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Supplementary Materials for

Deformed Wing Virus is a Recent Global Epidemic in Honeybees driven by Varroa Mites

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This PDF file includes:

Materials and Methods
Figs. S1 to S7
Tables S1 to S7
Captions for databases S1

Other Supplementary Materials for this manuscript includes the following:

Databases S1 to S5 as zipped archives:
Database S1: analysis_composition.txt
Database S2: lp_fragmentary.txt
Database S3: vp3_fragmentary.txt
Database S4: helicase_fragmentary.txt
Database S5: rdrp_fragmentary.txt

68 **Materials and Methods**

69 Bee and mite samples

70 A total of 398 honeybees (*A. mellifera* [n=285] and *A. cerana* [n=18]) and 95 mites (*Varroa*, n=86) and *Tropilaelaps*
71 *clareae* (n=9) were kindly donated by beekeepers from thirty-two geographic regions spread over four continents
72 from 1998 through to 2009, with the vast majority of samples collected during the spring and summer of 2009 (see
73 Supplementary Table 1 for details and genbank accession numbers; thanks to Mark Goodwin, Yves Le Conte,
74 Gloria Gonzalez, Adam Tofliski, Junichi Takahashi, Marie Pierce, Peter Rosenkranz, Grazyna Topolska, Elisabeth
75 Stephen, Luis Medina, Constantino Macias Garcia, Omar Arguello Najera, Peter Neumann, John McMullan, Jose
76 Flores, Michael Penck, Chris Tomlins, Marla Spivak, Allan Balata, Martin Kracher, Ethel Villabos, Steve Cooper,
77 Peter Rosenberg, Zoltan Sabo). *Tropilaelaps* mites, present on *A. mellifera* samples from Pakistan, share a similar
78 life history to *Varroa* and can vector DWV (40). Whenever possible, samples were collected into RNA later (Sigma)
79 filled tubes or in a few cases, treated with RNAlater®-ICE (Qiagen) upon receipt and frozen at -80°C until
80 processing.

81
82 To refine our estimate of the DWV evolutionary rate, we also used sequence data obtained from 145 *Bombus*
83 *terrestris/lucorum* bumblebee queens collected in Northern Switzerland during an early spring between 2001 and
84 2011. These queens were briefly maintained in the lab, were frozen at -80°C and maintained at -20°C until
85 processing.

86 RNA isolation, RT-PCR and Sequencing

87 Individual honeybees and pooled mites were homogenized in 500µl of TRIzol reagent (Invitrogen) using a
88 TissueLyser (Qiagen), according to the manufacturers instructions. Total RNA was extracted with an RNAeasy kit
89 (Qiagen) according to manufacturer's protocol and eluted into 50µl of RNase-free water (Ambion). The nucleic acid
90 concentration was determined using a NanoDrop™ (NanoDrop). For bumblebee queens, RNA was extracted using
91 the TRIzol protocol, with half-bees homogenized in 2 ml of TRIzol.
92

93
94 DWV contains a positive, single-stranded monocistronic RNA genome comprising 10,144 nucleotides (41). In a
95 preliminary study, 9 genomic regions of DWV were examined in specimens collected from 5 geographic locations
96 to assess sequencing efficiency and genomic diversity therein (data not shown). Using this approach, four genomic
97 regions - VP3, Helicase, L-protein and RdRp (41) – were selected and assayed via one-step PCR (Applied
98 Biosystems) using the following 4 DWV primer pairs, respectively: F1-B1 (42); 6285F-6693R (27); DWV-F1153
99 (5'-ATTAAAAATGGCCTTTAGTTG-3') with DWV-B1806 (5'-CTTTTCTAATTCAACTTCACC-3') and F15-
100 B23 (23). cDNA was synthesized from 1µg of RNA template using the OneStep RT-PCR Kit (Qiagen), according to
101 the manufacturer's specifications for viral RNA. PCR reactions were carried out in a Peltier Thermal Cycler using
102 2µl of cDNA and all PCR products were analysed by 1.5% agarose gel electrophoresis. Samples were purified using
103 ExoSAP-IT (Applied Biosystems).

104
105 Fluorescence-based direct sequencing of amplicons was performed using Big Dye Terminator v1.1 (for Helicase,
106 VP3 and RdRp amplicons) or v1.2 (L-protein amplicons) Cycle Sequencing Kit (Applied Biosystems) with Taq
107 DNA polymerase (Invitrogen) following standard procedure. The PCR products were purified with an
108 ethanol/EDTA/sodium acetate precipitation method (ABI Cycle Sequencing Kit manual) and directly sequenced in
109 both directions on an ABI 3730 Genetic Analyser using PCR primers.

110
111 For the bumblebee queens, a similar approach was taken, using primers DWV-F7993 (5'-
112 AACTGGCGAYCATACTCAGC-3') and DWV-R8577 (5'- WCCAGGCACMCCACATACAG-3') for direct
113 sequencing following an MMLV goScript (Promega) transcription with random hexamers following the

114 manufacturers protocol and using Sephadex purification and Big Dye Terminator v.3.1. All ABI trace files were
115 manually edited and all SNPs and Indels verified using Genious 6.1.4 before combining both reads into contigs.

116

117 Not all four genomic regions could be amplified from all 246 DWV-positive samples ($N_{lp}=153$, $N_{vp3}=171$,
118 $N_{helicase}=221$, $N_{rdp}=175$) (see Supplementary Table S1, including Genbank accession numbers). Therefore, distinct
119 data sets were used for further analyses, combining them with the available sequences from Genbank and optimizing
120 alignment lengths to maximize the available data: i) *lp* ($N = 234$ ($N_{new} = 122$), 328 nt; *vp3* ($N = 145$ ($N_{new} = 129$), 303
121 nt); iii) *helicase* ($N = 256$ ($N_{new} = 178$), 243 nt) *rdrp* ($N = 224$ ($N_{new} = 136$), 411 nt) (see database S1 for sample
122 information per data set). Because the *helicase* fragment had very low nucleotide diversity ($\pi = 0.013$, $N = 178$), we
123 did not include it in phylogenetic analysis.

124

125 We used BLAST to confirm that sequences belonged to the DWV group. We excluded sequences that aligned with
126 DWV's sister group VDV-1 (*lp*-gene = 20, *vp3*-gene = 40, *helicase*-gene = 0, *rdrp*-gene = 6) as these sequences
127 were limited to a small number of European populations and thus not informative for DWV's global epidemiology.
128 We used the SBP and GARD algorithms in the HyPhy package (43) as well as the RDP, GENECONV, MaxChi,
129 BootScan and SiScan algorithms in the rdp3 package (v. 3.3) (44) to confirm that there is no recombination within
130 fragments at a *p*-value of 0.05.

131

132 Phylogenetic reconstruction

133 To estimate the evolutionary rate of DWV and its subtypes, we collated three independent data sets with temporal
134 information for at least 1 population: 1) partial *lp*-gene including samples from the present study and genbank (10
135 populations, $n = 78$, 328 nt (bp 1323 – 1650; Genbank AJ489744, AY292384, GU109335, HM162355, JF346615-
136 JF346620, JF346624-JF346629, JF346633-JF346639, KF164292, KF164293, KJ437447, KP734726, KP734738,
137 KP734747, KP734765-KP734770, KP734774-KP734787, KP734817-KP734825, KP734827-KP734846); spanning
138 30 years); 2) partial *vp3*-gene comprising of samples from genbank (1 population, $n = 167$, 1215 nt (2634 – 3848
139 bp; Genbank AY292384, HQ655502-HQ655561, KF314827- KF314932); spanning 12 years); 3) partial *rdrp*-gene
140 in Swiss bumblebee queens (1 population, $n = 145$, 508 nt (bp 8016-8522; Genbank KP734326 - KP734470);
141 spanning 11 years)). These three temporal datasets directly relate to our global samples: the *lp*-fragment overlaps in
142 its entirety, the *vp3*-fragments (short and long) partly overlap with the temporal *vp3*-fragment and, while there is no
143 direct sequence overlap between the *rdrp*-fragment for the global and temporal data sets, they are part of the same
144 gene.

145 To test whether these fragments contain a molecular clock signal, we estimated the root-to-tip divergence using
146 Path-o-gen v.1.4 (<http://tree.bio.ed.ac.uk/software/pathogen/>) to estimate whether the genetic variation can be
147 explained by the sampling date. We constructed maximum likelihood phylogenetic trees without the assumption of a
148 molecular clock in Phylip v. 3.695 (45) and tested whether the regression between root-to-tip distance in these
149 maximum likelihood trees and the age of the samples indicated a clock-like signal. Additionally, we tested for a
150 significant temporal signal by randomizing the temporal information across each data set 100 times and compared
151 the resulting random evolutionary rates with the real dataset. A temporal signal is supported if there is a significant
152 difference between the real data set and the randomized data sets (46, 47). Both approaches (Fig. S1, S2) show that
153 the data sets contain temporal information and therefore allow the estimation of evolutionary rates.

154

155 Phylogenetic reconstruction: model selection and estimation of evolutionary rates

156 To determine the appropriate demographic and molecular clock models for each data set, we used the path sampling
157 maximum likelihood estimator implemented in BEAST 1.8 (48, 49). As this method is highly computationally
158 intensive, we first used a range of simpler tests to limit the number of models to be compared by this method (46,
159 50); these results are summarized in Supplementary Table S2. We used jModelTest v.2.1.1 (51) to compare
160 substitution models based on the Bayesian Information Criterion (46). We partitioned substitution rates between the
161 1st & 2nd and 3rd codon positions as, for all data sets, the 3rd codon position had a significantly higher rate. We tested
162 whether a strict clock rate can be excluded by running models with a lognormal relaxed clock; if the relaxed clock's
163 coefficient of variation statistic abuts the zero boundary, a strict clock cannot be excluded (52). We ran models with
164 exponential population growth for all models; if the exponential growth rate was significantly higher than zero, a

165 constant population size can be excluded. We then used path sampling to distinguish between clock models
166 (exponential and lognormal relaxed clock) and demographic models (a GMRF skyride (53, 54) and either a constant
167 population size or exponential population growth prior) as indicated for each data set by the initial analyses
168 (Supplementary material Tables S2 and S3).

169
170 Using Beast 1.8.1, we estimated the evolutionary rate for three fragments of the DWV genome, the partial *lp*-gene
171 ($U_{ced} = 9.097 \times 10^{-4}$ changes per site per year [95 % HPD = $4.412 \times 10^{-4} - 1.394 \times 10^{-3}$]), partial *vp3*-gene ($U_{ced} =$
172 1.845×10^{-3} [$1.159 \times 10^{-3} - 2.569 \times 10^{-3}$]) and partial *rdrp*-gene ($U_{cld} = 1.278 \times 10^{-3}$ ($4.131 \times 10^{-4} - 2.513 \times 10^{-3}$)). These
173 rates differ significantly between fragments ($p < 0.001$, $F_{(2, 26998)} = 8241$), with the evolutionary rate for the *vp3*-
174 fragment being twice as high as that for the *lp*-fragment. With an average of 1.35×10^{-3} changes per site per year,
175 these values are typical of picornaviruses (55). For the datasets for discrete phylogeographic analyses, we used path
176 sampling to compare the mean evolutionary rate prior across all three fragments using the GMRF skyride
177 (lognormal prior with a mean in real space of 1.35×10^{-3} changes per year per site ($\log(\text{stdev}) = 0.4$)) against the gene-
178 specific rates for each fragment (*lp*-fragment: normal prior with a mean of 0.91×10^{-3} ($\text{stdev} = 0.24 \times 10^{-3}$); *vp3*-
179 fragment: normal prior with a mean of 1.85×10^{-3} ($\text{stdev} = 0.35 \times 10^{-3}$); *rdrp*-fragment: lognormal prior with a mean in
180 real space of 1.28×10^{-3} ($\log(\text{stdev}) = 0.325$)).

181
182 Beast 1.8.1 was used for phylogenetic reconstruction. We ran all models long enough to obtain effective sample
183 sizes > 200 for all parameters, except for skyride population size parameters and discrete trait indicators, for which
184 we accepted effective sample sizes > 100 . Each model was run with a 10 % burn-in of MCMC generations,
185 sampling the chain at equal distances to obtain a total of 10'000 trees per analysis. We combined the two runs using
186 Tracer v.1.5 and examined them for convergence. We used TreeAnnotator v. 1.7.5 to produce Maximum Clade
187 Credibility (MCC) trees.

188
189 Migration routes and evolutionary rates
190 To infer migration rates and geographic origins of branches as well as changes in host species, we fitted a discrete
191 trait model with an asymmetric substitution model as described in (56) using Ferreira and Suchard's (57) conditional
192 reference prior for the change in location rate. The geographic location of samples was pooled by region (Australia,
193 East Asia, Europe, Hawaii, New Zealand, North America, Pakistan; for the *lp*-fragment only, samples from Thailand
194 and South America were available (the latter only present in a shorter partial alignment), see Supplementary Table
195 S1 and Supplementary Database S1. Well-supported rates were identified using a Bayes factors analysis based on
196 the Bayesian stochastic search variable selection (56), using a ln Bayes Factor of 3 as a cut-off. With the exception
197 of the uninformative *helicase*-fragment for one South African sample (KP765198), no African samples could be
198 obtained. There is however evidence that DWV may indeed not be prevalent in sub-Saharan Africa: (58) found no
199 DWV (but Black Queen Cell Virus) in an extensive survey of Ugandan apiaries and (59) found DWV only in
200 southern Kenya, not in remote northern Kenya. A recent survey of North-African and Middle-Eastern honeybee
201 populations showed no evidence for this region as a DWV-origin (60).

202
203 We used tip dates for all analyses, using the results from the temporal data sets as priors for the discrete trait models.
204 As the path sampling analysis indicated that the gene-specific rates were overall preferred (Supplementary Table
205 S3), we have used the gene-specific rates for all tests. Based on the preliminary tests (Table S2) and the path-
206 sampling analyses (Table S3), we used a relaxed exponential clock for all fragments together with an exponential
207 growth prior for the *lp*- and *vp3*-fragments, and a constant population size prior for the *rdrp*-fragment. We used the
208 same parameters for models that did not incorporate discrete traits, with the exception of the *vp3*-fragment, which
209 lacked exponential growth and indicated that a strict clock could not be excluded and was thus run with a constant
210 growth prior and a strict molecular clock. Additionally, we ran GMRF skyride models for all fragments for the
211 discrete trait analysis using a lognormal relaxed clock model (Table S3). Discrete trait analysis is vulnerable to
212 biased sampling, if this does not directly reflect differences in prevalence (61). To address the potential over-
213 sampling of European populations in our data set, we randomly down-sampled this population to match the next
214 largest population for each fragment (*lp*-fragment: reduction from 130 to 28 samples; *rdrp*-fragment reduction from
215 98 to 40 samples; *vp3*-fragment reduction from 40 to 16 samples; representation of different populations in table
216 S4). For each fragment, we produced 10 independent randomly down-sampled data files and conducted discrete trait
217 analysis with a GMRF skyride,

218
219 Population genetic measures

220 We calculated indicators of population structure and differentiation using DnaSP v5 (62): K_{ST} , a measure of
221 population differentiation based on the proportion of between-population nucleotide differences (63) and the
222 nearest-neighbour statistic SNN , which calculates the proportion at which genetic nearest neighbours are found
223 within the same population (64).

224

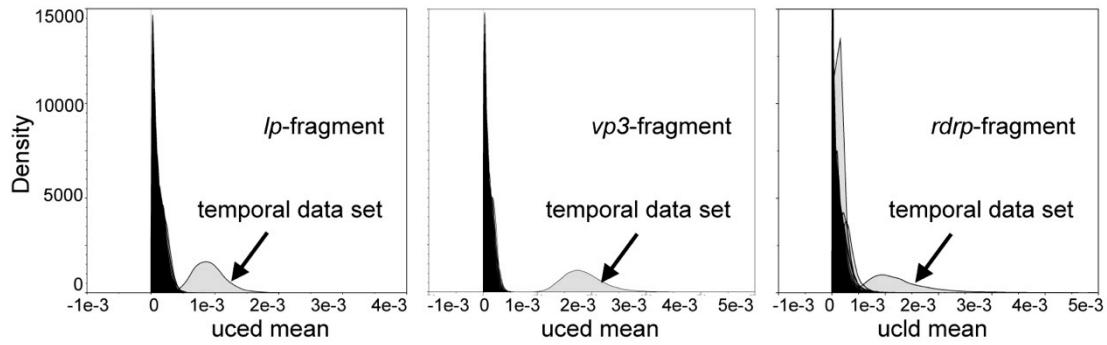
225 Mapping the spread of *Varroa*

226 We have based our map of the global spread of *V. destructor* as an *A. mellifera* parasite (Fig. 2b) on (65) (itself
227 based on data supplied by Diana Summataro). We have supplemented this dataset with all publicly available records
228 to date (29, 66-81). *V. destructor* was first described as a species separate from *V. jacobsoni* in 2000 (82) and we
229 follow the convention of attributing earlier records of *V. jacobsoni* in *A. mellifera* to *V. destructor*.

230

231

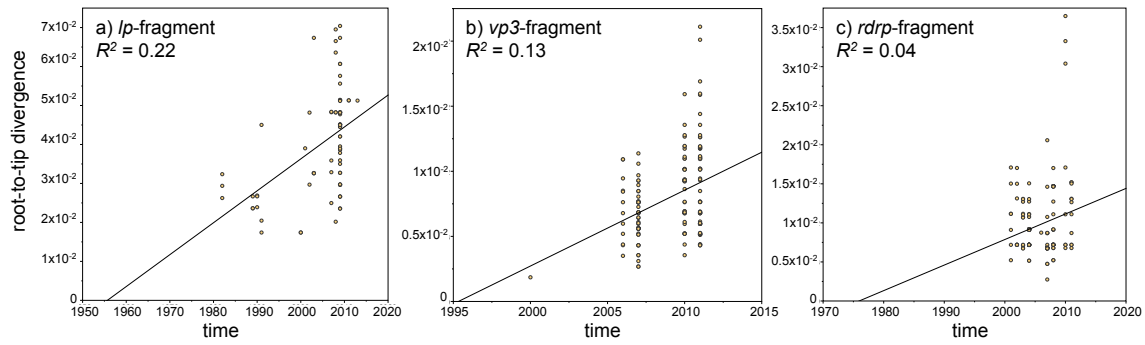
232 **Fig. S1.**



233 Fig. S1: Kernel density plots comparing the evolutionary rate for each temporal data set against 100 data sets with
234 randomized collection date information. These plots indicate a significant temporal signal for each fragment.
235
236

237

238 **Fig. S2**

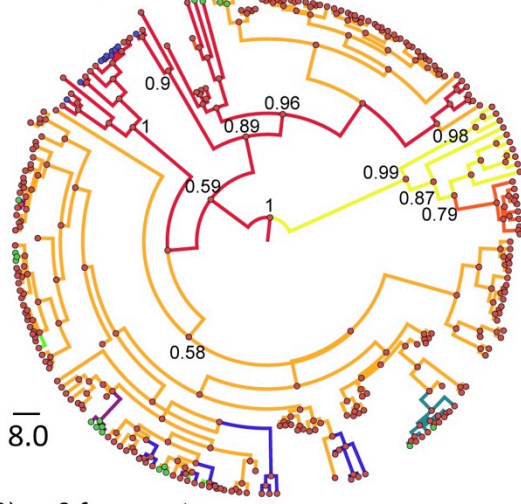


239

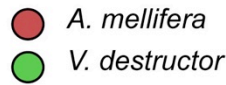
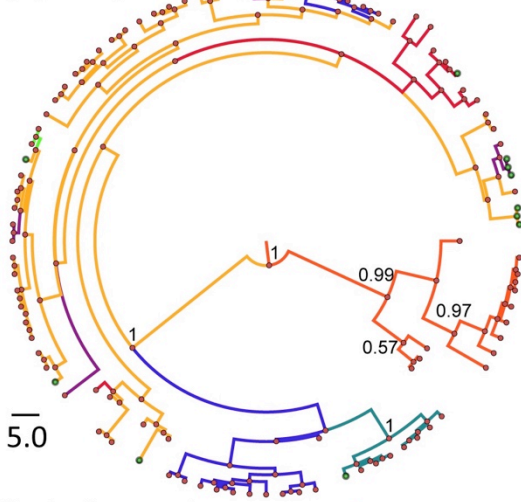
240 Fig. S2: Path-O-Gen plots of root-to-tip divergence, indicating temporal signal in the temporal
241 data sets

242

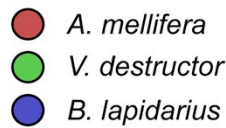
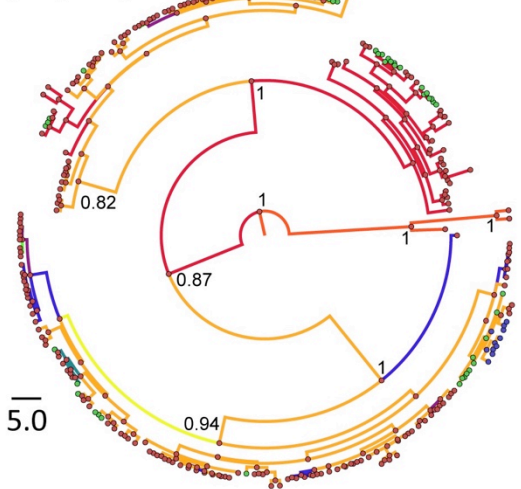
A) *lp*-fragment



B) *vp3*-fragment

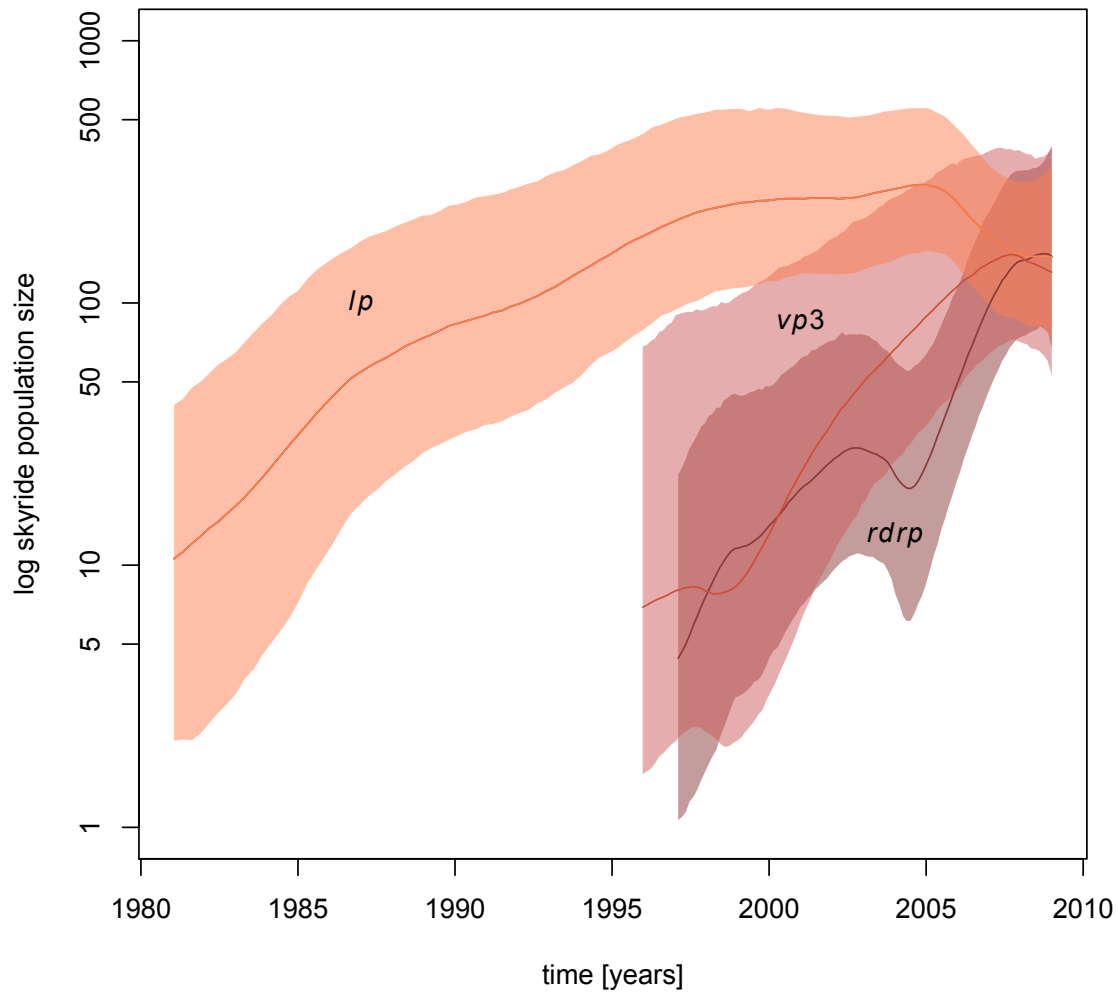


C) *rdrp*-fragment



245
246 Fig. S3 : Alternative representation of MCC trees shown in Fig. 2: Phylogenetic reconstruction of three fragments of
247 DWV showing host and geographic structure. The figure shows Maximum clade credibility (MCC) trees for the *lp*-
248 fragment (a), *vp3*-fragment (b) and the *rdrp*-fragment (c) of DWV. The branches are coloured according to the
249 lineages' inferred geographic origin and the nodes are coloured according to the inferred host species. Posterior
250 support >0.5 is indicated for nodes up to the 4th order; horizontal bars indicate the time scale in years. The x-Axis
251 shows time in years.
252

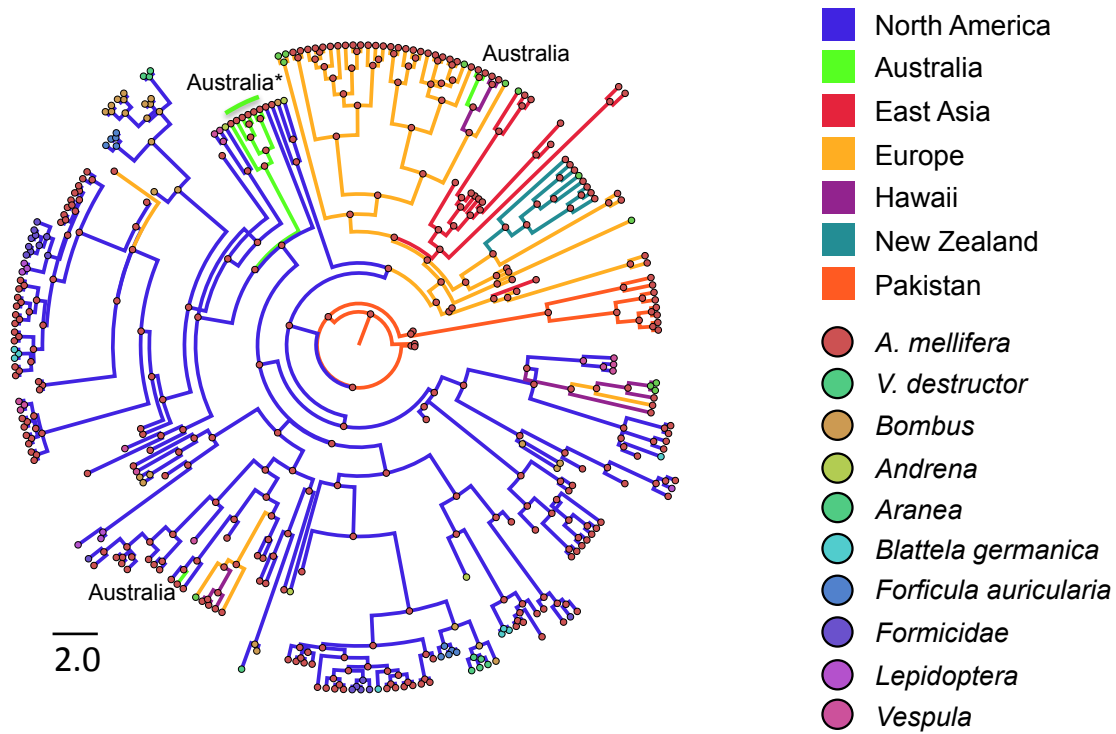
253 **Fig. S4**



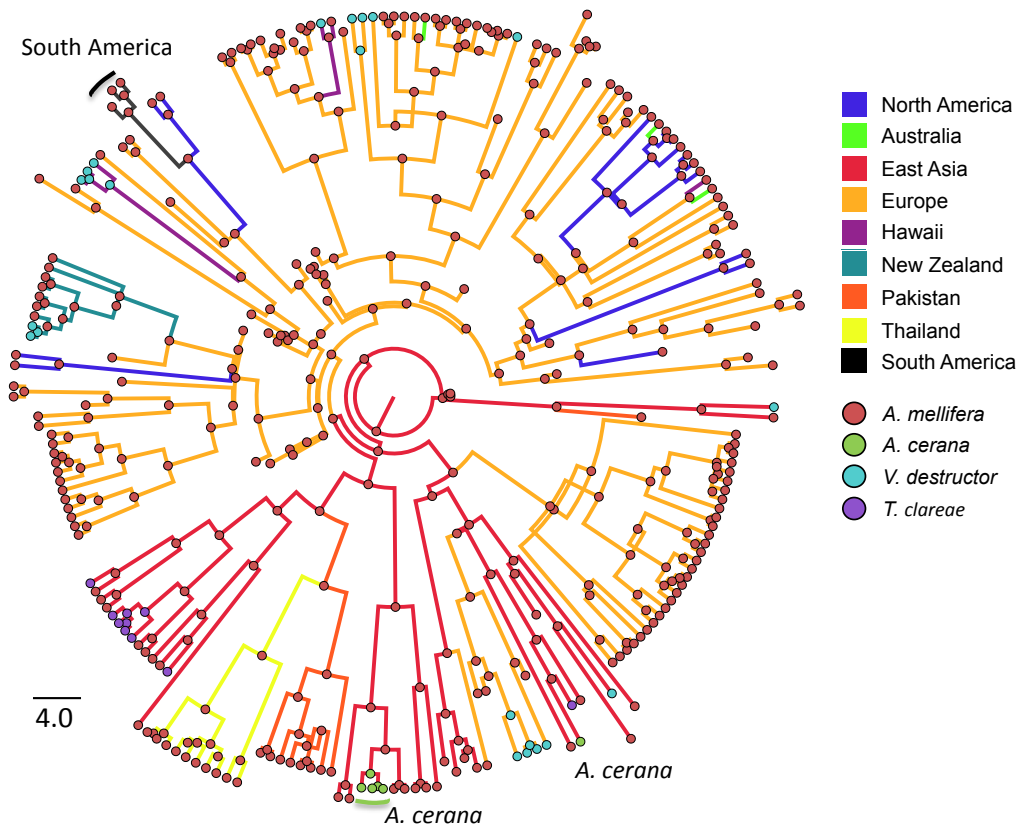
254

255 Fig. S4: Skyride plots, indicating recent population growth across fragments and populations
256 (curtailed in 2009). Population structure can produce an artificial signal of a declining population
257 (21); we have therefore excluded data post 2009, as only small and geographically disparate
258 population samples were available for that period (see Supplementary Database S1). When
259 including these, population size plummets post-2009, as predicted by Heller et al. (26).

260 **Fig. S5**

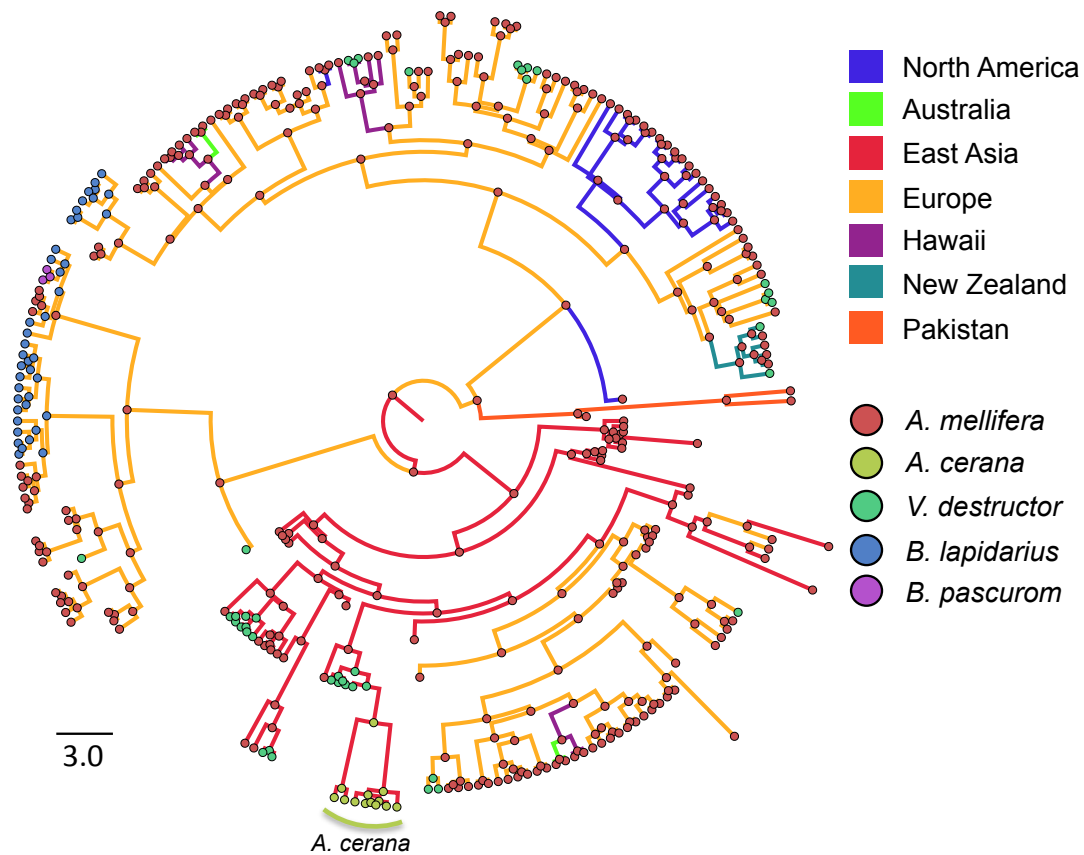


262 Fig. S5: MCC tree for a partial *vp3*-fragment (101 nt). This tree includes the sequences from
263 (23), including the only previously reported samples from Australia (HQ655496-HQ655501),
264 marked with an asterisk. This lends further support to Australia being a sink population, with
265 ancestral migration from Europe and America as shown in Fig. 1 & 2;



267
 268 Fig. S6: MCC tree for a partial *lp*-fragment (171 nt). This tree contains additional samples from *A. cerana*
 269 (HG779849, HG779850, HG779854, HG779856) as well as samples from South America (Peru: HG974552&
 270 HG974553; Chile: JQ413340). It demonstrates that *A. cerana* is not the ancestral DWV host and shows that South
 271 America is nested within a North American and European clade; BSSVS analysis shows significant transmission
 272 from North America (Bayes factor = 9.4) and Europe (Bayes factor = 4.4) to South America; horizontal bars indicate
 273 the time scale in years. The *Varroa* mite was first introduced to Paraguay in 1971 (62); the Andes isolate Eastern
 274 and Western South America, where the available DWV samples originate from. This may explain why the South
 275 American isolates of DWV are nested within a North American/European clade rather than a South East Asian
 276 clade. Collection dates for samples HG779848-HG974663 provided by Orlando Yanez.

277 **Fig. S7**



278
279 Fig. S7: MCC tree for a partial *rdrp*-fragment (303 nt). This tree includes sequences from *A. cerana* (*rdrp*-fragment,
280 303nt, JX679473 - JX679477 and JX679479 - JX679480) and demonstrates that this species is not the ancestral host
281 of DWV; horizontal bars indicate the time scale in years.

282

283 **Table S1.**

284 Table S1: Sample information, giving the country of origin, host species, collection year and Genbank accession
 285 number. 'short' indicates that DWV/VDV-1 positive sequence information was obtained, but the sequence was too
 286 short or of too low quality to be included in the analysis. This sequence data is available as supplementary databases
 287 S2-5.

sample name	country	host	year	bee status	lp-fragment	vp3-fragment	helicase-fragment	rdp-fragment
AliL1	UK	<i>A. mellifera</i>	2009	NA	KP734726	Short	KP765049	short
AustB1	Austria	<i>A. mellifera</i>	2009	NA	short	NA	KP765050	KP734665
AustB10	Austria	<i>A. mellifera</i>	2009	NA	NA	Short	KP765051	KP734663
AustB11	Austria	<i>A. mellifera</i>	2009	NA	NA	NA	KP765052	KP734668
AustB15	Austria	<i>A. mellifera</i>	2009	NA	NA	Short	KP765053	NA
AustB2	Austria	<i>A. mellifera</i>	2009	NA	NA	NA	KP765054	KP734667
AustB3	Austria	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
AustB4	Austria	<i>A. mellifera</i>	2009	NA	NA	NA	KP765055	KP734664
AustB5	Austria	<i>A. mellifera</i>	2009	NA	NA	NA	KP765056	KP734666
AustB6	Austria	<i>A. mellifera</i>	2009	NA	NA	NA	KP765057	NA
AustB7	Austria	<i>A. mellifera</i>	2009	NA	NA	NA	KP765058	NA
AustB8	Austria	<i>A. mellifera</i>	2009	NA	NA	NA	KP765059	NA
AUSTM1	Austria	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
AUSTM10	Austria	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
AUSTM11	Austria	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
AUSTM2	Austria	<i>V. destructor</i>	2009	NA	KP734727	NA	KP765060	KP734675
AUSTM5	Austria	<i>V. destructor</i>	2009	NA	NA	KP734471	KP765061	KP734674
AUSTM6	Austria	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
AUSTM7	Austria	<i>V. destructor</i>	2009	NA	KP734728	NA	KP765062	short
AUSTM9	Austria	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
AUSTMAC1	Austria	<i>V. destructor</i>	2009	NA	KP734729	KP734472	KP765063	KP734685
AUSTMAC2	Austria	<i>V. destructor</i>	2009	NA	KP734730	KP734473	KP765064	KP734686
AUSTMFRE1	Austria	<i>V. destructor</i>	2009	NA	KP734731	KP734474	KP765065	KP734683
AUSTMFRE2	Austria	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
DEVB2	UK	<i>A. mellifera</i>	2006	NA	NA	NA	NA	NA
DEVB3	UK	<i>A. mellifera</i>	2006	NA	NA	NA	NA	NA
DEVB4	UK	<i>A. mellifera</i>	2006	NA	NA	NA	NA	NA
FRAB1	France	<i>A. mellifera</i>	2009	NA	NA	VDV-1	KP765066	NA
FRAB21M	France	<i>V. destructor</i>	2009	NA	NA	VDV-1	KP765067	NA
FRAB21M_2	France	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
FRAMPB1	France	<i>A. mellifera</i>	2009	NA	VDV-1	VDV-1	KP765068	KP734678
FRAMPB2	France	<i>A. mellifera</i>	2009	NA	VDV-1	VDV-1	KP765069	KP734679
FRAMPB3	France	<i>A. mellifera</i>	2009	NA	NA	VDV-1	KP765070	KP734680
FRAMPB4	France	<i>A. mellifera</i>	2009	NA	VDV-1	VDV-1	KP765071	KP734681
FRAMPB5	France	<i>A. mellifera</i>	2009	NA	VDV-1	VDV-1	KP765072	short
FRAMPB6	France	<i>A. mellifera</i>	2009	NA	short	VDV-1	KP765073	KP734682
FRAMPB7	France	<i>A. mellifera</i>	2009	NA	VDV-1	VDV-1	KP765074	short
FRAPM2	France	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
FRAYD	France	<i>A. mellifera</i>	2009	NA	VDV-1	VDV-1	KP765075	KP734676
FRAYV	France	<i>A. mellifera</i>	2009	NA	short	VDV-1	KP765076	KP734677
FRMPB1H	France	<i>A. mellifera</i>	2009	healthy	short	VDV-1	KP765077	KP765048
FRMPB2H	France	<i>A. mellifera</i>	2009	healthy	NA	NA	short	NA
FRMPB3H	France	<i>A. mellifera</i>	2009	healthy	NA	VDV-1	NA	NA
FRMPB4H	France	<i>A. mellifera</i>	2009	healthy	NA	VDV-1	KP765078	NA
FRMPB5H	France	<i>A. mellifera</i>	2009	healthy	KP734738	VDV-1	short	KP734615
FRMPB6H	France	<i>A. mellifera</i>	2009	healthy	short	VDV-1	KP765079	short

FRMPM1	France	<i>V. destructor</i>	2009	NA	VDV-1	VDV-1	KP765080	short
FRMPM3	France	<i>V. destructor</i>	2009	NA	VDV-1	VDV-1	KP765081	KP734720
FRMPM4	France	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
FRMPM5	France	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
FRMPM6	France	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
FRYB1D	France	<i>A. mellifera</i>	2009	deformed	NA	VDV-1	KP765082	NA
FRYB2D	France	<i>A. mellifera</i>	2009	deformed	VDV-1	VDV-1	KP765083	KP734710
FRYB2H	France	<i>A. mellifera</i>	2009	healthy	short	VDV-1	KP765084	KP734709
FRYB3D	France	<i>A. mellifera</i>	2009	deformed	VDV-1	VDV-1	KP765085	NA
FRYB4D	France	<i>A. mellifera</i>	2009	deformed	VDV-1	VDV-1	short	KP734598
FRYM1	France	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
FRYM2	France	<i>V. destructor</i>	2009	NA	VDV-1	VDV-1	KP765086	KP734711
FRYM3	France	<i>V. destructor</i>	2009	NA	VDV-1	VDV-1	KP765087	NA
FRYM4	France	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
GEPRB1D	Germany	<i>A. mellifera</i>	2009	deformed	short	VDV-1	KP765088	NA
GEPRB1H	Germany	<i>A. mellifera</i>	2009	healthy	NA	Short	KP765089	KP734647
GEPRB2D	Germany	<i>A. mellifera</i>	2009	deformed	VDV-1	NA	KP765090	NA
GEPRB2H	Germany	<i>A. mellifera</i>	2009	healthy	KP734747	NA	KP765091	NA
GEPRB3D	Germany	<i>A. mellifera</i>	2009	deformed	VDV-1	VDV-1	short	NA
GEPRB3H	Germany	<i>A. mellifera</i>	2009	healthy	VDV-1	VDV-1	short	NA
GEPRB4D	Germany	<i>A. mellifera</i>	2009	deformed	NA	VDV-1	short	KP734600
GEPRB4H	Germany	<i>A. mellifera</i>	2009	healthy	NA	VDV-1	KP765092	NA
GEPRB5H	Germany	<i>A. mellifera</i>	2009	healthy	VDV-1	VDV-1	KP765093	KP734616
GEPRB6H	Germany	<i>A. mellifera</i>	2009	deformed	VDV-1	VDV-1	NA	short
GEPRM1	Germany	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
GEPRM2	Germany	<i>V. destructor</i>	2009	NA	NA	NA	KP765094	NA
GEPRM3	Germany	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
GEPRM4	Germany	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
GERB1	Germany	<i>A. mellifera</i>	2009	NA	NA	VDV-1	KP765095	KP734722
GERB21M	Germany	<i>A. mellifera</i>	2009	NA	NA	VDV-1	KP765096	KP734723
GERB22M	Germany	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
GERB41M	Germany	<i>A. mellifera</i>	2009	NA	NA	VDV-1	NA	KP734724
GERB42M	Germany	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
GERPRM1	Germany	<i>V. destructor</i>	2009	NA	VDV-1	VDV-1	KP765097	NA
GERPRM2	Germany	<i>V. destructor</i>	2009	NA	NA	VDV-1	KP765098	NA
GUB1D	Guernsey	<i>A. mellifera</i>	2009	deformed	KP734753	KP734512	KP765099	short
GUB1D	Guernsey	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
GUB2D	Guernsey	<i>A. mellifera</i>	2009	deformed	KP734754	KP734513	short	KP734634
GUB2D	Guernsey	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
GUB3D	Guernsey	<i>A. mellifera</i>	2009	deformed	KP734755	KP734514	short	KP734636
GUB3D	Guernsey	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
GUB4H	Guernsey	<i>A. mellifera</i>	2009	healthy	KP734756	KP734515	KP765100	KP734637
GUB4H2	Guernsey	<i>A. mellifera</i>	2009	healthy	KP734779	KP734516	KP765101	KP734638
GUB5H	Guernsey	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
GUERDB1	Guernsey	<i>A. mellifera</i>	2009	NA	NA	KP734517	KP765102	NA
GUERDB2	Guernsey	<i>A. mellifera</i>	2009	NA	KP734757	NA	KP765103	KP734670
GUERDB3	Guernsey	<i>A. mellifera</i>	2009	NA	KP734758	KP734518	KP765104	NA
GUERDB4	Guernsey	<i>A. mellifera</i>	2009	NA	KP734759	KP734519	KP765105	KP734671
GUERDB5	Guernsey	<i>A. mellifera</i>	2009	NA	KP734760	KP734520	KP765106	KP734672
GUERDB6	Guernsey	<i>A. mellifera</i>	2009	NA	KP734761	KP734521	KP765107	KP734673
GUERDB7	Guernsey	<i>A. mellifera</i>	2009	NA	KP734762	Short	KP765108	KP734669
GUERDWW	Guernsey	<i>A. mellifera</i>	2009	NA	KP734763	Short	KP765109	KP734651
GUERM1	Guernsey	<i>V. destructor</i>	2009	NA	KP734764	KP734522	KP765110	KP734649
GUERMDB4	Guernsey	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA

GUERMDB7	Guernsey	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
GUERWB1	Guernsey	<i>A. mellifera</i>	2009	NA	NA	KP734523	KP765111	KP734650
HAB17AM	Hawaii	<i>V. destructor</i>	2009	NA	NA	NA	KP765112	short
HAB1HL1	Hawaii	<i>A. mellifera</i>	2009	NA	NA	NA	KP765113	short
HAB1HM	Hawaii	<i>V. destructor</i>	2009	NA	NA	NA	short	NA
HAB1P1L1	Hawaii	<i>A. mellifera</i>	2009	NA	NA	NA	KP765114	NA
HAB3DL1	Hawaii	<i>A. mellifera</i>	2009	NA	NA	NA	short	NA
HABIL1	Hawaii	<i>A. mellifera</i>	2009	NA	NA	Short	short	KP734640
HABIL2	Hawaii	<i>A. mellifera</i>	2009	NA	NA	KP765227	KP765115	short
HABIL3	Hawaii	<i>A. mellifera</i>	2009	NA	NA	KP765228	KP765116	KP734641
HAL1	Hawaii	<i>A. mellifera</i>	2009	NA	KP734765	NA	KP765117	KP734622
HAL2	Hawaii	<i>V. destructor</i>	2009	NA	KP734766	Short	short	KP734623
HAL3	Hawaii	<i>A. mellifera</i>	2009	NA	short	KP765229	KP765118	KP734624
HAM1	Hawaii	<i>V. destructor</i>	2009	NA	KP734767	KP765230	KP765119	KP734625
HAM2	Hawaii	<i>V. destructor</i>	2009	NA	KP734768	NA	short	NA
HAM3	Hawaii	<i>V. destructor</i>	2009	NA	KP734769	KP765231	KP765120	short
HAWEV1M	Hawaii	<i>A. mellifera</i>	2009	NA	short	KP765232	KP765121	KP734687
HAWEV3B	Hawaii	<i>A. mellifera</i>	2009	NA	KP734770	KP765233	KP765122	KP734688
HAWEV3L	Hawaii	<i>A. mellifera</i>	2009	NA	short	Short	KP765123	KP734690
HAWEV3M	Hawaii	<i>A. mellifera</i>	2009	NA	short	KP765234	KP765124	KP734689
HAWEV3M2	Hawaii	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
HAWEV7A	Hawaii	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
HAWEV7G	Hawaii	<i>A. mellifera</i>	2009	NA	short	KP765235	KP765125	KP734691
HAWEVIP3	Hawaii	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
IOMB1H	Isle of Man	<i>A. mellifera</i>	2009	healthy	NA	Short	NA	KP734642
IOMB2H	Isle of Man	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	short
IOMB3H	Isle of Man	<i>A. mellifera</i>	2009	healthy	NA	Short	NA	KP734643
IOMB4H	Isle of Man	<i>A. mellifera</i>	2009	NA	NA	NA	KP765126	NA
IOMB5H	Isle of Man	<i>A. mellifera</i>	2009	NA	NA	NA	short	short
IOMB6H	Isle of Man	<i>A. mellifera</i>	2009	NA	NA	NA	KP765127	KP734648
IOMGLB1H	Isle of Man	<i>A. mellifera</i>	2009	NA	KP734771	Short	KP765128	KP734654
IOMGLB2H	Isle of Man	<i>A. mellifera</i>	2009	NA	NA	Short	KP765129	KP734655
IOMGLB3H	Isle of Man	<i>A. mellifera</i>	2009	NA	short	Short	KP765130	KP734656
IOMGLB4H	Isle of Man	<i>A. mellifera</i>	2009	NA	NA	Short	KP765131	KP734657
IOMGLB5H	Isle of Man	<i>A. mellifera</i>	2009	NA	KP734772	Short	KP765132	KP734658
IOMGLB6H	Isle of Man	<i>A. mellifera</i>	2009	NA	KP734773	NA	KP765133	NA
IREJMB1	Ireland	<i>A. mellifera</i>	2009	NA	KP734774	KP734524	KP765134	KP734704
IRJMB1H	Ireland	<i>A. mellifera</i>	2009	healthy	KP734775	KP734525	NA	KP734621
IRJMB2H	Ireland	<i>A. mellifera</i>	2009	healthy	KP734776	KP734526	KP765135	short
IRJMB3H	Ireland	<i>A. mellifera</i>	2009	healthy	KP734777	KP734527	KP765136	short
IRJMB4H	Ireland	<i>A. mellifera</i>	2009	healthy	KP734778	KP734528	KP765137	KP734631
ISGLB1H	Israel	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
ISGLB2H	Israel	<i>A. mellifera</i>	2009	healthy	NA	NA	short	short
ISGLB3H	Israel	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
ISGLB4H	Israel	<i>A. mellifera</i>	2009	healthy	NA	NA	KP765138	NA
ISGLB5H	Israel	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
ISGLB6H	Israel	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
IsrB1	Israel	<i>A. mellifera</i>	2009	NA	NA	NA	KP765139	NA
IsrB2	Israel	<i>A. mellifera</i>	2009	NA	NA	NA	KP765140	NA
ITB1H	Italy	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
ITB2H	Italy	<i>A. mellifera</i>	2009	healthy	KP734780	Short	short	KP734639
ITB3H	Italy	<i>A. mellifera</i>	2009	healthy	NA	Short	NA	NA
JA06SMB2H	Japan	<i>A. cerana</i>	2006	healthy	NA	NA	NA	NA
JA06SMB3H	Japan	<i>A. cerana</i>	2006	healthy	NA	NA	NA	NA

JA06SMB4H	Japan	<i>A. cerana</i>	2006	healthy	NA	NA	NA	NA
JA06SMB5H	Japan	<i>A. cerana</i>	2006	healthy	NA	NA	NA	NA
JA08SMB2H	Japan	<i>A. cerana</i>	2008	healthy	NA	NA	NA	NA
JA08SMB3H	Japan	<i>A. cerana</i>	2008	healthy	NA	NA	NA	NA
JA08SMB4H	Japan	<i>A. cerana</i>	2008	healthy	NA	NA	NA	NA
JA08SMB5H	Japan	<i>A. cerana</i>	2008	healthy	NA	NA	NA	NA
JA08TB1H	Japan	<i>A. mellifera</i>	2008	healthy	KP734781	KP734529	KP765141	short
JA08TB2H	Japan	<i>A. mellifera</i>	2008	healthy	KP734782	NA	short	NA
JA08TB3H	Japan	<i>A. mellifera</i>	2008	healthy	NA	NA	NA	NA
JA08TB4H	Japan	<i>A. mellifera</i>	2008	healthy	NA	NA	NA	NA
JA08TM1	Japan	<i>V. destructor</i>	2008	NA	NA	NA	NA	NA
JA08TM2	Japan	<i>V. destructor</i>	2008	NA	KP734783	NA	KP765142	NA
JA08TM3	Japan	<i>V. destructor</i>	2008	NA	NA	NA	NA	NA
JA08TM4	Japan	<i>V. destructor</i>	2008	NA	NA	NA	NA	NA
JA30SML1	Japan	<i>A. mellifera</i>	2004	NA	NA	KP734530	KP765143	KP734662
JA30SML2	Japan	<i>A. mellifera</i>	2004	NA	NA	NA	NA	NA
JAPACB1	Japan	<i>A. cerana</i>	2008	NA	NA	NA	KP765144	short
JAPACB2	Japan	<i>A. cerana</i>	2008	NA	NA	NA	NA	NA
JAPOTB1	Japan	<i>A. mellifera</i>	2009	NA	KP734784	KP734531	short	short
JASML2	Japan	<i>A. mellifera</i>	1998	NA	NA	NA	KP765145	short
JATB1H	Japan	<i>A. mellifera</i>	2009	healthy	short	Short	KP765146	KP734635
JATB2H	Japan	<i>A. mellifera</i>	2009	healthy	KP734785	NA	short	NA
JATB3H	Japan	<i>A. mellifera</i>	2009	healthy	NA	KP734532	KP765147	short
JATB4H	Japan	<i>A. mellifera</i>	2009	healthy	short	KP734533	KP765148	KP734599
JATB5H	Japan	<i>A. mellifera</i>	2009	healthy	KP734786	Short	short	KP734607
JATM2	Japan	<i>V. destructor</i>	2009	NA	short	Short	short	KP734715
JATM3	Japan	<i>V. destructor</i>	2009	NA	KP734787	KP734534	short	KP734719
JATM4	Japan	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
MEGVGL1D	Mexico	<i>A. mellifera</i>	2009	deformed	NA	NA	NA	NA
MEGVGL1H	Mexico	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
MEGVGL2D	Mexico	<i>A. mellifera</i>	2009	deformed	NA	NA	NA	NA
MEGVGL2H	Mexico	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
MEGVGL3D	Mexico	<i>A. mellifera</i>	2009	deformed	NA	NA	NA	NA
MEGVGL3H	Mexico	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
MEGVGL4D	Mexico	<i>A. mellifera</i>	2009	deformed	NA	NA	NA	NA
MEGVGL4H	Mexico	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
MEGVGM1	Mexico	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
MEGVGM2	Mexico	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
MEGVGM3	Mexico	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
MEGVGM4	Mexico	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
MELMB1H	Mexico	<i>A. mellifera</i>	2009	healthy	short	KP734535	KP765149	KP734608
MELMB2H	Mexico	<i>A. mellifera</i>	2009	healthy	KP734788	KP734536	KP765150	NA
MELMB3H	Mexico	<i>A. mellifera</i>	2009	healthy	KP734789	KP734537	short	NA
MELMB4H	Mexico	<i>A. mellifera</i>	2009	healthy	KP734790	KP734538	KP765151	NA
MELMB5H	Mexico	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	KP734609
MELMB6H	Mexico	<i>A. mellifera</i>	2009	healthy	short	NA	NA	KP734610
MELMB7H	Mexico	<i>A. mellifera</i>	2009	healthy	short	Short	KP765152	KP734611
MELMB8H	Mexico	<i>A. mellifera</i>	2009	healthy	KP734791	KP734539	KP765153	KP734612
MELMB9H	Mexico	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
MELMM1	Mexico	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
MELMM10H	Mexico	<i>A. mellifera</i>	2009	healthy	short	NA	KP765154	KP734614
MELMM2	Mexico	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
MELMM3	Mexico	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
MELMM4	Mexico	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA

MELMM5	Mexico	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
MELMM9H	Mexico	<i>A. mellifera</i>	2009	healthy	KP734792	KP734540	KP765155	KP734613
MEOAJB1H	Mexico	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	short
MEOAJB2H	Mexico	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	KP734617
MEOAJB3H	Mexico	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
MEOAJB4H	Mexico	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
MEXA1	Mexico	<i>A. mellifera</i>	2009	NA	KP734793	KP734541	KP765156	KP734700
MEXA4	Mexico	<i>A. mellifera</i>	2009	NA	short	KP734542	KP765157	KP734701
MEXB1	Mexico	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
MEXB2	Mexico	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
MEXB3	Mexico	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
MEXB4	Mexico	<i>A. mellifera</i>	2009	NA	KP734794	Short	short	KP734652
MEXLMB1	Mexico	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
MEXLMB2	Mexico	<i>A. mellifera</i>	2009	NA	NA	NA	KP765158	short
MEXLMB3	Mexico	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
MEXLMB4	Mexico	<i>A. mellifera</i>	2009	NA	KP734795	KP734543	KP765159	KP734707
MEXM29/6	Mexico	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
NZBH1	New Zealand	<i>V. destructor</i>	2008	NA	NA	NA	NA	NA
NZMGB1D	New Zealand	<i>A. mellifera</i>	2008	deformed	KP734796	KP734544	short	short
NZMGB1H	New Zealand	<i>A. mellifera</i>	2008	healthy	KP734797	KP734545	KP765160	NA
NZMGB2D	New Zealand	<i>A. mellifera</i>	2008	deformed	KP734798	KP734546	short	NA
NZMGB2H	New Zealand	<i>A. mellifera</i>	2008	healthy	NA	NA	NA	NA
NZMGB3D	New Zealand	<i>A. mellifera</i>	2008	deformed	KP734799	KP734547	KP765161	KP734717
NZMGB3H	New Zealand	<i>A. mellifera</i>	2008	healthy	KP734800	KP734548	KP765162	KP734716
NZMGB4D	New Zealand	<i>A. mellifera</i>	2008	deformed	KP734801	KP734549	KP765163	KP734593
NZMGB4H	New Zealand	<i>A. mellifera</i>	2008	healthy	KP734802	KP734550	KP765164	KP734592
NZMGBM6	New Zealand	<i>A. mellifera</i>	2008	healthy	NA	NA	NA	NA
NZMGBM7	New Zealand	<i>A. mellifera</i>	2008	deformed	NA	NA	NA	NA
NZMGM2	New Zealand	<i>V. destructor</i>	2008	NA	NA	NA	NA	NA
NZMGM3	New Zealand	<i>V. destructor</i>	2008	NA	KP734803	Short	short	KP734718
NZMGM4	New Zealand	<i>V. destructor</i>	2008	NA	NA	NA	NA	NA
NZMGM5	New Zealand	<i>V. destructor</i>	2008	NA	KP734804	KP734551	short	KP734597
NZMGM8	New Zealand	<i>V. destructor</i>	2008	NA	NA	NA	NA	NA
OZB1H	Australia	<i>A. mellifera</i>	2009	healthy	NA	Short	KP765165	short
OZB1H2	Australia	<i>A. mellifera</i>	2009	NA	KP734805	KP734552	KP765166	KP734698
OZB2H	Australia	<i>A. mellifera</i>	2009	healthy	NA	NA	KP765167	short
OZB2H2	Australia	<i>A. mellifera</i>	2009	NA	KP734806	NA	KP765168	KP734699
OZB3H	Australia	<i>A. mellifera</i>	2009	healthy	KP734807	KP734553	KP765169	KP734632
OZB4H	Australia	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
OZB5H	Australia	<i>A. mellifera</i>	2009	healthy	NA	KP734554	KP765170	KP734633
OZMPB1	Australia	<i>A. mellifera</i>	2009	NA	NA	NA	KP765171	NA
OZMPB2	Australia	<i>A. mellifera</i>	2009	NA	NA	NA	KP765172	NA
OZMPB3	Australia	<i>A. mellifera</i>	2009	NA	NA	NA	KP765173	NA
PA4SMB1	Pakistan	<i>A. mellifera</i>	1998	NA	NA	KP734555	KP765174	KP734692
PA4SMB2	Pakistan	<i>A. mellifera</i>	1998	NA	KP734808	NA	NA	NA
PA4SMB3	Pakistan	<i>A. mellifera</i>	1998	NA	NA	KP734556	NA	NA
PA4SMB4	Pakistan	<i>A. mellifera</i>	1998	NA	NA	KP734557	NA	NA
PAESB1D	Pakistan	<i>A. mellifera</i>	2009	deformed	KP734809	KP734558	KP765175	NA
PAESB2D	Pakistan	<i>A. mellifera</i>	2009	deformed	KP734810	Short	short	NA
PAESB3D	Pakistan	<i>A. mellifera</i>	2009	deformed	KP734811	Short	short	NA
PAESB4D	Pakistan	<i>A. mellifera</i>	2009	deformed	KP734812	Short	KP765176	NA
PAESB5D	Pakistan	<i>A. mellifera</i>	2009	deformed	KP734813	KP734559	KP765177	NA
PAESLA1	Pakistan	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
PAESM1	Pakistan	<i>T. clareae</i>	2009	NA	NA	NA	NA	NA

PAESM2	Pakistan	<i>T. clareae</i>	2009	NA	NA	NA	NA	NA
PAESM3	Pakistan	<i>T. clareae</i>	2009	NA	NA	NA	NA	NA
PAESM4	Pakistan	<i>T. clareae</i>	2009	NA	NA	NA	NA	NA
PAESM5	Pakistan	<i>T. clareae</i>	2009	NA	NA	NA	NA	NA
PAESP1	Pakistan	<i>A. mellifera</i>	2009	NA	KP734814	KP734560	short	NA
PAESP2	Pakistan	<i>A. mellifera</i>	2009	NA	KP734815	KP734561	KP765178	short
PAESP3	Pakistan	<i>A. mellifera</i>	2009	NA	KP734816	KP734562	short	short
PAK3A	Pakistan	<i>A. mellifera</i>	1998	NA	NA	NA	NA	NA
PAK4A	Pakistan	<i>A. mellifera</i>	1998	NA	NA	NA	NA	NA
PAKEB1	Pakistan	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
PAKEB2	Pakistan	<i>A. mellifera</i>	2009	NA	short	KP734563	KP765179	KP734705
PAKEB3	Pakistan	<i>A. mellifera</i>	2009	NA	short	KP734564	short	KP734706
PAKEB4	Pakistan	<i>A. mellifera</i>	2009	NA	NA	KP734565	KP765180	NA
PAKSJMB1	Pakistan	<i>A. cerana</i>	2003	NA	NA	NA	NA	NA
PAKSJMB2	Pakistan	<i>A. cerana</i>	2003	NA	NA	NA	NA	NA
PASMB1	Pakistan	<i>A. mellifera</i>	1998	deformed	NA	KP734566	NA	NA
PASMB2	Pakistan	<i>A. mellifera</i>	1998	NA	NA	NA	NA	NA
PASMM1	Pakistan	<i>T. clareae</i>	1998	NA	NA	NA	NA	NA
PASMM2	Pakistan	<i>T. clareae</i>	1998	NA	NA	NA	NA	NA
PASMM3	Pakistan	<i>T. clareae</i>	1998	NA	NA	NA	NA	NA
PASMM4	Pakistan	<i>T. clareae</i>	1998	NA	NA	NA	NA	NA
PHILACER2005	Phillipines	<i>A. cerana</i>	2005	NA	NA	NA	NA	NA
PHSMB2H	Phillipines	<i>A. cerana</i>	2000	healthy	NA	NA	short	short
PHSMB3H	Phillipines	<i>A. cerana</i>	2000	healthy	NA	NA	NA	NA
PHSMB4H	Phillipines	<i>A. cerana</i>	2000	healthy	short	NA	NA	short
PHSMB5H	Phillipines	<i>A. cerana</i>	2000	healthy	NA	NA	NA	NA
PHSMB6H	Phillipines	<i>A. cerana</i>	2000	healthy	NA	NA	NA	NA
POATB1D	Poland	<i>A. mellifera</i>	2009	deformed	NA	NA	NA	NA
POATB1H	Poland	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	NA
POATB2D	Poland	<i>A. mellifera</i>	2009	deformed	NA	NA	NA	NA
POATM1	Poland	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
POATM2	Poland	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
POATM3	Poland	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
POATM4	Poland	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
POGTB1D	Poland	<i>A. mellifera</i>	2003	deformed	KP734817	KP734567	KP765181	KP734712
POGTB1H	Poland	<i>A. mellifera</i>	2003	healthy	NA	NA	NA	NA
POGTB2D	Poland	<i>A. mellifera</i>	2003	deformed	short	Short	KP765182	KP734714
POGTB2H	Poland	<i>A. mellifera</i>	2003	healthy	NA	NA	KP765183	NA
POGTB3D	Poland	<i>A. mellifera</i>	2003	deformed	NA	KP734568	KP765184	KP734591
POGTB3H	Poland	<i>A. mellifera</i>	2003	healthy	NA	NA	KP765185	NA
POGTB4D	Poland	<i>A. mellifera</i>	2003	deformed	short	Short	NA	KP734596
POGTB4H	Poland	<i>A. mellifera</i>	2009	healthy	NA	KP734569	KP765186	KP734594
POGTB4H2	Poland	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
POGTB5D	Poland	<i>A. mellifera</i>	2003	deformed	NA	Short	KP765187	KP734603
POGTB5D2	Poland	<i>A. mellifera</i>	2003	deformed	KP734818	KP734570	KP765188	KP734605
POGTB5H	Poland	<i>A. mellifera</i>	2003	healthy	NA	NA	NA	NA
POGTB6D	Poland	<i>A. mellifera</i>	2003	deformed	KP734819	Short	KP765189	KP734604
POGTB6H	Poland	<i>A. mellifera</i>	2003	healthy	NA	NA	NA	NA
POGTB7D	Poland	<i>A. mellifera</i>	2003	deformed	KP734820	Short	NA	KP734606
POGTM1	Poland	<i>V. destructor</i>	2009	NA	KP734821	KP734571	KP765190	KP734713
POGTM2	Poland	<i>V. destructor</i>	2009	NA	KP734822	Short	short	short
POGTM3	Poland	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
POGTM4	Poland	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
POGTM5	Poland	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA

POGTM5	Poland	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
POGTM6	Poland	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
POGTM6	Poland	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
POOGTB1D	Poland	<i>A. mellifera</i>	2009	deformed	NA	NA	NA	NA
POOGTB2D	Poland	<i>A. mellifera</i>	2009	deformed	KP734823	NA	NA	NA
POOGTB3D	Poland	<i>A. mellifera</i>	2009	deformed	KP734824	KP734572	KP765191	KP734725
POOGTB4D	Poland	<i>A. mellifera</i>	2009	deformed	short	KP734573	KP765192	KP734595
POOGTB5D	Poland	<i>A. mellifera</i>	2009	deformed	NA	Short	KP765193	KP734602
POOGTB6D	Poland	<i>A. mellifera</i>	2009	deformed	NA	NA	NA	NA
ROMB1	Romania	<i>A. mellifera</i>	2009	NA	NA	VDV-1	KP765194	NA
ROMB2	Romania	<i>A. mellifera</i>	2009	NA	NA	NA	KP765195	NA
ROMM1	Romania	<i>V. destructor</i>	2009	NA	NA	NA	KP765196	NA
ROMM2	Romania	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
ROMM3	Romania	<i>V. destructor</i>	2009	NA	NA	VDV-1	KP765197	KP734708
SAB1	South Africa	<i>A. mellifera</i>	2009	NA	NA	NA	KP765198	NA
SASM2	South Africa	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
SASM3	South Africa	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
SASM4	South Africa	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
SASMM1	South Africa	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
SASMM55	South Africa	<i>V. destructor</i>	2009	NA	NA	NA	NA	NA
ShfAnchB1	UK	<i>A. mellifera</i>	2001	NA	NA	NA	KP765199	NA
ShfAnchB2	UK	<i>A. mellifera</i>	2001	NA	NA	NA	KP765200	NA
ShfAnchB3	UK	<i>A. mellifera</i>	2001	NA	NA	NA	short	NA
SHHLB1D	UK	<i>A. mellifera</i>	2008	deformed	NA	NA	NA	NA
SHHLB2D	UK	<i>A. mellifera</i>	2008	deformed	KP734825	NA	KP765201	NA
SHHLB3D	UK	<i>A. mellifera</i>	2008	deformed	NA	NA	KP765202	KP734721
SHHLB4D	UK	<i>A. mellifera</i>	2008	deformed	NA	Short	KP765203	KP734601
SHHLM1	UK	<i>V. destructor</i>	2008	NA	VDV-1	VDV-1	KP765204	KP734684
SHHLM2	UK	<i>V. destructor</i>	2008	NA	NA	NA	NA	NA
SHHLM3	UK	<i>V. destructor</i>	2008	NA	NA	NA	NA	NA
SHHLM4	UK	<i>V. destructor</i>	2008	NA	NA	NA	NA	NA
SHSMAB2H	UK	<i>A. mellifera</i>	2001	healthy	KP734827	NA	KP765205	short
SHSMAB3H	UK	<i>A. mellifera</i>	2001	healthy	NA	NA	NA	NA
SHSMAB4H	UK	<i>A. mellifera</i>	2001	healthy	NA	NA	NA	NA
SLB1H	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
SLB2H	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	short	NA
SLB3H	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
SLB4H	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
SLB5H	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
SlovB3a	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
SlovB3b	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
SlovB3c	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
SlovB5a	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
SlovB5b	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
SlovB5c	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	KP765206	NA
SLOVB6	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	short	NA
SLOVB7	Slovenia	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
SPJM1H	Spain	<i>A. mellifera</i>	2009	healthy	short	KP734577	short	KP734626
SPJM2H	Spain	<i>A. mellifera</i>	2009	healthy	KP734828	KP734578	KP765207	KP734627
SPJM3H	Spain	<i>A. mellifera</i>	2009	healthy	KP734829	KP734579	short	KP734628
SPJM4D	Spain	<i>A. mellifera</i>	2009	deformed	short	KP734580	short	KP734629
SPJM5D	Spain	<i>A. mellifera</i>	2009	deformed	KP734830	KP734581	short	KP734630
SWBDB1H	Switzerland	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	short
SWBDB2H	Switzerland	<i>A. mellifera</i>	2009	healthy	short	NA	NA	KP734618

SWBDB3H	Switzerland	<i>A. mellifera</i>	2009	healthy	NA	NA	NA	short
SWBDB4D	Switzerland	<i>A. mellifera</i>	2009	deformed	KP734831	KP734582	KP765208	KP734619
SWBDB5D	Switzerland	<i>A. mellifera</i>	2009	deformed	KP734832	Short	KP765209	KP734620
SwissB1	Switzerland	<i>A. mellifera</i>	2009	NA	KP734833	KP734583	KP765210	KP734661
SwissB2	Switzerland	<i>A. mellifera</i>	2009	NA	KP734834	Short	KP765211	short
SwissB3	Switzerland	<i>A. mellifera</i>	2009	NA	KP734835	Short	KP765212	short
SWISSBD1	Switzerland	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
SWISSBD2	Switzerland	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
SWISSBD3	Switzerland	<i>A. mellifera</i>	2009	NA	KP734836	KP734584	KP765213	KP734702
SWISSBD4	Switzerland	<i>A. mellifera</i>	2009	NA	NA	NA	KP765214	KP734703
TaptB1	UK	<i>A. mellifera</i>	2009	NA	KP734837	Short	KP765215	short
TaptB2	UK	<i>A. mellifera</i>	2009	NA	KP734838	Short	KP765216	short
TaptB3	UK	<i>A. mellifera</i>	2009	NA	short	Short	KP765217	KP734653
TAPTGL1	UK	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
TAPTGL2	UK	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
TaptP1	UK	<i>A. mellifera</i>	2008	NA	KP734839	Short	KP765218	short
TaptP2	UK	<i>A. mellifera</i>	2008	NA	KP734840	Short	KP765219	KP734659
TaptP3	UK	<i>A. mellifera</i>	2008	NA	KP734841	Short	KP765220	KP734660
UoM4	USA	<i>A. mellifera</i>	2009	NA	NA	NA	KP765221	NA
UOMBA	USA	<i>A. mellifera</i>	2009	NA	short	Short	KP765222	KP734693
UOMBB	USA	<i>A. mellifera</i>	2009	NA	KP734842	KP734585	KP765223	KP734694
UOMBC	USA	<i>A. mellifera</i>	2009	NA	NA	NA	NA	NA
UOMBD	USA	<i>A. mellifera</i>	2009	NA	KP734843	KP734586	KP765224	KP734695
UOMBE	USA	<i>A. mellifera</i>	2009	NA	KP734844	KP734587	KP765225	KP734696
UOMBF	USA	<i>A. mellifera</i>	2009	NA	KP734845	KP734588	KP765226	KP734697
UoMMSB1	USA	<i>A. mellifera</i>	2009	NA	NA	KP734589	short	KP734644
UoMMSB2	USA	<i>A. mellifera</i>	2009	NA	NA	NA	short	KP734645
UoMMSB3	USA	<i>A. mellifera</i>	2009	NA	KP734846	KP734590	NA	KP734646

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289

290 **Table S2.**

291 Table S2: First stage of model selection. Substitution model based on jmodeltest (51), clock model and exponential
 292 growth prior based on BEAST analyses. Note that exponential growth is significant for the *rdrp*-fragment when
 293 curtailing data in 2009 to exclude populations with strong population structure and low sample sizes.
 294

Fragment	Substitution model	Strict clock	Exponential population growth
dated <i>lp</i> -fragment	TrN+G	no	yes
dated <i>vp3</i> -fragment	TrN+I+G	no	yes
dated <i>rdrp</i> -fragment	TrN+I	no	no
<i>lp</i> DWV	TrN+I+G	no	yes
<i>vp3</i> DWV	HKY+I	no	yes
<i>rdrp</i> DWV	HKY+G	no	no

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298 **Table S3.**
 299 Table S3: Results of path sampling maximum likelihood estimator analysis comparing demographic and molecular
 300 clock models.

Fragment	Clock model and prior	Constant pop. size	Exponential pop. Growth	301 Skyride ₃₀₂	
dated <i>lp</i> fragment	Exponential clock	NA	-2003.80	-2008.64	
	Lognormal clock	NA	-2006.82	-2010.48	
dated <i>vp3</i> -fragment	Exponential clock	NA	-5905.28	-5922.11	
	Lognormal clock	NA	-5905.44	-5928.43	
dated <i>rdrp</i> -fragment	Exponential clock	-1857.80	NA	-1865.98	
	Lognormal clock	-1850.13	NA	-1860.15	
<i>lp</i> -fragment	Exp. clock	mean	NA	-4368.23	
		<i>lp</i>	NA	-4327.47	
	Log. clock	mean	NA	NA	-4364.63
		<i>lp</i>	NA	-4330.91	-4363.68
<i>vp3</i> -fragment	Exp. clock	mean	NA	-1844.62	
		<i>vp3</i>	NA	-1841.40	
	Log. clock	Mean	NA	-1844.42	-1865.29
		<i>vp3</i>	NA	-1843.75	-1863.13
<i>rdrp</i> -fragment	Exp. clock	mean	-2754.91	NA	
		<i>rdrp</i>	-2752.95	NA	
	Log. clock	mean	-2755.09	NA	-2770.03
		<i>rdrp</i>	-2876.71	NA	-2767.01

303 **Table S4.**
 304 Table S4: Geographic composition of data sets per fragment, indicating down-sampled sample size for European
 305 samples
 306

<i>area</i>	<i>lp</i>	<i>vp3</i>	<i>rdrp</i>
Australia	3	3	4
East Asia	28	8	40
Europe	130/28	40/16	98/40
Hawaii	6	9	11
New Zealand	9	8	6
North America	14	16	21
Pakistan	9	12	3
Thailand	10	NA	NA

307

308 **Table S5.**

309 Table S5: Bayes factors for asymmetric migration model a) *lp*-fragment; b) *vp3*-fragment; c) *rdrp*-fragment.

310 a) *lp*-fragment

		Recipient							
		America	Australia	East Asia	Europe	Hawaii	New Zealand	Pakistan	Thailand
donor	America	NA	23.08	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
	Australia	n.s.	NA	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
	East Asia	n.s.	n.s.	NA	370.52	n.s.	n.s.	103.56	4.94
	Europe	7058.77	53.78	n.s.	NA	1171.71	44.55	n.s.	n.s.
	Hawaii	n.s.	n.s.	n.s.	n.s.	NA	n.s.	n.s.	n.s.
	New Zealand	n.s.	n.s.	n.s.	n.s.	n.s.	NA	n.s.	n.s.
	Pakistan	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	NA	3.37
	Thailand	n.s.	n.s.	3.42	n.s.	n.s.	n.s.	18.01	NA

311 b) *vp3*-fragment

		Recipient							
		America	Australia	East Asia	Europe	Hawaii	New Zealand	Pakistan	Thailand
donor	America	NA	8.2	n.s.	n.s.	n.s.	4.02	n.s.	NA
	Australia	n.s.	NA	n.s.	n.s.	n.s.	n.s.	n.s.	NA
	East Asia	n.s.	n.s.	NA	n.s.	n.s.	n.s.	n.s.	NA
	Europe	19.25	19.16	136.04	NA	267.61	3.64	n.s.	NA
	Hawaii	n.s.	n.s.	n.s.	n.s.	NA	n.s.	n.s.	NA
	New Zealand	n.s.	n.s.	n.s.	n.s.	n.s.	NA	n.s.	NA
	Pakistan	n.s.	n.s.	n.s.	7.53	n.s.	n.s.	NA	NA
	Thailand	NA	NA	NA	NA	NA	NA	NA	NA

312 c) *rdrp*-fragment

		Recipient							
		America	Australia	East Asia	Europe	Hawaii	New Zealand	Pakistan	Thailand
donor	America	NA	3.75	n.s.	5.36	3.98	n.s.	n.s.	NA
	Australia	n.s.	NA	n.s.	n.s.	n.s.	n.s.	n.s.	NA
	East Asia	n.s.	n.s.	NA	16.3	n.s.	n.s.	n.s.	NA
	Europe	159.02	23.11	12.79	NA	282.5	88.94	n.s.	NA
	Hawaii	n.s.	4.52	n.s.	n.s.	NA	n.s.	n.s.	NA
	New Zealand	n.s.	n.s.	n.s.	n.s.	n.s.	NA	n.s.	NA
	Pakistan	n.s.	n.s.	4.17	3.19	n.s.	n.s.	NA	NA
	Thailand	NA	NA	NA	NA	NA	NA	NA	NA

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314

315 **Table S6.**
 316 Table S6: Bayes factors and repeatability data for asymmetric migration models, correcting for oversampling
 317 European populations by using 10 randomly downsampled data sets per fragment a) *lp*-fragment; b) *vp3*-fragment;
 318 c) *rdrp*-fragment; the left-hand number indicates the median significant bayes factor for a migration event, the
 319 right-hand number indicates in how many of the randomly downsampled datasets the interaction was found (Bayes
 320 factor cutoff = 3).
 321

322 a) *lp*-fragment

		recipient							
		America	Australia	East Asia	Europe	Hawaii	New Zealand	Pakistan	Thailand
donor	America	NA	121.5 - 10/10	n.s.	n.s.	13.1 - 3/10	n.s.	n.s.	n.s.
	Australia	n.s.	NA	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
	East Asia	n.s.	n.s.	NA	629.7 - 10/10	n.s.	n.s.	32.6 - 10/10	11.6 - 10/10
	Europe	1074 - 10/10	11.1 - 10/10	n.s.	NA	147.5 - 10/10	21.1 - 10/10	n.s.	n.s.
	Hawaii	n.s.	n.s.	n.s.	n.s.	NA	n.s.	n.s.	n.s.
	New Zealand	n.s.	n.s.	n.s.	n.s.	n.s.	NA	n.s.	n.s.
	Pakistan	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	NA	n.s.
	Thailand	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	38.9 - 10/10	NA

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326 b) *vp3*-fragment

		recipient							
		America	Australia	East Asia	Europe	Hawaii	New Zealand	Pakistan	Thailand
donor	America	NA	7.7 - 10/10	n.s.	6.6 - 6/10	14.3 - 10/10	3.4 - 10/10	n.s.	NA
	Australia	n.s.	NA	n.s.	n.s.	n.s.	n.s.	n.s.	NA
	East Asia	n.s.	n.s.	NA	5.5 - 3/10	n.s.	n.s.	n.s.	NA
	Europe	5.4 - 7/10	9.6 - 10/10	21.3 - 10/10	NA	18.7 - 10/10	3.7 - 8/10	n.s.	NA
	Hawaii	3.5 - 2/10	4.9 - 10/10	n.s.	5.2 - 6/10	NA	n.s.	n.s.	NA
	New Zealand	n.s.	n.s.	n.s.	n.s.	n.s.	NA	n.s.	NA
	Pakistan	3.6 - 9/10	n.s.	n.s.	4.0 - 5/10	n.s.	n.s.	NA	NA
	Thailand	NA	NA	NA	NA	NA	NA	NA	NA

327

328 c) *rdrp*-fragment

		recipient							
		America	Australia	East Asia	Europe	Hawaii	New Zealand	Pakistan	Thailand
donor	America	NA	3.5 - 5/10	n.s.	10.4 - 10/10	12.5 - 10/10	n.s.	n.s.	NA
	Australia	n.s.	NA	n.s.	n.s.	n.s.	n.s.	n.s.	NA
	East Asia	5.3 - 1/10	n.s.	NA	29.4 - 10/10	n.s.	n.s.	5.5 - 9/10	NA
	Europe	9.7 - 7/10	6.3 - 10/10	12.3 - 1/10	NA	45.8 - 10/10	35.8 - 10/10	4.7 - 1/10	NA
	Hawaii	7.6 - 10/10	n.s.	n.s.	n.s.	NA	n.s.	n.s.	NA
	New Zealand	n.s.	n.s.	n.s.	4.4 - 2/10	n.s.	NA	n.s.	NA
	Pakistan	5.2 - 8/10	n.s.	6.6 - 9/10	n.s.	n.s.	n.s.	NA	NA
	Thailand	NA	NA	NA	NA	NA	NA	NA	NA

329
 330

331 **Additional Data table S1 (separate file)**

332 Analysis composition table: this table gives the genbank accession numbers, collection year, area and host
333 information of the samples included in any one analysis; 'analysis' refers to the fragment and the particular subset of
334 samples (partial: shorter alignment with additional samples (Fig. S5-7); random: randomly down-sampled data sets
335 (table S6); temporal: data sets used to infer evolutionary rates)

336 **Additional Data table S2 (separate file)**

337 *lp*_fragmentary alignment: Alignment of DWV-positive samples for the *lp*-fragment which were too short or too low
338 in quality to be included in the phylogeographic analysis
339

340 **Additional Data table S2 (separate file)**

341 *vp3*_fragmentary alignment: Alignment of DWV-positive samples for the *vp3*-fragment which were too short or too
342 low in quality to be included in the phylogeographic analysis
343

344 **Additional Data table S2 (separate file)**

345 *helicase*_fragmentary alignment: Alignment of DWV-positive samples for the *helicase*-fragment which were too
346 short or too low in quality to be included in the phylogeographic analysis
347

348 **Additional Data table S2 (separate file)**

349 *rdrp*_fragmentary alignment: Alignment of DWV-positive samples for the *rdrp*-fragment which were too short or
350 too low in quality to be included in the phylogeographic analysis