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vol 27 (1, 2) : 44-48, 1984

DIFFERENT RATES OF GENOME DIVERGENCE PRESUMED BETWEEN TWO SPECIES GROUPS IN THE GENUS *ORYZA**

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Two independent species groups in the genus *Oryza* are widely distributed throughout the tropics from Southern China to Northern Australia and to Pakistan as well as in intertropical Africa and America.

One, the *O. sativa* group, comprises, as is suggested in its name, all cultivated forms and their closest wild relatives. They are

all diploid and share only one genome AA as reported in the literature on the basis of chromosome pairing at meiosis in F_1 hybrids. The cultivated forms will not be considered here but it should be emphasized that many wild plants collected from Asia are rather weedy.

The other *O. latifolia* group includes no domesticated form but four genomes are recognized: B, C, D and E. The B, C and

*Presented at Symposium on Chromosomes, 1983.

Such a programme needs time not only 3. BRÜCHER H (1958) Beiträge zur Abstammung

with maximum distribution in Africa, South Asia and Australia, respectively. The D genome is not known at diploid level; it was assumed to correspond to *O. officinalis* in China (5) although this remains to be proven as its cytogenetic relationship with other genomes has not been studied yet. Two allotetraploid genomes are known in nature: BBCC in Africa and Asia and CCDD mainly in America but probably in Asia.

Most of the available world collection (except from China) were studied at a few discriminant isozyme loci and a condensed collection was constituted on the basis of the taxonomical classification, the geographical and ecological origins and preliminary isozyme survey on a few polymorphic loci. The condensed assembly of strains was further studied for additional isozyme loci.

For the *O. sativa* group, 181 strains were analyzed at 24 isozyme loci. In order not to make any *a priori* classification, Nei's standard genetic distances (D) were computed strain to strain in all possible combinations and the matrix of these distances was analyzed by a Principal Coordinate Analysis computer programme.

The clusters of strains assembled on the plane defined by the two first components extracted are shown on figure 1-A. The Australian strains formed a cluster with some of New Guinean origin although morphologically they differ. They are at a maximum genetic distance from all others with a value of D up to 1.26 for some of the Australian strains. Another cluster consisted of the African perennial species *O. longistaminata* only. The third cluster was composite, comprising all Asian and American strains (*O. rufipogon*), some New Guinean strains and the annual African species *O. breviligulata*. It was a surprise that the morphologically divergent American strains could not be distinguished clearly from their Asian counterparts. *O. breviligulata* could be clearly isolated on the basis of some specific

electromorphs as well as morphological characters. Also, when only Asian strains were considered, it appeared that some Chinese strains were clearly distinguished from their South Asian counterparts as shown in figure 1-B. These were strains collected in remote areas, isolated from cultivated rice fields.

In short, 4 main areas of geographic differentiation appear in the Old World: Africa, South Asia, China and Australasia. The American taxa are not clearly distinguishable from the Asian ones and only in Africa can the annual and perennial life forms be distinguished.

The largest genetic distances found between the Australian and other strains point to many millions years of divergence assuming the calibration of the molecular clock adopted in other organisms. The primitive features and wide diversity of the genus *Oryza* among grasses allow to assume its existence in the widely distributed tropical paleoenvironment of tertiary era. It is thus plausible that migration of *Oryza* to Australasia occurred at the time of its collision with South East Asia, that is around 15 million years (m.y.) ago. Rice could have remained isolated in Australia until the present Era. It is remarkable that, assuming such calibration of the isozyme clock, the genetic structure of the *O. sativa* group can be understood as resulting primarily of the isolation of four areas in the Old World through tectonic or climatic events as follows:

- (i) Progressive appearance of inhospitable land for rice between Africa and Asia, due to the aridity and/or cooling of climate. In accordance with the observed genetic distances, it is logical that migration might have been interrupted earlier (10 m.y.) for the perennial life forms adapted to flooded areas than for the annual life forms adapted to temporary pools in arid savannahs (2 or 3 m.y.).
- (ii) Progressive emergence of the Himalayan mountain range known to be geologically very young mountain. It seems to have stopped the migration of Hipparion fauna across it, hence of wild rice, only 2 or 3 m.y. ago.

O. sativa sp.g. (genome AA) wild forms only

Asia only

II ↑

World

with the fact that intermediate genomes CC₁ and CC₂ are found in areas where about twice as rich in DNA as the latter

If we recall that the extension of temperate and mediterranean climate areas is relatively recent while the tropical and subtropical ones have been retreating, it makes sense that species with large DNA amount were selected during this climate shift as they had the ability to speciate more rapidly. This could be an alternative hypothesis (although not exclusive) to the direct adaptative significance of DNA amount proposed by Bennett (1).

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vol 27 (1,2) : 48-63, 1984

CYTOTAXONOMY OF THE OCTOPOLOID AND DECAPLOID SPECIES OF HIBISCUS SECT. FURCARIA (MALVACEAE)*

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The genus *Hibiscus* L. contains 350-400 described species of which about 50 may be assigned to sect. *Furcaria* DC. as defined by Hochreutiner (3). The name *Furcaria* derives from the forked involucreal bracteoles that characterize some but not all of the species, a trait that is usually dominant or epistatic in hybrids between species with forked and unforked bracteoles. The section comprises an extended allopolyploid series (2x to 10x) based on x = 18 small metacentric to submetacentric chromosomes of rather uniform size.

Thirty-eight species studied in the living collection at Florida State University include 10 diploid, 15 tetraploid, eight hexaploid, four octoploid and one decaploid species. Analysis of morphology, chromosome numbers, and geographical distribution of species, chromosome pairing in about 125 different types of interspecific hybrids (4-12), pollen exine morphology (1, 2) and isozyme profiles (Hancock *et al*, unpub) led to a general understanding of relationships among the diploid, tetraploid and hexaploid species. Diploids and tetraploids occur mainly in Africa and South America, whereas the hexaploids are confined to Australia and New Guinea (see 5). Relationships among the higher polyploids, the subject

*Presented at symposium on *Chromosome research—present trend and scope*, Calcutta, 23-26 December, 1983. It was supported partly by US-NSF Grant