

	Genome Size (Mbp)	Scaffolds	N50 (L50) (Kbp)	Contigs	G+C %	Gene Models	CEGMA C   P %	BUSCO C   D   F   M %	Repeats Total   Transposable Elements %	Introns Σ Total x Length	Exons
<i>Pythium aphanidermatum</i>	35.9	1,774	37.38 (0.27)	5,487	53.8	● 12,312	89   95	80   14   4.8   14	1.4   0.26	24,475   - 115   498	
<i>Phytophthora sojae</i>	82.6	83	7609 (0.004)	863	54.6	● 26,584	90   95	84   13   2.5   12	39   -	-   63,535 174   494	
<i>Saprolegnia parasitica</i>	53.09	1,442	280.94 (0.04)	4,125	58	● 20,113	91   95	75   10   9.5   15	40   -	-   68,260 75   337	
<i>Hyphochytrium catenoides</i>	65.7*	4,758	35.57 (0.39)	8,490	49.3	● 18,075	89   93	52   5   11.0   35	9.53   1.79	67,332   85,813 208   228	
<i>Thalassiosira pseudonana</i>	31	27	1992 (0.007)	45	31	● 11,390	89   91	72   10   4.6   22	-   2.0	15,946   28,930 125   613	
<i>Nannochloropsis gaditana</i>	28.4	1,844	38.08 (0.25)	4,045	54.2	● 9,053	73   80	60   17   9.0   30	-   -	14,665   - 220   -	
<i>Ectocarpus siliculosus</i>	195.8	1,561	497.38 (0.11)	13,304	53.6	● 16,788	71   87	43   2.5   22   34	22.7   -	113,619   129,875 703   242	

Numbers in italics are inferrd from scaffold data.

CEGMA: C = Complete, P = Partial

BUSCO: C = Complete, D = Duplicated, F = Fragmented, M= Missing

\* K-mer estimation

All numbers are gathered from the genome portlas of each taxa.