Nucleotide sequence of the 5.8S and 25S rRNA genes and of the internal transcribed spacers from *Arabidopsis thaliana*

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From a genomic library of *Arabidopsis thaliana* (Brassicaceae) constructed in the phage lambda vector EMBL3 we have isolated and subcloned a complete rRNA gene unit. The intergenic region (IGR; 1) and the region coding for 18S rRNA (2) were published previously. Here we present the nucleotide sequences of the 5.8S rRNA and the 25S rRNA genes as well as of the internal transcribed spacers (ITS).

The 5.8S coding region shows 97.0% homology with the 5.8S gene from *Sinapis alba* (Brassicaceae; 3) and 96.9% homology with the 5.8S gene from tomato (4). The 25S coding region has 93.3% homology with the analogous gene from tomato (5).

ITS1 and ITS2, which are regarded as not being evolutionarily conserved, are 75.7% (ITS1) and 81.1% (ITS2) homologous between the two Brassicaceae mustard and *Arabidopsis*, whereas the IGR's of the two Brassicaceae *Raphanus sativus* and *Arabidopsis* show no significant homology. This may indicate that most of the ITS's could be important for post-transcriptional processing.

ACKNOWLEDGEMENTS

REFERENCES

1. Gruendler,P., Unfried,I., Pointner,R. and Schweizer,D. (1989) *Nucl. Acids Res.* **17**, 6395–6396.
2. Unfried,I. and Gruendler,P. (1989) *Nucl. Acids Res.* **17**, 7513.
3. Rathgeber,J. and Capesius,I. (1989) *Nucl. Acids Res.* **17**, 7522.
4. Kiss,T., Kiss,M., Abel,S. and Solymosy,F. (1989) *Nucl. Acids Res.* **17**, 2127.
5. Kiss,T., Kiss,M. and Solymosy,F. (1989) *Nucl. Acids Res.* **17**, 796.

Figure 1. Nucleotide sequences of the 5.8S and 25S coding regions and of ITS1 and ITS2. ITS1 and ITS2 are in upper case, the 5.8S coding region is in upper case and underlined, and the 25S coding region is in upper case and bold.