

Table 1 | General characteristics of the genomes of *E. intestinalis* and other microsporidia.

	<i>Encephalitozoon intestinalis</i>	<i>Encephalitozoon cuniculi</i> *	<i>Enterocytozoon bieneusi</i>	<i>Octospora bayeri</i>
Chromosomes (#)	11	11	≥6	Unknown
Genome size (Mbp)	2.3	2.9	6	≤24.2
Assembled (Mbp)	2.2	2.5	3.86	13.3
Genome coverage (%)	96	86	64	55
G + C content (%)	41.4	47	25	26
Gene density (gene per kbp)	0.86	0.84	0.87	0.23
Mean intergenic length	115 bp	119 bp	127 bp	429 bp
Presence of overlapping genes	Yes	Yes	Yes	No
SSU-LSU rRNA genes	22	22	Unknown	≥2
5S rRNA genes	3	3	Unknown	≥2
tRNAs	46	46	46	37
tRNA synthetases	21	21	21	21
tRNA introns (size)	2 (16, 42 bp)	2 (16, 42 bp)	2 (13, 30 bp)	≥1 (50 bp)
Spliceosomal introns (size)	14 (23–47 bp)	14 (23–49 bp)	0	≥6 (24–33 bp)
Predicted ORFs	1,833	1,999	3,804	2,174
ORFs with assigned functional categories	886 (48%)	894 (45%)	669 (39%)	894 (41%)
Mean size of CDS	1,041 bp	1,041 bp	1,002 bp	1,056 bp

Abbreviations: CDS, coding sequences; LSU, large subunit ribosomal RNA gene; ORF, open reading frames; rRNA: ribosomal RNA; SSU, small subunit ribosomal RNA gene; tRNA, transfer RNA.
*Values for *E. cuniculi* differ from those reported in the genome because our reannotation of the genome based on *E. intestinalis* (see Supplementary Data 1) altered the previous annotation of several *E. cuniculi* genes. Values for *E. bieneusi* and *O. bayeri* have been previously reported elsewhere^{26,18}.