the common conclusion that the tektite ejection process selectively samples only the top ~ 100 m of target material and, therefore, a thin veneer of carbonate over siliceous materials may be sufficient to produce the observed trends of chemical variation between the glasses. Proposed impact sites at both Manson, Iowa, and Chicxulub, Mexico, are in geologic terranes where appropriate mixtures of carbonate and silicate target materials are present (1-4).

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- 17. The uncertainty associated with the reported δ¹8O values is estimated to be ±0.2 per mil based on three independent experiments: (i) a rather large (10 mg) K-T glass spherule (sample A4a) was broken into three pieces and each was analyzed separately (Table 1); (ii) pairs of analyses made on two Australasian Muong Nong-type tektites (samples 8301 and 8319) agreed within 0.1 per mil (Table 1); and (iii) 30 replicate laser analyses of a quartz standard (38) with a conventional δ¹8O = 11.7 per mil (1a)
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Scale and Structure in Natural Food Webs

Karl Havens

The degree to which widely accepted generalizations about food web structure apply to natural communities was determined through examination of 50 pelagic webs sampled consistently with even taxonomic resolution of all trophic levels. The fraction of species in various trophic categories showed no significant overall trends as the number of species varied from 10 to 74. In contrast, the number of links per species increased fourfold over the range of species number, suggesting that the link-species scaling law, defined on the basis of aggregated webs, does not reflect a real ecological trend.

For over two decades, ecologists have tried to establish generalizations about the structure of natural food webs. From trends in published webs, three scaling laws (1-3)have been proposed. The first, the species scaling law, proposes that the basal (autotrophs and detritus), intermediate (preying on others and themselves preved upon), and top (having no predators) fractions of species do not vary with the total number of species (S) in the web. The second, the link scaling law, proposes that the fractions of top-intermediate, top-basal, intermediateintermediate, and intermediate-basal links do not vary with S. The third, the linkspecies scaling law, proposes that the total number of links (L) is proportional to S and that linkage density (d = L/S) does not vary with S.

These laws have been supported by studies, each including up to 113 webs (1–5). They have also been criticized for lack of uniformity in data collection, linkage criteria, and species aggregation in the food webs used to develop and test the laws (6, 7). For example, some webs present "whales" as several distinct trophic groups, whereas others make whales a single group that feeds on plankton, macroinvertebrates, and seals. Ag-

Department of Biological Sciences and Water Resources Research Institute, Kent State University, Kent, OH 44242.

gregation tends to be uneven across trophic levels; basal species are often lumped into categories such as "plankton" while top species are aggregated only slightly or not at all (8). To address this problem, Briand and Cohen developed scaling laws for webs where biological taxa were first aggregated into "trophic species," those having identical pred-"trophic species," those having identical predators and prey (1). Others have argued that this aggregation disguises trophically important interactions (6, 9), and it remains uncertain whether the scaling laws reflect trends in natural nonaggregated webs. Recently Martinez (10) suggested that they do not, and Briand, Cohen, and others have proposed that link-species scaling in particular might be scale-dependent (2, 4, 11, 12). However, investigations have used either descriptions of webs from various sources that differ in sampling methods and completeness (13, 14) or a single, highly resolved web successively aggregated by computer algorithms (10).

I have analyzed the scaling laws using a large group of nonaggregated natural webs sampled consistently and constructed from identical linkage criteria (15, 16). The 50 webs represent the pelagic communities of small lakes and ponds in New York State sampled as part of the Adirondack Biota Project (17). Taxa at all trophic levels (fish, invertebrate predators, zooplankton, and phytoplankton) are resolved to genus

cannibalistic interactions were not considered when assigning species to the three trophic categories. Had they been included, none of the webs would have contained top species. In the smallest webs (S < 20) there is evidence of a reduced fraction of intermediate species and an increased fraction of basal species. These trends are not statistically significant but have been reported previously (1, 2, 10). The trends coincide with a reduction in the number of intermediate trophic levels from two to one.

The results in Fig. 2 support the link scaling law (1–3). The fractions of top-inter-

ing cannibals (10). By convention (1-5),

The results in Fig. 2 support the link scaling law (1-3). The fractions of top-intermediate (Lti/L), top-basal (Ltb/L), intermediate-intermediate (Lii/L), and intermediatebasal (Lib/L) links are scale invariant, with means of 0.10, 0.05, 0.32, and 0.53, respectively. Cohen and Briand (2) reported scaleinvariant fractions with means of 0.35, 0.08, 0.30, and 0.27. More links to top species and \aleph fewer intermediate-basal links reflect inflated α values for the fraction of top species in their webs (10). In the smallest webs herein, the fraction of top-basal links is increased while the fraction of intermediate-intermediate links is reduced to zero. The trends are not of statistically significant but have been previously observed (1, 2, 10). In this case, they reflect the loss of intermediate-intermediate links in webs where the number of trophic levels is less than four.

Overall, the results support Briand and

600

500

400

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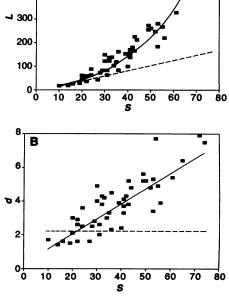
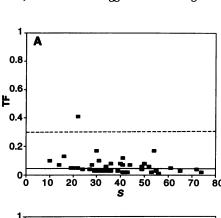
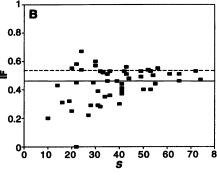


Fig. 3. (A) Links (L) and (B) linkage density (d) as a function of S. The solid lines are fitted to the data points; the dashed lines indicate the relations predicted by the link-species scaling law.

or species and further resolved into life history stages where ontogenic changes in diet occur (for example, cyclopoid nauplii and larval fish). A total of 220 taxa are represented. The webs range in size from 10 to 74 species (Table 1), approximately the same range of S covered by the nonaggregated webs of Sugihara *et al.* (13) and a much greater range than covered by the original Briand (18) webs.

The data from the 50 natural webs (Fig. 1) support the species scaling law (1–3). The fractions of top (TF), intermediate (IF), and basal (BF) species are scale invariant, with means of 0.06, 0.44, and 0.50, respectively. Cohen and Briand (2) reported scale-invariant fractions with means of 0.19, 0.53, and 0.29. Martinez (10) reported means of 0.01, 0.86, and 0.13 and suggested that the greater





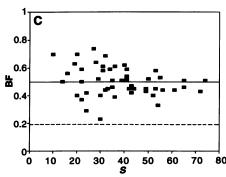
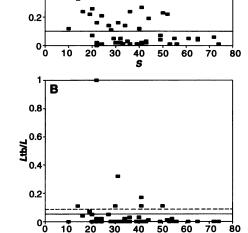


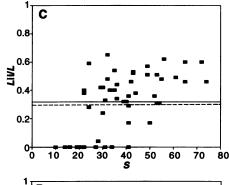
Fig. 1. Fraction of species in (**A**) top (TF), (**B**) intermediate (IF), and (**C**) basal (BF) trophic categories as a function of *S*. The solid lines represent the fraction means; the dashed lines indicate the fraction means predicted by the species scaling law.

fraction of top species given by Cohen and Briand was an artifact of aggregation. The present results indicate that for pelagic webs that view is correct; only a small fraction of species are top predators. Indeed, it is questionable whether any natural food webs contain top species as defined by Cohen and Briand (1, 2), which lack all predators includ-

0.8

0.6· **TI**





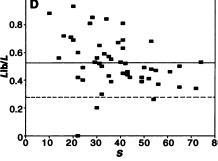


Fig. 2. Fraction of **(A)** top-intermediate (Lti/L), **(B)** top-basal (Ltb/L), **(C)** intermediate-intermediate (Lii/L), and **(D)** intermediate-basal (Lib/L) links as a function of S. The solid lines represent the fraction means; the dashed lines indicate the fraction means predicted by the link scaling law.

Table 1. Properties of the 50 food webs (22).

Lake name S L d TF IF BF LiVL Lib/L											
Balsom 50 261 5.2 0.08 0.4 0.52 0.23 0.11 0.17 0.48 Beaver 55 267 4.9 0.03 0.44 0.53 0.05 0 0.48 0.47 Bridge Brook 74 553 7.5 0.02 0.47 0.51 0.01 0 0.46 0.53 Brandy 30 121 4 0.17 0.6 0.23 0.45 0.11 0.24 0.25 Brook Trout 14 19 1.4 0.07 0.43 0.5 0.33 0.11 0 0.56 Buck Burthridge 53 183 3.7 0.07 0.41 0.52 0.02 0.17 0 0.56 Burthridge 53 183 3.4 0.02 0.4 0.58 0.01 0 0.44 0.55 Chub 36 83 2.3 0.03 0.46 0.51 0.01 0 0.44	Lake name	S	L	d	TF	IF	BF	Lti/L	Ltb/L	Lii/L	Lib/L
Beaver 55 267 4.9 0.03 0.44 0.53 0.05 0 0.48 0.47 Big Hope 61 328 5.4 0.05 0.51 0.44 0.05 0 0.49 0.46 Brandy 30 121 4 0.17 0.6 0.23 0.45 0.11 0.24 0.25 Brook Trout 14 19 1.4 0.07 0.41 0.52 0.02 0.17 0 0.56 Burk 41 153 3.7 0.07 0.41 0.52 0.02 0.17 0 0.81 Burntbridge 53 183 3.4 0.02 0.4 0.55 0.03 0.16 0.51 0.03 0.14 0.57 Chub Pond 54 416 7.7 0.17 0.5 0.33 0.41 0.02 0.4 0.5 Constable 31 61 2 0.1 0.29 0.61 0.16	Alford	56	220	3.9	0.01	0.55	0.44	0.01	0	0.62	0.37
Big Hope 61 328 5.4 0.05 0.51 0.44 0.05 0 0.49 0.46 0.53 Bridge Brook 74 553 7.5 0.02 0.47 0.51 0.01 0 0.46 0.53 Brook Trout 14 19 1.4 0.07 0.43 0.5 0.33 0.11 0 0.56 Buck 41 153 3.7 0.07 0.41 0.52 0.02 0.17 0 0.81 Burk Discoper 35 118 3.3 0.03 0.46 0.51 0.03 0 0 0.4 0.55 Chub 36 83 2.3 0.03 0.46 0.51 0.04 0 0.44 0.55 Chub Pond 54 416 7.7 0.17 0.5 0.33 0.41 0.02 0.31 0.66 Constable 31 61 2 0.1 0.29 0.61 0.16	Balsom	50	261	5.2	0.08	0.4	0.52	0.23	0.11	0.17	0.49
Bridge Brook 74 553 7.5 0.02 0.47 0.51 0.01 0 0.46 0.53 Brancy 30 121 4 0.17 0.6 0.23 0.45 0.11 0.24 0.2 Brancy 14 19 1.4 0.07 0.43 0.5 0.33 0.11 0.24 0.2 Brook Trout 14 19 1.4 0.07 0.43 0.5 0.33 0.11 0 0.56 Buck 41 153 3.7 0.07 0.41 0.52 0.02 0.17 0 0.81 Burntbridge 53 183 3.4 0.02 0.4 0.58 0.01 0 0.31 0.68 Cascade 35 118 3.3 0.03 0.36 0.61 0.01 0 0.44 0.57 Chub 36 83 2.3 0.03 0.36 0.61 0.01 0 0.44 0.55 Chub Pond 54 416 7.7 0.17 0.5 0.33 0.41 0.02 0.31 0.26 Connery 65 418 6.4 0.03 0.46 0.51 0.04 0 0.46 0.5 Constable 31 61 2 0.1 0.29 0.61 0.16 0.32 0 0.52 Deep 19 28 1.5 0.05 0.32 0.63 0.22 0.07 0 0.71 Emerald 22 58 2.9 0.05 0.45 0.5 0.16 0.02 0.4 0.42 Falls 39 152 3.9 0.03 0.46 0.51 0.01 0 0.32 0.67 Fawn 32 122 3.8 0.03 0.46 0.51 0.01 0 0.32 0.67 Fawn 32 122 3.8 0.03 0.46 0.51 0.01 0 0.32 0.67 Fawn 32 122 3.8 0.03 0.46 0.51 0.01 0 0.32 0.67 Fawn 32 122 3.8 0.03 0.58 0.37 0.02 0 0.48 0.5 Federation 22 57 2.6 0.05 0.58 0.37 0.02 0 0.48 0.5 Federation 22 57 2.6 0.05 0.58 0.37 0.02 0 0.48 0.5 Gaull 44 212 4.8 0.07 0.48 0.45 0.19 0.01 0.32 0.67 Gaull 44 212 4.8 0.07 0.48 0.45 0.19 0.01 0.32 0.52 0.46 Gull North 16 25 1.6 0.13 0.31 0.56 0.24 0.04 0 0.72 Helidiver 41 169 4.1 169 4.1 0.12 0.37 0.51 0.27 0.11 0.17 0.45 High 24 87 3.6 0.04 0.67 0.29 0.01 0 0.59 0.4 Horseshoe 49 255 5.2 0.06 0.49 0.45 0.59 0.14 0.02 0 0.65 0.44 0.04 0.35 0.44 0.08 0.3 0.53 0.44 0.02 0 0.05 0.44 0.04 0.05 0.04 0.59 0.44 0.04 0.05 0.05 0.05 0.05 0.05 0.05	Beaver	55	267	4.9	0.03	0.44	0.53	0.05	0	0.48	0.47
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	Twin West	20	60	3	0.05	0.25	0.7	0.07	0	0	0.93
Wolf 27 42 1.6 0.04 0.22 0.74 0.14 0.05 0 0.81	Whipple	32	136	4.3	0.03	0.28	0.69	0.05	0	0.65	0.3
	Wolf	27	42	1.6	0.04	0.22	0.74	0.14	0.05	0	0.81

Cohen's view (1-5) that the "shape" of food webs as described by both the species and link fractions is a scale-invariant property. The results also demonstrate the validity of community assembly models, which have predicted similar scale-invariant patterns (19, 20).

The results do not support the linkspecies scaling law. In these natural nonaggregated pelagic webs, linkage density is not scale invariant (Fig. 3). The relation between L and S can instead be approximated by a power function $(L = S^{1.4})$, as proposed by Pimm, Lawton, and Cohen (12) and recently demonstrated by Martinez (14) for a set of 175 aggregated food webs taken from previous findings. Such a scale-variant relation is likely to exist in all food webs having indiscriminant herbivores. Particle feeders including many planktivorous fish and zooplankton consume a potentially limitless number of prey species because linkage is not so much a species-dependent phenomenon as it is a size-dependent one.

Powerful patterns in community structure do exist in nature, albeit some are independent of scale and others are not. Ecologists must now turn to the more interesting question of what causes those patterns.

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- 15. The 50 lakes sampled were selected by a stratified random design (17) with samples taken once during the summer 1984. Phytoplankton samples were taken from mid-epilimnion: zooplankton N were collected with vertical tows of a plankton net (76 µm for rotifiers and 158 µm for crustaceans). Fish were sampled with overnight gill nets and minnow traps. The first step in constructing the food webs was to produce a cumulative list of species collected in the 50 lakes. Diet information was obtained from Martinez (10), Havens (21), W. B. Scott and E. J. Crossman [Freshwater Fishes of Canada (Fisheries Research Board of Canada) Ottawa, 1973)], K. Bogdan and J. J. Gilbert [Proc. Natl. Acad. Sci. U.S.A. 81, 6427 (1984)], K. Havens and J. DeCosta [J. Plankton Res. 7, 207 (1985)], and W. G. Sprules and J. E. Bowerman [Ecology 69, 418 (1988)] and used to construct a cumulative matrix of predator-prey interactions among the 220 taxa. Individual matrices for the 50 lakes were derived from the rows and columns corresponding to the species present. In some cases the lake matrices were edited by removal of 'dangling species" (11) that lacked trophic links to the web. The cumulative web approach was taken because direct measurements of feeding relations were not taken in the 50 lakes. To do so would have required gut content analyses of all predators and limited the study to a small number of lakes. Predator selectivity does not vary from lake to lake, according to the cumulative web approach. That is, if species A eats species B in one community, it eats B in all other communities where both are present, regardless of availability of alternate prey. This assumption may not be entirely valid. However, because the web models include only data on the existence (or lack thereinteraction strength, the assumption is more robust.
- 16. The food webs used herein were not aggregated into trophic species because the objective was to determine whether the scaling laws accurately predict trends in the natural biological communi-
- ties and not in their aggregates.

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