

**TITLE:** COMPARISON OF MOLECULAR IDENTITY IN DIFFERENT DATABASES OF THE SPECIES *Fusarium* spp

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## **ABSTRACT**

The genus *Fusarium* has recently emerged as an important human pathogen, and its identification to the species level requires training and professional experience to characterize the morphology of the fungus through characteristics such as measurement of mycelial growth, conidial dimensions, colony pigmentation and molecular identification, making this process difficult. *Fusarium*-ID and *Fusarium* MLST databases, open access sites on the internet, are used to identify this species. Until then, the most used databases for the molecular comparison were BLAST and BLAST strain type (ST), and the most widely used gene for *Fusarium* is the ITS, known as the bar code of fungi. The objective of our work was to compare the results between these databases and to define which of them are best for *Fusarium* identification. The DNA was extracted from the 32 *Fusarium* samples using the Mini Kit-Qiagen and amplified by the Polymerase Chain Reaction (PCR) using the ITS primers 1 and 4, according to methodology already described by White et al. 1990. The amplified products were separated on 1.5% agarose gel and quantified compared to Low Mass (Invitrogen). Subsequently, they were purified using the enzyme EXOSAP and sequenced by UAMP at Hospital of Clinics of Porto Alegre. The sequences obtained were edited in the CHROMAS PRO program and then compared with the databases BLAST, BLAST strain type, *Fusarium* ID and MLST, with only species having  $\geq 99\%$  similarity accepted. When comparing the results obtained in the database search, it was found that 100% of the results diverged when comparing the BLAST ST base with BLAST and BLAST ST with *Fusarium*-ID, as well as 94% of the BLAST ST results when compared to MLST. Comparing the BLAST base with *Fusarium*-ID, we obtained a 50% concordance result, but when comparing *Fusarium*-ID with MLST, the agreement improved to 59%. The best combination found was between BLAST and MLST bases, resulting in a 69% agreement. These data allow us to conclude that the BLAST and MLST bases are the two best bases for *Fusarium* identification, however, more studies are needed to increase the safety of this data, such as using other genes that are more informative for the species level identification, such as *TEF1 $\alpha$* , *RPB1* and / or *RPB2*.

**Key-words:** *Fusarium* spp., MLST, ITS.

**Development agencies:** Fapergs, CNPQ.