

Summary: Comparative analysis of different parameters between sexual and asexual species of Chalcidoidea

Species used for comparisons:

Manual dataset:

- In total: 133 species (50 asexual, 83 sexual)
- Reported into 32 pairs.

Family	Genus	Asex	Sex	Total
Aphelinidae	Aphelinus	2	9	11
	Aphytis	20	35	55
	Encarsia	7	8	15
	Eretmocerus	2	3	5
Torymidae	Megastigmus	7	11	18
	Torymus	1	2	3
Trichogrammatidae	Megaphragma	1	1	2
	Trichogramma	10	12	22
	Trichogrammatoidea	0	2	2

Comparison groups inferred based on either morphological or genetic data:

Genus	Morphologically inferred	Genetically inferred	% genetically inferred
Aphelinus	4	7	64%
Aphytis	41	14	25%
Encarsia	0	16	100%
Eretmocerus	0	5	100%
Megastigmus	0	18	100%
Torymus	3	0	0%
Megaphragma	2	0	0%
Trichogramma	0	22	100%
Trichogrammatoidea	0	2	100%

Automated dataset:

- In total: 8357 species (136 asexual, 8221 sexual) from 66 genera in 11 families.
- No pairs, using genera instead.

Family	Asexual	Sexual	Total
Aphelinidae	46	1006	1052
Chalcididae	1	304	305
Encyrtidae	22	1314	1336
Eulophidae	22	2148	2170
Eupelmidae	1	481	482
Eurytomidae	3	879	882
Leucospidae	1	117	118
Mymaridae	12	528	540
Pteromalidae	6	680	686
Torymidae	8	517	525
Trichogrammatidae	14	247	261

Family	Genus	Sexual	Asexual	Percentage.of.asexuals
Aphelinidae	Aphelinus	88	3	3.3%
Aphelinidae	Aphytis	83	15	15.31%
Aphelinidae	Coccophagus	263	0	0%
Aphelinidae	Encarsia	410	20	4.65%
Aphelinidae	Eretmocerus	76	4	5%
Aphelinidae	Paraphytis	16	3	15.79%
Aphelinidae	Pteroptrix	70	1	1.41%
Chalcididae	Brachymeria	304	1	0.33%
Encyrtidae	Adelencyrtus	33	1	2.94%
Encyrtidae	Anagyrus	276	1	0.36%
Encyrtidae	Anicetus	50	1	1.96%
Encyrtidae	Arrhenophagus	3	0	0%
Encyrtidae	Blepyrus	17	1	5.56%
Encyrtidae	Clausenia	11	1	8.33%
Encyrtidae	Coccidoxenoides	0	1	100%
Encyrtidae	Comperiella	8	1	11.11%
Encyrtidae	Copidosoma	200	1	0.5%
Encyrtidae	Diaphorencyrtus	1	1	50%
Encyrtidae	Diversinervus	11	1	8.33%
Encyrtidae	Encyrtus	86	2	2.27%
Encyrtidae	Habrolepis	15	2	11.76%
Encyrtidae	Hambletonia	9	0	0%
Encyrtidae	Microterys	200	1	0.5%
Encyrtidae	Ooencyrtus	306	2	0.65%
Encyrtidae	Plagiomerus	9	1	10%
Encyrtidae	Prochiloneurus	32	1	3.03%
Encyrtidae	Protyndarichoides	4	0	0%
Encyrtidae	Pseudleptomastix	4	1	20%
Encyrtidae	Trechnites	24	1	4%
Encyrtidae	Zaplatycerus	15	1	6.25%
Eulophidae	Aprostocetus	770	4	0.52%
Eulophidae	Baryscapus	120	1	0.83%
Eulophidae	Ceranisus	36	3	7.69%
Eulophidae	Galeopsomyia	19	1	5%
Eulophidae	Holarcticesa	1	1	50%
Eulophidae	Necremnus	37	2	5.13%
Eulophidae	Neochrysocharis	49	0	0%
Eulophidae	Omphale	256	8	3.03%

Family	Genus	Sexual	Asexual	Percentage.of.asexuals
Eulophidae	Oomyzus	25	1	3.85%
Eulophidae	Pediobius	219	0	0%
Eulophidae	Pnigalio	60	0	0%
Eulophidae	Tamarixia	50	1	1.96%
Eulophidae	Tetrastichus	506	0	0%
Eupelmidae	Anastatus	146	1	0.68%
Eupelmidae	Eupelmus	335	0	0%
Eurytomidae	Bephratelloides	6	0	0%
Eurytomidae	Eurytoma	675	1	0.15%
Eurytomidae	Tetramesa	198	2	1%
Leucospidae	Leucospis	117	1	0.85%
Mymaridae	Anagrus	82	5	5.75%
Mymaridae	Anaphes	218	1	0.46%
Mymaridae	Caenomymar	0	1	100%
Mymaridae	Polynema	223	4	1.76%
Mymaridae	Stephanocampta	5	1	16.67%
Pteromalidae	Mesopolobus	123	1	0.81%
Pteromalidae	Muscidifurax	4	1	20%
Pteromalidae	Nasonia	3	1	25%
Pteromalidae	Pteromalus	483	0	0%
Pteromalidae	Spalangia	58	3	4.92%
Pteromalidae	Trichilogaster	9	0	0%
Torymidae	Ditropinotus	2	0	0%
Torymidae	Megastigmus	126	7	5.26%
Torymidae	Torymus	389	1	0.26%
Trichogrammatidae	Megaphragma	12	3	20%
Trichogrammatidae	Trichogramma	208	11	5.02%
Trichogrammatidae	Trichogrammatoidea	27	0	0%

First impressions:

- No effect on body length.
- Seems to have an effect on number of host species.

Notes

- Some of the species are not in a relation group yet, either because they have both reproduction modes, or because there was no “hard proof” that they were related to any other species
- Species from the Trichogrammatoidea family are clustered with other species of the Trichogramma family because they were really closely related on ITS2 phylogenies.

Variables analysed:

Geographical distribution: Locations at which species were sampled have been extracted from the nhm database. Used an automatic script to compute the geographical center of each location. Locations are in latitude; longitude decimal format.

Number of locations: Number of different locations at which species were sampled.

Reproduction mode: Coded as sexual, asexual, or both. Both means there are sexual and asexual populations in a given species. These species are excluded from analyses.

Body length: The length of the body, excluding the ovipositor. Accuracy of the values varies between authors. Min and Max known values are stored when a range is given. If a single value is given, Min and Max are the same. Values are given in millimeters.

Biogeographic regions: [indicative, temporary] World was divided in 7 biogeographic regions and species presence was recorded in a binary fashion.

Extreme coordinates: Max and Min longitude and latitude at which each species has been encountered. These values were extracted from the geographical distribution, meaning they do not represent exact values, but rather geographical center of the most accurate definition of the sampling site.

Number of host species: Overall number of host species for a given wasp species.

Host orders/families: Host range recorded in a binary fashion, hosts orders are given except when an order is especially relevant, in which case families are given.

Development time: Time from oviposition to emergence of adult. This data is indicative and should be used with care since experimental conditions (i.e. Temperature, day/night cycles, host species, host age, humidity) strongly affect results. Values are given in days.

Ecology: Encoded as parasitoid or phytophagous. This value is roughly estimated per genus in the automated dataset, but is more accurately determined in the manual dataset.

Analyses performed

Overall: These analyses include all species independantly of their genera or families. They are not very informative since the effect of reproduction is masked by the inter-family difference.

Within Family: Same, Inter-genus difference might hide the effect of reproduction mode.

Within genus: More accurate, but some species might still be quite distant. This is the most accurate analysis that can be performed with the automated dataset.

Per comparison group: Only comparing species that are known to be closely related, either on the basis of morphological studies, or phylogenetics studies (Generally CO1 or 18S / 28S rDNA). This is the most accurate analysis performed and is only available with the manual dataset.