Application of the calculations of genetic distance for flagellate Systematics

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Summary

The author proposes to assay a phylogenic classification for flagellates based on estimations of genetic distance.
Key words : Flagellates – Natural classification – Genetic distance – Isoenzymes.

Résumé

APPLICATION DES CALCULS DE DISTANCE GÉNÉTIQUE A LA SYSTÉMATIQUE DES FLAGELLÉS

L'auteur propose de tenter une classification phylogénique des flagellés, basée sur les calculs de distance génétique.
Mots-clés : Flagellés – Classification naturelle – Distance génétique – Isoenzymes.

Nei's calculations of genetic distance (Nei, 1972) were previously used rather for sexual organisms. However, nothing forbids their application for asexual animals (Nei, 1972 and personnal communication).

PRINCIPLE OF THE CALCULATIONS

Genetic distance (D) allows to estimate, with electrophoretic data, the number of codon differences per gene between two populations. The rate of protein evolution does not seem to depend on frequency of generations (Wilson *et al.*, 1977) and neither on speciation rate in a given phylad (Avise & Ayala, 1975). The rate seems to be constant, at least in a given class of proteins (Wilson *et al.*, 1977), so genetic distance shows indirectly the time of genetic divergence between 2 populations.

APPLICATION FOR FLAGELLATES

Given two strains X and Y, both be genetically homogeneous (cloning), one may test two enzymes A and B, whose activity, dependant on the genes A and B, gives one band for each enzyme. Band *a* of enzyme A is common for the 2 strains. Enzyme B gives band *b* for X, band *b'* (whose migration is different from that of *b*) for Y.

One may assimilate each strain into a homozygote population, generically monomorphic. For X, frequencies of band *a* ($= x_1$) and band *b* (x_2) are 1. That of *b'* (x_3) is 0. For Y, frequencies are for *a* (y_1) and *b'* (y_3) : 1, and for *b* (y_2) : 0. $\Sigma x^2 = x_1^2 + x_2^2 + x_3 = 2$; $J_x = \Sigma x^2/$number of loci (here, 2) $= 1$. Likewise, $J_Y = 1$. $J_{XY} = \Sigma xy/2 = 0,5$. « Normalized identity » $J_{XY}/(J_X J_Y)^{1/2}$ is equal to J_{XY}, here 0,5. One can deduce $D = Log_e I = 0,692$.

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DISCUSSION

With zymograms of flagellates, one cannot. to elucidate genetic control, make verifications of formal genetics with cross-breedings. For these studies, one actually has the situation which is that for sexual organisms before the genetic control of isozymes has been known. This ignorance did not prevent an estimation of genetic identities for *Drosophila* (Hubby & Throckmorton, 1965 and 1968) with a further estimation of genetic distance (Nei, 1971).

CONCLUSION

For flagellates, principal specific criterion (genetic isolation) is invalid, because each clone is genetically separated from the others. Genetic distances would allow to elucidate the real relationships between the different strains (date or at least order of separation of the different clones from each other) and ultimately elaborate true phylogenic trees.

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