

## **5: Conclusion and future work**

The results presented in this research showed a partial compatibility between ITS regions including 5.8S region with morphological data in the context of species identification. Further research is needed to clarify precisely the taxonomic relationships of these species. This study showed that ITS marker could be used for classification of nematode species that were available for this project. This molecular marker represents just a small variable part of the nematode genome and can be altered by some molecular events in the cells like endoreduplication and genomic rearrangement as discussed earlier.

There are some other high polymorphic and helpful molecular marker which can be used in additional research that are at times more polymorphic and informative than nuclear ITS such as mitochondrial DNA. Small and large subunit of mitochondrial DNA are found to be a more precise candidate compared to nuclear ITS even though it is less polymorphic in nature due to its uniparental way of inheritance. Because a progeny inherits one of the mitochondrial type from its mother, nematode mitochondria contain more homogeneity compared to genomic ITS regions.

The low polymorphism and low nucleotide divergence among some isolates can be justified as that the existing variants of ITSs that was identified in this research may be the result of some mutations that happened in an ancestral ITS region in a single nematode colony that gave rise to intra-individual variation of the ITS sequences. However the work has to be continue to get more precise data and should be confirmed with other molecular markers as well.