

F323 RFLP Analysis of the Intergenic Spacer in the rDNA of *Fusarium* spp.

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The Intergenic Spacer (IGS), which separates rDNA repeat units, appears to be the most rapidly evolving spacer region and closely related species may show considerable divergence in IGS, often reflection both length and sequences variation. Because of the potential for intra- and interspecific variation within the IGS, we compared this region of the rDNA from 9 formae speciales of *Fusarium oxysporum* (Section *Elegans*) and from eleven species of *Fusarium* belonging to Section *Liseola*. Primer CNL12 and CNS1 were used to amplified the IGS region of *Fusarium*. An amplification product was approximately 2.6 Kb that varied somewhat in size depending on the strain. When PCR products were digested with *Bam*HI, *Eco*RV, *Sph*I, *Xba*I, *Hind*III, *Stu*I, *Sac*I and *Xho*I, there were not observed distinct restriction fragments. Digestion of the amplified IGS with *Sma*I and *Hind*II showed a very similar restriction patterns among *F. oxysporum* formae speciales, but different from those of species belonging to Section *Liseola*. When isolates were digested with *Bgl*II, *Kpn*I and *Pst*I, the former two enzymes (*Bgl*II, *Kpn*I) appeared one restriction site in *Elegans* but no site in *Liseola*. The latter enzyme *Pst*I showed one restriction site in section *Liseola* but no site in section *Elegans*. In case of *Eco*RI and *Nru*I, all strains belong to two sections had similar band patterns which could not distinguish section *Elegans* from section *Liseola*. The all strains of *Fusarium* exhibited different *Hin*II, *Alu*I, *Hae*III, *Msp*I and *Taq*I patterns. In general, IGS divergence within the section was more variable than within the species. Comparison of IGS restriction patterns will provide more phylogenetic information in *Fusarium* spp.

F324 Redox-sensitive Modulation of an Anti-Sigma Factor RsrA from *Streptomyces coelicolor* (RsrA, an anti-sigma factor, regulated by redox change in *Streptomyces coelicolor*)

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SigR (σ^R) is a sigma factor in *Streptomyces coelicolor* responsible for inducing *trxBA* gene encoding thioredoxin/thioredoxin reductase upon oxidative stress. We identified an anti-sigma factor for σ^R (RsrA) which binds and inhibits σ^R -directed transcription *in vitro* under reduced conditions. Exposure to H₂O₂ or diamide resulted in dissociation of σ^R from σ^R -RsrA, allowing σ^R -dependent transcription. Thioredoxin was able to reduce RsrA, thus completing the feedback regulatory loop in response to oxidative stress. The result presents a novel example of modulating anti-sigma activity in a redox-dependent manner.