

A Meta-analysis of Longevity Estimates of Mosquito Vectors of Disease: Supplementary Figures

Ben Lambert, Ace North, Charles Godfray

December 10, 2020

S1 Lifespan estimates

Genus	Species	5%	25%	50%	75%	95%	Mean	Std. dev.
<i>Aedes</i>	<i>simpsoni s.l.</i>	6.3	11.3	18.3	31.8	75.0	26.9	29.5
<i>Aedes</i>	<i>communis</i>	10.0	13.2	15.4	18.2	24.3	16.2	5.2
<i>Anopheles</i>	<i>koliensis</i>	6.7	10.5	15.2	24.0	56.5	21.9	25.2
<i>Anopheles</i>	<i>punctulatus</i>	7.2	10.7	15.1	22.8	48.9	20.3	28.6
<i>Aedes</i>	<i>cantans</i>	9.7	12.0	13.9	16.1	20.6	14.4	4.7
<i>Aedes</i>	<i>albopictus</i>	8.0	10.0	11.6	13.7	17.7	12.1	3.4
<i>Anopheles</i>	<i>albimanus</i>	5.9	8.6	11.6	16.9	35.7	15.2	18.7
<i>Anopheles</i>	<i>darlingi</i>	4.9	7.3	10.2	16.0	37.5	14.5	14.8
<i>Anopheles</i>	<i>maculatus</i>	5.7	7.9	10.2	13.7	24.3	12.2	8.7
<i>Anopheles</i>	<i>culicifacies s.l.</i>	4.6	7.3	9.1	11.4	18.2	10.1	6.9
<i>Anopheles</i>	<i>sergenti</i>	3.6	5.9	8.7	13.8	32.6	12.4	13.4
<i>Aedes</i>	<i>triseriatus</i>	5.6	6.6	7.5	8.5	10.7	7.7	1.8
<i>Anopheles</i>	<i>farauti s.l.</i>	4.2	5.4	6.4	7.7	10.5	6.8	2.1
<i>Aedes</i>	<i>africanus</i>	3.4	5.1	6.2	7.8	11.9	7.0	9.3
<i>Aedes</i>	<i>aegypti</i>	2.8	4.5	6.2	8.5	13.9	7.0	3.8
<i>Culex</i>	<i>quinquefasciatus</i>	4.3	5.2	5.9	7.0	9.4	6.3	1.8
<i>Culex</i>	<i>nigripalpus</i>	3.5	4.6	5.8	7.5	11.3	6.4	3.1
<i>Aedes</i>	<i>notoscriptus</i>	2.9	4.0	5.4	8.2	20.2	7.9	9.5
<i>Culex</i>	<i>pipiens</i>	3.4	4.4	5.2	6.4	9.0	5.6	2.0
<i>Anopheles</i>	<i>saperoi</i>	3.5	4.2	4.9	5.8	8.2	5.2	2.0
<i>Anopheles</i>	<i>gambiae s.l.</i>	3.0	3.8	4.4	5.1	6.4	4.5	1.1
<i>Aedes</i>	<i>melanimon</i>	3.3	3.9	4.3	4.8	5.7	4.4	1.0
<i>Anopheles</i>	<i>funestus s.l.</i>	2.9	3.6	4.2	4.8	6.0	4.3	1.0
<i>Anopheles</i>	<i>lesteri</i>	2.4	3.2	3.9	5.0	7.5	4.4	2.1
<i>Anopheles</i>	<i>quadrimaculatus</i>	3.3	3.6	3.9	4.2	4.8	4.0	0.5
<i>Anopheles</i>	<i>pseudopunctipennis s.l.</i>	2.3	2.9	3.5	4.3	6.7	3.8	1.9
<i>Aedes</i>	<i>vexans</i>	1.9	2.3	2.6	3.0	4.1	2.8	1.0
<i>Culex</i>	<i>tarsalis</i>	1.9	2.1	2.3	2.4	2.7	2.3	0.3
<i>Anopheles</i>	<i>vestitipennis</i>	1.3	1.8	2.2	2.9	4.4	2.5	1.2
<i>Anopheles</i>	<i>albitarsis s.l.</i>	1.3	1.6	1.9	2.2	2.9	2.0	1.0
<i>Culex</i>	<i>tritaeniorhynchus</i>	0.7	0.9	1.1	1.2	1.6	1.1	1.0
<i>Anopheles</i>	<i>subpictus s.l.</i>	0.4	0.6	0.8	1.1	2.4	1.1	2.6
<i>Aedes</i>		2.8	4.8	6.9	10.0	17.2	8.1	4.9
<i>Anopheles</i>		1.5	3.0	5.0	8.4	17.8	6.8	6.4
<i>Culex</i>		1.1	1.8	2.5	3.5	5.6	2.9	1.5
Overall		1.4	2.8	4.6	7.5	15.4	6.0	5.2

Table S1: **MRR: mean unfed female mosquito lifespan estimates.** The 5%, 25%, 50%, 75% and 95% columns indicate the respective quantiles of the posterior distribution for mean lifespan, and the ‘Mean’ and ‘Std. dev.’ columns indicate the posterior mean and standard deviation of mean lifespan. Units of lifespan are days.

Genus	Species	5%	25%	50%	75%	95%	Mean	Std. dev.
<i>Anopheles</i>	<i>sergentii</i>	1.0	1.9	2.5	3.4	6.2	3.0	2.5
<i>Anopheles</i>	<i>gambiae s.l.</i>	0.7	1.2	1.9	2.9	5.4	2.4	1.9
<i>Culex</i>	<i>thalassius</i>	1.1	1.6	1.8	2.1	2.9	1.9	1.0
<i>Anopheles</i>	<i>farauti s.l.</i>	1.5	1.6	1.7	1.7	1.9	1.7	0.1
<i>Anopheles</i>	<i>minimus</i>	0.7	1.2	1.7	2.2	4.1	2.0	2.2
<i>Anopheles</i>	<i>maculipennis</i>	0.8	1.1	1.4	1.8	2.9	1.6	0.7
<i>Culex</i>	<i>pipiens</i>	1.1	1.3	1.4	1.5	1.7	1.4	0.2
<i>Mansonia</i>	<i>uniformis</i>	0.9	1.1	1.1	1.2	1.4	1.1	0.2
<i>Anopheles</i>	<i>rivulorum</i>	0.8	1.0	1.1	1.1	1.4	1.1	0.2
<i>Anopheles</i>	<i>melas</i>	0.8	1.0	1.0	1.1	1.3	1.0	0.2
<i>Anopheles</i>	<i>culicifacies</i>	0.9	1.0	1.0	1.1	1.2	1.0	0.1
<i>Anopheles</i>	<i>subpictus</i>	0.6	0.9	1.0	1.2	2.1	1.2	2.0
<i>Aedes</i>	<i>aegypti</i>	0.5	0.8	1.0	1.2	2.0	1.2	3.0
<i>Anopheles</i>	<i>quadrimaculatus</i>	0.7	0.9	1.0	1.1	1.3	1.0	0.2
<i>Anopheles</i>	<i>stephensi</i>	0.6	0.8	1.0	1.1	1.6	1.0	0.4
<i>Anopheles</i>	<i>darlingi</i>	0.7	0.8	0.9	1.0	1.3	1.0	0.2
<i>Culex</i>	<i>quinquefasciatus</i>	0.4	0.7	0.9	1.3	2.2	1.1	0.6
<i>Aedes</i>	<i>polynesiensis</i>	0.8	0.9	0.9	0.9	1.0	0.9	0.1
<i>Culex</i>	<i>tritaeniorhynchus</i>	0.3	0.6	0.9	1.3	4.2	2.5	30.8
<i>Culex</i>	<i>annulirostris</i>	0.5	0.8	0.9	1.0	1.4	0.9	0.5
<i>Aedes</i>	<i>samoanus</i>	0.6	0.7	0.8	0.9	1.0	0.8	0.2
<i>Aedes</i>	<i>sollicitans</i>	0.4	0.5	0.6	0.8	1.3	0.7	0.5
<i>Aedes</i>	<i>vexans</i>	0.4	0.5	0.6	0.7	0.9	0.6	0.7
<i>Anopheles</i>	<i>cruzii</i>	0.3	0.5	0.5	0.7	1.1	0.6	0.4
<i>Anopheles</i>	<i>bellator</i>	0.3	0.4	0.5	0.6	1.0	0.6	1.8
<i>Anopheles</i>		0.6	1.0	1.4	1.9	3.2	1.6	0.9
<i>Mansonia</i>		0.9	1.1	1.1	1.2	1.4	1.1	0.2
<i>Culex</i>		0.5	0.8	1.0	1.4	2.3	1.2	0.6
<i>Aedes</i>		0.6	0.7	0.8	0.9	1.1	0.8	0.2
Overall		0.5	0.8	1.2	1.7	2.7	1.3	0.7

Table S2: **Polovodova dissection: mean female mosquito lifespan in terms of gonotrophic cycles.** The 5%, 25%, 50%, 75% and 95% columns indicate the respective quantiles of the posterior distribution for mean lifespan, and the ‘Mean’ and ‘Std. dev.’ columns indicate the posterior mean and standard deviation of mean lifespan.

Genus	Species	5%	25%	50%	75%	95%	Mean	Std. dev.
<i>Anopheles</i>	<i>gambiae</i> (Form M)	0.9	1.8	2.6	3.6	6.7	3.2	4.6
<i>Anopheles</i>	<i>gambiae</i>	0.6	1.1	1.7	2.7	5.6	2.2	2.2
<i>Anopheles</i>	<i>arabiensis</i>	0.4	0.9	1.5	2.6	6.3	2.3	3.9
<i>Anopheles</i>	<i>gambiae</i> s.l.	0.7	1.7	3.1	6.3	21.2	7.3	56.1
<i>Anopheles</i>	<i>moucheti</i>	1.0	1.9	2.8	4.2	8.9	3.8	6.3
<i>Anopheles</i>	<i>funestus</i>	0.8	1.6	2.7	4.4	10.6	4.0	10.6
<i>Anopheles</i>	<i>funestus</i> s.l.	0.6	1.2	2.1	3.7	9.8	3.3	4.8
<i>Anopheles</i>	<i>nili</i> s.l.	1.0	1.4	1.7	2.1	2.8	1.8	0.6
<i>Anopheles</i>	<i>subpictus</i> s.l.	0.9	1.5	2.1	2.8	4.8	2.4	1.8
<i>Anopheles</i>	<i>dirus</i> (formerly Sp. A)	0.5	1.0	1.5	2.2	4.2	1.8	1.5
<i>Anopheles</i>	<i>dirus</i> s.l.	0.6	1.2	2.0	3.1	7.4	2.9	6.8
<i>Anopheles</i>	<i>aconitus</i>	0.5	1.1	1.8	2.8	6.3	2.5	4.7
<i>Anopheles</i>	<i>sundaicus</i> s.l.	0.4	0.9	1.6	2.9	7.5	2.7	7.4
<i>Anopheles</i>	<i>minimus</i> s.l.	0.5	1.1	1.6	2.5	5.8	2.3	5.6
<i>Anopheles</i>	<i>fluvialis</i> s.l.	0.4	0.9	1.4	2.3	5.1	2.0	3.0
<i>Anopheles</i>	<i>maculatus</i> s.l.	0.6	1.0	1.2	1.6	2.5	1.4	0.8
<i>Anopheles</i>	<i>farauti</i> s.l.	0.3	0.7	1.2	2.0	4.9	1.8	2.3
<i>Anopheles</i>	<i>annularis</i> s.l.	0.3	0.7	1.2	2.0	4.7	1.7	1.9
<i>Anopheles</i>	<i>sinensis</i>	0.4	0.8	1.1	1.7	3.0	1.4	1.0
<i>Anopheles</i>	<i>culicifacies</i> s.l.	0.5	0.8	1.1	1.5	2.3	1.2	0.6
<i>Anopheles</i>	<i>anthropophagus</i> (lesteri)	0.4	0.9	1.4	2.3	5.1	2.0	3.0
<i>Anopheles</i>	<i>lesteri</i> s.l.	0.3	0.6	1.1	1.9	4.7	1.7	2.4
<i>Anopheles</i>	<i>barbirostris</i> s.l.	0.4	0.7	1.0	1.4	2.8	1.2	1.3
<i>Anopheles</i>	<i>albitarsis</i> (formerly Sp C)	0.8	2.0	3.9	8.4	32.6	13.3	>100
<i>Anopheles</i>	<i>albitarsis</i> (formerly Sp A)	0.2	0.4	0.6	1.0	2.3	0.8	0.9
<i>Anopheles</i>	<i>albitarsis</i> (Sp. B)	0.1	0.3	0.6	0.9	1.9	0.7	0.8
<i>Anopheles</i>	<i>albitarsis</i> s.l.	0.4	0.9	1.5	3.0	8.3	2.8	5.8
<i>Anopheles</i>	<i>nuneztovari</i> s.l.	0.3	0.6	1.1	1.9	4.4	1.6	2.3
<i>Anopheles</i>	<i>darlingi</i>	0.2	0.7	1.2	2.4	6.7	2.2	4.2
<i>Anopheles</i>	<i>albimanus</i>	0.2	0.5	0.9	1.6	3.6	1.3	1.6
<i>Anopheles</i>	<i>aquasalis</i>	0.3	0.6	1.1	1.8	4.4	1.6	4.0
<i>Anopheles</i>	<i>aquasalis</i> s.l.	0.2	0.4	0.7	1.0	2.4	0.9	1.3

Table S3: **Detinova dissection: mean female mosquito lifespan estimates in terms of gonotrophic cycles.** The 5%, 25%, 50%, 75% and 95% columns indicate the respective quantiles of the posterior distribution for mean lifespan, and the ‘Mean’ and ‘Std. dev.’ columns indicate the posterior mean and standard deviation of mean lifespan.

Genus	Species	5%	25%	50%	75%	95%	Mean	Std. dev.
<i>Culex</i>	<i>thalassius</i>	5.7	8.2	9.4	11.0	15.6	10.1	5.2
<i>Anopheles</i>	<i>sergentii</i>	3.7	6.4	8.5	11.5	20.6	10.1	8.1
<i>Culex</i>	<i>pipiens</i>	5.7	6.6	7.2	7.8	8.9	7.2	1.0
<i>Anopheles</i>	<i>gambiae s.l.</i>	2.4	4.3	6.4	9.8	18.3	8.0	6.3
<i>Anopheles</i>	<i>farauti s.l.</i>	4.8	5.5	5.9	6.3	6.9	5.9	0.6
<i>Anopheles</i>	<i>minimus</i>	2.7	4.4	5.8	7.7	13.7	6.9	8.1
<i>Anopheles</i>	<i>maculipennis</i>	2.8	4.0	5.1	6.4	9.6	5.5	2.3
<i>Culex</i>	<i>quinquefasciatus</i>	2.0	3.4	4.8	6.9	11.7	5.6	3.3
<i>Aedes</i>	<i>aegypti</i>	2.3	3.7	4.7	5.6	9.3	5.6	12.3
<i>Culex</i>	<i>annulirostris</i>	2.7	3.9	4.6	5.4	7.5	4.9	2.4
<i>Culex</i>	<i>tritaeniorhynchus</i>	1.6	3.2	4.6	7.2	22.8	13.0	174.0
<i>Mansonia</i>	<i>uniformis</i>	3.4	4.0	4.4	4.9	5.5	4.5	0.7
<i>Aedes</i>	<i>polynesiensis</i>	3.2	3.7	4.1	4.5	5.1	4.1	0.6
<i>Anopheles</i>	<i>rivulorum</i>	2.8	3.4	3.8	4.2	5.0	3.9	0.7
<i>Anopheles</i>	<i>melas</i>	2.8	3.3	3.7	4.1	4.8	3.8	0.7
<i>Anopheles</i>	<i>culicifacies s.l.</i>	2.8	3.3	3.7	4.1	4.7	3.7	0.6
<i>Anopheles</i>	<i>subpictus s.l.</i>	2.2	3.1	3.7	4.5	7.0	4.3	6.6
<i>Aedes</i>	<i>samoanus</i>	2.7	3.2	3.6	4.0	4.9	3.7	1.0
<i>Anopheles</i>	<i>quadrimaculatus</i>	2.4	3.1	3.5	4.0	4.8	3.6	0.8
<i>Anopheles</i>	<i>stephensi</i>	2.1	2.9	3.5	4.2	5.7	3.7	1.5
<i>Anopheles</i>	<i>darlingi</i>	2.3	2.9	3.4	3.8	4.7	3.4	0.9
<i>Aedes</i>	<i>sollicitans</i>	1.6	2.3	2.9	3.6	6.1	3.3	2.5
<i>Aedes</i>	<i>vexans</i>	1.7	2.2	2.7	3.1	4.2	3.0	3.3
<i>Anopheles</i>	<i>cruzii</i>	1.2	1.6	2.0	2.5	4.0	2.2	1.3
<i>Anopheles</i>	<i>bellator</i>	1.0	1.4	1.7	2.1	3.6	2.1	5.4
<i>Culex</i>		2.5	4.0	5.4	7.6	12.3	6.2	3.2
<i>Anopheles</i>		2.1	3.6	4.9	6.8	10.8	5.5	2.9
<i>Mansonia</i>		3.3	4.0	4.5	4.9	5.6	4.5	0.8
<i>Aedes</i>		2.5	3.3	3.8	4.3	5.2	3.8	0.9
<i>Overall</i>		2.0	3.3	4.7	6.4	10.2	5.2	2.6

Table S4: **Polovodova dissection: mean female mosquito lifespan estimates in terms of chronological time.** The 5%, 25%, 50%, 75% and 95% columns indicate the respective quantiles of the posterior distribution for mean lifespan, and the ‘Mean’ and ‘Std. dev.’ columns indicate the posterior mean and standard deviation of mean lifespan. Units of lifespan are days.

Genus	Species	5%	25%	50%	75%	95%	Mean	Std. dev.
<i>Anopheles</i>	<i>gambiae</i> (Form M)	3.3	6.2	8.7	11.9	22.3	10.7	14.9
<i>Anopheles</i>	<i>gambiae</i>	2.0	3.8	5.8	9.0	18.4	7.6	7.1
<i>Anopheles</i>	<i>arabiensis</i>	1.4	3.2	5.3	8.8	20.8	7.7	11.9
<i>Anopheles</i>	<i>gambiae</i> s.l.	2.5	5.7	10.3	20.6	68.4	23.9	>100
<i>Anopheles</i>	<i>moucheti</i>	3.5	6.4	9.2	13.9	29.0	12.5	19.7
<i>Anopheles</i>	<i>funestus</i>	2.9	5.7	9.0	14.5	34.4	13.4	31.0
<i>Anopheles</i>	<i>funestus</i> s.l.	2.0	4.3	7.1	12.5	32.2	11.1	15.6
<i>Anopheles</i>	<i>nili</i> s.l.	3.6	4.8	5.8	7.1	9.6	6.1	2.0
<i>Anopheles</i>	<i>subpictus</i> s.l.	3.4	5.3	7.1	9.5	16.2	8.2	6.2
<i>Anopheles</i>	<i>dirus</i> (formerly Sp. A)	1.9	3.6	5.1	7.4	13.8	6.2	5.0
<i>Anopheles</i>	<i>dirus</i> s.l.	2.0	4.4	6.8	10.5	24.1	9.8	23.0
<i>Anopheles</i>	<i>aconitus</i>	1.9	4.0	6.2	9.6	20.7	8.5	15.4
<i>Anopheles</i>	<i>sundaicus</i> s.l.	1.5	3.4	5.6	9.7	24.7	9.1	23.6
<i>Anopheles</i>	<i>minimus</i> s.l.	1.9	3.8	5.5	8.3	19.2	7.9	17.8
<i>Anopheles</i>	<i>fluvialis</i> s.l.	1.6	3.2	5.0	7.8	16.9	6.8	9.6
<i>Anopheles</i>	<i>maculatus</i> s.l.	2.2	3.5	4.5	5.6	8.6	4.9	2.6
<i>Anopheles</i>	<i>farauti</i> s.l.	1.2	2.6	4.3	6.9	16.0	6.1	7.5
<i>Anopheles</i>	<i>annularis</i> s.l.	1.1	2.5	4.3	6.9	15.6	5.8	6.2
<i>Anopheles</i>	<i>sinensis</i>	1.6	2.8	4.1	5.9	10.3	4.8	3.2
<i>Anopheles</i>	<i>culicifacies</i> s.l.	1.9	3.0	4.0	5.2	8.0	4.3	2.0
<i>Anopheles</i>	<i>anthropophagus</i> (lesteri)	1.6	3.2	5.0	7.7	16.9	6.8	9.9
<i>Anopheles</i>	<i>lesteri</i> s.l.	0.9	2.2	3.9	6.5	15.6	5.7	7.8
<i>Anopheles</i>	<i>barbirostris</i> s.l.	1.4	2.5	3.5	4.9	9.6	4.3	4.1
<i>Anopheles</i>	<i>albitarsis</i> (formerly Sp C)	3.0	6.8	13.0	27.3	>100	44.2	>100
<i>Anopheles</i>	<i>albitarsis</i> (formerly Sp A)	0.6	1.3	2.2	3.7	7.7	3.0	3.1
<i>Anopheles</i>	<i>albitarsis</i> (Sp. B)	0.5	1.2	2.0	3.3	6.6	2.6	2.6
<i>Anopheles</i>	<i>albitarsis</i> s.l.	1.2	3.1	5.4	9.9	26.9	9.3	18.6
<i>Anopheles</i>	<i>nuneztovari</i> s.l.	1.0	2.3	3.9	6.4	14.7	5.6	7.6
<i>Anopheles</i>	<i>darlingi</i>	0.9	2.4	4.5	8.1	22.0	7.4	13.6
<i>Anopheles</i>	<i>albimanus</i>	0.9	2.0	3.3	5.4	12.0	4.5	5.3
<i>Anopheles</i>	<i>aquasalis</i>	1.0	2.3	3.9	6.3	14.4	5.6	12.9
<i>Anopheles</i>	<i>aquasalis</i> s.l.	0.8	1.6	2.4	3.8	8.2	3.3	4.1

Table S5: **Detinova dissection: mean female mosquito lifespan estimates in terms of chronological time.** The 5%, 25%, 50%, 75% and 95% columns indicate the respective quantiles of the posterior distribution for mean lifespan, and the ‘Mean’ and ‘Std. dev.’ columns indicate the posterior mean and standard deviation of mean lifespan. Units of lifespan are days.

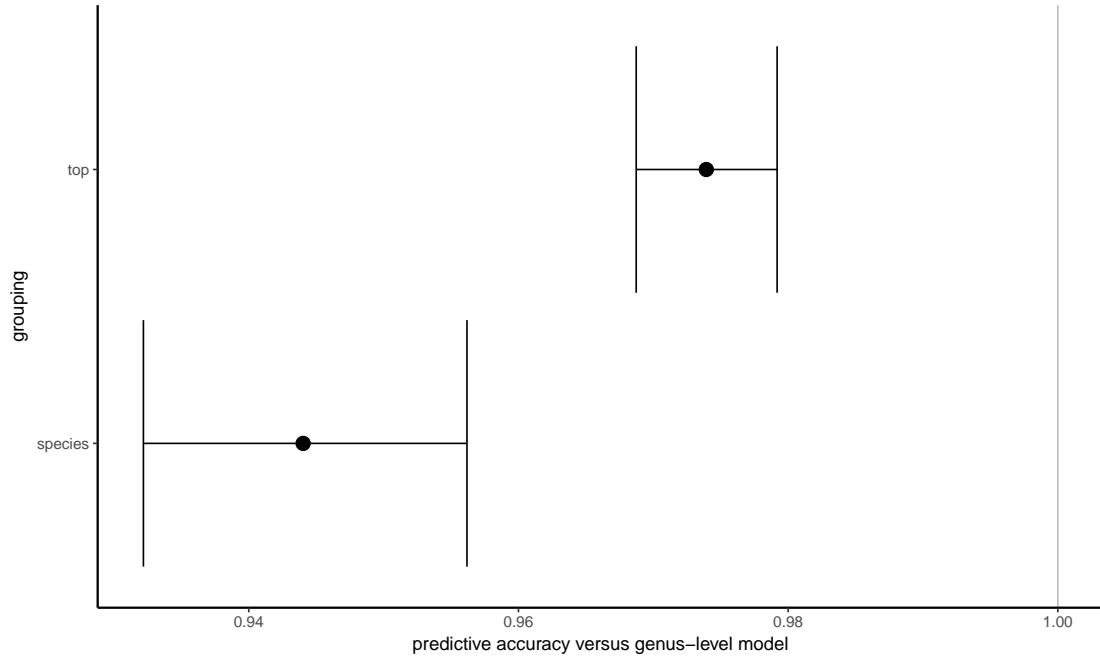


Figure S1: **MRR: predictive accuracy of the species- and overall-level models relative to the genus-level model.** The predictive accuracy was determined using K-Fold cross-validation as described in SOM; the measure of accuracy presented here by the central dots is the difference in estimated expected log pointwise predictive density compared to the exponential model. The lower and upper whiskers represent the lower and upper bounds of the 95% confidence interval in predictive accuracy.

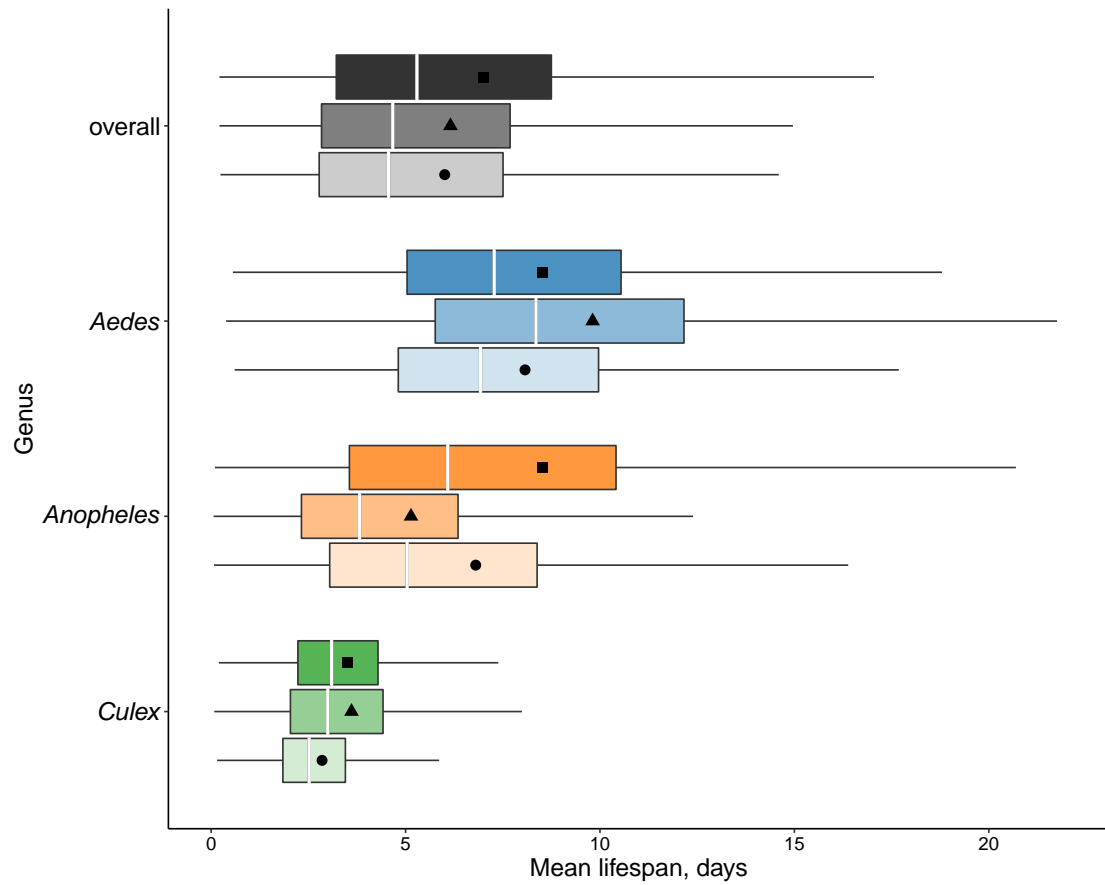


Figure S2: **MRR: female mosquito mean lifespan by pre-release feeding status.** The lifespans shown are for mosquitoes that were not fed with sugar or blood (for females) before release. The middle line in each box shows the median estimates and the solid dot indicates the mean. The left and right box edges show the 25%, and 75% posterior quantiles respectively. The whiskers show the range of the data, excluding points lying more than 1.5 times the interquartile range away from each edge of the box. The numbers before the start of the left whisker indicate the number of individual time-series within each species. All estimates were obtained using the hierarchical exponential survival model.

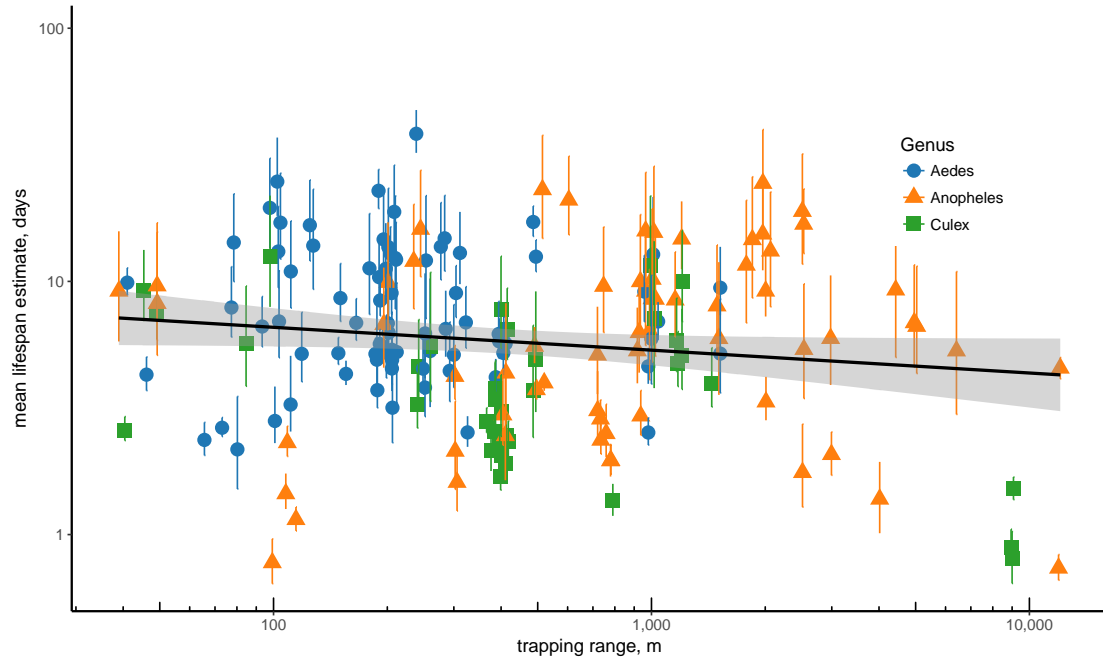


Figure S3: **MRR: mean mosquito lifespan versus trapping range.** The markers show the median posterior lifespan estimates for each time series with the lower and upper bounds indicating the 25% and 75% quantiles, respectively. The black line shows a linear regression line estimated using the median posterior lifetimes, with the grey shading indicating 95% confidence intervals. All estimates were obtained using the non-hierarchical exponential survival model.

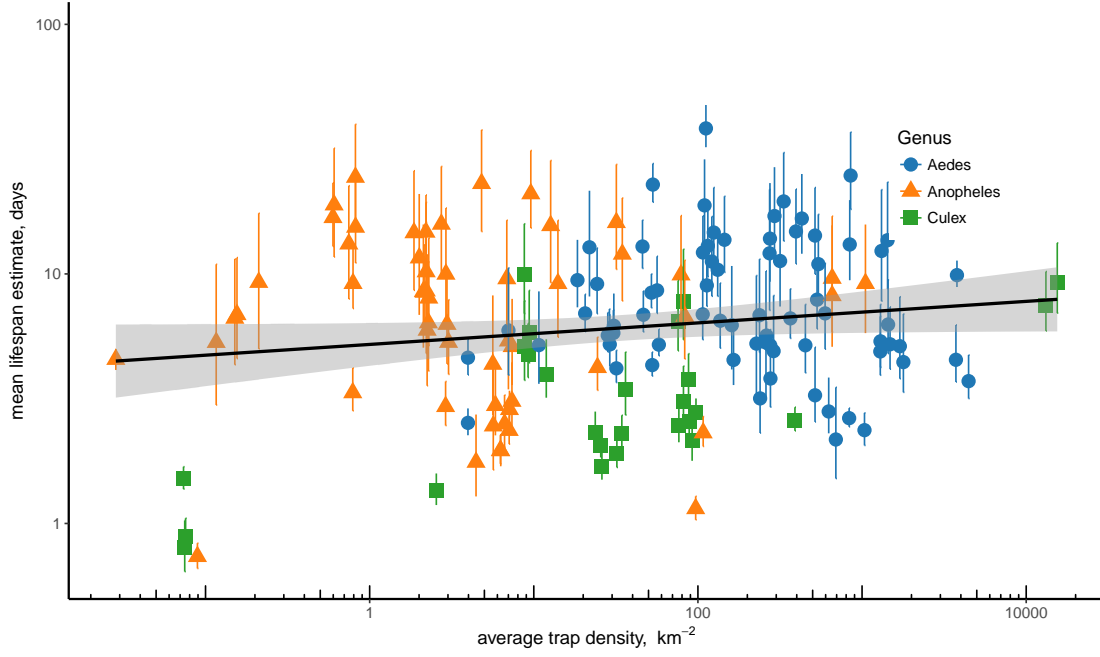


Figure S4: **MRR: mean mosquito lifespan versus trapping density.** The markers show the median posterior lifespan estimates for each time series with the lower and upper bounds indicating the 25% and 75% quantiles, respectively. The trap density was estimated assuming traps were contained within a circular area with radius equal to the trapping range. The black line shows a linear regression line estimated using the median posterior lifetimes, with the grey shading indicating 95% confidence intervals. All estimates were obtained using the non-hierarchical exponential survival model.

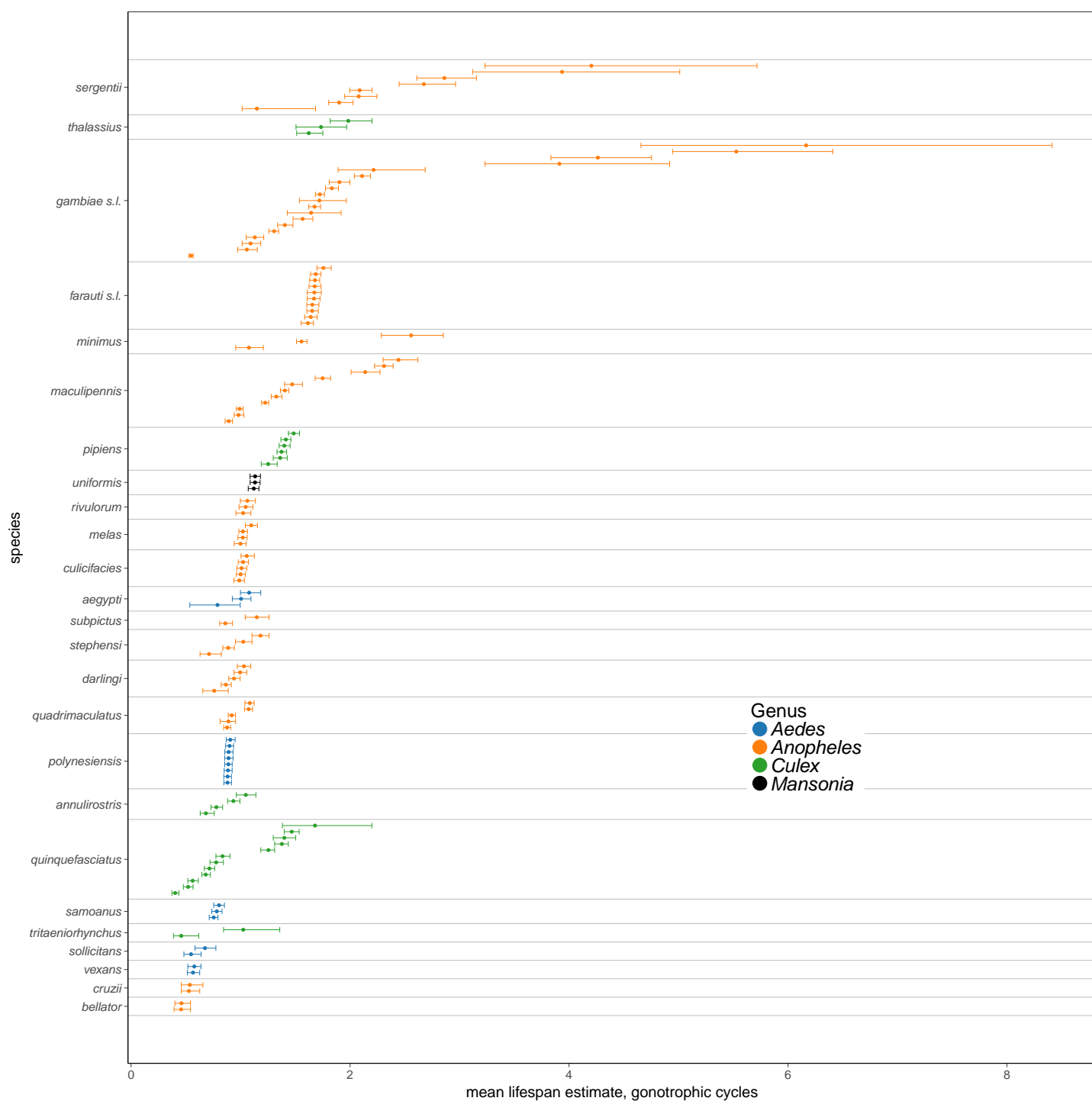


Figure S5: **Polovodova dissection: individual time-series estimates of adult mosquito mean lifespan.** The middle line in each box shows the median estimates. The left and right box whiskers show the 25%, and 75% posterior quantiles respectively. All estimates were obtained using the non-hierarchical exponential survival model.

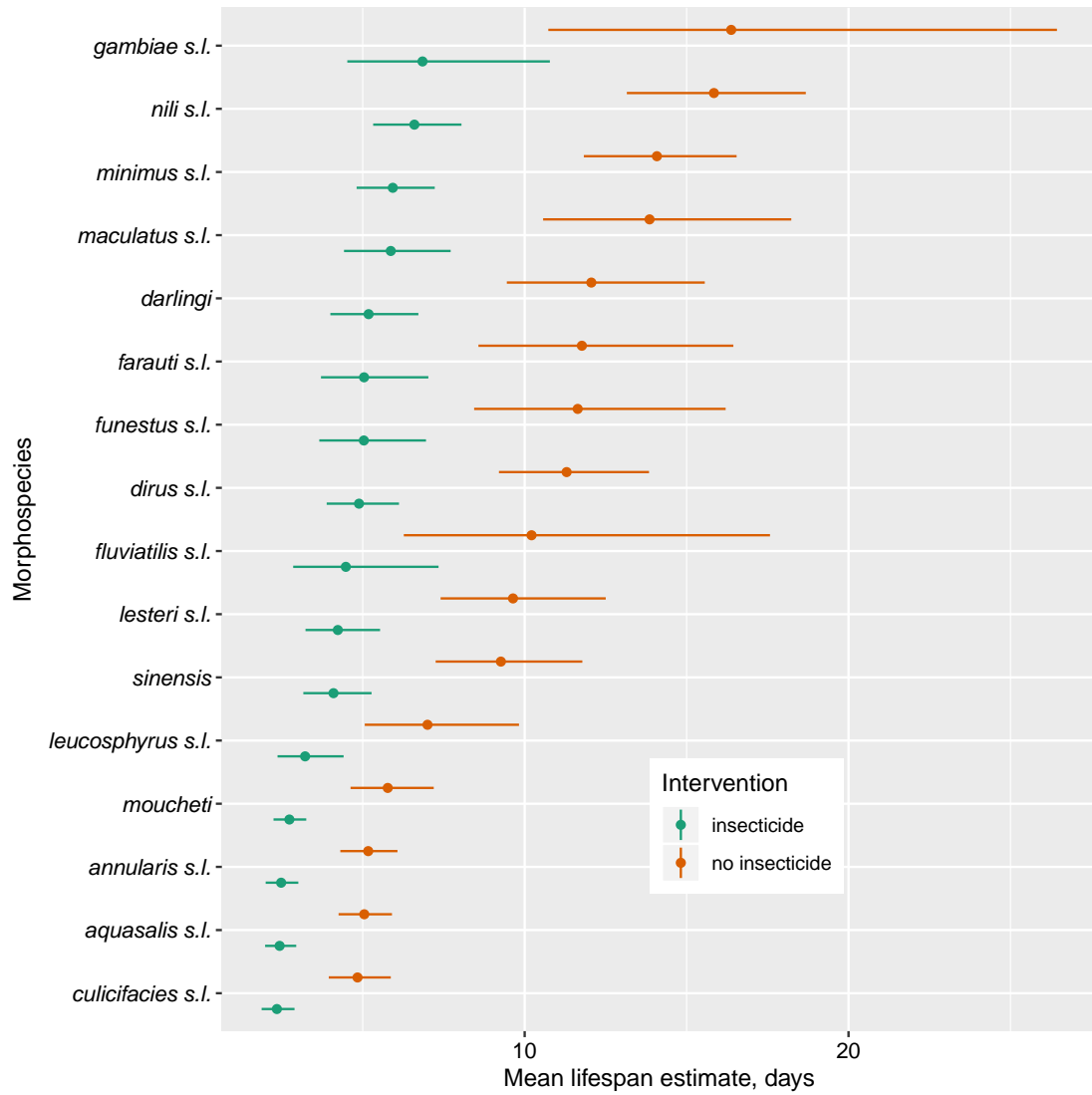


Figure S6: **Detinova dissection: estimated impact of insecticide on lifespan.** The middle line in each box shows the median estimates. The left and right box whiskers show the 10%, and 90% posterior quantiles respectively.

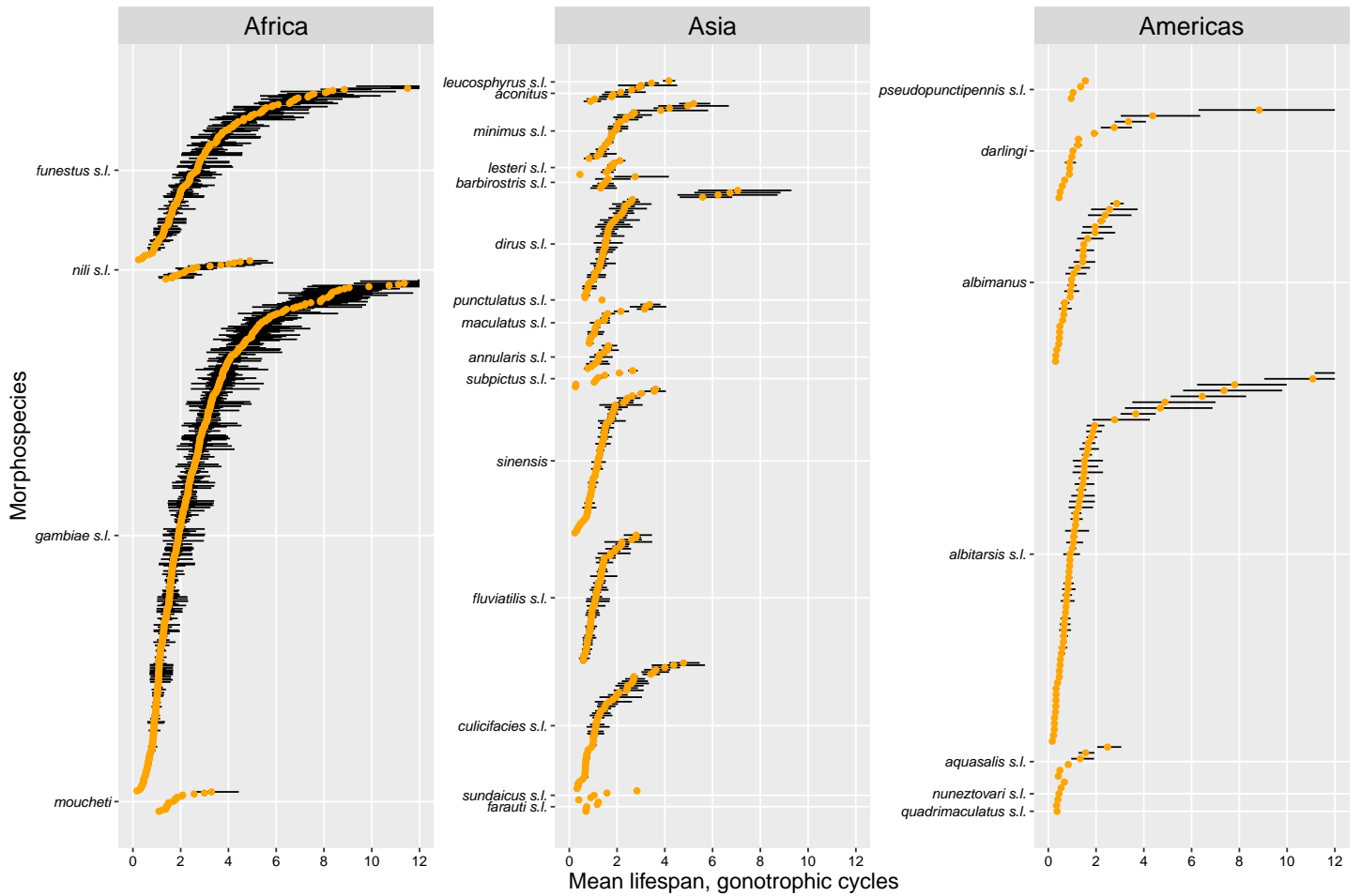


Figure S7: **Detinova dissection: individual time-series estimates of adult mosquito mean lifespan.** The middle line in each box shows the median estimates. The left and right box whiskers show the 25%, and 75% posterior quantiles respectively. Note, that a handful of observations are not shown in the plot since their estimates exceeded the reasonable range (here deemed to be up to 12 cycles).

S2 Evidence for senescence

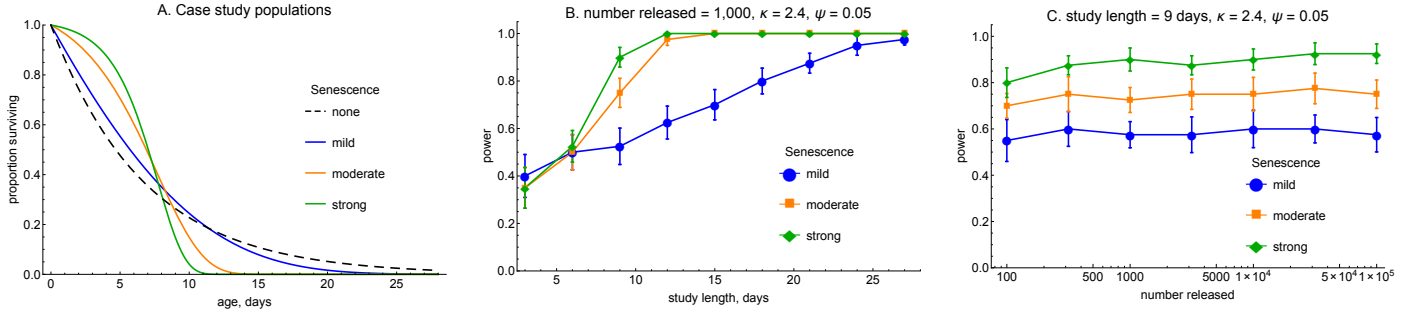


Figure S8: **MRR: statistical power analysis for senescence detection.** The plot shows the statistical power to detect senescence for A. three case study populations as a function of B. study length and C. number released. For each parameter set we generated 500 simulated data series using the negative binomial sampling model with a gompertz hazard function ($\lambda(t) = \alpha e^{\beta t}$), and estimated the β parameter using maximum likelihood and tested the null hypothesis $\beta = 0$ (constant mortality risk) against the alternative $\beta > 0$ using an likelihood ratio test with a 5% test size. The error bars show the standard deviation in the power for each parameter set. The recapture probability parameters (ψ and κ) used were the averages of those estimated for the actual data.

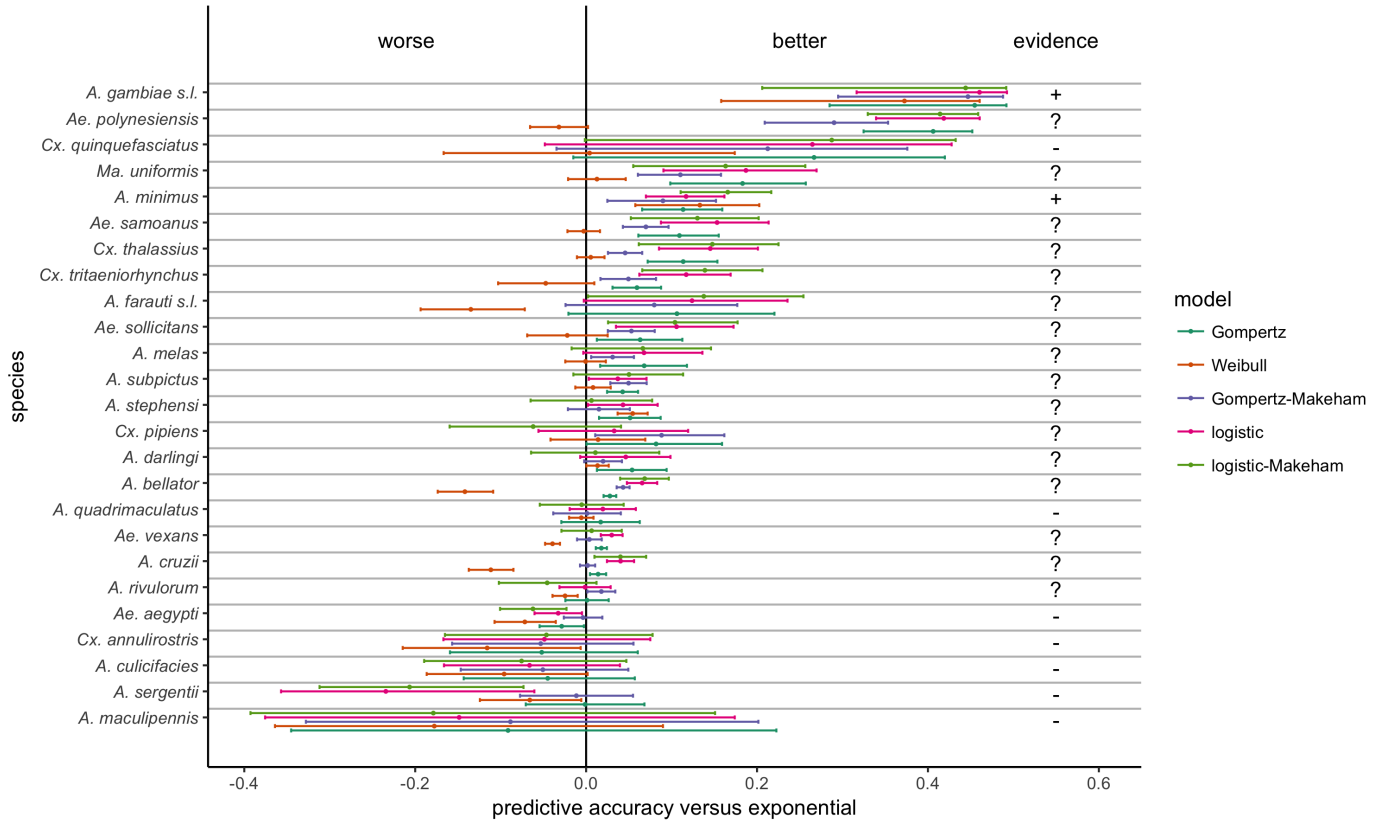


Figure S9: **Polovodova dissection: evidence for senescence.** Here, we consider the predictive accuracy of age-dependent models of mortality versus the exponential model by species. The predictive accuracy was determined using K-Fold cross-validation as described in SOM; the measure of accuracy presented here by the central dots is the difference in estimated expected log pointwise predictive density compared to the exponential model. The lower and upper whiskers represent the lower and upper bounds of the 95% confidence interval in predictive accuracy. The species have been ordered so that those with the highest average predictive accuracy across all age-dependent models compared to the exponential model appear at the top. If all age-dependent models outperform the exponential, we deem this as evidence for age-dependent mortality ('+'); if a subsample of models perform better, we deem the evidence ambiguous ('?'); and if no age-dependent model exceeds the performance of the exponential, we conclude no evidence in favour of senescence ('-').

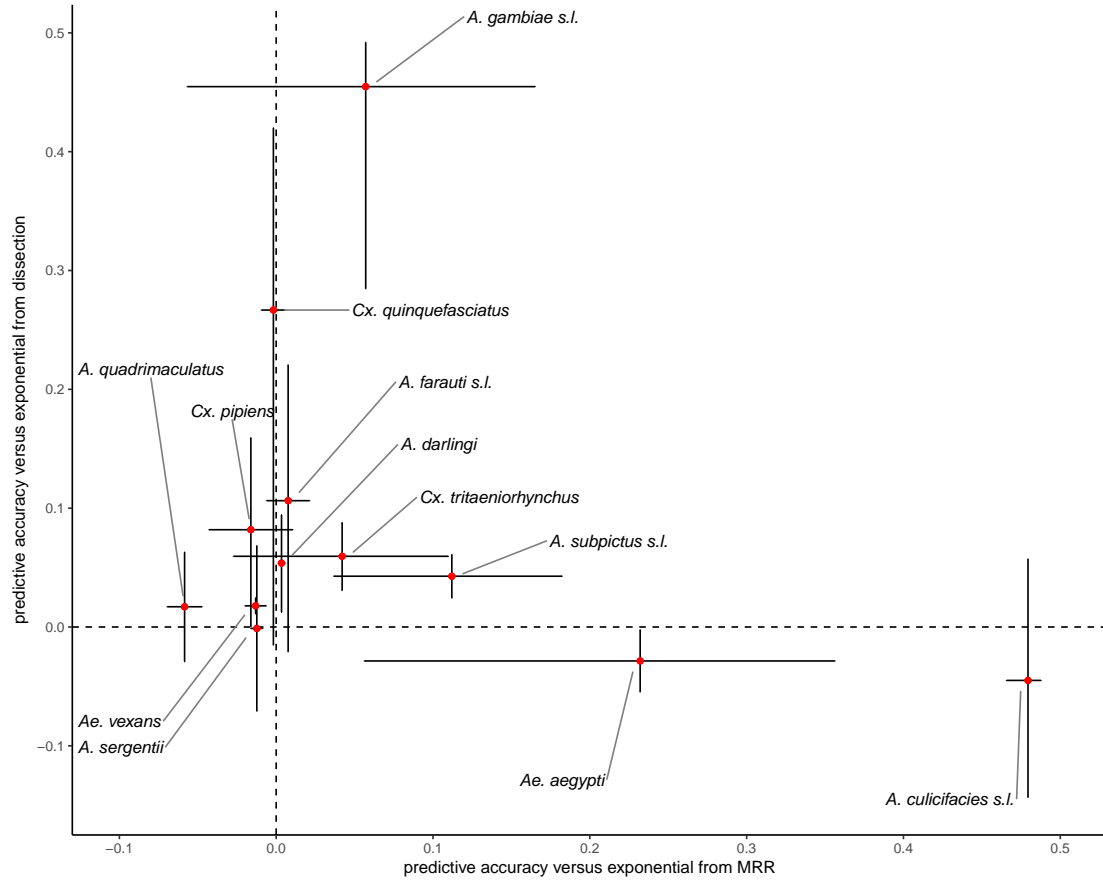


Figure S10: **Evidence for senescence: comparing evidence from Gompertz model across MRR and Polovodova dissection analyses.** The points indicate the estimated predictive accuracy compared with the exponential model (see SOM Methods) and the lower and upper whiskers represent 2.5% and 97.5% quantiles on this quantity.

S3 Power analysis of MRR studies

Consider an ideal MRR experiment, where the assumptions of no emigration and harmless marking are fully satisfied. With these data, how accurately can we estimate mosquito lifespan? To address this question we generated artificial MRR data and attempted to estimate the (known) parameters by maximum likelihood (a ‘Monte Carlo’ analysis). Specifically, we simulated releases of N mosquitoes that are monitored for m days in each case, and determined how statistical power to estimate lifespan depends on these two parameters (Fig. S11). In order to focus on estimating lifespan, we assumed the mosquitoes experience constant mortality, and recaptures follow the negative binomial sampling model (eqn. 1) where the recapture probability parameters (ψ and κ) were the averages of those estimated for the actual data.

Unsurprisingly, the error in predicting lifespan declines as the duration of study is increased (Fig. S11A). However once a study length is much longer than the lifespan of the majority of mosquitoes, the predictive power cannot be improved by extending the study duration. The effect of increasing release size (while holding study length constant) is similarly a case of diminishing returns (Fig. S11B). For the parameters we use, there are significant gains in accuracy from releasing 1,000 rather than 100 mosquitoes, but modest gains from releasing 10,000 rather than 1000 mosquitoes.

We also conducted a power analysis for the detection of senescence in MRR experiments (Fig. S8). Here we calculated the power of a maximum likelihood estimator of the ‘senescence parameter’ β of the Gompertz survival function (see Table SM3) for case study populations with three different levels of senescence (Fig. S8A.). These indicate that the power to detect senescence is strongly dependent on study length (Fig. S8B.), but is insensitive to release size (Fig. S8C.). ? conducted a meta-analysis of MRR and dissection-based experiments and found evidence of senescence that is, at least, qualitatively similar in magnitude to that of the ‘mild’ case considered above. For this case detecting senescence with a power of 80% requires a study length of at least 18 days. Since the median study length for experiments included in our analysis was 10 days (Table SM1) this could partly explain our failure to detect senescence at the species level.

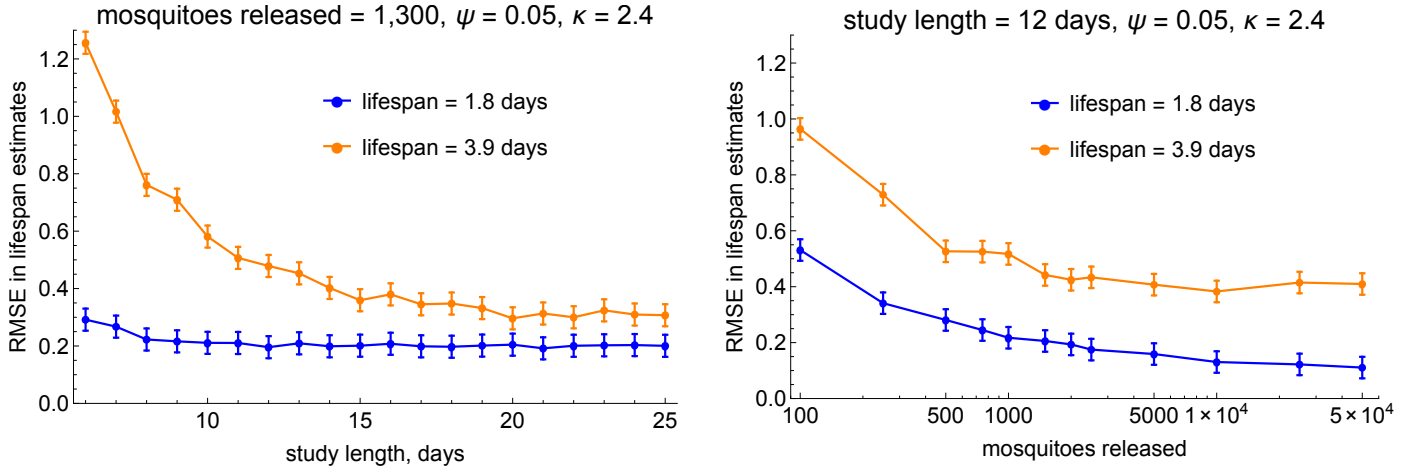


Figure S11: **MRR: Monte Carlo analysis of errors in predicting mean lifespan.** This shows the Root Mean Square Error (RMSE) in predicting mean lifespan as a function of study length (left) and number of released mosquitoes (right) in a Monte Carlo analysis. For each parameter set we generated 400 simulated data series using the negative binomial sampling model with an exponential survival function as described in the text, and estimated the mean lifespan using maximum likelihood. The error bars show the standard deviation in the prediction error.