Linear growth rates of strains representing 10 Neurospora species

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Abstract
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36. Cleaning up new mutants. Before being subjected to extensive genetic or phenotypic analysis, new mutant strains from mutant hunts or other sources should be monitored for the presence of (1) secondary mutations or modifiers (by crossing by standard wild type and recovering the single mutant as an f1), and (2) chromosome rearrangements (by examining ascospores in a cross of the mutant by fluffy or another standard tester).

37. Gene order and map distance. Whenever possible, establish gene order using 3-point data in preference to combining 2-point data from separate crosses. rec genes are polymorphic in stocks of different parentage, and these can result in local differences up to 10 or 20 fold in recombination in specific regions, depending on differences in rec genotype. (For example, see Catchetside 1973 Aust. J. Biol. Sci. 26, p. 1342).

Don't base gene order just on the 'distance' apparent in your cross from markers in a "standard" published map. There is no 'standard' map so far as distances are concerned, because the maps are based on crosses which were highly heterogenous with respect to rec genotypes. In contrast, gene order from 3-point or multiple-point crosses is reliable and doesn't depend on absolute values.

In calculating recombination values (map distances) from 3-point data, double cross-overs contribute to each component interval. One must add the double crossovers to the single crossovers to obtain the value for each segment.

38. Nomenclature and conventions. With new mutants, assign a unique allele (isolation) number to each occurrence. Allele numbers should be preceded by a letter or letters indicating your name or institution, e.g. CB1, CB2, etc. if your name were Charley Brown. Choose a combination not already preempted (see FGSC stocklist for list of prefixes in use. Allele numbers of markers should be recorded for all stocks maintained or sent to others. Do not confuse allele (isolation) number (e.g. CB513) with locus number (e.g., - in al-2), or with accession (stock or strain) number (e.g., FGSC no. 2583). Assign new locus numbers (e.g. al-4) only when allelism with previously established loci (al-1, al-2, al-3) has been excluded. For summary and references on nomenclature see Compendium pp. 427-428 and Barratt et al. 1965 N.N. 8:23-24. — — Department of Biological Sciences, Stanford University, Stanford, California 94305
TABLE I

Linear growth of strains representing all the known Neurospora species. Rate is mm/h at 25°C on minimal medium N in 30 cm long growth tubes. Each value is based on the linear phase of growth in a single tube.

| SPECIES       | STOCK NO. | NAME OF STRAIN          | RATE | GRAPH OF LINEAR RATES |
|---------------|-----------|-------------------------|------|-----------------------|
| N. crassa     | 8203      | ORS-SL6 a               | 3.7  |                       |
|               | 2149      | fl-P A                  | 3.8  |                       |
|               | P538      | Mauriceville-1c A       | 3.7  |                       |
|               | 8063      | Adiopodoume A           | 3.9  |                       |
|               | 9359      | Adiopodoume V7 A        | 4.0  |                       |
| N. intermedia | P420      | Clewiston-1h A          | 4.0  |                       |
|               | P405      | Labelle-1b a            | 4.0  |                       |
|               | 8136      | Shp-1 a                 | 4.1  |                       |
|               | 8135      | Shp-1 A                 | 4.2  |                       |
|               | P60       | Kao-shong-1 a (ylo ecotype) | 3.3 |                       |
|               | P201      | Kelungkung-1 a (ylo ecotype) | 3.4 |                       |
| N. sitophila  | P8085     | Arlington A (Sk-1k)     | 3.8  |                       |
|               | P8086     | Arlington a (Sk-1k)     | 3.8  |                       |
|               | 8112      | Sk-1s A                 | 3.9  |                       |
|               | 8111      | Sk-1s a                 | 3.9  |                       |
|               | 8222      | fl Sk-1k A              | 4.0  |                       |
| N. tetrasperma| 8055      | 85 A                    | 3.3  |                       |
|               | 8056      | 85 a                    | 3.5  |                       |
|               | 8219      | 85 A+a                  | 3.6  |                       |
|               | P2300     | Waitakere, N.Z. A+a     | 4.0  |                       |
|               | P202      | Gianjor-1 A+a           | 4.0  |                       |
| N. discreta   | P851      | Kirbyville-6 A          | 1.5  |                       |
|               | P846      | Kirbyville-1 a          | 1.4  |                       |
|               | P390      | Homestead-1k a          | 2.8  |                       |
|               | P755      | Santa Maria a           | 2.8  |                       |
| homothallics  | 8058      | N. africana             | 1.7  |                       |
|               | 8059      | N. dodgei               | 2.1  |                       |
|               | 8060      | N. galapagosensis       | 1.5  |                       |
|               | D301      | "", var. dominicana     | 1.8  |                       |
|               | FGSC 1889 | N. terricola            | 0.8  |                       |
|               | FGSC 1910 | N. lineolata            | 1.7  |                       |
Rather than prepare tubes in duplicate or triplicate for individual tests, only a single race tube was used for each strain, and rates were determined using several different strains to represent each species. This could not be done for the homothallic species where only a single isolate was available.

_N. crassa, N. intermedia, N. sitophila, and N. tetrasperma_ differ little in rate of linear growth. An apparent exception is the yellow ecotype of _N. intermedia_ (represented by P60, P201) which is found characteristically on nonburned substrates in the Eastern hemisphere.

In contrast, the five homothallic species grow at only half the speed of the heterothallics, or less. The slowest species, _N. terricola_, from soil in Wisconsin, is also set off from the others morphologically by having rounded ascospores with a single germ pore. Strain D301 from Dominica, West Indies, has been diagnosed as a variety of _N. galapagosensis_ (H.L. Huang, personal communication). All the homothallic strains are devoid of conidia.

Representative strains of the new species _N. discreta_ are also distinctly slower than the other heterothallic species. The Kirbyville isolates from Texas are slowest. P390 (Florida) and P755 (Guatemala) are somewhat faster.

Our growth-rate determinations based on single tubes are certainly not definitive. However, these results agree well with the more extensive data of other workers for species tested previously. Our 25°C rates compare with those of Ryan et al. (1943) as follows: 3.7-4.0 vs 3.7-4.2 mm/h for _N. crassa_; 3.8-4.0 vs 4.1-4.2 mm/h for _N. sitophila_. For _N. intermedia_, our 4.0-4.2 mm/h compares with about 4.2 mm/h of Griffiths et al. (personal communication). Ryan et al. calculated that a difference of less than 0.4 mm/h between two single race tubes is probably not significant. - Department of Biological Sciences, Stanford University, Stanford, California 94305

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**Scharf, C. and B.L. Seidel**

Computer analysis of _N. crassa_ growth curves.

The determination of the best fit line to a growth curve has been difficult because of its sigmoidal nature. A number of equations have been developed which attempt to describe growth curves. These include the logistic, Gompertz, von Bertalanffy, and Richardson equations (Ricklefs, 1967, Ecology 48:978-983; Richardson, 1984, Bull. Southern Calif. Acad. Sci. 83:101-115). Several statistical packages are available which allow the use of these equations for computer analysis of the data, including the SAS system; BMDP (Bio-Medical Data Processing), and Systat (IBM). All packages can be run on an IBM microcomputer, but require a hard disk drive. We describe here the use of the SAS system for the analysis of _N. crassa_ growth curve data.

The SAS system is an all-purpose system designed for data analysis and is available through SAS institute, Inc. Box 8000; Cary, NC 27511-8000 (919-467-8000). The software is compatible with IBM 370/30XX/43XX; Digital Corporation VAX 11/7XX; and Data General ECLIPSE series to name a few. We used the Data General System available through the Academic Computer Center at SUNY-Plattsburgh.

The particular procedure used was PROC NLIN and is written as shown in Table I. This is a least-squares procedure for estimating parameters for non-linear models. Data is entered into the program using the DATA statement. This is accomplished by retrieving data stored in a separate file or by typing the data directly into the program as was done here. PROC NLIN invokes the SAS procedure. BEST = 10 requests that the residual sums of squares for only the best iterations are printed. PARMS sets the starting values for the parameters. In this case, _B_0 = asymptote and is set at 50 mg dry weight; _B_1 = growth rate constant: the program will iterate from a value of 0 to 0.99 in increments of 0.05; _B_2 = inflection point: the program will iterate from a value of 15 to 30 in increments of 1.0. The MODEL statement is the equation for the logistic curve written in SAS nomenclature. The remaining statements involve instructions for output of the analysis. Since no method was chosen, the default method DUD was used as the iterative procedure. Several other methods of iteration are possible. The above procedures and statements can be modified for use with the Gompertz, von Bertalanffy, and Richardson equations. As a result, one can determine the equation which best describes the data.