Supporting Text

Recursions. We developed a model to investigate the evolution of ploidy levels in the presence of host-parasite interactions between a focal and nonfocal species. The focal species is assumed to have two loci, a ploidy modifier locus with alleles C_1 and C_2 and an interaction locus with alleles A and a. Thus there are four haploid gamete types in the focal species: AC_1 with frequency X_1, aC_1 with frequency X_2, AC_2 with frequency X_3, and aC_2 with frequency X_4. The modifier locus influences ploidy levels by altering the timing of meiosis; diploid zygotes of genotype C_iC_j have a probability, d_{ij}, of undergoing meiosis late in life, thus experiencing host-parasite selection as a diploid, versus early in life, thus experiencing selection as a haploid (Fig. 2).

The nonfocal species is assumed to be a sexual diploid, having only a brief haploid stage, although results derived with a haploid nonfocal species were similar. For clarity, we assume that the A locus in the focal species interacts with a B locus in the nonfocal species, with alleles B and b. Note that Table 1 differs from this convention by referring to alleles in both species as A and a. We use a different notation here to avoid additional subscripts in the equations. The frequencies of alleles are denoted by p_A, p_a, p_{C1}, and p_{C2} in the focal species and p_B and p_b in the nonfocal species, all measured at the gamete stage of the life cycle (Fig. 2). Also measured at this stage is $D = (X_1 X_4 - X_2 X_3)$, the disequilibrium between the modifier and selected loci in the focal species.

Assuming an infinite population size and random mating, ignoring mutation, and following earlier work by Otto and Goldstein (1), we can write down recursions for the focal and nonfocal species after one round of selection and recombination:

$$TX_1' = X_1X_1(W_{AA}d_{11} + (1-d_{11})W_A) + X_1X_2(W_{Aa}d_{11} + (1-d_{11})W_A) +$$
$$X_1X_3(W_{AA}d_{12} + (1-d_{12})W_A) + X_1X_4(1-r)(W_{Aa}d_{12} + (1-d_{12})W_A) + \qquad \text{(S1a)}$$
$$X_2X_3r(W_{Aa}d_{12} + (1-d_{12})W_A)$$

$$TX_2' = X_1X_2(W_{Aa}d_{11} + (1-d_{11})W_a) + X_1X_4\,r(W_{Aa}d_{12} + (1-d_{12})W_a) +$$
$$X_2X_2(W_{aa}d_{11} + (1-d_{11})W_a) + X_2X_3(1-r)(W_{Aa}d_{12} + (1-d_{12})W_a) + \qquad \text{(S1b)}$$
$$X_2X_4(W_{aa}d_{12} + (1-d_{12})W_a)$$

$$TX'_3 = X_1 X_3 (W_{AA} d_{12} + (1 - d_{12}) W_A) + X_1 X_4\, r(W_{Aa} d_{12} + (1 - d_{12}) W_A) +$$
$$X_2 X_3 (1 - r)(W_{Aa} d_{12} + (1 - d_{12}) W_A) + X_3 X_3 (W_{AA} d_{22} + (1 - d_{22}) W_A) +$$
$$X_3 X_4 (W_{Aa} d_{22} + (1 - d_{22}) W_A) \tag{S1c}$$

$$TX'_4 = X_1 X_4 (1 - r)(W_{Aa} d_{12} + (1 - d_{12}) W_a) + X_2 X_3\, r(W_{Aa} d_{12} + (1 - d_{12}) W_a) +$$
$$X_2 X_4 (W_{aa} d_{12} + (1 - d_{12}) W_a) + X_3 X_4 (W_{Aa} d_{22} + (1 - d_{22}) W_a) +$$
$$X_4 X_4 (W_{aa} d_{22} + (1 - d_{22}) W_a) \tag{S1d}$$

$$p'_B = \left(p_B^2 W_{BB} + p_B p_b W_{Bb} \right) / \overline{W} \tag{S1e}$$

where T is the sum of the right hand sides of Eqs. **S1 a-d**, r is the recombination rate between the ploidy and interaction loci in the focal species, and $\overline{W} = p_B^2 W_{BB} + 2 p_B p_b W_{Bb} + p_b^2 W_{bb}$ is the mean fitness of the nonfocal species.

We incorporate host-parasite coevolution into our model by allowing the fitnesses of the various genotypes to depend on the genetic composition of the interacting species. We assume that encounters between species occur at random, that at most one interaction occurs per generation per individual, and that the probability of the nonfocal species encountering the focal species in its diploid vs. haploid phase is directly proportional to d_{ij}. Defining W_{UIV} as the fitness of genotype U when it interacts with genotype V (Table 1), the fitnesses of the various focal species genotypes are:

$$W_{AA} = p_B^2 W_{AAIBB} + 2 p_B p_b W_{AAIBb} + p_b^2 W_{AAIbb} \tag{S2a}$$

$$W_{Aa} = p_B^2 W_{AaIBB} + 2 p_B p_b W_{AaIBb} + p_b^2 W_{AaIbb} \tag{S2b}$$

$$W_{aa} = p_B^2 W_{aaIBB} + 2 p_B p_b W_{aaIBb} + p_b^2 W_{aaIbb} \tag{S2c}$$

$$W_A = p_B^2 W_{AIBB} + 2 p_B p_b W_{AIBb} + p_b^2 W_{AIbb} \tag{S2d}$$

$$W_a = p_B^2 W_{aIBB} + 2 p_B p_b W_{aIBb} + p_b^2 W_{aIbb}. \tag{S2e}$$

The fitnesses of the nonfocal species genotypes are:

$$W_{BB} = h_A W_{BBIA} + h_a W_{BBIa} + X_1 X_1 d_{11} W_{BBIAA} + 2 X_1 X_2 d_{11} W_{BBIAa} + 2 X_1 X_3 d_{12} W_{BBIAA}$$
$$+ 2 X_1 X_4 d_{12} W_{BBIAa} + X_2 X_2 d_{11} W_{BBIaa} + 2 X_2 X_3 d_{12} W_{BBIAa} + 2 X_2 X_4 d_{12} W_{BBIaa} \tag{S3a}$$
$$+ X_3 X_3 d_{22} W_{BBIAA} + 2 X_3 X_4 d_{22} W_{BBIAa} + X_4 X_4 d_{22} W_{BBIaa}$$

$$W_{Bb} = h_A W_{BbIA} + h_a W_{Bbla} + X_1 X_1 d_{11} W_{BbIAA} + 2 X_1 X_2 d_{11} W_{BbIAa} + 2 X_1 X_3 d_{12} W_{BbIAA}$$
$$+ 2 X_1 X_4 d_{12} W_{BbIAa} + X_2 X_2 d_{11} W_{Bblaa} + 2 X_2 X_3 d_{12} W_{BbIAa} + 2 X_2 X_4 d_{12} W_{Bblaa} \quad \text{(S3b)}$$
$$+ X_3 X_3 d_{22} W_{BbIAA} + 2 X_3 X_4 d_{22} W_{BbIAa} + X_4 X_4 d_{22} W_{Bblaa}$$

$$W_{bb} = h_A W_{bbIA} + h_a W_{bbla} + X_1 X_1 d_{11} W_{bbIAA} + 2 X_1 X_2 d_{11} W_{bbIAa} + 2 X_1 X_3 d_{12} W_{bbIAA}$$
$$+ 2 X_1 X_4 d_{12} W_{bbIAa} + X_2 X_2 d_{11} W_{bblaa} + 2 X_2 X_3 d_{12} W_{bbIAa} + 2 X_2 X_4 d_{12} W_{bblaa} \quad \text{(S3c)}$$
$$+ X_3 X_3 d_{22} W_{bbIAA} + 2 X_3 X_4 d_{22} W_{bbIAa} + X_4 X_4 d_{22} W_{bblaa}$$

where h_A and h_a are the frequencies of A and a, respectively, among individuals that undergo meiosis early in the life cycle and experience selection as haploids:

$$h_A = X_1 X_1 (1 - d_{11}) + X_1 X_2 (1 - d_{11}) + 2 X_1 X_3 (1 - d_{12}) + X_1 X_4 (1 - d_{12})$$
$$+ X_2 X_3 (1 - d_{12}) + X_3 X_3 (1 - d_{22}) + X_3 X_4 (1 - d_{22})$$
$$h_a = X_1 X_2 (1 - d_{11}) + X_1 X_4 (1 - d_{12}) + X_2 X_2 (1 - d_{11}) + X_2 X_3 (1 - d_{12}) + 2 X_2 X_4 (1 - d_{12})$$
$$+ X_3 X_4 (1 - d_{22}) + X_4 X_4 (1 - d_{22})$$

Quasi-Linkage Equilibrium Approximations. A direct mathematical analysis of Eq. **S1** using fitnesses (Eqs. **S2-S3**) is not feasible without making simplifying assumptions. We assume that the selection coefficients are small in both the host (γ_h, ξ_h, α_h <<1) and parasite (γ_p, ξ_p, α_p <<1; see Table 1), that costs of resistance and virulence in the GFG model are small (c_h, c_p <<1) when present, and that recombination is frequent relative to the selection coefficients. Under these assumptions, we can make a quasi-linkage equilibrium (QLE) approximation, where the disequilibrium reaches a steady-state level that depends on the current allele frequencies and is on the order of the selection coefficients, with this process occurring at a time scale that is fast relative to selection (2, 3). At QLE, we can derive conditions for the spread of a modifier that alters the probability of being in the diploid phase by calculating the per-generation change in the frequency of allele C_1. It is worth pointing out that the following results are not driven by the disequilibrium, which contributes only smaller order terms to changes at the ploidy modifier locus.

The GFG Model. First, we modeled GFG interactions (Table 1), where infection reduces host fitness by γ_h and resistance reduces parasite fitness by γ_p. We considered two

different scenarios: (*i*) the focal species is the host, and (*ii*) the focal species is the parasite. When the focal species is the host, the change in the frequency of the C_1 modifier allele is to leading order in the selection coefficients:

$$\Delta p_{C1} = \delta \gamma_h p_A p_a (1 + p_B) p_b p_{C1} p_{C2} \qquad \text{(S4a)}$$

where δ is the effect of carrying a C_1 allele instead of C_2 on the average probability of being diploid during selection ($\delta = p_{C1}(d_{11} - d_{12}) + p_{C2}(d_{12} - d_{22})$). Thus, the C_1 allele will spread only if it increases the probability that the host is diploid ($\delta > 0$). If the focal species is the parasite, the change in the frequency of the modifier is approximately:

$$\Delta p_{C1} = -\delta \gamma_p p_A p_a p_B (1 + p_b) p_{C1} p_{C2} \qquad \text{(S4b)}$$

Thus, C_1 will spread only if it increases the probability that the parasite is haploid ($\delta < 0$).

The GFG Model With Costs. Next, we modeled GFG interactions (Table 1), incorporating a cost of resistance, c_h, in the host, and a cost of virulence, c_p, in the parasite. These costs were assumed to follow the same pattern of dominance as the beneficial effects of these alleles, so that costs were dominant in the host, but recessive in the parasite. Relaxing this assumed pattern of dominance in costs makes it more likely that our general results apply, that is, that diploidy evolves in hosts and haploidy evolves in parasites. When the focal species is the host, the change in the frequency of the C_1 modifier allele is approximately:

$$\Delta p_{C1} = \delta \gamma_h p_A p_a [\gamma_h (1 - p_B^2) - c_h] p_{C1} p_{C2} \qquad \text{(S5a)}$$

Thus, the C_1 allele spreads if it increases the probability that the host is diploid ($\delta > 0$) and $c_h \leq \gamma_h (1 - p_B^2)$. It is reasonable to assume that c_h is less than γ_h at any locus contributing to disease resistance because only then can resistant alleles become established within the population. Nevertheless, c_h can be greater than $\gamma_h (1 - p_B^2)$ at times

when virulence alleles are common in the parasite (p_B near one). If the focal species is the parasite, the change in the frequency of the modifier is approximately:

$$\Delta p_{C1} = -\delta\, \gamma_p p_A p_a [\gamma_p p_B (1 + p_b) - c_p] p_{C1} p_{C2} \qquad \text{(S5b)}$$

Thus, C_1 will spread if it increases the probability that the parasite is haploid ($\delta < 0$) and $c_p \leq \gamma_p p_B (1 + p_b)$. Again, it is reasonable to assume that c_p is less than γ_p because only then can virulence alleles become established within the population. Nevertheless, c_p can be greater than $\gamma_p p_B (1 + p_b)$ at times when resistance alleles are rare in the host (p_B near zero).

The MAM. We next considered the MAM (Table 1), where infection reduces host fitness by ξ_h and resistance reduces parasite fitness by ξ_p. If the focal species is the host, the change in the frequency of the modifier is approximately:

$$\Delta p_{C1} = -\delta\, \xi_h p_A p_a (1 + 2 p_B p_b) p_{C1} p_{C2} \qquad \text{(S6a)}$$

Thus, C_1 is favored only if it increases the probability that the host is haploid ($\delta < 0$). If the focal species is the parasite, the change in the frequency of the modifier is approximately:

$$\Delta p_{C1} = -\delta\, \xi_p p_A p_a (p_B^2 + p_b^2) p_{C1} p_{C2} \qquad \text{(S6b)}$$

Again, C_1 is favored only if it increases the probability that the parasite is haploid ($\delta < 0$).

The Inverse MAM. Finally, we modeled inverse matching alleles interactions (Table 1), where infection reduces host fitness by α_h and resistance reduces parasite fitness by α_p. If the focal species is the host, the change in the frequency of the modifier is approximately:

$$\Delta p_{C1} = \delta\, \alpha_h p_A p_a (p_B^2 + p_b^2) p_{C1} p_{C2} \qquad \text{(S7a)}$$

Thus, C_1 is favored only if it increases the probability that the host is diploid ($\delta > 0$). If the focal species is the parasite, the change in the frequency of the modifier is approximately:

$$\Delta p_{C1} = -\delta\,\alpha_p p_A p_a (p_B^2 + p_b^2) p_{C1} p_{C2} \qquad\qquad\qquad \text{(S7b)}$$

Once again, C_1 is favored only if it increases the probability that the parasite is haploid ($\delta < 0$).

Simulations. Simulations were performed by directly iterating the exact recursions (**S1**). These simulations assume an infinite population size, random mating, and an absence of mutation. For each model of coevolution and combination of parameters, simulations were run three times with initial allele frequencies at the loci under direct selection chosen at random. The initial frequency of the modifier allele C_1 was set at 0.5 in all simulations, and we set $d_{11} = 0.55$, $d_{12} = 0.30$, and $d_{22} = 0.05$. All simulations were run for 3,000 generations and the modifier was considered to have increased in frequency if its average frequency over the 3,000 generations exceeded its initial frequency.

In the GFG model with costs, the ploidy alleles cycle in frequency, as expected from **S5**. Consequently, the changes observed after 3,000 generations might reflect the current phase of the cycle rather than the overall trend in the modifier frequency. As this should bias the results toward diploidy and haploidy being equally favored, it is likely that haploidy is even more favored among parasites than suggested by the simulation results (Table 2).

Statistical Issues with Correlation Between Ploidy and Parasitism. The correlation between haploidy and parasitic life cycles among protists is highly significant if based on the raw numbers of species ($P \ll 0.001$; χ^2 contingency test of Table 3). This is misleading, however, because many of the data points are not statistically independent but come from closely related species (see *Supporting Data*). If we assumed that the

entries in Table 1 are nearly independent because they are distantly related (and/or because they differ in associations), then we can compare the χ^2 statistic from the data to that from randomized data sets (obtained by sampling with replacement from the entries). In this case, the observed data fall at about the 70th percentile of the randomized data sets. This is almost certainly too conservative, however, because it fails to take into account the fact that multiple evolutionary transitions occur within these taxonomic groups. Parasitism, in particular, is a fairly labile trait in many of the protistan groups. Consequently, there are >22 evolutionarily independent data points in the table. From this point of view, it becomes significant that few ciliates are parasites because we can presume that several more transitions to parasitism arose than established, and it becomes significant that most apicomplexa are parasites, because we can presume that several transitions to nonparasitism arose but failed to establish. A refined analysis awaits more data on the ploidy levels and phylogenetic relationships among and within the taxa summarized in Table 3.

1. Otto, S. P. & Goldstein, D. B. (1992) *Genetics* **131,** 745-751.

2. Kirkpatrick, M., Johnson, T. & Barton, N. (2002) *Genetics* **161,** 1727-1750.

3. Nagylaki, T. J. (1993) *Genetics* **134,** 627-647.

Supplementary Figure 2: The life cycle of the focal species. The life cycle starts at the gamete stage (Left) and proceeds through random union of gametes, early meiosis (with probability 1- d_{ij}), selection resulting from host-parasite interactions, late meiosis (with probability d_{ij}), and gametogenesis (Right). It is assumed that gamete production is synchronous for all genotypes. Haploid phases are drawn in single red lines, and diploid phases are drawn in double blue lines.
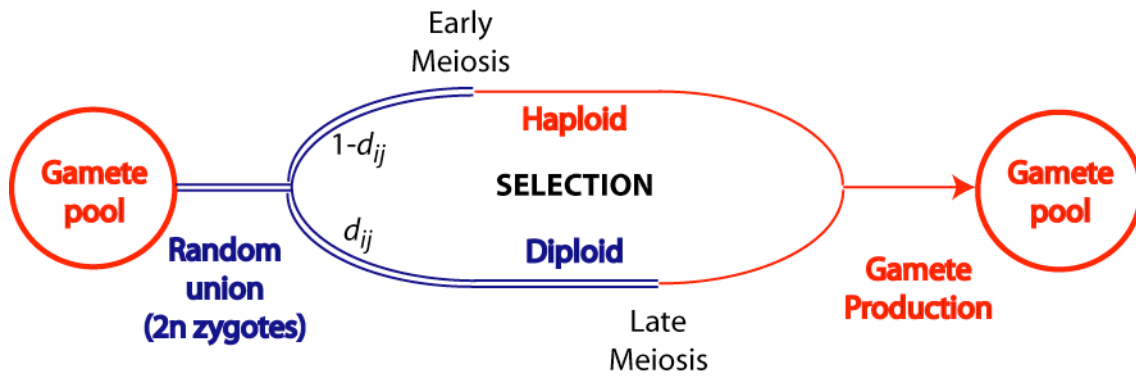
PROTISTS GROUPS (ref. 1)

Cercozoa	Apusozoa
	Heliozoa
	Phytomyxids
	Haplosporidia
	Filosa
	Foraminifera
	Radiolaria
Opisthokonts	Fungi
	Animals
	Nuclearids
	Ichthyosporea
	Choanoflagellates
Amoebozoa	Lobosea
	Slime Molds
	Archamoebae
Excavates	Oxymonads
	Trimastix
	Hypermastigotes
	Trichomonads
	Retortamonads
	Diplomonads
	Carpediamonas
	Jakobids (core)
Discicristates	Kinetoplastids
	Diplonemids
	Euglenids
	Heterolobosea
Chromists	Cryptomonads
	Haptophytes
	Opalinids
	Bicosoecids
	Oomycetes
	Diatoms
	Brown Algae
Alveolates	Ciliates
	Colpodellids
	Apicomplexa
	Dinoflagellates
	Oxyrrhis
	Perkinsus
Plantae	Plants
(Plants and other autotrophs ignored.)	Charophytes
	Chlorophytes
	Red Algae
	Glaucophytes

P. Keeling 2004
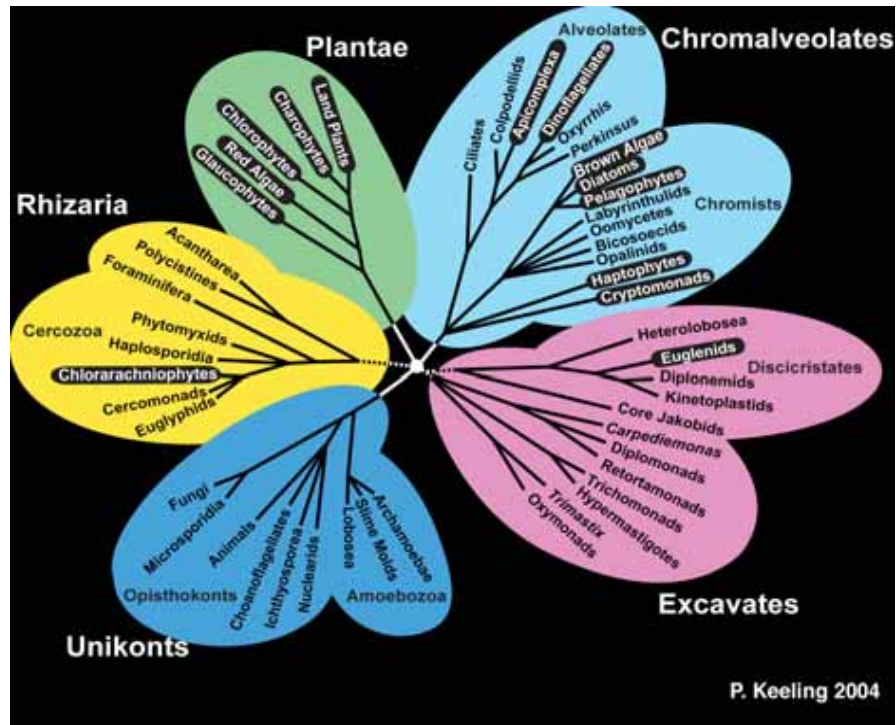
SUMMARY: NUMBER OF SPECIES IN EACH GROUP CONTAINING INFORMATION ON PLOIDY AND LIFE STYLE

Diploid Parasite (~1468-1963 species)
Some Lobosea (<10 species?, ref. 2, p. 7-8)
Some Diplomonads (~8 species, ref. 2, p. 202)
Some Trypanosomes (unknown fraction of ~495 species are diploid, ref. 2, p. 218)
Some Oomycetes (>250 species, ref. 2, p. 672-678)
Some Ciliates (~1200 species; ref. 3, p. 40)

Haploid Parasite (~2573-3068 species)
All Phytomyxids (~29 species, ref. 2, p. 399)
Some Trichomonads (~4 species, ref. 4)
Some Trypanosomes (unknown fraction of ~495 species are haploid, ref. 2, p. 218)
All Apicomplexa (~2400 species, ref. 2, p. 549)
Some Dinoflagellates (~140 species, ref. 5, p. 1)

Diploid Non-Parasite (~7284 species)
All Heliozoa (~90 species, ref. 2, p. 347)
Most Lobosea (~200 species, ref. 2, p. 3)
Some Oxymonads (~20 species, ref. 6)
Some Hypermastigotes (~4 species, ref. 6)
Most Diplomonads (~100 species, ref. 2, p. 202)
Most Ciliates (>6300 species = 85% of 7500, ref. 2, p. 498)
All Opalinids (~400 species, ref. 2, p. 239)
Some Oomycetes (>170 species, ref. 2, p. 672-678)

Haploid Non-Parasite (~1465 species)
Dictyostelium (~50 species, ref. 2, p. 88)
Most Trichomonads (~250 species, ref. 4, 6)
Most Dinoflagellates (~1000 species, ref. 7)
Some Oxymonads (~35 species, ref. 6)
Most Hypermastigotes (~130 species, ref. 6)

Cercozoa

Group	Life style	Reference	Ploidy	Example	Reference	
Apusozoa	Predator	ref. 4, p. 1309				
Heliozoa	Predator		Diploid - selfer	2	ref. 8	
Phytomyxids	Intracellular parasites	ref. 4, p. 1342	Haploid	3	ref. 9, 10	
Haplosporidia	Parasite	ref. 4, p. 1328	Debated		ref. 4, p. 1330	
Filosea (Euglyphids; filoamoeba)	Herbivore/Bacterivore	ref. 4, p. 1055		5		
Foraminifera	Predator		HaploidDiploid	6	ref. 11	
Radiolaria (Polycystinea)	Planktonic; predators	ref. 4, p. 996	Unknown/Multinucleate	7		

NOTE (ORDER)	GENUS	SPECIES	PLOIDY	HAPLOID n	REFERENCE	LIFE STYLE	REFERENCE
2							
Actinophryida	Actinophrys	sol	Diploid - selfer	22	ref. 11	Freshwater Planktonic; Predator	ref. 8, p. 866
Heliozoa	Actinosphaerium		Diploid - selfer			Freshwater Planktonic	ref. 8
3							
Plasmodiophora	*Plasmodiophora (grouped here as phytomyxid, following Cavalier-Smith, ref. 12)						
	Plasmodiophora	brassicae	Haploid		ref. 9, 10	Parasites (obligate, intracellular)	ref. 4, p. 1342
	Spongospora	subterranean					
6							
Foraminiferida	Ovammina	opaca	HaploidDiploid	3	ref. 11		
	Discorbis	vilardeboanus	HaploidDiploid	6	ref. 11	Marine Planktonic	
	Cibicides	lobatulus	HaploidDiploid	6	ref. 11		
	Rubratella	intermedia	HaploidDiploid	8	ref. 11	Marine Planktonic	ref. 8
	Rotaliella	roscoffensis	HaploidDiploid	9	ref. 11	Marine Planktonic	ref. 8
	Rotaliella	heterocaryotica	HaploidDiploid (selfer)	18	ref. 11	Marine Planktonic	ref. 8
	Glabratella	sulcata	HaploidDiploid	9	ref. 11	Marine Planktonic	
	Allogromia	laticollaris	HaploidDiploid (selfer)	10	ref. 11	Marine Planktonic	ref. 8
	Patellina	corrugata	HaploidDiploid (selfer)	24	ref. 11	Marine Planktonic	ref. 8, 13
	Iridia		HaploidDiploid		ref. 8	Marine Planktonic	ref. 8
	Metarotaliella		HaploidDiploid		ref. 8	Marine Planktonic	ref. 8
	Myxotheca		HaploidDiploid (selfer)		ref. 8	Marine Planktonic	ref. 8, 13
	Tretomphalus		HaploidDiploid		ref. 8	Marine Planktonic	ref. 8
7							
Polycystinea			Unknown?		ref. 4, p. 996	Planktonic; predator*	ref. 4, p. 996
Acantharea			Multinucleate**			Marine Planktonic	
Phaeodarea						Marine Planktonic	

* http://www.ucmp.berkeley.edu/protista/radiolaria/rads.html
** http://www.palaeos.com/Eukarya/Units/Acantharea/Acantharea.000.html

Opisthokonts

Group	Life style	Reference	Ploidy	Example	Reference	
Fungi	Not considered					
Animals	Not considered					
Nuclearids	Predatory amoeba	ref. 4, p. 818		3		
Ichthyosporea (Mesomycetozoea)	Parasitic		(sex unknown)	4	ref. 14	
Choanoflagellates	Bacteriovore	ref. 3, p. 31		5		

NOTE (ORDER)	GENUS	SPECIES	PLOIDY	HAPLOID n	REFERENCE	LIFE STYLE	REFERENCE
3							
	Nuclearia						
4 ("DRIPs" clade)							
Dermocystida	Dermocystidium					Parasitic	
	Rhinosporidium	seeberi				Parasitic	ref. 15
Ichthyophonida	Ichthyophonus					Parasitic	
	Psorospermium					Parasitic	
5							
	Corallochytrium						

Amoebozoa

Group	Life style	Reference	Ploidy	Example	Reference
Lobosea (Gymnamoebae?)	Mixed		(sex rare, mixed)	1	
Slime Molds (Mycetozoa)	Detritivores; Predators (bacteriovores)		Mixed	2	
Archamoebae (Pelobionts [Karyoblastea])	free-living heterotrophs	ref. 4, p. 1097	(sex unknown)	3	*

NOTE (ORDER)	GENUS	SPECIES	PLOIDY	HAPLOID n	REFERENCE	LIFE STYLE	REFERENCE
1							
	Acanthamoeba		Polyploid		ref. 16, 17		
	Amoeba	proteus	Polyploid		ref. 16	Predators (Parasitic on coelenterates)	ref. 4, p. 1040
	Entamoeba	histolica	Diploid	14	ref. 18	Parasitic (ordinarily so)	
	Chaos					Predatory	
	Vannella					Predatory	
	Sappinia	diploidia	Dikaryotic		ref. 8	Freshwater predator**	ref. 8
	Hydramoeba	hydroxena					
	Naeglaria	gruberi	HaploidDiploid?		ref. 16		
	Arcella	vulgaris	Diploid (selfer)		ref. 19		
2							
Dyctyosteliida (subclass protostelia)			Primarily haploid				
	Dictyostelium	discoideum	haploid (asexual)				
Subclass Myxogastria [Myxomycota]			Primarily diploid				
	Physarum		haploid (amoebae) diploid (plasmodium)				
3							
	Mastigella						
	Mastigoamoeba						
	Mastigina						
	Pelomyxa						

* http://comenius.susqu.edu/bi/202/Protists/schizomastigotista.htm
** One known opportunistic infection of humans.

Excavates

Group	Life style	Reference	Ploidy	Example	Reference	
Oxymonads	Endocommensal or symbiotic	ref. 2	Mixed	1	ref. 11	
Trimastix	Heterotroph	ref. 4, p. 1326	(sex unknown)			
Hypermastigotes	Symbiotic	ref. 4, p. 1221	Mixed	3		
Trichomonads	Mixed		Haploid	4		
Retortamonads	Parasitic (mostly)	ref. 4, p. 1250	(sex unknown)	5	ref. 20	
Diplomonads	Mixed	ref. 4, p. 1126	doubled haploid (sex absent?)	6		
Carpediemonas	Heterotrophic	ref. 4, p. 1310	?			
Jakobids (core)	Heterotrophic	ref. 4, p. 1316	(sex unknown)		ref. 4, p. 1316	

NOTE (ORDER)	GENUS	SPECIES	PLOIDY	HAPLOID n	REFERENCE	LIFE STYLE	REFERENCE
1							
Oxymonadida	Notila	proteus	Diploid	14	ref. 11, 21	Symbiotic	ref. 8
	Oxymonas	doroaxostylus	Haploid (selfer?)	~25	ref. 11, 21	Symbiotic	ref. 8
	Saccinobaculus	ambloaxostylus	Haploid (selfer?)	~30	ref. 11, 21	Symbiotic	ref. 8
	Pyrsonympha/Dinenympha		Polyploid		ref. 21		
3							
Hypermastigida	Holomastigotoides	tusilata	Haploid	2	ref. 11		
	Holomastigotoides	psammotermitidis	Haploid	2	ref. 11		
	Spirotrichonympha	polygyra	Haploid	2	ref. 11		
	Urinympha	talea	Diploid (selfer)	8	ref. 11, 21	Symbiotic	ref. 8
	Rhynchonympha	tarda	Diploid (selfer)	10	ref. 11		
	Leptospironympha	wachula	Haploid	10	ref. 11, 21	Symbiotic	ref. 8
	Spirotrichosoma	normun	Haploid	12	ref. 11		
	Spirotrichosoma	submagnum/promagnum	Haploid	24	ref. 11		
	Spirotrichosoma	paramagnum	Haploid	48	ref. 11		
	Spirotrichosoma	magnum	Haploid	60	ref. 11		
	Barbulanympha	wenyoni	Haploid (selfer?)	12	ref. 11, 21	Symbiotic	ref. 8
	Barbulanympha	estaboga	Haploid (selfer?)	16	ref. 11, 21	Symbiotic	ref. 8
	Barbulanympha	laurabuda	Haploid (selfer?)	20	ref. 11, 21	Symbiotic	ref. 8
	Barbulanympha	ufalula	Haploid (selfer?)	26	ref. 11, 21	Symbiotic	ref. 8
	Trichonympha	okolona & others	Haploid	24	ref. 11, 21	Symbiotic	ref. 8
	Eucomonympha	imla	Haploid	~50	ref. 11, 21	Symbiotic	ref. 8
	Macrospironympha		Diploid		ref. 21	Symbiotic	ref. 8
	Rhynchonympha		Diploid		ref. 21	Symbiotic	ref. 8
4							
Trichomonadida	Trichomonas	caviae	Haploid	4	ref. 11	Parasite (Commensal?)	
	Trichomonas	vaginalis	Haploid		ref. 22	Parasite (humans)	ref. 23
	Tritrichomonas	batrachorum	Haploid	6	ref. 11	Parasite (Commensal?)	ref. 24
	Dientamoeba	fragilis	Haploid	4	ref. 11	Commensal	ref. 4, p. 1207
	Mixotricha	paradoxa				Symbiont	ref. 2
5							
	Retortamonas						
	Chilomastix						
6							
	Hexamita						
	Giardia	intestinalis				Parasite	ref. 4, p. 1126
	Giardia	lamblia					

Discicristates

Group	Life style	Reference	Ploidy	Example	Reference	
Kinetoplastids	Mixed		Haploid (sex generally not observed)	1	ref. 11	
Diplonemids	Mixed	ref. 4, p. 1157	?	2		
Euglenids	Predators/auxotrophs	ref. 3, p. 28	(sex unknown)	3		
Heterolobosea	Mixed	ref. 4, p. 1107	?	4	ref. 11	

NOTE (ORDER)	GENUS	SPECIES	PLOIDY	HAPLOID n	REFERENCE	LIFE STYLE	REFERENCE
1							
Of the two unifamily suborders of kinetoplastids, ploidy levels have only been mentioned for the Trypanosomatina and not for the Bodonina. Thus, only trypanosomes are reported.							
Trypanosomatina	Trypanosoma	equiperdum	Haploid	3	ref. 11	Parasite	
	Trypanosoma	lewisi	Haploid	3	ref. 11	Parasite	
	Trypanosoma	cruzi	Diploid/aneuploid		ref. 25, 26	Parasite	
	Trypanosoma	brucei gambiense/brucei rhodesiense	Diploid (in humans?; sex rare)		ref. 27	Parasite	
	Leishmania		Diploid (in humans?; sex rare)			Parasite	
Bodonina	Bodo	saltans				Bacteriovore	ref. 3, p. 29
2							
	Diplonema						
	Rhynchopus						
3							
	Paranema						
	Euglena						
4							
	Naegleria	gruberi	?				

Chromists

Group	Life style	Reference	Ploidy	Example	Reference		
Cryptomonads	Autotroph*	ref. 4, p. 1116	(sex largely unknown)	1	ref. 28		
Haptophytes (prymnesiida)	Autotroph**	ref. 4, p. 1273	HaploidDiploid	2	ref. 4, p. 1274		
Opalinids	Commensal***	ref. 2	Diploid	3	ref. 10		
Bicosoecids	Heterotroph	ref. 4, p. 752	(sex unknown)		****		
Oomycetes	Mixed (saprophytes & parasites*)	ref. 2	Diploid	5	ref. 2, 10, 30		
Diatoms	Autotroph		Diploid				
Brown Algae	Autotroph		HaploidDiploid				

NOTE (ORDER)	GENUS	SPECIES	PLOIDY	HAPLOID n	REFERENCE	LIFE STYLE	REFERENCE
1							
	Proteomonas	sulcata	HaploidDiploid		ref. 28	Autotroph	
	Goniomonas		unknown		ref. 28	Heterotroph	
	Chilomonas		unknown		ref. 28	Heterotroph	
2							
Prymnesiomonads						Autotrophs**	ref. 4, p. 1273
	Hymenomonas		HaploidDiploid		ref. 10		
	Pleurochrysis		HaploidDiploid		ref. 10		
Coccolithophorids	Coccolithophorids		HaploidDiploid		*****		
3						Commensals***	ref. 2
Opalinida	Zelleriella	(5 species)	Diploid	24	ref. 11		
	Opalina	ranarum	HaploidDiploid (primarily diploid, ref. 4, p. 755)	9	ref. 11		
	Opalina		Diploid		ref. 8		
	Protoopalina						
5							
	Phytophthora	infestans					
	Phytophthora	cambivora	Diploid	10-12	ref. 30	Pathogen	ref. 30
	Phytophthora	fragariae	Diploid	10-12	ref. 30	Pathogen	ref. 30
	Pythium	irregulare	Diploid		ref. 31	Pathogen	

* Except Goniomonas and Chilomonas are heterotrophs
** Many supplement autotrophy with heterotrophy; some coccolithophorids are obligate heterotrophs. Symbionts also known. (See also ref. 2.)
*** Although generally classified as parasitic because they live on their hosts, opalinids are more likely commensals, as there is no evidence that they harm their hosts (ref. 2).
**** http://comenius.susqu.edu/bi/202/Protists/bicoflagellota.htm
*****http://www.uga.edu/~protozoa/portal/Radiolaria_captions.html

ALVEOLATES

Group	Life style	Reference	Ploidy	Example	Reference	
Ciliates	Mixed*	ref. 3, p. 40	Diploid	1	ref. 32	
Colpodellids	Predator	ref. 4, p. 370	?	2		
Apicomplexa	Intracellular parasites		Haploid	3	ref. 3, p. 43	
Dinoflagellates	Mixed**	ref. 2, 7	Haploid	4	ref. 7, 11	
Oxyrrhis	Predator; saprobe	ref. 4, p. 686	?	5		
Perkinsus	Parasite	ref. 4, p. 200	Debated	6	ref. 33	

NOTE (ORDER)	GENUS	SPECIES	PLOIDY	HAPLOID n	REFERENCE	LIFE STYLE	REFERENCE
1	Diploid according to ref. 32;	dikaryotic according to ref. 4.					
Karyorelictida	Tracheloraphis	phoenicopterus	Diploid	17	ref. 11		
	Tracheloraphis	caudatus	Diploid	22	ref. 11		
	Trachelocerca	coluber	Diploid	~27	ref. 11		
	Trachelonema	sulcata	Diploid	28	ref. 11		
Nassulida	Nassula	ornata	Diploid	~20	ref. 11		
Hymenostomatida	Tetrahymena	thermophila	Diploid (selfer?)	5	ref. 11	Freshwater	ref. 8
	Colpidium	campylum	Diploid	21	ref. 11	Freshwater	ref. 8
	Paramecium	tetraurelia	Diploid (selfer?)	35-50	ref. 11	Freshwater	ref. 8
	Paramecium	primaurelia	Diploid (selfer?)	43-63	ref. 11	Freshwater	ref. 8
	Paramecium	triaurelia	Diploid (selfer?)	77-85	ref. 11	Freshwater	ref. 8
	Paramecium	jenningsi	Diploid (selfer?)	~64	ref. 11	Freshwater	ref. 8
	Paramecium	bursaria (raceFD)	Diploid (selfer?)	~40	ref. 11	Freshwater	ref. 8
	Paramecium	bursaria (2 strains)	Diploid (selfer?)	~52	ref. 11	Freshwater	ref. 8
	Paramecium	caudatum	Diploid (selfer?)	~165	ref. 11	Freshwater	ref. 8
	Ichthyophthirius		Diploid			Parasitic	ref. 8
	Ophryoglena		Diploid			Parasitic	ref. 8
Peritrichida	Vorticella	campanula	Diploid	~75	ref. 11	Freshwater Epi	ref. 8
	Zoothamnion		Diploid		ref. 8	Freshwater Epi	ref. 8
	Opercularia		Diploid		ref. 8	Freshwater Epi	ref. 8
Heterotrichida	Blepharisma	japonixcum	Diploid	~59	ref. 11		
	Spirostomum	ambiguum	Diploid	18-24	ref. 11		
	Climacostomum	virens	Diploid	~60	ref. 11		
Hypotrichida	Euplotes	woodruffi	Diploid	~16	ref. 11		
	Euplotes	patella	Diploid	~24	ref. 11		
	Euplotes	aediculatus	Diploid	50-60	ref. 11		
	Kahlia	sp.	Diploid	~25	ref. 11		
	Stylonychia	mytilus	Diploid	125-150	ref. 11		
Haptorida	Didinium		Diploid		ref. 8	Freshwater	ref. 8
?	Gymnodinioides		Diploid		ref. 8	Parasitic	ref. 8
Armorphorida	Metopus		Diploid		ref. 8	Freshwater	ref. 8
Exogemmida	Spirochona		Diploid		ref. 8	Freshwater Epi	ref. 8
Endogenida	Tokophyra		Diploid		ref. 8	Freshwater Epi	ref. 8
Evaginogenida	Stylocometes		Diploid		ref. 8	Freshwater Epi	ref. 8
Exogenida	Ephelota		Diploid		ref. 8	Freshwater Epi	ref. 8

2

	Colpodella	edax					

3

	Mattesia	trogodermae	Haploid	2	ref. 11	Parasitic	ref. 8
Gregarinia							
	Diplocystis	schneideri	Haploid	3	ref. 11		
	Gregarina	blattarum	Haploid	3	ref. 11	Parasitic	ref. 8
	Actinocephalus	parvus	Haploid	4	ref. 11		
	Stylocephalus	longicollis	Haploid	4	ref. 11	Parasitic	ref. 8
	Stylocephalus	mesomorphi	Haploid	4	ref. 11	Parasitic	ref. 8
	Stylocephalus	conoides	Haploid	8	ref. 11	Parasitic	ref. 8
	Stylocephalus	elongatus	Haploid	9	ref. 11	Parasitic	ref. 8
	Zygosoma	globosum	Haploid	6	ref. 11		
	Lipocystis	polyspora	Haploid		ref. 13	Parasitic	ref. 8
Coccidia	Coelotropha	durchoni	Haploid	3	ref. 11		
	Klossia	helicina	Haploid	4	ref. 11	Parasitic	ref. 8
	Eimeria	maxima	Haploid	5	ref. 11	Parasitic	ref. 8
	Eimeria	tenella	Haploid	5	ref. 11	Parasitic	ref. 8
	Karyolysus	lacertae	Haploid	5	ref. 11	Parasitic	ref. 8
	Eucoccidium	dinophili	Haploid	5	ref. 11	Parasitic	ref. 8
	Aggregata	eberthi	Haploid	6	ref. 11	Parasitic	ref. 8
	Merocystis	kathae	Haploid	6	ref. 11		
	Adelea	cryptocerci	Haploid	8	ref. 11		
	Adelina	deronis	Haploid	10	ref. 11	Parasitic	ref. 8
	Plasmodium	berghei	Haploid	8	ref. 11	Parasitic	ref. 8
	Haemoproteus		Haploid		ref. 8	Parasitic	ref. 8
	Toxoplasma	gondii	Haploid		ref. 34	Parasitic (intracellular pathogen)	ref. 34
Piroplasmida	Babesia		Haploid		ref. 10		
	Theileria		Haploid		ref. 10		

4   Margulis (2) notes that parasitic dinoflagellates are "common", although their hosts are often other protists & algae.

			Mostly haploid except:				
	Noctiluca		Diploid		ref. 10		

5

	Oxyrrhis	marina					

6

	Perkinsus	marinus	Debated		ref. 33		

* Predators; 15% are parasites, many ectoparasites (ref. 3)
** Photoauxotrophs (~50%); heterotrophs; parasites (ref. 2)

For those groups in which species counts were needed:

Oomycete species numbers (ref. 2)

		# Species Parasitic	# Species Saprophytic	# Species Both
Peronnosporomycetidae	Leptomitales		8	
	Rhipidiales		13	
	Sclerosporiales	21		
	Pythiaceae			159
	Peronosporales	141-326		
Saprolegniomycetidae	Saprolegniales	some	147	
Mixed	ref. 2, Table 2, p. 673	97	5	40
	TOTAL	259-444	173	199

Excavate species numbers (ref. 2, 3, 6)

700 species of "Retortomonads and axostylata" including diplomonads, retortamonads, oxymonads, parabasalia (trichomonads, hypermastigotes), ref. 3.
Retortamonads ~50 species, ref. 2, p. 259.
Oxymonads/pyrsonymphida ~68 species (from lower termites), ref. 6.
Diplomonads ~108 species, ref. 2, p. 202
Hypermastigotes ~191 species (from lower termites), ref. 6
Trichomonads ~175 species(from lower termites), ref. 6.

Oxymonad species numbers (ref. 6)
(any member of same
genus considered)

			# Species	
	Notila	Diploid	1	
	Oxymonas	Haploid (selfer?)	30	
	Saccinobaculus	Haploid (selfer?)	5	
	Pyrsonympha/Dinenymph:	Polyploid	21	(higher ploidy levels counted as "diploid" for the purpose of our hypothesis)

Hypermastigida species numbers (ref. 6)
(any member of same
genus considered)

		# Species	
Holomastigotoides	Haploid	36	130
Spirotrichonympha	Haploid	29	
Leptospironympha	Haploid	12	
Spirotrichosoma	Haploid	12	
Barbulanympha	Haploid (selfer?)	4	
Trichonympha	Haploid	35	
Eucomonympha	Haploid	2	
Macrospironympha	Diploid	1	4
Urinympha	Diploid (selfer)	2	
Rhynchonympha	Diploid (selfer)	1	

Trichomonadida ~175 species in termites & ~80 species in non-termites

~175 species in termites	ref. 6 (considered to be haploid non-parasitic species, although ploidy levels are not well known)
~80 species in non-termites	ref. 4 (considered to be haploid non-parasitic species, although ploidy levels are not well known)
Parasitic species:	Trichomonas vaginalis
	Trichomonas gallinae
	Tritrichomonas foetus
	Histomonas meleagridis

Although trichomonads are found in vertebrates and invertebrates, pathogenic effects are not demonstrated in most.

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