caryophyllaceae	4	14.81	15.38	15.63	18.52	15.38	0.00	4.54	0.47
Crassulaceae*	2	0.00	7.69	0.00	0.00	0.00	0.00	*	
Cyperaceae	1	11.11	23.08	9.38	14.81	50.00	0.00	6.9	0.22
Ericaceae	4	18.52	7.69	0.00	26.92	25.00	0.00	2.94	0.7
Fagaceae*	1	3.70	0.00	0.00	0.00	0.00	0.00	*	
Gentianaceae*	2	3.70	0.00	0.00	0.00	0.00	0.00	*	
Geraniaceae*	1	3.70	0.00	0.00	3.85	0.00	0.00	*	
Hypericaceae*	1	0.00	0.00	0.00	50.00	0.00	0.00	*	
Lamiaceae*	1	0.00	0.00	0.00	3.85	0.00	0.00	*	
Onagraceae	3	18.52	23.08	6.25	46.15	0.00	0.00	3.14	0.2
Papilionaecae*	2	11.11	0.00	0.00	0.00	0.00	0.00	*	
Poaceae	10	96.26	100.00	25.00	100.00	100.00	25.00	179.23	<0.0001
Polygonaceae	4	0.00	30.77	6.25	3.85	0.00	0.00	2.32	0.31
Primulaceae	2	51.85	98.27	34.38	22.22	7.69	3.13	13.93	<0.001
Ranunculaceae	4	59.26	92.31	9.38	30.77	25.00	12.50	41.89	<0.0001
Rosaceae	6	96.30	92.31	56.25	92.31	100.00	25.00	210.07	<0.0001
Rubiaceae	1	3.70	0.00	6.25	0.00	0.00	0.00	1.4	0.49
Salicaceae*	1	0.00	0.00	0.00	3.85	0.00	0.00	*	
Saxifragaceae	2	7.41	7.69	3.13	11.54	0.00	0.00	1.78	0.41
Scrophulariaceae	2	25.93	30.77	9.38	23.08	50.00	0.00	18.7	<0.002
Orobanchaceae	1	18.52	15.38	3.13	3.85	0.00	0.00	4.2	0.11
Urticaceae*	1	0.00	0.00	3.13	3.85	0.00	0.00	*	
Violaceae*	1	0.00	0.00	3.13	3.00	0.00	0.00	*	
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1012	Table 2: Model-averaged predictive models for effect of each parameter on plant diet
1013	richness with AIC < 2 and relative importance (RI) of each parameter.
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			7				
	Parameter	Estimate (β)±SE	Lower	ower Upper		P value	RI
			(2.5%)	5%) (97.5%)			
	Intercept	1.65±0.04	1.56	1.73	37.87	0.001	
	Talus area cover	0.17±0.04	0.07	0.27	3.50	0.001	1.00
	Depth of crevices	-0.13±0.04	-0.22	-0.03	2.78	0.01	1.00
	Talus area cover*						
	Depth of crevices	-0.009±0.0 3	-0.03	0.16	0.27	0.78	0.29
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044			
045	List of Figures		
046			
047			
048	Figure 1 Faecal pellet sa	mpling sites in Garhwa	al, Uttarakhand, India
049			
050	Code site name	Altitude (above sea	level a.s.l) Long / Lat
051	TUN Chopta-Tungnath	2,600–3,680 m,	30°28' to 31°32' N, 79°13' to 79°14' E
052	RUD Rudranath	2,900–3,500 m,	30°28' to 31°31' N, 78°18' to 79°19' E
053	MAD Madmaheshwar	3,000–3,300 m,	30°37'to 31°38' N, 78°12' to 79°13' E,
054	HAR Har ki Doon	2,700–3,800 m,	31°06' to 31°09' N, 78°19' to 78°26' E,
)55	NAN Bedni-Roopkund	2,700–4,450 m,	30°11' to 30°15' N, 79°31' to 79°44' E.
)56			
057			
058	Figure 2 Plant diet richne	ess across an elevatior	gradient in pre-monsoon (Premon) and post-
)59	monsoon season (Postm	ion) (HAK= Har ki door	; MAD= Madmaheshwar; TUN=Tungnath;
060	RUD=Rudranath; NAN=B	edni-roopkund; full de	etails of the study sites are provided in Figure
)61	1)		, , , , , ,
)62			
)63			
064	Figure 3 Evolutionary or	igin of plants per pelle	t sampled in pre-monsoon (A) and post-
065	monsoon (B) diet of Roy	les's pika in the wester	rn Himalaya (CA: Centrasiatic; EH: Himalayan
066	Endemic; HO: Holarctic;	MA: South East Asiation	Malaysian; SJ: Sino Japanese or Eastern
)67	Asiatic; TR: Tropical; YU:	South East Chinese; d	etails of the study sites are provided in Figure
)68	1)		
)69			
)70			
)71	Figure 4 Upper distribut	ion limit of plants dete	ected per sample in pre-monsoon (A) and post-
72	monsoon (B) diet of Roy	les's pika across elevat	tion (Low=2,500–3,500 m; Medium=3,500–
73	4,500 m; High=4,500–6,0	000 m; details of the st	tudy sites are provided in Figure 1)
74			
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)76	Figure 5 Lower distributi	on limit of plants dete	cted in pre-monsoon (A) and post-monsoon
)77	(B) diet of Royle's pika a	cross elevation (Low=5	500–1,000 m; Medium=1,000–2,000 m; High
78	=> 2,000 m; details of th	e study sites are provi	ded in Figure 1)
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1089	Figure 1 Faecal pellet sampling sites in Garhwal region of Uttarakhand, India							
1090								
1091	<u>Code</u>	site name	Altitude (above sea leve	el a.s.l)	Long / Lat			
1092	TUN	Chopta-Tungnath	2,600–3,680 m,	30°28′	to 31°32′ N, 79°13′	to 79°14' E		
1093	RUD	Rudranath	2,900–3,500 m,	30°28′ t	to 31°31′ N, 78°18′	to 79°19′ E		
1094	MAD	Madmaheshwar	3,000–3,300 m,	30°37′t	o 31°38′ N, 78°12′	to 79°13' E,		
1095	HAR	Har ki Doon	2,700–3,800 m,	31°06′	to 31°09' N, 78°19'	to 78°26' E,		
1096	NAN	Bedni-Roopkund	2,700–4,450 m,	30°11′	to 30°15′ N, 79°31′	' to 79°44' E.		
1097								









1137 Figure 3 Evolutionary origin of plants per pellet sampled in pre-monsoon (A) and post-

1138 monsoon (B) diet of Royles's pika in the western Himalaya (CA: Centrasiatic; EH: Himalayan

- 1139 Endemic; HO: Holarctic; MA: South East Asiatic Malaysian; SJ: Sino Japanese or Eastern Asiatic;
- 1140 TR: Tropical; YU: South East Chinese; details of the study sites are provided in Figure 1)





**Figure 4** Upper distribution limit of plants detected per sample in pre-monsoon (A) and post monsoon (B) diet of Royles's pika across elevation (Low=2,500–3,500 m; Medium= 3,500–

- 1150 4,500 m; High =4,500–6,000 m; details of the study sites are provided in Figure 1)





1161 Figure 5 Lower distribution limit of plants detected in pre-monsoon (A) and post monsoon (B)

1162 diet of Royle's pika across elevation (Low= 500–1000 m; Medium=1,000–2,000 m; High =>

1163 2,000 m; details of the study sites are provided in Figure 1)



