

The relationship between the regional number of aphid species and plant species diversity

AULAY MACKENZIE¹, ANTHONY F.G. DIXON² and PAVEL KINDLMANN³

¹Department of Biology, University of Essex, Colchester CO4 3SQ, United Kingdom

²School of Biological Sciences, University of East Anglia, Norwich NR4 7TJ, United Kingdom

³Czech Academy of Sciences, Branišovská 31, 370 05 České Budějovice, Czech Republic

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Abstract. The relationship between the regional number of aphid species to the number of plant species in the same area was assessed. A simple power model was statistically fitted to data from 35 countries, spanning six continents. The maximum aphid species diversity was found to occur at an intermediate plant species diversity.

INTRODUCTION

In a previously presented model (Dixon et al., 1987), it was suggested that the regional species diversity of aphids was maximal at some intermediate plant species richness, and declined in areas of high vegetational complexity. This pattern, in apparent contrast to more mobile herbivorous insects such as butterflies, implies that aphid speciation has been limited by aphid's weak locomotory powers to the exploitation of plant resources which are readily located. As vegetation types increase in species complexity, the mean distance between individuals of the same species increases, and the necessary search effort increases. This model is a simple and powerful indicator of the evolutionary constraints acting upon these insects.

In this paper we statistically validate this model, using an extended dataset, and confirm its conclusions.

METHODS

The data is based on that used in Dixon et al. (1987), with additional aphid species number estimates included for Brazil (Costa et al., 1993), Canada, Chile (Philippi, 1981), Cuba (Smith & Cermeli, 1979), Denmark, Hungary, Korea, Indonesia (Noordham & Hille Ris Lambers, 1985), Puerto Rico (Smith et al., 1971), Sardinia (Barbagallo, 1985), Sicily (Barbagallo & Stroyan, 1980; Patti, 1983), Venezuela (Cermeli, 1965; 1970; 1973) and the United States of America (Smith & Parron, 1978). Plant species diversity estimates are from Frodin (1984).

The model used here is identical to that developed in Dixon et al. (1987), which relates the area-adjusted regional species numbers of plants and aphids (S_p and S_a respectively) to two constants, C_{crit} , the minimum proportional plant representation required to support aphids and K , the average number of species of aphids per plant (of those whose abundance exceeds C_{crit}) across all regions. However, to avoid problems of visual interpretation of the figures, it was decided to avoid using one factor (S_a) on both sides of the equation (and hence, both graph axes).

Dividing by this factor compresses the data into the lower left of the graph, such that even random variates would appear to weakly follow the model. Thus, the equation is expressed as:

$$S_a = S_p K e^{C_{crit} S_p}$$

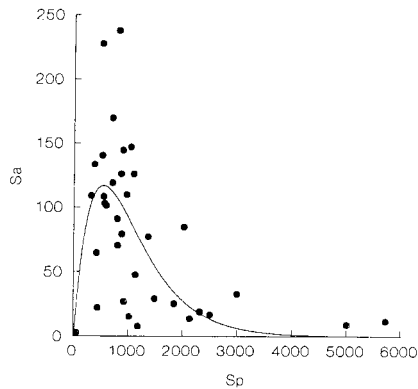


Fig 1. The relationship between area-adjusted species diversity across countries in aphids (S_a) and plants (S_p).

A statistical fit of this model to the data is achieved by bootstrapping (Efron & Gong, 1983). From the observed sample of n S_p and S_a pairs, a pseudosample of size n is taken by random choice of paired values with replacement from the observed sample and the least sum of squares of deviates calculated for the model (across all parameter values). This procedure is repeated many times (10,000 here), and the resulting distribution of sums of squares compared to the observed sum of squares. If the observed deviation from the model is below the five percentile level of the bootstrapped distribution, the fit is taken to be significantly better than that expected by chance. Random choice of data was made using the Standard Apple Numeric Environment (SANE) random number generator, called from a Pascal program.

RESULTS

The best least squares fit of the model to the raw data is shown in Fig. 1. The bootstrapped deviate is non-significant, as indicated by the wide scattering of the data, clearly apparent by omitting the S_p divisor on the y axis. Whilst it is clear that the highest values of S_a do occur at intermediate levels of S_p , the variation between countries is high. To overcome this regional variation, the average S_a value across S_p classes of width 250 was considered (Fig. 2). After this modification the model is a very good descriptor of the distribution ($P = 0.0016$).

It has been suggested that aphids originated in the northern hemisphere and have not achieved an equivalent diversity in the southern hemisphere due to the barrier of low aphid species diversity in the tropics. By considering each country's deviation from the model, this regional deficit or excess of aphid species over the global norm can be considered.

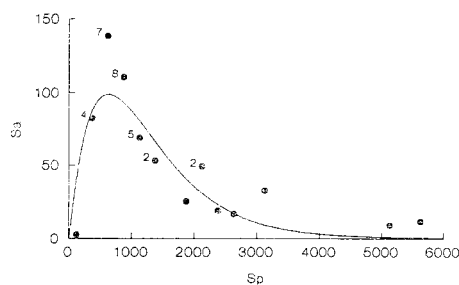


Fig 2. The relationship between average area-adjusted species diversity in aphids (S_a) and plants (S_p). Number represent sample sizes where greater than one.

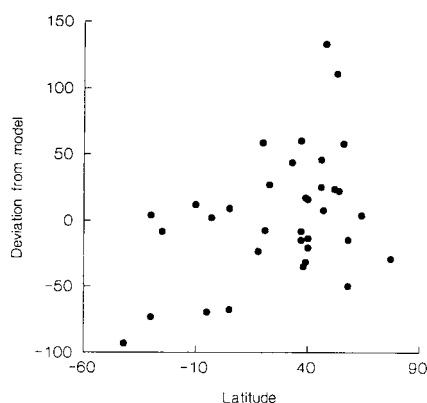


Fig 3. The effect of latitude on deviation from the model.

Because error will exist in estimates of both aphid and plant numbers, it is appropriate to consider the deviation from the data point to the nearest part of the function curve, rather than the y axis deviate. The comparison between these and each country's mean latitude is shown in Fig. 3. Whilst the representation of the southern hemisphere is limited, there is a significant positive correlation ($r_{1331} = 0.413$, $P < 0.02$), indicating a deficit of aphid species in southern latitudes.

CONCLUSION

The model clearly is a good predictor of aphid species diversity when averaged across countries, and strongly suggests that aphid speciation has been fundamentally determined by the limited host location abilities of this taxon. There are, however, local factors which give rise to variation from this general picture, one of which appears to be latitude, due to constraints imposed by the area of evolutionary origin.

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