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Recovery and nonrecovery of freshwater food webs effects of

5 acidification

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SUMMARY

33 Many previous attempts to understand how ecological networks respond to 34 and recover from environmental stressors have been hindered by poorly resolved 35 and unreplicated food web data. Few studies have assessed how the topological 36 structure of large, replicated collections of food webs recovers from perturbations. 37 We analysed food web data taken from 23 UK freshwaters, sampled repeatedly over 38 24 years, yielding a collection of 442 stream and lake food webs. Our main goal was 39 to determine the effect of acidity on food web structure and to analyse the way food 40 web structure recovered from the effects of acidity over time.

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41 Long-term monotonic reversals of acidification were evident at many of the sites, but

42 the ecological responses were generally far less evident than chemical changes, or

43 absent. Across the acidity gradient, food web linkage density and network efficiency

44 declined with increasing acidity, while node redundancy (i.e. trophic similarity

45 among species within a web) decreased. Within individual sites, connectance,

46 linkage density, trophic height, resource vulnerability and network efficiency tended

to increase over time as sites recovered from acidification, while consumer generalityand node redundancy tended to decrease. There was evidence for a lag in biological

and node redundancy tended to decrease. There was evidence for a lag in biological
recovery, as those sites showing a recovery in both their biology and their chemistry

50 were a nested subset of those which only showed a chemistry trend.

51 These findings support the notion that food web structure is fundamentally 52 altered by acidity, and that inertia within the food web may be hindering biological 53 recovery. This suggestion of lagged recovery highlights the importance of long-term 54 monitoring when assessing the impacts of anthropogenic stressors on the natural 55 world. This temporal dimension, and recognition that species interactions can shape 56 community dynamics, is missing from most national biomonitoring schemes, which 57 often rely on space-for-time proxies. I. INTRODUCTION
Natural ecosystems are increasingly exposed to anthropogenic stressors, such
as habitat modification, pollution and global climate change (Steffen *et al.* 2011;
Smith & Zeder 2013; Sutherland *et al.* 2016). A deeper understanding of how they
respond to and recover from such perturbations is important if we are to manage
our natural resources effectively in the coming decades (Pimm *et al.* 1995; Woodward *et al.* 2010a).

65 Biological recovery from the effects of stressors does not necessarily follow 66 from the removal of that stressor, as there may be time lags or ecological hysteresis, 67 even to the extent that alternative equilibria are possible for otherwise identical 68 environmental conditions (O'Neill 1998; Scheffer & Carpenter 2003; Feld et al. 2011; Battarbee et al. 2014; Murphy et al. 2014). These may arise via species interactions, 69 70 which can alter the rate and/or trajectory of recovery (Scheffer & Carpenter 2003) 71 and confound attempts to scale up predictions made from individuals or species 72 populations to the whole-community or ecosystem, because of the increasing scope 73 for "ecological surprises" to be manifested via complex indirect pathways in the 74 food web (Ings et al. 2009; Thompson et al. 2012). For instance, artificially high 75 nutrient concentrations can trigger regime shifts in shallow lakes, which may persist 76 even long after nutrient loads have been reduced (Scheffer & Carpenter 2003).

77

A.Food web recovery research

78 Due to the difficulties in constructing highly-resolved food webs, however, 79 very few studies have examined how trophic network structure responds to, and 80 recovers from, perturbations, and fewer still have a replicated design. Field 81 experiments have revealed how replicated freshwater food webs respond to 82 drought, through the loss of rare and rare-for-size consumers, as well as the larger 83 taxa high in the food web (e.g. eight stream food webs; Ledger et al. 2012; Woodward 84 et al. 2012). Other studies have economised on effort and increased their sample 85 sizes, and hence ability to detect responses statistically, by making assumptions about the diet of consumers. Thus, O'Gorman and Emmerson (2010) used 144 86 87 marine food webs in a mesocosm study across a range of experimental treatments to 88 investigate how their structure responded to the removal of keystone species. Very 89 few examples exist where the recovery of replicated, natural food webs following a 90 perturbation has been studied, although McLaughlin, Emmerson and O'Gorman 91 (2013) constructed a collection of 96 terrestrial food webs which tracked the recovery 92 of sixteen riparian food webs after a flood over the course of a year. Often, a space-93 for-time substitution approach is used: for instance, Layer et al (2010b) studied the

structure of 20 freshwater food webs sampled once from 20 sites distributed across a
wide pH gradient, and this was subsequently set in the context of long-term change
in the single model system of Broadstone Stream over four decades of rising pH
(Layer *et al.* 2011). However, no studies of which we are aware have analysed the

- 98 long-term recovery from perturbation of replicated food webs distributed across
- 99 wide ecological gradients.
- 100 B. Freshwater acidification

Freshwater acidification is usually caused by atmospheric pollution (though 101 102 there are naturally rather acidic systems), in which strong mineral acids emitted 103 from industrial sources are deposited on the landscape (e.g. Driscoll et al. 2001). 104 Where soils and geology have an insufficient supply of base cations to buffer acidity, 105 runoff to streams and lakes become strongly acidic. At a pH of 5.5, alkalinity falls to 106 zero and inorganic aluminium concentration rises to become toxic to many forms of 107 life, including almost all fish (Sutcliffe & Hildrew 1989). Such anthropogenic 108 acidification has profound ecological impacts, including the loss of many acid-109 sensitive species from all trophic levels (e.g. Dillon et al. 1984; Schindler 1988). 110 Evidence for the causes and consequences of acidification and its effect on species 111 assemblages is long-standing and overwhelming (e.g. Likens & Bormann 1974; 112 Schindler 1988; Hildrew & Ormerod 1995) and comes primarily from north-western 113 Europe and much of north and eastern USA and Canada. This ranges from 114 palaeolimnological reconstructions of lake pH (e.g. Battarbee et al. 1988), widespread 115 surveys and descriptions (e.g. Townsend, Hildrew & Francis 1983; Henriksen et al. 1990), experimental acidification of whole systems (e.g. Hall et al. 1980; Webster et al. 116 117 1992; Findlay et al. 1999), and biogeochemical modelling (e.g. Jenkins et al. 1990). In 118 the UK, intensive research on the long-term and large-scale ecological consequences 119 of acidification on running waters was concentrated in three main study systems: 120 Llyn Brianne in south-west Wales (Durance & Ormerod 2007), the Ashdown Forest 121 of south-eastern England (Hildrew 2009), and via the nationally covering UK Acid 122 Waters Monitoring Network (UKAWMN), which interdigitated to a limited extent 123 by sharing three sites with the other two (Layer et la 2010).

In the face of such evidence, reductions of polluting emissions were agreed upon in both Europe and North America, which have resulted in dramatically reduced depositions since the 1970s (Stoddard *et al.* 1999; RoTAP 2012). In 1988, the UK Government set up UKAWMN (incorporated within the latterly expanded Upland Waters Monitoring Network – or UWMN, in 2014) to assess the effectiveness of these measures, which came at considerable economic and social costs. The 130 Network was designed explicitly to detect any recovery in the quality of surface 131 waters at its 23 stream and lake sites, as well as any shifts in their biology and 132 ecology that might be expected to accompany chemical recovery. The network's sites 133 are distributed across acid sensitive (base poor) regions of the UK (Figure 1), mainly 134 in the uplands areas of the north and west where precipitation and wet deposition of 135 acidity tend to be high, although some are in small, acid sensitive areas in the south 136 and east. A few sites are located in the extreme north and west of Scotland and 137 Northern Ireland which were thought sufficiently remote from industrial pollutant 138 sources to have been significantly affected by acid deposition (Patrick et al. 1991).

139 Substantial (though not complete) chemical recovery from acidification has 140 now occurred at most sites that had been acidified at the outset (Monteith et al. 2014). 141 This has included large reductions in inorganic aluminium concentrations in the 142 most acidified waters and more widespread but gradual increases in water pH, 143 while Acid Neutralising Capacity (ANC) has increased in proportion to the rate of 144 reduction in acid anions. Ubiquitous increases in dissolved organic carbon 145 concentration also appear to be part of the biogeochemical response, leading to a partial replacement of mineral acidity by organic acidity that has tempered the pH 146 response (Evans et al. 2008). Evidence for biological recovery, in terms of the 147 148 establishment of acid-sensitive assemblages of species, has been much less obvious 149 (Battarbee et al. 2014), but most evident in the diatoms of the epilithon and from the 150 colonisation of recovering sites by some species of macrophytes. In the last UWMN 151 data interpretation report (Kernan et al. 2010), invertebrate assemblages showed 152 signs of partial recovery at around half of the chemically recovering sites. Only two 153 of those sites, both of which were particularly severely acidified at the onset of 154 monitoring, showed any evidence of recovery of salmonid populations, another 155 indicator of decreasing acidity (Murphy et al. 2014; Malcolm et al. 2014). Similar, 156 "sluggish" biological recovery has also been reported in other acidified systems 157 elsewhere globally (e.g. Nedbalová et al. 2006; Keller et al. 2007).

158 Several hypotheses have been put forward to explain these delays in the 159 anticipated simple reversal of acidification, including dispersal limitations, pollutant 160 legacies and attendant recurring acid episodes (e.g. Kowalik et al. 2007), interactions 161 with other stressors (e.g. climate change; Johnson & Angeler 2010), and indirect 162 food-web effects (Yan et al. 2003; Ledger & Hildrew, 2005; Monteith et al. 2005). 163 These mechanisms are not necessarily mutually exclusive explanations and there are differing levels of support for each. For instance, the role of dispersal is still 164 165 uncertain for differing biological components, with evidence for and against its role:

166 Gray & Arnott (2011) suggested it may constrain the recovery of lake zooplankton in 167 Canadian lakes, contrary to previous findings (Keller et al. 2002; Yan et al. 2004). 168 Evidence for more mobile taxa, such as benthic insects with flying adults, however, 169 suggests that dispersal is usually sufficient to allow rapid recolonisation and thus 170 unlikely to explain delayed biological recovery (Masters et al. 2007; Hildrew 2009). 171 The type of waterbody also affects both its rate of chemical recovery and its 172 recolonisation potential: lakes are larger and thus better able to absorb spikes of run-173 off that can create acid episodes than streams (Evans, Monteith & Harriman 2001) 174 and yet they show similarly limited biological recovery and so acidic episodes alone 175 cannot explain the lag in biological recovery. In addition, these hypotheses may 176 operate additively or even synergistically.

177 To date, no evidence has been found for differing rates of recovery between 178 streams and lakes. Given the evidence that persistent acidic episodes in stream 179 systems can limit biological recovery (Lepori & Ormerod 2005; Kowalik et al. 2007) 180 one might expect stream systems to recover more slowly than lakes, although 181 Monteith et al., 2014 found that the magnitude of acid pulses at UWMN sites had declined at a similar rate to mean acidity. Conversely, the dynamic nature of 182 183 streams, with a natural regime of frequent flow disturbances, and downstream 184 connectivity to pools of less acid-sensitive species in the lower reaches might render 185 them naturally more resilient (e.g. Hildrew & Giller 1994). Thus, we had no clear a priori hypothesis or expectations of the relative rates of recovery in the communities 186 187 of lakes and streams.

188

C. The recovery of acidified food webs

189 The possibility that species interactions within the food web might inhibit 190 ecological recovery requires further testing (Webster et al. 1992; Frost, Montz & Kratz 191 1998). Circumstantial evidence from streams suggests that generalist, non-predatory 192 invertebrates (e.g., stoneflies of the families Leuctridae and Nemouridae), that are 193 acid-tolerant and often dominate the benthos of acid streams, may fill the feeding 194 niche of specialist, acid-sensitive grazers and inhibit their return (Ledger & Hildrew 195 2005; Layer, Hildrew & Woodward 2013). Further, dynamic modelling found that 196 the reticulate acidified food webs are more robust, suggesting that they might be 197 more inherently stable and thus less prone to (re)invasion (Laver et al. 2010b). 198 Finally, the common reliance on space-for-time proxies may miss the transient 199 dynamics and the possible existence of alternate stable states of a system responding 200 to stress. For instance, if the strong effects of pH on food web properties reported in 201 the space-for-time survey of 20 sites by Layer et al. (2010b) are not evident in systems

202 undergoing actual changes in pH over time, then the expected mapping of the biota 203 onto the environmental template might not be evident, and its absence would 204 indeed indicate ecological inertia. This has wider implications for biomonitoring 205 science in general, which is underpinned by space-for-time approaches and rarely 206 has access to truly long-term (i.e. multidecadal) high quality biological time series 207 (Friberg et al. 2011). Mismatches between temporal and space-for-time data may provide evidence for time lags or hystereses resulting from the system's own 208 209 internal dynamics, although the potential importance of biogeographic constraints 210 should also not be discounted. On the other hand, if the two data types match 211 perfectly then indirect food web effects - which would otherwise reshape the simple 212 biota-environment relationship - can effectively be discounted.

213 Repeated assessment of the topology of a large collection of food webs, as 214 they recover from the effects of acidification, is needed to complement previous 215 work, which dealt with single, 'model' systems (e.g. Layer et al. 2010a, 2011), or 216 relied on space-for-time substitutions. At present examples of the former case are 217 lacking, but in the latter, Layer et al.'s (2010b) suggested the smaller but more interconnected acidified webs had more stable configurations of trophic linkages 218 219 across a pH gradient of <5 to >8. Linkage density and connectance are both common 220 measures of web complexity, and an abundance of "redundant" interactions can 221 help stabilise the network's structure in the face of perturbations, by preventing the 222 secondary extinctions that arise when consumers are left without resources (Dunne, 223 Williams & Martinez 2002; Thébault & Fontaine 2010). Indeed, linkage density 224 increased with stream pH across the spatial gradient of the 20 sites, which included 225 10 of the UWMN streams used in the current study.

226 Mean food chain length (the number of steps between a basal resource and a 227 particular consumer, see Text Box) gives a measure of the trophic height of the web 228 as a whole (Williams & Martinez 2004), which tends to shorten as environmental 229 stress increases and productivity declines (Woodward et al. 2005). Food chains are 230 generally assumed to be shorter than six links, and omnivory, which is 231 commonplace in aquatic systems, tends to truncate them further (Pimm 1980; 232 Hildrew, Townsend & Hasham 1985; Lawton 1989; Yodzis 1989; Williams & 233 Martinez 2000). Although long-term data are still scarce, there is some evidence that 234 suggests that increasing pH leads to higher productivity and an overall lengthening 235 of food chains (Gerson, Driscoll & Roy; Grahn, Hultberg & Landner 1974; 236 Woodward et al. 2005; Hildrew 2009). For instance, progressively larger and more 237 acid-tolerant predators have (re)invaded Broadstone Stream as pH has risen since

the 1970s, culminating in the recent return of the apex predator, the brown trout(*Salmo trutta*) (Layer *et al.* 2011).

In addition to simple food chain metrics, the range of both resources and 240 consumers each species is connected to in the web has important implications for the 241 242 overall network's dynamical and structural stability, and its ability to respond to or 243 resist environmental change. *Generality* (see Text Box) is a substructural measure of 244 the dietary breadth of a consumer, derived statistically from its number of resources. 245 If a consumer is a specialist (i.e. narrow diet), then it might be more vulnerable to 246 extinction as the loss of only a few species will leave it with insufficient resources. 247 *Vulnerability* (see Text Box) is the converse measure of *Generality*; it is derived from 248 the number of consumers feeding on a particular resource species, and indicates how important that resource is in terms of the consumers it supports. Freshwater 249 250 predators are commonly gape-limited generalists, so the size and diversity of prev 251 increases with consumer size (Woodward & Hildrew 2002; Woodward et al. 2010b). 252 Similarly, the herbivorous consumers in acidified streams are also generalists, 253 feeding on a wide range of detritus and algae (e.g. Ledger & Hildrew 2005; Layer, 254 Hildrew & Woodward 2013). As acidity decreased and acid sensitive, but more 255 specialist, species re-invade, the average generality of consumers (i.e., normalised to 256 the size of the food web) should decrease. The average vulnerability of resources 257 (again normalised to the size of the food web) should increase with decreasing 258 acidity as the consumer guild becomes more speciose (Layer et al. 2010b). However, 259 Layer et al. (2010b), found that normalised consumer generality and resource 260 vulnerability did not change systematically, and there was no relationship between 261 either the variation (standard deviation) in consumer generality or resource 262 vulnerability and pH, although the sample size was rather small.

Under acidified conditions, generalist primary consumers can partially 263 264 occupy the niche left by the loss of specialist herbivorous species, potentially 265 creating 'ecological inertia' within the food web by slowing the return of the latter as 266 pH rises (Ledger & Hildrew 2005). The effect of acidity on this redundancy of 267 feeding pathways within the whole food web has not been investigated previously 268 using network-based approaches. As acidified systems tend to be species poor, and 269 dominated by generalist consumer species and few specialists (e.g. Hämäläinen & 270 Huttunen 1996; Ledger & Hildrew 2005), there should be greater trophic redundancy 271 (i.e. species of acid streams should have more similar diets and share more predators 272 than more speciose webs of relative specialists), which could make them resistant to

perturbations and hence more robust to the loss of food resources than those at
higher pH (Naeem 1998; Solé *et al.* 2003; Peralta *et al.* 2014).

As with other features of the whole network (such as connectance) or parts of 275 276 the network (e.g. generality) the so-called 'small-world' properties of food webs 277 have also been linked to stability (Watts & Strogatz 1998; Montoya & Solé 2002) and 278 to the rate at which perturbations propagate (Montoya, Pimm & Solé 2006). 279 Essentially, if species are highly connected to the rest of the food web in a 'small-280 world' network, then perturbations may spread (and dissipate) rapidly, but if there 281 are less well connected (more degrees of separation) this may lead to longer-lived 282 oscillatory dynamics and feedbacks that require a long time to reach equilibrium. 283 Thus, it is not simply the linkage density or strength of connections that are important for determining stability or food-web inertia, but their particular 284 285 configuration. Even large food webs from circumneutral or higher pH systems can 286 exhibit these properties, with most species being only 1-2 degrees of separation from 287 the rest of the web (Thompson et al. 2015). Network efficiency (see Text Box) is a 288 measure of how well connected a network is, as well as the distribution of those 289 connections across a network (Latora & Marchiori 2001), and can enable inferences 290 to be made about the small-world properties of food webs. Although rarely applied 291 to date in food web studies, this metric derived from the wider field of network 292 science could provide new insights into how these small-world aspects of food web 293 topology itself might shape the trajectory of biological recovery (Monteith et al. 2005; 294 Layer et al. 2010b). The lengthening of food chains associated with the re-invasion of 295 consumers might be expected to increase the overall efficiency of the network, as the 296 wider breadth of diet of new, large, top predators effectively reduces the distance (in 297 terms of number of links) between resources.

298

D. The Upland Waters Monitoring Network

299 The data analysed here (from the UWMN) consist of repeated observations on 300 the same 23 sites (Figure 1) over 24 years (1988 – 2012). Spatially, the sites 301 encompass a wide range of pH (from 3.71 to 7.49), and include some that were 302 strongly acidified at the onset of monitoring (e.g. Old Lodge) and others that were 303 circumneutral and have changed little (e.g. Allt na Coire nan Con). The gradual 304 long-term chemical recovery of many of these sites, particularly among those 305 formerly the most acidic, provides a unique and large-scale picture of the chemical 306 drivers and biological responses in the network over both space and time. 307 Characterizing the 'baseline' variation in food web structure in the near absence of 308 changes in environmental stress is crucial for our understanding of how a

- community recovers from that stressor and, more broadly, for gauging its potential
 responses to future environmental changes. The food webs compiled from these data
 provide the replication and statistical power that has previously been insufficient for
 rigorous analysis food web responses to acidification and chemical recovery.
- 313



Figure 1. The Upland Waters Monitoring sites, consisting of 11 lakes (dark blue squares) and 12
streams (light blue circles).

- We aimed to describe changes in food web structure as water chemistry recovered over three decades of chemical and biological monitoring. Our emphasis was on structural changes in binary networks of the presence/absence of nodes and
- 321 links, rather than the effects of acidity on the dynamical stability of species

populations *per se*. To determine the effect of environmental variables on food web
structure, we tested the following hypotheses, using data gathered across all sites
and years:

- When analysed across the entire acidity gradient, food web structure will be directly affected by acidity. Food webs of less-acidified systems should exhibit higher linkage density, food chain length and network efficiency but lower connectance consumer generality and redundancy (Table 1).
- 3293292. There will be directional and predictable changes in food web structure at330ach site through time as acidity decreases (Table 1).
- 331 3. If indirect food-web effects arising from biotic interaction are unimportant,
 332 changes in network structure through time will match recovery from
 333 acidification; i.e. those sites which experience change in their chemistry will
- also change at a comparable pace in their food web attributes. (Figure 2).

Additionally, in order to investigate if the rates of recovery were different between
stream and lake sites, the two ecosystem types were analysed both together and
separately.

- 338
- 339
- 340



342 *Figure 2. A conceptual figure of the possible outcomes for biological (thick, blue line) and chemical*

- 343 (thin, red line) recovery at the UWMN sites over time.
- *Table 1. Summary of predicted relationships between acidity and food web structure.*

Food web metric	Predicted relationship with decreasing acidity
Connectance	\checkmark
Linkage density	\wedge
Mean trophic height	\wedge
Maximum trophic height	\wedge
Resource vulnerability	\wedge
Consumer generality	\checkmark
Standard deviation in vulnerability	no change
Standard deviation in generality	no change
Network efficiency	\wedge
Redundancy	\checkmark

II. METHODS

347 A.Sites

346

348 The UWMN consists of 11 streams and 12 lakes from across the UK (Figure 1): 349 full site descriptions and sampling methodologies are provided in Patrick, Monteith 350 & Jenkins (1995) and Kernan et al. (2010). Water chemistry, epilithic diatom, 351 macroinvertebrate and fish sampling began in spring 1988 and has continued 352 annually at most sites up to 2012, except for a few exceptions when access was 353 occasionally restricted (see Kernan et al. 2010). The sites are distributed along a 354 latitudinal gradient across the UK, which can be interpreted as a proxy for the 355 degree of acid deposition at the outset: sites at high latitude were exposed to 356 relatively little acid deposition, whilst those sites at lower latitudes were generally 357 more acidified (Patrick et al. 1991). One lake site, Loch Coire nan Arr, was affected by 358 damming that increased the water level, so it was replaced in 2001 by the nearby 359 Loch Coire Fionnaraich, which has comparable characteristics (Figure 1).

360 B. Chemistry

361 Water samples for chemical analysis were taken in acid-rinsed bottles monthly 362 from streams and quarterly from lakes. A large number of chemical determinands 363 were recorded at each site: for more details see Kernan et al. (2010) and Monteith et 364 al. (2014). In total 13 variables that are considered key drivers or indicators of 365 acidification (Monteith et al. 2014) were used here: pH, alkalinity, H⁺, conductivity, nitrate (NO₃), non-labile aluminium, soluble aluminium, labile aluminium, 366 367 Dissolved Organic Carbon (DOC), sodium (Na+), sulphate (SO4²⁻), calcium (Ca²⁺) 368 and chloride (Cl-). With the exception of pH, we used the annual arithmetic mean of all chemical data as summary statistics for each site. Annual average pH was 369 370 calculated by first converting pH to H⁺ concentration, calculating the annual 371 arithmetic mean, and then converting back to pH.

372 C. Biota

373 Benthic diatoms, macroinvertebrates and fish were sampled annually from 374 1988-2012. Benthic diatoms were sampled according to standard UWMN protocols 375 (Patrick et al. 1991), by selecting five cobble-sized stones from the streambed, or from 376 the permanently submerged littoral zone in lakes. Three samples were taken from 377 each site, in streams at the top, middle and bottom of fixed 50m reaches, and in the 378 lakes from three discrete locations on the shoreline (away from inflow or outflow 379 streams). The biofilm on the surface of the stone was scrubbed into a funnel, washed 380 into a plastic vial with stream or lake water, and immediately preserved in Lugol's 381 iodine solution. In the laboratory, samples were prepared by digestion in hydrogen

peroxide (H₂O₂) and diluted with distilled water. To enable subsequent examination
by light microscopy at 1000x magnification, a sub-sample was pipetted onto a
coverslip, dried and mounted onto a slide using Naphrax (Battarbee *et al.* 2001).
Three hundred diatom valves from each sample were identified to species to give
the diatom species assemblage per site per year.

387 Macroinvertebrates were sampled according to standard UWMN protocols 388 (Patrick et al. 1991), by taking five separate one-minute kick samples with a standard 389 hand net (330µm mesh) from riffle sections of streams and from the dominant littoral 390 habitat of lakes. Macroinvertebrates were subsequently sorted and preserved with 391 70% Industrial Methylated Spirit. Oligochaeta, Diptera and Bivalvia were identified 392 to class, family and genus, respectively, while all others were identified to species. All taxa were counted and the counts from the five samples summed to represent the 393 394 macroinvertebrate assemblage per site per year.

395 Annual electrofishing surveys were conducted according to standard UWMN 396 protocols (Patrick et al. 1991). Surveys were undertaken between mid-September and 397 mid-October at each stream site or, for lakes, in the outflow stream immediately 398 downstream. It was assumed that composition of the fish assemblage in lake 399 outflows could serve as a proxy for that of fish in the lake itself. Three 50m reaches, 400 distributed across 500m of the stream or lake outflow, were isolated using stop nets 401 and electrofished. Depletion electrofishing was employed and all salmonids were 402 counted, while the presence of any other fishes was also recorded.

403

D.Food web construction

Species lists were compiled for each site in each year for which there was 404 405 complete biological and chemical data, yielding 442 food webs. Binary food webs 406 were constructed using the WebBuilder function in R (Gray et al. 2015) and the 407 database of freshwater aquatic trophic interactions contained therein, based on the 408 presence/absence of species (nodes) at each site in each year and the occurrence of a 409 trophic linkage in the feeding link database. This method is based on the assumption 410 that all feeding links between specific pairs of species that have been reported 411 previously would be realized, wherever and whenever both species co-exist at a 412 study site (Hall & Raffaelli 1991; Martinez 1991; Layer et al. 2010b; Pocock, Evans & 413 Memmott 2012), although many of the feeding links within that database were, in 414 fact, derived from direct observation from previous UWMN surveys (Ledger & 415 Hildrew 2005; Layer et al. 2010b; a, 2011). When species-specific trophic interactions 416 had not previously been described for some rare or understudied taxa (nodes), 417 feeding links were assigned on the basis of taxonomic similarity; for instance, by

- 418 assuming that different species within the same genus consumed and were
- 419 consumed by the same species. This method is often used when constructing
- 420 freshwater food webs as in these systems consumer diets tend to be highly
- 421 generalist, and determined primarily by the size of their prey (e.g. Layer *et al.* 2010b;
- 422 a; Layer, Hildrew & Woodward 2013). Food webs built in this manner are
- 423 structurally comparable to those built solely through analysis of consumers gut
- 424 contents; for instance, the method has predicted the links of four well documented
- 425 freshwater food webs with 40-60% accuracy (on a scale from -100% to 100%, Gray *et*426 *al.* 2015).
- 427 E. Network metrics

428 Several commonly used metrics were calculated for each food web, including: connectance ($C = L/S^2$; where L= the number of trophic links, S = the number of 429 430 species) and linkage density (LD = L/S), mean trophic height (after Levine 1980: 431 defined as 1 plus the mean trophic level of a consumer's resources, averaged across 432 all consumers) and maximum trophic height (defined in the same way, except that 433 the maximum value across all consumers was taken). Mean generality (G; number of 434 resources per consumer, see Text Box) and vulnerability (V; number of consumers 435 per resource, see Text Box) was calculated, as was normalised *G* and *V* for each taxon 436 *k*, as:

$$G_k = \frac{1}{L/S} \sum_{i=1}^S a_{ik} \tag{1}$$

$$V_{k} = \frac{1}{L/S} \sum_{j=1}^{S} a_{jk}$$
(2)

437

Where *S* is the number of nodes and *L* the number of links in a food web. $a_{ik} = 1$ if taxon k consumes taxon i (otherwise $a_{ik} = 0$), and $a_{jk} = 1$ if taxon k is being consumed by taxon j (otherwise $a_{jk} = 0$). Mean G_k and V_k in any given food web equal 1, making their standard deviations, which give an indication of the variability in *G* and *V* respectively across a network, comparable across networks of different size. These metrics were all calculated using the R package cheddar (Hudson *et al.* 2013).

445 Network efficiency (Latora & Marchiori 2001, see Text Box) describes the
446 'reachability' of each node by any other node, and is a measure of overall
447 connectivity, and was calculated using the sna R package (Butts 2013) as:

$$E = \frac{1}{S(S-1)} \sum_{i \neq j \in G} \frac{1}{d_{ij}}$$
(3)

449 Where d_{ij} is the shortest path length between node *i* and *j*.

The proportional node redundancy (see Text Box) of each network was
calculated by grouping nodes into trophic species (i.e. nodes with common resources
and consumers) and then calculated as:

$$Redundancy = 1 - \frac{T}{S}$$
(4)

453

454 Where *T* is the number of trophic species within the network. Redundancy was

455 calculated using functions from the cheddar package (Hudson *et al.* 2013) in R.

456

457 F. Statistical analyses

458 All statistical analyses were done in R version 3.1.1 (R Core Team 2013), 459 PRIMER-E with PERMANOVA + (2006). To simplify the chemical data, Principal 460 Component Analysis (PCA) was performed on all 13 water chemistry variables 461 across all sites and years, using a resemblance matrix constructed from Euclidean 462 distances. As some of the variables were measured on different scales (i.e. NO₃ vs 463 pH), and to reduce the influence of extremely large or small values, each variable 464 were centred to zero and scaled by their standard deviations (van den Berg et al. 465 2006). Sample scores on the first PC axis (PC1) were extracted for use as a proxy for a 466 general gradient in overall acidity in further analysis.

467 *Effects of acidity on food web structure*

For data-visualisation purposes only, as we were unable to fully account for 468 both temporal and spatial pseudoreplication of our data simultaneously using 469 470 multivariate analysis, principal coordinates analysis was used on all data across all 471 sites and time points. The resemblance matrix of food web metrics was constructed 472 from square root transformed variables, using Bray-Curtis distances. More rigorous 473 statistical inferences were drawn from univariate approaches, in which 474 pseudoreplication was addressed within the variance structure of the relevant 475 model(s), as explained below.

476 To assess the effect of acidity on food web structure (our first hypothesis), 477 each network metric was regressed against the derived acidity gradient (PC1), and 478 any trend assessed with Generalised Linear Mixed Effects models. Alongside acidity 479 (PC1), site type (lake or stream) was fitted as a fixed effect, and any potential 480 interactions with acidity (PC1) were assessed on the basis of stepwise model simplification and model AIC (Crawley 2013). For each model, site was fitted as 481 482 having a random effect on the intercept of the model, and year was fitted to have a 483 random effect on the slope and intercept of the model.

484 Directional change in food web structure

Mann-Kendall trend tests were used to determine if there were significant monotonic trends in the acidity and food web structure over time at each site (our second hypothesis). The acidity gradient (PC1) extracted from the PCA above, and all the network metrics described above, were calculated for each site in each year. These variables were then assessed for monotonic trends over time at each site.

490 Food web recovery from acidification

To test our third hypothesis we used χ^2 contingency tests to assess the extent 491 492 to which sites that exhibited clear decreases in acidity also showed evidence of 493 directional change in their food web structure (as in Murphy et al. 2014). For acidity (PC1), and for each network metric, we counted the number of sites (out of 23) that 494 495 exhibited (a) a biological and a chemical trend, (b) a biological but not a chemical 496 trend, (c) a chemical but not a biological trend (i.e., evidence for ecological inertia), 497 and (d) neither a biological nor a chemical trend (Figure 2). The χ^2 test assessed 498 whether the distribution of sites across these four categories was due to chance.

499

III. RESULTS

500 The PCA of the chemical variables revealed that the first axis was strongly 501 correlated with pH, H⁺ ions and SO₄. It was therefore was used a proxy for the 502 acidity-related stress to which each food web was exposed (Figure 3), as it 503 encompassed the variation in these pH related chemistry variables. From here on 504 PC1 is called 'acidity' and refers not only to pH, but to the chemical stress associated 505 with low pH.

	0.15		Variable	Correlation
				with PC1
	9		рН	0.311
	0	the state of the s	Alk	0.147
		Ань Са	HION	-0.336
	0.05	nin Dgr	Cond	-0.337
		pH Na Cl	NO3	-0.225
PC	PC2	S04	Nl_Al	-0.278
	0.0	NLAI	Sol_Al	-0.317
		NO3 HION	DOC	-0.141
	0.05	. Salar and a start of Salar	L_Al	-0.281
	Ŧ		Na	-0.309
	0	i di Barra d	Ca	-0.198
-0.10	-0.10		Cl	-0.299
			SO4	-0.321
		-0.10 -0.05 0.00 0.05 0.10 0.15		
		PC1		

507 Figure 3. PCA ordination of chemical variables. The correlation between each variable and acidity

508 (PC1) is given in the accompanying table. The first axis, PC1, is strongly related to pH, SO₄ and 509 aluminium such that PC1 can be interpreted as an 'acidity gradient'.

510 A. Effects of acidity on food web structure

511 When the food web data were analysed at the regional (UK) scale, and modelled

against the acidity gradient extracted from Figure 3, some clear trends in food web

513 structure emerged, although several did not match or even ran counter to our initial

514 hypotheses. Contrary to our expectations (Table 1) connectance, and trophic height

515 were unrelated to the acidity gradient (

- Table 2; more acid sites are to the right in Figure 5). As predicted, linkage density increased with decreasing acidity (517

- 518 Table 2; Figure 5), lake food webs had lower linkage density than stream food webs
- 519 (Figure 5). Normalised consumer generality and normalised vulnerability did not
- 520 change (

- 521 Table 2; Figure 6), nor did their standard deviations, across the acidity gradient. As
- 522 predicted, however, network efficiency was lower in more acidified conditions (

- 523 Table 2; Figure 7), suggesting that more acidified food webs were connected such
- 524 that the average path length between nodes was greater than for circumneutral food
- 525 webs. Node redundancy was highest in more acidified food webs (

- 526 Table 2; Figure 7), suggesting that circumneutral food webs had more unique
- 527 feeding pathways, confirming our prediction. Overall, lake food webs had lower
- 528 network efficiency and higher node redundancy than streams (

529 Table 2; Figure 7). Figure 4 indicates more variation in lake food web structure 530 along PCO1, contrasting with our expectation that stream food webs might be more 531 dynamic and variable than lake food webs.



532

533 Figure 4. Ordination of food webs (points) based on the resemblance matrix created from food web 534 metrics using Bray-Curtis distances, which was analysed with PERMANOVA. Site type is shown as 535 either black points (streams) or grey points (lakes). This plot allows comparison of food web metrics 536 (blue vectors and names) with the predictor variable PC1 extracted from Figure 3, in multivariate 537 space. Longer vectors indicate a stronger correlation. The blue circle indicates the boundary for a 538 correlation of 1. *C* = connectance, *LD* = linkage density, meanTH = mean trophic height, maxTH = 539 *maximum trophic height, Vul = resource vulnerability, Gen = consumer generality, E = network* 540 *efficiency, Red = node redundancy* 541

543 Table 2. Statistics of fit for the multiple mixed effects models. All models include a random effect of

544 site on the intercept of the linear relationship, and year on the slope of the linear relationship. Bold p-545 values indicate significance at $\alpha = 0.05$.

Response	Predictor variable	d.f.	F-value	P-value
variable				
Commentance	PC1	99	-1.537	0.1270
Connectance	type	1	7.991	<0.0001
Linkaga dangitu	PC1	72	-3.902	<0.0001
Linkage density	type	1	2.686	0.0130
Mean trophic	PC1	76	-0.017	0.9864
height	type	1	4.294	0.0003
Maximum trophic	PC1	74	1.407	0.1640
height	type	1	-0.068	0.9460
Network efficiency	PC1	101	-2.306	0.0231
	type	1	8.288	< 0.0001
Normalised	PC1	54	-0.264	0.7929
vulnerability	type	1	-2.478	0.0208
Normalised	PC1	67	1.122	0.2666
generality	type	1	-6.531	<0.0001
ad (Verle anability)	PC1	115	-0.395	0.6940
sd(Vulnerability)	type	1	-0.450	0.6570
ad (Comorrality)	PC1	112	1.952	0.0534
su(Generality)	type	1	-7.228	< 0.0001
Dodundanay	PC1	91	3.577	0.0005
Kedundancy	type	1	-5.269	< 0.0001



548

549 Figure 5. The relationship between connectance, linkage density, mean and maximum trophic height, 550 and environmental stress. The acidity gradient is PC1 extracted from Figure 3, and is strongly related 551 to pH, SO₄ & labile aluminium, with increasing environmental stress (acidity) from left to right, such 552 that the most acidified food webs are to the right of each plot. Lines indicate fitted values from 553 *GLMM*; where p < 0.05, the conditional R^2 as an indication of overall model explanatory power is 554 shown (Johnson 2014). Where site type (lake or stream) was found to be a significant predictor 555 variable, separate lines are given for each site type. Lake food webs are indicated by dark blue squares, 556 while streams are light blue circles.



Figure 6. Variation in resource vulnerability and consumer generality (both normalised to species

richness) across the stress (acidity) gradient (greater acidity to the right, see Figure 5). Lake food webs

are indicated by dark blue squares, while streams are light blue circles.



Figure 7. Network efficiency increases with decreasing environmental stress (acidity, greater acidity
to the right, see Figure 5), node redundancy decreases with decreasing environmental stress. Lines
indicate fitted values from GLMM; where p < 0.05 the conditional R² as an indication of overall
model explanatory power is shown (Johnson 2014). Where site type (lake or stream) was found to be a
significant predictor variable, separate lines (light blues streams; dark blue lakes) are given for each
site type. Lake food webs are indicated by dark blue squares, while streams are light blue circles.

571

572 B. Directional change in food web structure

There was overall a clear directional trend in chemical recovery: eighteen of the 573 574 23 sites exhibited a monotonic declining trend in their PC1 axis scores (i.e. 575 decreasing acidity) over time (Figure 8; Figure 9). Three of the five sites which 576 showed no trend in their PC1 scores (i.e. no directional change in acidity over time) 577 were located in the north of Scotland, which always experienced less acid deposition 578 and so were not highly acidified at the outset of monitoring (Figure 1)(Patrick, 579 Monteith & Jenkins 1995). This suggests that at least partial chemical recovery from 580 acidification has occurred at most sites at which it was expected (Monteith et al. 581 2014).



583

584 Figure 8. Trends in overall acidity (PC1 extracted from Figure 3) at each of the UWMN lake sites.

585 For those sites showing significant monotonic temporal trends (as determined through Mann–Kendall

586 trend tests, see Methods) the test statistic and associated p-value are shown. Sites are arranged in

587 order of their decreasing latitude, which can be used as a proxy for their initial acidified state, more

588 acidified sites were generally in the south (bottom panels), while the least acidified sites were more

589 *northern (top panels).*



591 *Figure 9. Trends in overall acidity (PC1 extracted from Figure 3) at each of the UWMN stream sites.*

592 For those sites showing significant monotonic temporal trends (as determined through Mann–Kendall

593 *trend tests, see Methods) the test statistic and associated p-value are shown. Sites are arranged in*

594 order of their decreasing latitude, which can be used as a proxy for their initial acidified state, more

acidified sites were generally in the south (bottom panels), while the least acidified sites were more

596 northern (top panels).

597 Directional change in food web structure was also evident across many of the 598 UWMN sites, in line with the chemical trends and with our second main hypothesis, 599 although it was far from ubiquitous. Of the eighteen sites showing chemical 600 recovery, around half also showed significant increasing trends in connectance (9 601 sites; Table 3; Table 4), linkage density (7 sites; Table 3; Table 4), mean trophic height 602 (8 sites; Table 3; Table 4), resource *Vulnerability* (6 sites; ; Table 3; Table 4), standard 603 deviation in resource *Vulnerability* (5 sites, Figure 10; Figure 11) and network 604 efficiency (7 sites; Table 3; Table 4). Of the eighteen showing chemical recovery, significant declines were evident in consumer Generality (10 sites; Table 3; Table 4), 605 606 redundancy (10 sites; Table 3) and the standard deviation of *Generality* (10 sites; 607 Figure 10; Figure 11). Maximum trophic height increased in one site, decreased in 608 two, and showed no trend in the other 20 (Figure 10; Figure 11). See Appendices for 609 more detailed plots of each trend over time.

610 There was evidence for a delay in food web recovery after chemical recovery 611 at the UWMN sites; most sites occupied the 'both biological and chemical recovery' 612 or 'chemical but no biological recovery' portions of the conceptual recovery figure 613 (Figure 2) for each of their food web metrics (Table 3; Table 4). Very few sites 614 exhibited change in their food web structure in the absence of directional change in 615 their acidity (PC1); the food webs of Loch Coire Fionnaraich and Allt na Coire nan 616 Con both showed increasing linkage density and resource vulnerability over time, in 617 the absence of a significant temporal trend in acidity (Figure 10, Figure 11). Similarly, 618 the food web of Coneyglen Burn decreased in redundancy over time, despite no

- 619 significant temporal trend in acidity (Figure 10, Figure 11).
- 620
- 621
- 622
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- 624
- 625
- 626
- 627
- 628

- 630 Table 3. The number of the twelve lake sites showing a significant temporal trend in their food web
- *metrics over time, as determined by Mann–Kendall trend tests (see Methods). Chemical recovery here*
- *is indicated by a significant temporal trend in acidity (PC1). C = connectance, LD = linkage density,*
- *meanTH = mean trophic height, maxTH = maximum trophic height, Vul = resource vulnerability,*
- $634 \qquad Gen = consumer generality, E = network efficiency, Red = node redundancy.$

Biological & chemical		Biological but no chemical	
recovery		recovery	
C = 6	LD = 2	C = 0	LD = 1
meanTH = 4	maxTH = 0	meanTH = 0	maxTH = 0
Vul = 3	Gen = 6	Vul = 0	Gen = 1
E = 4	Red = 4	$\mathbf{E} = 0$	Red = 0
Chemical but no biological		No biological or chemical	
recovery		recovery	
C = 4	LD = 8	C = 2	LD = 1
meanTH = 6	maxTH = 8	meanTH = 2	maxTH = 2
Vul = 6	Gen = 4	Vul = 2	Gen = 1
E = 6	Red = 6	E = 2	Red = 2

- 637 Table 4. The number of the eleven stream sites showing a significant temporal trend (in the direction
- 638 predicted in hypotheses; recovery) in their food web metrics over time, as determined by Mann-
- 639 Kendall trend tests (see Methods). Chemical recovery here is indicated by a significant temporal trend
- *in acidity (PC1). C = connectance, LD = linkage density, mean.TH = mean trophic height, max.TH =*
- *maximum trophic height, Vul = resource vulnerability, Gen = consumer generality, E = network*
- *efficiency, Red = node redundancy.*

Biological & chemical		Biological but no chemical	
recovery		recovery	
C = 3	LD = 5	C = 0	LD = 1
meanTH = 4	maxTH = 1	meanTH = 0	maxTH = 0
Vul = 3	Gen = 4	Vul = 1	Gen = 0
E = 3	Red = 6	$\mathbf{E} = 0$	Red = 1
Chemical but no biological		No biological or chemical	
recovery		recovery	
C = 5	LD = 3	C = 3	LD = 2
meanTH = 4	maxTH = 7	meanTH = 3	maxTH = 3
Vul = 5	Gen = 4	Vul = 2	Gen = 3
E = 5	Red = 2	E = 3	Red = 2



646 Figure 10. Trends in food web metrics at each of the UWMN lake sites. Sites are arranged in order of 647 their decreasing latitude (top left to bottom right; see Figure 1), which can be used as a proxy for their initial acidified state (generally least acid to the top left, more acidified sites at the bottom). Site names 648 649 in green indicate a monotonic decreasing trend in acidity over time at that site, site names in black 650 indicate no trend in acidity. Points on the inner ring of each radial plot indicated a negative trend in 651 that variable at that site over time, points on the middle ring indicate no significant trend while 652 points on the outer ring indicate a positive trend. C = connectance, LD = linkage density, mean.TH = 653 *mean trophic height, max.TH = maximum trophic height, E = network efficiency, Vul = resource* 654 vulnerability, Gen = consumer generality, sd.V = standard deviation in resource vulnerability, sd.G 655 = standard deviation in consumer generality, Red = node redundancy. See Appendices for detailed 656 plots of each trend over time.



658 Figure 11. Trends in food web metrics at each of the UWMN stream sites. Sites are arranged in order 659 of their decreasing latitude (top left to bottom right; see Figure 1), which can be used as a proxy for 660 their initial acidified state (generally least acid to the top left, more acidified sites at the bottom). Site 661 names in green indicate a monotonic decreasing trend in acidity over time at that site, site names in 662 black indicate no trend in acidity. Points on the inner ring of each radial plot indicated a negative 663 trend in that variable at that site over time, points on the middle ring indicate no significant trend 664 while points on the outer ring indicate a positive trend. C = connectance, LD = linkage density, 665 mean.TH = mean trophic height, max.TH = maximum trophic height, E = network efficiency, Vul = 666 resource vulnerability, Gen = consumer generality, sd.V = standard deviation in resource 667 vulnerability, sd.G = standard deviation in consumer generality, Red = node redundancy. See

668 *Appendices for detailed plots of each trend over time.*

669 C. Food web recovery from acidification

Trends in chemistry over time were not linearly related to shifts in food web 670 671 structure, or at least have not yet related to the latter, strengthening the evidence for 672 inertia in food web recovery. The χ^2 tests revealed that there was little congruence 673 between those sites exhibiting chemical and biological recovery (Table 5). However, 674 the χ^2 tests did reveal that those sites showing a trend in standard deviation in 675 consumer *Generality* also tended to show a trend in acidity (Table 5). This generally 676 refutes our third hypothesis, and provides more evidence for a lag or inertia in food 677 web recovery; those sites recovering from acidification over time showed little 678 systematic change in their food web structure, suggesting that biological recovery (in 679 terms of food web structure) does not directly track chemical recovery at these sites.

680

681 Table 5. Results from the χ^2 contingency test (see main text). Bold p-values indicate significance at α 682 = 0.05. See the legend of Table 3 for abbreviations.

	PC1
С	0.113
LD	1
mean.TH	0.123
max.TH	0.574
Е	0.146
Vulnerability	1
Generality	1
sd.V	1
sd.G	0.046
Redundancy	0.325

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IV. Discussion 688 689 Our analyses reveals fundamental structural changes occurring in food web 690 structure in response to decreasing acidity over the three decades of the study. These 691 structural changes could have profound implications for the stability of the systems' 692 food webs, and could be hindering biological recovery. Confirming our hypotheses, 693 when analysed at the regional (UK) scale, acidified food webs had lower linkage 694 density, and network efficiency but had more redundancy within their feeding 695 pathways. Contrary to our other hypotheses, we found no effect on connectance, 696 trophic height, nor on resource Vulnerability and consumer Generality or the standard 697 deviations of both. When analysed at the site scale some further trends in network 698 metrics over time became clearer, but overall these were mixed and often harder to 699 associate with decreasing acidity *per se*. There was strong evidence for a lag in 700 biological recovery, as those sites showing a recovery in both their biology and their 701 chemistry tended to be a nested subset of those that only showed a chemical trend.

702 703

A.Food web recovery across the UWMN sites and acidity gradient

The general increasing mean trophic height of food webs over time at each 704 705 site (see also Figure D Appendices) reflected the reverse of the typical responses to 706 acidification, where species are lost throughout the food web, but top predators such 707 as fish (Henriksen, Fjeld & Hesthagen 1999) and many predatory macroinvertebrates 708 are especially vulnerable (Layer et al. 2011). The return of these acid-sensitive species 709 over time causes food chain lengths and the trophic height of the web as a whole to 710 increase (Woodward & Hildrew 2001; Layer et al 2011) - in our dataset all of the sites 711 which experienced this lengthening of food chains were also decreasing in their 712 acidity. However, not all sites with falling acidity also exhibited increases in trophic 713 height, which is again suggestive of food-web inertia. Often site-specific trends were 714 not evident, but were when the data were analysed across the full acidity gradient, 715 also suggesting that other environmental drivers might be modulating the 716 relationship with the food web. For instance DOC, which was closely related to PC2, 717 is known to limit secondary production in lakes (Finstad et al. 2014).

Along the derived acidity gradient, normalised *Vulnerability* and *Generality* were unchanged. Over time at individual sites, however, the latter tended to decrease and the former to increase, but across the 23 sites as a whole only seven showed increasing *Vulnerability* and most showed complex and non-linear patterns over time (see Appendices). Decreasing *Generality* and increasing *Vulnerability* with decreasing acidity is consistent with the proposition that specialist consumers and 724 also larger top predators re-colonise communities following chemical recovery 725 (Woodward & Hildrew 2001; Layer, Hildrew & Woodward 2013). This should result 726 in increased Vulnerability (more consumers per resource due to greater consumer 727 species richness) and reduced Generality (fewer resources per consumer due to 728 increased specialism). The reappearance of acid-sensitive consumers including both 729 invertebrates (such as species of the mayflies *Baetis spp.* and *Caenis spp.*, or the snail 730 *Radix balthica*) and salmonid fish at high pH should lead to both a general elongation 731 and greater compartmentalisation in the web and specialism becomes more 732 prevalent both within and across trophic levels.

733 The connectivity of the food webs as a whole changed across the derived 734 acidity gradient: network efficiency, which describes how 'reachable' each node is 735 from every other, increased with decreasing acidity. If pockets of species are poorly 736 connected to other species, the average shortest path length between all pairs of 737 nodes will increase. Thus, species within more acidified food webs were less well-738 connected on average across the whole network. The increased species richness and 739 addition of top predators such as salmonid fish to the system (Woodward & Hildrew 740 2001) may explain the increased efficiency of these less-acidified food webs. The top 741 predator of these freshwater systems, the brown trout (*Salmo trutta*) is a highly 742 generalist engulfing predator which will consume anything within a given size 743 range of prey. The addition of these (acid-sensitive) generalist interactions between 744 top predators and those macroinvertebrates within its prey-size range may well 745 increase the reachability between those resource nodes, as well as ultimately linking 746 together different feeding pathways (e.g., the allochthonous vs autochthonous 747 resource base of the food web), even though these may be becoming more 748 compartmentalised horizontally among their increasingly specialist primary 749 consumers.

Acidified food webs contained proportionally more redundant feeding pathways than their circumneutral counterparts, the proportion of 'trophic species', nodes feeding on and being fed on by the same species, is larger in the smaller, more acidified food webs. This is consistent with the increase is specialist consumers as acidity decreases. Additionally, acidified food webs tend to have few species and few links (Layer *et al.* 2010b), making the scope for unique feeding pathways small.

Contrasting trends emerged when our data were analysed at the site or
regional scale. When our data were analysed at the individual site scale, trends were
mixed and were not necessarily always related to decreasing acidity, while clearer
trends often emerged from the regional scale analysis. This could arise if

760 communities are highly variable when released from a stressor, and other drivers 761 (e.g. nutrients) that were previously uninfluential start to shape local habitat filtering 762 (e.g. Micheli et al. 1999). Additionally, site scale sources of variation, such as 763 potentially powerful contingent site characteristics, might have swamped potential 764 underlying trends in food web structure over time. Indeed, site identity was a 765 necessary variable in our models that encompassed a range of site specific variables, such as latitude. Additionally, weather conditions were uncontrolled and extreme 766 767 events close to the small sampling widow for each site, has caused some sites to lose and regain their significant trends in biotic recovery over time (Monteith & Evans 768 769 1998, 2005; Kernan et al. 2010). Additionally, the portion of the acidity gradient that 770 each site is exposed to is small relative to that of the whole dataset.

771

B. The recovery of freshwater food webs from acidification

772 Although some clear responses were evident, the food web metrics used here 773 might not be the most appropriate for detecting recovery from acidification. There 774 were considerable inter-site differences in food web structure, but not all were 775 sensitive to changes in acidity and there was still considerable unexplained variation 776 in the models. It seems likely that, as our understanding grows, more sensitive 777 measures of food web structure will emerge, perhaps through analysis of 778 substructure rather than 'whole network' properties, and that these might be better 779 at capturing ecological responses to environmental change.

780 That acidified ecosystems might exhibit 'ecological inertia' has increasingly been 781 suggested as mechanism to explain the delay in biological recovery (Lundberg, 782 Ranta & Kaitala 2000; Ledger & Hildrew 2005; Kernan et al. 2010; Layer et al. 2010b). 783 Various lines of evidence are increasingly suggesting that acidified food webs are 784 dynamically stable and resistant to re-colonisation by acid-sensitive species, even as 785 chemical conditions start to improve. Townsend et al. (1987) measured the 786 persistence of 27 stream invertebrate communities across a pH gradient, and found 787 that those communities from the most acidified sites were indeed the most 788 persistent, although data on species interactions and network structure were not 789 available at the time. Later, Layer et al. (2010b) used dynamic modelling to determine 790 the robustness of stream food webs to species extinctions, and found that food webs 791 from more acidified conditions were more robust, but the long-term temporal data 792 were not available to test this prediction empirically. Here we provide the largest 793 scale evidence to test these ideas, which broadly support the general notion that 794 redundancy is an important component of stability that could confer robustness on 795 the system. In ecosystems redundancy can increase the reliability of process rates

and buffer the effects of species loss (Naeem 1998; Peralta et al. 2014): we found that 796 797 food webs from acidified waters had higher redundancy, suggesting that they might 798 be more robust, and might therefore provide more stable (albeit often slower) 799 process rates (Naeem 1998; Peralta et al. 2014). As acidity decreases in fresh waters, 800 decomposition of leaf-litter, which fuels much of the food web, does indeed 801 accelerate (Jenkins, Woodward & Hildrew 2013), although the extent to which 802 species richness modulates this relationship is still largely unknown (but see Jonsson 803 et al. 2002). Additionally, we found that more acidified food webs had lower global efficiency, which is associated with reduced small-world properties. Ecological 804 805 networks that are small worlds are often relatively stable (Solé & Montoya 2001; 806 Dunne, Williams & Martinez 2002), as they offer many alternative pathways of 807 interaction. These apparently contrasting responses to different dimensions of 808 stability warrant further investigation to reveal if acidified food webs are indeed 809 more (or less) stable in some regards and not others (e.g. Donohue et al. 2013).

810

C. Caveats and future directions

811 The use of inferred feeding links in food web studies has been criticised on 812 the basis that they might over estimate diet breadth, and fail to detect behavioural 813 differences between sites (Hall & Raffaelli 1997; Raffaelli 2007), yet to build complete 814 food webs *de novo* from replicated natural systems is simply logistically unfeasible, 815 so a trade-off between replication and realism is inevitable. The use of 'summary' 816 food webs, which include the full complement of known possible tropic interactions 817 can still be a useful tool for understanding community structure, especially as in 818 freshwaters most species are highly generalist and their diets are largely size-driven 819 and consistent among systems when presented with the same potential prey species 820 (Woodward et al. 2010b; Layer, Hildrew & Woodward 2013; Gray et al. 2015). Indeed, 821 given the nature of building summary food webs, that they tend to overestimate 822 interactions between species, they are more likely to be insensitive to environmental 823 change rather than reveal erroneous trends (i.e. it is more likely that the structure of 824 summary food webs is conserved given that any changes will be entirely driven by 825 changes in species composition rather than feeding behaviour). Hence, we contend 826 that the trends revealed here are broadly realistic, and warrant further examination, 827 especially as the feeding links described in many of our webs had been observed in 828 the same system, albeit only for a snapshot of the full set of sampling occasions. 829 Future work could involve a more formal validation of randomly selected portions of the network via direct analysis of gut contents (as in Woodward, Speirs & 830 831 Hildrew 2005; Layer et al. 2010b) and also the application of new molecular

approaches that could potentially capture a more complete picture of the entire foodweb with a fraction of the current effort required (Gray *et al.* 2014).

834 Another potential limitation to the food webs produced here is that they do 835 not include the full freshwater community, in particular the meiofauna and 836 microfauna (e.g. Schmid-Araya et al. 2002) and true apex predators such as the 837 European Dipper (*Cinclus cinclus*) or Otter (*Lutra lutra*). Top predators can have 838 varying effects on food web structure in these systems (Woodward & Hildrew 2001; 839 Layer et al. 2011), and so their exclusion may be omitting an important source of 840 variation in this data. However, this was unavoidable in this study, as in almost all 841 other food webs described to date, because the presence of these cryptic or very rare 842 species has not been systematically recorded. Additionally, although the fish 843 assemblage of the lakes were sampled from the lake outflows, all these low-844 productivity upland sites are typically dominated by brown trout (Salmo trutta) and 845 the occasional European eel (Anguilla anguilla) in both the running and standing 846 waters across the acidity gradient: of the 434 sampling occasions on which fish were 847 present at a site, brown trout were always present, reflecting its dominance in these systems. The next most common species was the European eel (Anguilla anguilla), 848 849 was found on 136 occasions and all other species (Esox lucius, Gasterosteus aculeatus, 850 *Lampetra spp., Phoxinus phoxinus and Salmo salar*) were found on <60 sampling 851 occasions.

852

853 D.Conclusion

It is clear from this study that both spatial and temporal scales are important 854 855 considerations when assessing food web responses to environmental change in real 856 time (Chave 2013). When our data were analysed at the individual site scale, trends 857 were mixed and were not necessarily always related to decreasing acidity. When the 858 data were analysed at the regional (UK) scale, some clear and significant trends 859 emerged, highlighting the need for large, replicated collections of food webs as well 860 as the need for caution when extrapolating from small collections or individual food 861 webs. Identifying the effects of individual chemical drivers was often challenging 862 given the range of potential drivers in a nationwide dataset that also spans several 863 decades.

To the best of our knowledge this is the largest collection of food webs that span both large temporal and spatial gradients: the next largest set of empirical food webs from natural systems of which we are aware is less than half the size (the 170 867 soil webs described by Mulder et al. 2011) and the remainder are far smaller still, 868 with most studies being conducted on unreplicated singletons (Ings et al 2009). Our 869 study is thus one of the first to address macroecological questions relating to the 870 structure of food webs across time and a broad environmental gradient in a 871 (relatively) standardised manner. Our analysis reveals fundamental structural 872 changes occurring in the food webs as they respond to changes in acidity, these 873 structural changes could have profound implications for the stability of the system, 874 and may be limiting biological recovery. It would be instructive to investigate 875 further the stability of these food webs, in order to explore more fully whether 876 intrinsic inertia is indeed limiting their recovery, and how that might possibly be 877 manipulated to accelerate the rate of recovery.

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VII. Text Box

1239 Definitions of food web metrics used in this study

Food Web metric	Definition
Connectance (C)	Number of links (L) / Number of species (S) ² . The proportion of potential trophic links that do occur (Warren 1994).
Linkage density	L/S. Number of links per taxon. A measure of average diet specialisation across the food web (Tylianakis, Tscharntke & Lewis 2007).
Generality (G)	The mean number of prey per consumer (Schoener & Schoenerz 1989).
Vulnerability (V)	The mean number of consumers per prey (Schoener & Schoenerz 1989).
Mean food chain length	Average number of links found in a food chain across a food web (Levine 1980; Williams & Martinez 2000).
Maximum food chain length	The maximum number of links found in any food chain in a food web (Levine 1980; Williams & Martinez 2000).
Efficiency	How well connected a network is, as well as the distribution of those connections across a network. High efficiency indicates that the species of a food web are all closely connected to one another (Latora & Marchiori 2001)
Redundancy	The trophic similarity among species within a web, high redundancy indicates that many of the species in a food webs are the same resources and consumers; many of the feeding pathways are the same (Briand & Cohen 1984; Cohen & Briand 1984).

II. Appendices



1244 Figure A. Trends in connectance at each of the UWMN sites. Sites are arranged in order of their

decreasing latitude, which can be used as a proxy for their initial acidified state, more acidified sites

1246 were generally in the south (bottom of plot), while the least acidified sites were more northern (top of

plot). See Figure 1 for site name abbreviations.



Figure B. Trends in linkage density at each of the UWMN sites. Site ordering is explained in the

legend of Figure A. See Figure 1 for site name abbreviations.



Figure C. Trends in mean trophic height at each of the UWMN sites. Site ordering is explained in the

legend of Figure A. See Figure 1 for site name abbreviations.



Figure D. Trends in maximum trophic height at each of the UWMN sites. Site ordering is explained

in the legend of Figure A. See Figure 1 for site name abbreviations.



1259 Figure E. Trends in average food web vulnerability at each of the UWMN sites. Site ordering is

explained in the legend of Figure A. See Figure 1 for site name abbreviations.



Figure F. Trends in the standard deviation of food web vulnerability at each of the UWMN sites. Site

1263 ordering is explained in the legend of Figure A. See Figure 1 for site name abbreviations.



1265 Figure G. Trends in food web generality at each of the UWMN sites. Site ordering is explained in the

legend of Figure A. See Figure 1 for site name abbreviations.



Figure H. Trends in the standard deviation of food web generality at each of the UWMN sites. Site

1269 ordering is explained in the legend of Figure A. See Figure 1 for site name abbreviations.



Figure I. Trends in food web efficiency at each of the UWMN sites. Site ordering is explained in thelegend of Figure A. See Figure 1 for site name abbreviations.



Figure J. Trends in food web redundancy at each of the UWMN sites. Site ordering is explained in the

legend of Figure A. See Figure 1 for site name abbreviations.