Fig. S1. Phylogeny of Oonopidae and related families based on *28S* sequence data. Majority rule consensus Bayesian tree is shown. Squares represent bootstrap values of BI, ML and MP analyses respectively with strong support (black: BI ≥ 0.95; ML, MP ≥ 0.70), moderate support (grey: 0.75 ≤ BI < 0.95; 0.60 ≤ ML, MP < 0.70), weak support (white: 0.50 < BI < 0.75; 0.50 < MP, ML < 0.60) and no support (square with diagonal line).

Table S1. Estimates of average evolutionary divergence calculated as the number of base differences per site averaging over all sequence pairs within each species, genus and family in MEGA5 (TAMURA et.al. 2011, option: pairwise deletion).

	18S		28S	
	taxa	p	taxa	p
Paradysderina vlad	2	0.002		
Orchestina communis	2	0.008		
Neotrops waorani	2	0.001	2	0.005
Heteroonops spinimanus	2	0.000	2	0
Brignolia kapit	3	0	3	0.001
Tapinesthis inermis	2	0	2	0.002
Oonops	2	0.019	3	0
Orchestina	16	0.039	5	0.074
Tridysderina	3	0.006	3	0.010
Paradysderina	5	0.016	4	0.044
Scaphidysderina	2	0.017	2	0.052
Opopaea	7	0.012	5	0.017
Xyphinus	3	0.030	2	0.063
Ischnothyreus	4	0.029	2	0.125
Neotrops	6	0.022	4	0.071
Scaphiella	2	0.028	4	0.130
Escaphiella	4	0.012		
Niarchos	2	0.037		
Scaphios	2	0.022		
Lucetia	2	0.004		
Silhouttella	2	0.051		
Aschnaoonops	3	0.012		
Australoonops	2	0.005		
Birabenella	2	0.007		
Melchisedec	2	0.013		
Unicorn	2	0.006		
Triaeris	4	0.000		
Brignolia	3	0.000	3	0
Dysdera	3	0.005		
Ariadna	3	0.002	2	0.016
Segestria	2	0.006		
Dysderidae	7	0.008		
Segestriidae	5	0.007		
Filistatidae	2	0.010		
Oonopidae	102	0.064	57	0.119