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## Genetic approach in *Fusarium* genus concept

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In examining of the generic concepts in mycology, it appear useful to consider the biological evolutionary process among taxa, resulting from heritable change made possible by mutation and natural selection. The anamorphic *Fusarium* genus has been classified traditionally according to various morphological characteristics, but it sometimes presents some limitations such as the subjective interpretation. Moreover, the absence of teleomorphic state in some taxa and the fact that some strains can mutate or degenerate in axenic culture can lead to further difficulties for a correct taxonomic placement. Most of the morpho-classification systems consider the *Fusarium* genus subdivided in several sections solely on the basis of anamorph characters (Wollenweber & Reinking, 1935; Booth, 1971; Gerlach & Nirenberg, 1982; Nelson et al, 1983).

If the *Fusarium* taxonomist aim, besides a morpho-taxonomic identification, has also been to classify the taxa from relationship point of view (phylogeny), we are only partially agree. The fact that some sections may include taxa with different teleomorphic state is not obvious. A attempt on the sectional relationships within the genus *Fusarium*, basing on morphological features, has been made by Booth (1971), but also in this case no perfect correlation exist between sectional relationships and the respective teleomorphic state. In addition, both the subdivision of the anamorph genus *Fusarium* into three distinct teleomorph genera (*Gibberella*, *Calonectria* and *Nectria*) and the fact that *Calonectria* and *Nectria* include species belonging also to different anamorphic genera (e.g. *Cylindrocarpon*, *Tubercularia*, *Dendrodochium*) (Subramanian, 1983) led us to suspect the taxonomic validity of the anamorphic nomenclature. In fact, just little morphological differences it is possible to distinguish between *Fusarium* section *Martiella* and *Cylindrocarpon* genus (Domsch et al., 1980), both belonging to *Neetria* teleomorphie genus. On the other hand, the characteristic fusiform conidia do not necessary represent a related link among *Fusarium* taxa. At this regard, teleomorphic (Müller, 1977) and genetic (Guadet et al.,

1989) studies are agree into remove *Fusarium nivale* (Fr.) Ces. from the anamorph genus *Fusarium* and reassign it to *Microdochium* (Samuels and Hallett, 1983) corresponding to the teleomorphic genus *Monographella*. These results have also been conformed by genetical and toxigenic study of a *Microdochium nivale* (Fries) Samuel & Hallett strain NRRL-3289 (Logrieco et al. 1991b). The molecular biological studies led us to clarify the evolutionary lines in/among each fungal group (phenetic tree), since they are mostly independent from personal interpretation.

Recently, the genetical analysis, with particular reference to molecular biological studies (e.g. sequence comparison of ribosomal RNAs or DNA, variability of the mitochondrial DNA, DNA/DNA hybridization), have proved to be helpful in mycology, including *Fusarium* genus [e.g. taxonomic placement of atypical strain (Logrieco et al., 1990b), in understanding the phylogenetic relationship among fungal taxa (Ellis, 1988; Guadet et al., 1989; Logrieco et al. unpublished), also in relation with their secondary metabolites (Logrieco et al., 1991a)]. Sequence comparisons of large (25S) subunit ribosomal RNA among species in *Fusarium* section *Sporotrichiella* (*F. poae* (Peck) Wollenw., *F. tricinctum* (Corda) Sacc., *F. sporotrichioides* Sherb., *F. chlamydo-sporum* Wollenw. & Reiking) showed a positive correlation between phylogeny based on rRNA sequence and secondary metabolites biochemical data of these species. *Fusarium poae* and *F. sporotrichioides* were the most closely related phylogenetically in accordance with their common ability to produce trichothecenes (Thrane, 1989; Logrieco et al., 1990a). The phylogenetic studies by ribosomal RNA relatedness appear to offer a mean for assessing affinities also above the species level, in *Fusarium* genus. Ribosomal RNA is among the most highly conserved genes known, and its sequence is potential source of information for inferring patterns of evolutionary relationships among taxa. Interpreting rRNA data in relationship to taxonomic level depends greatly upon the level of intraspecific/generic rRNA sequence variation. Dover (1982) used the term molecular drive for the phenomenon of nucleotide sequence identity among the multiple copies of ribosomal RNA in individual organisms and discussed the mechanisms which maintain sequence homogeneity among populations of species.

In anamorphic *Fusarium* genus, the sequence comparison of a select region from large subunit ribosomal RNA (25 S-635) (Logrieco et al., 1991a) showed that the most of *Fusarium* species clustered into main three groups, corresponding to the teleomorphic genera (*Gibberella*, *Calonectria*, *Nectria*) (Guadet et al., 1989; Logrieco et al., unpublished).

Finally, can the molecular techniques be useful in the taxonomic placement (in the evolutionary line) of taxa without a perfect state? In case of their phylogenetic placement has still value to maintain the anamorphic *Fusarium* name? In our preliminary calibration studies the genetic relatedness among *F. graminearum* (Group 1) Schwabe [teleomorphic state *Gibberella zeae* (Schw.) Petch.] *F. crookwellense* (Burgess, Nelson and Toussoun) and *F. culmorum* (W. G. Smith) (both of them without teleomorphic state), showed no base change in large-subunit ribosomal RNA (25S-635) sequence comparison and high nuclear DNA relatedness (> 75%). These findings indicate that the three taxa represents variants of a single taxon (teleomorphic species *Gibberella zeae*) (Logrieco et al., unpublished).

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