

Unequal Weighting in Numerical Taxonomy

IN the Fungi Imperfecti, the system of classification which has evolved over the past 150 years involves the recognition of 'form species' and 'form genera' which lack any established genetic basis. Thus it is possible to speak of 'similarity' but not of 'relationship'. This system, though admittedly artificial, is at present essential to sorting and identification procedures.

As no more natural scheme is yet in prospect, any consistent and reasonably objective way of placing an unknown or undescribed fungus within the existing framework would be useful both to the non-taxonomist attempting identifications, and to the scientific historian trying to explain the rationale of the present system.

We have accordingly attempted to apply the numerical approach to taxonomy within the existing scheme, as a first step toward making mathematics an operational tool in the taxonomy of the Fungi Imperfecti.

The method originally tested was that described by Sneath¹ in which coefficients of similarity are formed between pairs of organisms or taxa by the comparison of large numbers (at least 40 and preferably more than 60) of equally weighted qualitative and quantitative characters. Our initial work used a small group of Fungi Imperfecti comprising the genera *Haplobasidium*, *Lacellinopsis* and *Lacellina*, each with three species. The data were derived from a taxonomic treatment by Ellis², a list of 70 features being compiled for use in the numerical scheme.

When Sneath's method was followed, it was found that similarity coefficients between 'form species' from different existing 'form genera' were in some cases higher than those between 'form species' now considered congeneric (Table 1), and no acceptable alternative classification could be visualized. Consequently, it was felt that the method in its original form was unsuitable for this application.

In most discussions of numerical taxonomy¹⁻³ equal weighting of all characters has been a prerequisite, because of the difficulty of devising any rational criteria for differential weighting.

The principal differences between *Haplobasidium*, *Lacellinopsis* and *Lacellina* are that only the first two possess swollen sporiferous vesicles at the apex of the conidiophore, and only the last two possess setae. In organisms like the Fungi Imperfecti, which are described

Table 1. SIMILARITY COEFFICIENTS WITH EQUAL WEIGHTING

Species	1b	1c	2a	2b	2c	3a	3b	3c
1a	60	59	71	67	61	44	54	61
1b		68	58	59	67	50	50	54
1c			73	68	62	58	54	58
2a				74	72	70	73	71
2b					70	64	62	66
2c						63	57	64
3a							90	78
3b								79

Table 2. SIMILARITY COEFFICIENTS WITH DIFFERENTIAL WEIGHTING

Species	1b	1c	2a	2b	2c	3a	3b	3c
1a	78	78	73	71	69	50	54	57
1b		83	67	68	71	53	53	54
1c			75	72	69	56	54	56
2a				86	85	74	76	75
2b					84	71	70	72
2c						71	68	71
3a							95	88
3b								88

Key to species: 1a, b, c, *Haplobasidium thalictri*, *H. telebae*, *H. musae*. 2a, b, c, *Lacellinopsis sacchari*, *L. levispora*, *L. spiralis*. 3a, b, c, *Lacellina graminicola*, *L. macrospora*, *L. leonensis*.

largely in morphological terms, those terms may conveniently be divided into primary and secondary characters. Primary characters are those organs (setae, vesicles, conidia) which require further characterization or description. This is supplied by a variable number of secondary descriptive features (width, septation, pigmentation). Differences in secondary characters will naturally lower the similarity coefficient, and since secondary characters considerably outnumber primary characters, such differences can sometimes outweigh similarities in primary characters. Where a species lacks a primary character, the associated secondary characters are not considered when making comparisons with other species and hence do not affect the similarity coefficients. It seems unsatisfactory that it is possible for two species, both possessing a given primary character, to appear less similar to each other than to a third species lacking the primary character entirely, because of differences in secondary features of that character. This anomalous situation seems, in fact, to have arisen in the Fungi Imperfecti, although it has not apparently been encountered in other groups to which the method has been applied.

To obtain more realistic coefficients of similarity in the Fungi Imperfecti, an amended scoring system was devised. To each primary character was added a weighting of unity for each secondary character needed to describe it. The primary character 'setae present' is described by a maximum of eight secondary characters in any individual. In *Lacellinopsis sacchari*, for example, these are as follows:

- (1) simple, (2) straight, (3) subulate, (4) thick-walled, (5) pigmented, (6) septate, (7) 400–700 μ long (max.), (8) 7–9 μ thick (max.).

Under the modified scheme, the presence of setae in *Lacellinopsis* and their absence from *Haplobasidium* was now scored as nine character differences.

When this weighting system was used, the classification obtained was in accordance with present-day practice, the 'form genera' being clearly delimited (Table 2). While this was to be expected, since the weighting system was devised for this particular group of organisms, a more recent and larger analysis (which will be discussed in detail elsewhere), involving intraspecific as well as interspecific and intergeneric comparisons, has confirmed the usefulness of the modified method in the Fungi Imperfecti.

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¹ Sneath, P. H. A., *J. Gen. Microbiol.*, **17**, 201 (1957).

² Michener, C. D., and Sokal, R. R., *Evolution*, **11**, 130 (1957).

³ Sneath, P. H. A., and Sokal, R. R., *Nature*, **193**, 855 (1962).

⁴ Ellis, M. B., *Commonw. Mycol. Inst., Mycol. Pap.*, **67** (1957).