

Table A1: Virus isolates

Population	Sampling	N _{months}	N _{isolates}	Reference
Germany – Southwest	04/2008	6	4	Wilfert & Jiggins (2010)
Germany – Southeast	04/2008	7	7	Wilfert & Jiggins (2010)
Greece – Athens	04/2008	30	6	Wilfert & Jiggins (2010)
Greece – Athens	04/2008	18	2	Carpenter <i>et al.</i> (2007)
Greece – Athens	04/2008	4	52	Carpenter <i>et al.</i> (2007)
Ghana – Accra	02/2010	1	1	-
Kenya – Thika	02/2009	1	2	-
Spain – Galicia	04/2008	30	2	Carpenter <i>et al.</i> (2007)
Sweden – Uppsala	04/2008	7	4	Wilfert & Jiggins (2010)
UK – Cambridgeshire	09/2009	1	51	-
UK – Derby	04/2008	6	1	Wilfert & Jiggins (2010)
UK – Essex	04/2008	31	6	Wilfert & Jiggins (2010)
UK – Essex	04/2008	7	9	Carpenter <i>et al.</i> (2007), Wilfert & Jiggins (2010)
UK – Essex	09/2009	1	5	-
UK – Kent	04/2008	7	1	Wilfert & Jiggins (2010)
USA – California	09/2008	3	8	-
USA – Florida	04/2008	30	1	Carpenter <i>et al.</i> (2007)
USA – North Carolina	04/2008	5	1	Wilfert & Jiggins (2010)
Lab – Hap23	-	-	1	Wilfert & Jiggins (2010)

‘Sampling’ gives the time point at which samples were frozen for RNA extraction and ‘N months’ indicates the time period for which isolates were maintained in fly lines prior to this time-point. Additional sequences obtained from Genbank (3 samples from Athens, Greece: AM689323, AM689330, AM689331; 4 from Essex, UK: AM689310, AM689314, AM689317, AM689318; and 1 from Georgia, USA: AM689320) were sampled in November 2005 and had been maintained in the lab for up to 6 months.

Table A2: primers used for amplifying DMelSV; Primer pairs 2 and 5 were used to amplify partial sequences for the *p*- and *g*-gene respectively. Where specific primers were used for subsets of viral isolates, the alternative primers are given with their name indicating which isolates they were used for (i.e. ‘rare’ or US-type). The primers bind with an annealing temperature of 55° C.

Name	Sequence
Sigma_1F	5'-CCATATAGACACCAAGACCGAGT-3'
Sigma_1R	5'-GCCATTTTATTGCGTCTGCT-3'
Sigma_2F	5'- AAGATTCCCCTCGCATGG -3'
Sigma_2R	5'- ACCCTTTCGGAAGGTTTGAG -3'
Sigma_3F	5'- GGTTGGCTAGCGGAATATCA -3'
Sigma_3R	5'- TGCCATATCAGAGGTTTCACC -3'
Sigma_4F	5'- GGACCAGGGTAATGAGAGCA -3'
Sigma_4R	5'- TTCTGTGGCACATTGAGGAG -3'
Sigma_5F	5'- TGTTCACATCCACCAGACAA -3'
Sigma_5R	5'- AATCCCTCTTGTGCCTGCTT -3'
Sigma_6F	5'- CATTGACTCGCTTCACCAA -3'
Sigma_6R	5'- GATCGTGAGATGCGACTTGA -3'
Sigma_7F	5'- GCGGTGAGAAAACCACAGAG -3'
Sigma_7R	5'- TCAGTGCCAACATCCAGAGA -3'
Sigma_7R_rare	5' – TGGGGTCGTAGGACTGAAAG – 3'
Sigma_8F	5'- GGAGGGCGTTATGTTATCCA -3'
Sigma_8R	5'- CAGAGCATTCTGGGCTCACT -3'
Sigma_9F	5'- CGAAGGCGTACGAGGATATT -3'
Sigma_9R	5'- GTCGGTGAATCGCTCCAT -3'
Sigma_10F	5'- GGTGTCTTGTACCAAAGTGTCG -3'
Sigma_10R	5'- TGGGTCCAAATATGTGTCCAT -3'
Sigma_11F	5'- CCTGAAACTGGGGACAGGTA -3'
Sigma_11R	5'- GTCCTCTCTTGGTTCGGTTGA -3'
Sigma_11F_rare	5'- CCACCTCTGCTGTTGTGTAGG -3'
Sigma_11R_rare	5'- CACATGTGCAATTCACAAA -3'
Sigma_11F_UStype	5'-ACAACCTTGGAACAGGGGTGT -3'
Sigma_11R_UStype	5'- TTCCTCTGGCAAGGTGATCT -3'

Table A3: The number of sequence changes that occurred in sigma virus isolates maintained in laboratory *Drosophila* lines. The Genbank accession number is for the initial sequence obtained in 2005.

Virus isolate	Accession number	Length [bp]	Mutations
E021	AM689311	1226	0
E023	AM689312	1209	0
E024	AM689313	1208	0
E027	AM689315	1227	0
E029	AM689316	1225	0
E032	AM689319	1227	0
Gc20	AM689322	1209	0
Gc174	AM689321	1209	1
PF107	AM689324	1217	0
PF108	AM689325	1208	0
Pf119	AM689327	1208	0
PF136	AM689328	1209	0
PF139	AM689329	1213	1
PF115	AM689326	5626	3
AP30	HQ655101	5729	1

Carpenter JA, Obbard DJ, Maside X *et al.* (2007) The recent spread of a vertically transmitted virus through populations of *Drosophila melanogaster*. *Molecular Ecology*, **16**, 3947-3954.

Wilfert L, Jiggins FM (2010) Host-parasite coevolution: genetic variation in a virus population and the interaction with a host gene. *Journal of Evolutionary Biology*, **23**, 1447-1455.