

Figure S4. Screenshot of utilities of the Sym-ITS2 database web portal. The "Dataset" section (section 1) contains ITS2 sequences in the reference core and in the additional GenBank dataset. Information pertinent to these distinct ITS2 variants, such as the position within the original GenBank record, host organism, isolation source, cluster information, and secondary structure, can be viewed by clicking the corresponding sequence in the dropdown list, or searched via text input in the "Search" field. In the "Tools" section, for any user-provided ITS2 region sequence, the cropped ITS2 and the 5.8S and 28S borders are specified. Pressing the "Hybridize" button prompts a visual representation of the proximal stem as shown in section 2. It is also possible for users to run a "BLAST" search against both the core and the extended databases, to find the best match to the unknown sequence and possibly to assign an ITS2 type to it, as shown in section 3. Furthermore, secondary structure of the query sequence can be predicted through homology modeling using structures template archived in the core database, and the result is instantly displayed to allow direct verification of the annotation as shown in section 4.