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A NUMERICAL TAXONOMICAL STUDY OF *ARTHROBACTER*

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INCREASED interest in the use of the computers has led us to process the properties recorded of a large collection of freshly isolated cultures of *Arthrobacter* (170 strains) on a IBM 1620 computer. It may be pointed out here that the present-day trend in bacterial systematics is in the direction of recording as many properties of bacteria as possible on their morphology, physiology, nutrition and metabolism. In computing the similarity between two taxonomic entities, numerical taxonomy treats all the taxonomic characters as of equal value and importance. This approach to bacterial systematics has indeed yielded encouraging results in the hands of many investigators.

Among the recently reported investigations on the numerical taxonomy may be mentioned those of Liston,¹ Klinge,² Colwell and Liston³ and Lysenko⁴ on the Gram-negative pseudomonads and related forms and those of Focht and

Lockhart⁵ on the bacterial taxa of both Gram-positive and negative organisms, and of Hill,⁶ Pohja and Gyllenberg,⁷ Cheeseman and Berridge⁸ and Sneath⁹ on the Gram-positive genera. The taxonomy of even Streptomycetes has been examined by Silvestri *et al.*¹⁰ and Hill and Silvestri.¹¹ Numerical taxonomy of the more difficult species as those represented by coryneform bacteria has also been carried out more recently by da Silva and Holt¹² and Harrington.¹³

The present report describes the procedure employed for computer analysis of data recorded for 170 strains of bacteria isolated from glycine enrichments in this laboratory. All the strains were identified as belonging to the genus *Arthrobacter*. A few strains, established by others as those of *Arthrobacter*, were also included in this study. Various characters employed in numerical taxonomy are recorded

in Table I. The methods employed for determining these properties were essentially those recommended in the *Manual of Methods*¹⁴ and reported earlier by Mullakhanbhai and Bhat.^{15,16}

TABLE I
Properties used in the computer analysis for numerical taxonomy of Arthrobacter

1. Gram stain	25. Reduction of tellurite
2. Pleomorphism	26. Utilization of citrate
3. Fragmentation	27. Utilization of ammonium salts
4. Branching	28. Utilization of phenol
5. Motility	29. „ benzoate
6. Surface ring in broth	30. „ asparagine
7. Pellicle in broth	31. „ glycine
8. Turbidity in broth	32. Changes in bromocresol-purple milk
9. Growth in NaCl at concentration of 5%	33. Requirement of growth factors
10. Growth at 37°C.	34. Pigmentation
11. Growth at pH 9.0	35. Acid from arabinose
12. Gelatin hydrolysed	36. „ glucose
13. Starch hydrolysed	37. „ galactose
14. Casein hydrolysed	38. „ rhamnose
15. Tyrosinase produced	39. „ fructose
16. Arginine hydrolysed	40. „ glycerol
17. Urease produced	41. „ mannitol
18. Catalase produced	42. „ sorbitol
19. NH ₄ from peptone	43. „ raffinose
20. Trybutyrin hydrolysed	44. „ lactose
21. H ₂ S produced	45. „ maltose
22. Nitrates reduced	46. „ sucrose
23. M.R. Positive	
24. Indole produced	

For computing percentage similarity (%S) of each isolate in relation to all other isolates, the formula used was:

$$\%S = \frac{NS}{NS + ND} \times 100$$

where NS is the number of features in which the two organisms were alike and ND is the number of features in which they differed. The analysis of the data was carried out in the IBM 1620 and the programme followed was the one kindly furnished by Dr. Colwell. Each of the characters were punched on IBM code cards as 0 for negative, 1 for positive and 3 for not tested; 3 cards were punched for each strain and for all the 46 characters. Thus a total of 570 (510 for 170 new isolated strains and 60 for the 20 established strains) were punched, processed, and the data were got printed on IBM 704 machine and arranged in $t \times t$ table to form a triangular matrix.

The results presented in Table II are the %S values for only 36 representative strains selected from those analysed on the computer. It may be seen from the results that the strains within a group gave %S values between 95 and 100 showing a perfect matching with each other whereas those for individual pairs of strains for different groups were between 40 and 100% showing thereby the diversity among strains belonging to different groups. From the triangular matrix it is evident that the %S values between pair 1 and 9 is 62%, between 1 and 11 is 65%, and 1 and 24 is 68% and so on. Thus the symmetrical matrix provides a ready reference to obtain %S values of any pair of strains listed, besides offering the advantage that it can be used, as and when necessary, to accommodate new entries in appropriate groups.

The results presented here, when examined together with the *Arthrobacter* systematics worked out in this laboratory¹⁷ on the basis of recommendations of the *Bergey's Manual*¹⁸ as well as percentage occurrence of other characters of taxonomic importance, have led the authors to the conclusions that the genus *Arthrobacter* represents a homogeneous group and that Conn and Dimmick¹⁹ were justified in bestowing the taxonomic status to the genus *Arthrobacter* albeit it was done for the convenience of segregating the saprophytic coryneform bacteria from those causing diseases of plants and animals.

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GENERALIZED MEAN-SQUARE AMPLITUDES OF VIBRATION AND SHRINKAGE EFFECT IN LINEAR AND PLANAR XYZ TYPE OF MOLECULES

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SPECTROSCOPIC calculations of mean amplitudes of vibration and shrinkage effects are of great interest in modern electron diffraction studies on gas molecules. In the present investigation, the theory of mean-square amplitudes of vibration is applied to four molecules of the linear XYZ type and two molecules of planar XYZ and their generalized mean-square amplitudes of vibration namely, parallel and perpendicular mean-square amplitudes and mean cross products at 300° K. are evaluated for all the bonded and non-bonded distance deviations.

The perpendicular mean-square amplitudes are determined by Morino's method.¹ The

molecular parameters, frequencies, and kinetic energy matrix elements are taken from references (2) and (3). The parallel mean-square amplitude values for these molecules have been evaluated earlier.⁴ The generalized mean-square amplitudes evaluated for linear and planar XYZ molecules are reported in Tables I and II.

The deviation in the distance between two atoms from the sum of the distances between the atom pairs composing it is called the shrinkage effect. For linear XYZ molecules, using the perpendicular mean-square amplitudes and by applying the theory developed by

TABLE I
Generalized mean-square amplitudes at 300° K. for linear XYZ molecules (Å^2)

Bond	Mean-square amplitude	HN ₃	DN ₃	HNCO	HNCS
X-Y	$\langle(\Delta Z)^2\rangle$	0.001471	0.001478	0.001436	0.001412
	$\langle(\Delta X)^2\rangle$	0.003733	0.003135	0.003302	0.004549
	$\langle(\Delta Y)^2\rangle$	0.000777	0.000829	0.000917	0.001180
	$\langle(\Delta Z\Delta X)\rangle$	0.000312	-0.000253	-0.000031	-0.000032
Y-Z	$\langle(\Delta Z)^2\rangle$	0.001266	0.001272	0.001226	0.001586
	$\langle(\Delta X)^2\rangle$	0.004767	0.004590	0.003828	0.003435
	$\langle(\Delta Y)^2\rangle$	0.000825	0.000881	0.000887	0.000722
	$\langle(\Delta Z\Delta X)\rangle$	-0.000096	-0.000068	0.000003	0.000001
A-X	$\langle(\Delta Z)^2\rangle$	0.005526	0.004025	0.005503	0.005510
	$\langle(\Delta X)^2\rangle$	0.018194	0.012798	0.02288	0.027229
	$\langle(\Delta Y)^2\rangle$	0.000081	0.000087	0.000081	0.000125
	$\langle(\Delta Z\Delta X)\rangle$	-0.000587	-0.010353	-0.001104	-0.001489
X...Z	$\langle(\Delta Z)^2\rangle$	0.003048	0.003172	0.003164	0.003244
	$\langle(\Delta X)^2\rangle$	0.000161	0.000411	0.000202	0.000185
	$\langle(\Delta Y)^2\rangle$	0.000001	0.000001	0.000000	0.000542
	$\langle(\Delta Z\Delta X)\rangle$	-0.000174	-0.000150	-0.000033	-0.000057
A...Y	$\langle(\Delta Z)^2\rangle$	0.011190	0.009797	0.012170	0.012130
	$\langle(\Delta X)^2\rangle$	0.005061	0.004458	0.010456	0.013078
	$\langle(\Delta Y)^2\rangle$	0.000356	0.000380	0.000453	0.000537
	$\langle(\Delta Z\Delta X)\rangle$	-0.000681	-0.002563	-0.007808	-0.010446
A...Z	$\langle(\Delta Z)^2\rangle$	0.014750	0.013360	0.016650	0.017020
	$\langle(\Delta X)^2\rangle$	0.005771	0.005782	0.009339	0.011979
	$\langle(\Delta Y)^2\rangle$	0.000097	0.000104	0.000072	0.000014
	$\langle(\Delta Z\Delta X)\rangle$	-0.001126	0.000145	-0.004334	-0.006066