

The diagram shows a linear arrangement of rDNA repeat units. From left to right, the components are: 5S (transcribed left), NTS2, 5'-ETS, 18S (transcribed right), ITS1, 5.8S (transcribed right), ITS2, 28S (transcribed right), 3'-ETS, and NTS1. Below this diagram is a table comparing the lengths of these regions and the total repeat unit size for three species: *Ag* (*A. gossypii*), *Ecym* (*E. cymbalariae*), and *Sc* (*S. cerevisiae*). Percentages in the table indicate pairwise identity of rRNAs between *E. cymbalariae* and *A. gossypii*, and between *E. cymbalariae* and *S. cerevisiae*.

Ag	121	734	618	1795	207	158	210	3390	964	8197bp
	100%			99%		97%		97%		
Ecym	121	696	625	1796	206	158	210	3391	858	8061bp
	100%			97%		92%		94%		
Sc	121	1243	701	1800	361	158	232	3396	1125	9137bp

Figure S3 Comparison of the rDNA repeat units of *A. gossypii* and *S. cerevisiae* (Wendland *et al.*, 1999) with the rDNA-repeat of *E. cymbalariae*. A single repeat unit (not to scale) is shown starting with the 5S rRNA gene that is divergently transcribed from the precursor 35S pre-rRNA (running from 5'-ETS to 3'-ETS). This precursor contains the 18S, 5.8S, and 25S rRNA genes separated by internal transcribed spacers (ITS1, ITS2) and flanked by external transcribed spacers (5'ETS, 3'ETS). The 5S rRNA gene and the 35S pre-rRNA are separated by non-transcribed spacers (NTS1, NTS2). Length of the individual mature rRNAs and spacer regions is indicated. Using pairwise comparisons % identity of rRNAs between *E. cymbalariae* and *A. gossypii* and between *E. cymbalariae* and *S. cerevisiae* is indicated.