

1 **Advancing insect vector biology research: a community survey for future**
2 **directions, research applications and infrastructure requirements.**

3

4 Alain Kohl^{1*}, Emilie Pondeville¹, Esther Schnettler¹, Andrea Crisanti², Clelia Supparo²,
5 George K. Christophides², Paul J. Kersey³, Gareth L. Maslen³, Willem Takken⁴,
6 Constantianus J. M. Koenraad⁴, Clelia F. Oliva⁵, Núria Busquets⁶, F. Xavier Abad⁶,
7 Anna-Bella Failloux⁷, Elena A. Levashina⁸, Anthony J. Wilson⁹, Eva Veronesi¹⁰, Maëlle
8 Pichard¹¹, Sarah Arnaud Marsh¹¹, Frédéric Simard¹², Kenneth D. Vernick^{11, 13*}

9

10 ¹ MRC-University of Glasgow Centre for Virus Research, Glasgow G61 1QH, Scotland,
11 UK; ² Department of Life Sciences, Imperial College London, London SW7 2AZ; ³ The
12 European Molecular Biology Laboratory - The European Bioinformatics Institute,
13 Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK; ⁴ Laboratory
14 of Entomology, Wageningen University and Research Centre, P.O. Box 16, 6700 AA
15 Wageningen, The Netherlands; ⁵ Polo d'Innovazione di Genomica, Genetica e
16 Biologia, P.zza Gambuli, Edificio D, 3° Piano, 06132 Perugia, Italy; ⁶ Centre de Recerca
17 en Sanitat Animal (CRESA)—Institut de Recerca i Tecnologia Agroalimentàries (IRTA),
18 Campus UAB, 08193 Bellaterra, Barcelona, Spain; ⁷ Arboviruses and Insect Vectors
19 Unit, Department of Virology, Institut Pasteur, 25-28 rue du Docteur Roux, 75724
20 Paris cedex 15, France; ⁸ Department of Vector Biology, Max-Planck-Institut für
21 Infektionsbiologie, Campus Charité Mitte, Charitéplatz 1, 10117 Berlin, Germany; ⁹
22 Integrative Entomology Group, Vector-borne Viral Diseases Programme, The
23 Pirbright Institute, Ash Road, Pirbright, Woking, Surrey GU24 0NF, UK; ¹⁰ Swiss
24 National Centre for Vector Entomology, Institute of Parasitology, University of
25 Zürich, 8057 Zürich, Switzerland; ¹¹ Department of Parasites and Insect Vectors,
26 Institut Pasteur, Unit of Insect Vector Genetics and Genomics, 28 rue du Docteur
27 Roux, 75015 Paris cedex 15, France; ¹² MIVEGEC "Maladies Infectieuses et Vecteurs:
28 Ecologie, Génétique, Evolution et Contrôle", UMR IRD224-CNRS5290-Université de
29 Montpellier, 911 Avenue Agropolis, 34394 Montpellier, France; ¹³ CNRS Unit of
30 Hosts, Vectors and Pathogens, Paris, France (URA3012), 28 rue du Docteur Roux,
31 75015 Paris cedex 15, France.

32

33 *To whom correspondence should be addressed: alain.kohl@glasgow.ac.uk;

34 kvernick@pasteur.fr

35

36 **Abstract**

37 **Background:** Vector-borne pathogens impact public health and economies
38 worldwide. It has long been recognized that research on arthropod vectors such as
39 mosquitoes, ticks, sandflies and midges which transmit parasites and arboviruses to
40 humans and economically important animals is crucial for development of new
41 control measures that target transmission by the vector. While insecticides are an
42 important part of this arsenal, appearance of resistance mechanisms is an increasing
43 issue. Novel tools for genetic manipulation of vectors, use of *Wolbachia*
44 endosymbiotic bacteria and other biological control mechanisms to prevent
45 pathogen transmission have led to promising new intervention strategies. This has
46 increased interest in vector biology and genetics as well as vector-pathogen
47 interactions. Vector research is therefore at a crucial juncture, and strategic
48 decisions on future research directions and research infrastructures will benefit from
49 community input.

50 **Methodology/Principal Findings:** A survey initiated by the European Horizon2020
51 INFRAVEC-2 consortium set out to canvass priorities in the vector biology research
52 community and to determine key issues that should be addressed for researchers to
53 efficiently study vectors, vector-pathogen interactions, as well as access the
54 structures and services that allow such work to be carried out.

55 **Conclusions/Significance:** We summarize the key findings of the survey which in
56 particular reflect priorities in European countries, and which will be of use to
57 stakeholders that include researchers, government, and research organizations.

58

59

60 **Author Summary**

61 Research on arthropod vectors that transmit so-called arboviruses or parasites, such
62 as mosquitoes, ticks, sandflies and midges is important for the development of
63 control measures that target transmission of these pathogens. Important
64 developments in this research area, for example vector genome sequencing, genome
65 manipulation and use of transmission-blocking endosymbionts such as *Wolbachia*
66 have increased interest in vector biology. As such, strategic decisions on research
67 directions as well as research infrastructures will benefit from community input. A
68 survey initiated by the European Horizon2020 INFRAVEC-2 consortium set out to
69 investigate priorities in the vector biology research community as well as key issues
70 that impact on research, and access to the structures and services that allow such
71 studies to be carried out. Here we summarize the key findings of this survey, which
72 in particular reflect priorities in European countries. The survey data will be of use to
73 decision makers such as governments and research organizations, but also
74 researchers and others in the field.

75 **Introduction**

76 Vector-borne diseases such as those transmitted by mosquitoes have a major impact
77 on human and animal health. Among the many examples, malaria (caused by
78 *Plasmodium* parasites) and dengue (caused by four serotypes of dengue virus,
79 *Flaviviridae*) stand out as major diseases that affect populations worldwide, but new
80 threats such chikungunya virus (*Togaviridae*) and more recently Zika virus
81 (*Flaviviridae*) have emerged [1-4]. Both known and emerging pathogens put huge
82 pressure on communities and public health systems. Vaccine development against
83 key threats to human health such as dengue virus and *Plasmodium* parasites may
84 offer tools against transmission and disease, and progress is encouraging [5-8].
85 However, issues such as pathogen strain variation and vaccine or drug
86 production/distribution costs will remain as challenges [9], and even with vaccines
87 vector control will be a crucial part of a multivalent arsenal. Although drugs against
88 malaria parasites are on the market, availability, administration and resistance are
89 problematic [10-12]. Drugs targeting dengue virus are in the development stages
90 [13-16]. In the case of chikungunya virus vaccine candidates and drugs are now in
91 development [17]. Only veterinary vaccines are currently in use for the animal
92 pathogen Rift Valley fever virus (*Bunyaviridae*) and efforts to produce human
93 vaccines are urgently needed [18, 19].

94 Many ongoing efforts to control vector-borne diseases rely on control measures that
95 target mosquitoes including control of larval breeding sites, use of insecticides, use
96 of bed nets (often used in combination with insecticides) (see for example, [20-25]).
97 These efforts have been successful when implemented consistently, although issues
98 such as insecticide resistance, changes in vector behavior, and difficulties with

99 breeding site control (see for example [26-35]) require that research in vector
100 biology and control is continuously developed and strengthened. Technological
101 developments over the last decade are transforming modern vector research. These
102 include: vector genome sequences, high-throughput genomics, transcriptomics, and
103 population genetics with results in public databases [36], improved methods for
104 genetic manipulation of arthropods (that have led to field trials) [37-43], studies on
105 the influence of the mosquito midgut microbiome on pathogen transmission [44-46],
106 studies on the impact of the insect-specific viruses on arbovirus transmission [47,
107 48], and the use of *Wolbachia* endosymbiotic bacteria that prevent pathogen
108 transmission [37, 49-52]. Nonetheless the opportunity to access and make best use
109 of ongoing research can be difficult, given the specialized knowledge, costs and
110 infrastructures required.

111

112 The European Union (EU) has identified access to specialized Research
113 Infrastructures (RIs) as a key to producing high quality science. RIs are defined as
114 “Tools for science....RIs offer **unique research services** to users from different
115 countries, attract young people to science, and help to shape scientific
116 communities..... RIs may be ‘**single-sited**’ (a single resource at a single location),
117 ‘**distributed**’ (a network of distributed resources), or ‘**virtual**’ (the service is provided
118 electronically)” [53]. Such RIs can be research facilities, resources and related
119 services. Within the Framework Programmes (FP) of the EU, Research Infrastructure
120 projects support the improvement of key high-level facilities for research, and allow
121 access to the facilities by researchers in Europe and eligible member states. A wide
122 range of research disciplines have been targeted by RI projects, including physics,

123 information science, earth science and medicine. One such Research Infrastructure
124 project under EU FP7 was Infravec, which focused on developing and providing
125 research resources for insect vector biology from 2009-2014. Infravec, which was
126 constituted as an EC Starting Community under FP7, obtained the opportunity to
127 renew the project as an Advanced Community (AC) called INFRAVEC-2 under the
128 Horizon 2020 framework. Research Infrastructure projects are not research
129 networks, but rather are tasked to identify the key unique and rare research
130 infrastructures necessary for a research community, and organize them so that
131 researchers at institutes lacking the Research Infrastructures can access the facilities
132 in order to expand the scope of their research. Thus, Research Infrastructures are
133 exceptional facilities that permit experiments that could not routinely be done
134 without this structure. Use of Research Infrastructure facilities by external
135 researchers is provided as so-called “Transnational Access” (TNA), with access costs
136 reimbursed by the Research Infrastructure project, thus provided at no cost to the
137 end-user.

138

139 Conditions have changed since the inception of the FP7 Infravec project, including
140 the emergence and transmission of arboviruses in Europe and elsewhere, as well as
141 widening the project scope to include vector-borne diseases of economically
142 important animals and the most recently developed innovative technologies.
143 Collecting information about the current and perceived future infrastructure needs
144 of the vector biology research community and other stakeholders is an important
145 step to ensure that the services offered via Transnational Access reflect actual needs
146 of the advanced community. Here we present the findings of a survey of scientists

147 and associated stakeholders in the field of vector biology or fields that are linked to
148 vector biology such as pathogen studies, which will help to define priorities and
149 requirements within INFRAVEC-2 but should also be of interest to governments,
150 research organizations and researchers in the field. Participation numbers suggest
151 that in particular European research priorities are reflected in the results, but the
152 data can inform stakeholders worldwide.

153

154 **Materials and Methods**

155 **Survey structure.** A questionnaire (S1 Table) was sent to organizational email lists
156 (European Society for Vector Ecology; the journal Pathogens and Global Health;
157 National Center of Expertise in Vectors (CNEV, France); CIRM-Italian Malaria
158 Network; FP7 Infravec mail list; International Meeting on Arboviruses and their
159 Vectors mail list; BioInsectes; EU/DEVCO MEDILABSECURE network), as well as to
160 other lists owned by the authors. The questionnaire was sent as a URL link to the
161 online form along with an explanatory note to scientists in the vector biology field
162 and associated stakeholders. The questionnaire request was spontaneously
163 retransmitted by an unknown number of recipients to organizational and other lists.

164

165 Briefly, the cover note explained the aims of the INFRAVEC-2 community, followed
166 by a series of questions. The key areas covered by the survey are as follows: 1)
167 vectors and vector-borne pathogens studied by survey participants, 2) research area
168 (with several responses allowed), 3) infrastructures available at the respondents
169 home institution including those for vector and animal research, 4) ease of access to
170 vector research facilities outside the survey participants' home institution, 5)

171 infrastructures that participants would use, offered by the facilities at no cost to
172 user, 6) identification of research priorities over the next 5-10 years, and 7)
173 additional feedback. The survey was carried out from October to November 2015.
174 Respondents were given the opportunity to provide their name and institution,
175 although this was not required for completion of the questionnaire. However, all
176 respondents (n=211) identified themselves, indicating that repeat voting or vote
177 stuffing is not a concern for interpretation of the results. All results shown here are
178 anonymized, and no survey participant details published.

179

180 **Results and Discussion**

181 In total 211 responses were obtained (see S2 Table). Approximately 88% of
182 respondents were from countries across Europe, with France, and then the UK
183 providing the highest numbers of responses. This suggests that the results reflect a
184 good overview of current priorities in European vector biology and vector research
185 areas. Below we summarize and analyze the data obtained in the survey.

186

187 **Research areas: arthropods and pathogens relevant to survey participants.**

188 Our goal was to obtain an overview of the research areas and work of survey
189 participants, which are thus likely to guide their future research needs (S1 Table,
190 Survey Questionnaire). First, respondents indicated vectors relevant to their
191 research as major or minor area of interest (Table 1). *Aedes* species mosquitoes were
192 the top field, followed by *Anopheles* and *Culex* species. The strong interest in aedine
193 species may reflect the emergence of arboviruses such as chikungunya transmitted
194 by *Ae. aegypti* and *Ae. albopictus* as well as the expansion of the latter species in

195 Europe (and other areas) and acting as arbovirus vector [54-60]. Despite their
196 importance in the European context as major vectors of pathogens, comparatively
197 little research is carried out on ticks and *Culicoides* midges. This suggests that the
198 European vector biology community presently lacks sufficient opportunities and
199 resources for research on these vectors. Among the category “Other”, comments by
200 participants indicated phlebotomines/sand flies as a key area, with tsetse flies, fleas,
201 triatomines and tabanids/horse flies also mentioned.

202

203 **Table 1. Research areas and interests of the survey participants.** Numbers of
204 responses are indicated as Major or Minor depending on vector listed, or in the
205 category “Other” which incorporates other vectors not specifically listed (selection of
206 responses shown).

Arthropod	Major	Minor
<i>Aedes spec.</i>	102	38
<i>Culex spec.</i>	66	46
<i>Anopheles spec.</i>	79	42
<i>Culicoides spec.</i>	24	32
Ticks	55	44
Other	42	49
Vectors mentioned under “Other” (selection of most mentioned): phlebotomines/sandflies (33), fleas (13), tsetse flies (7), triatomines (4), tabanids/horse flies (6)		

207

208 We also quantified the major and minor interests of survey participants (Table 2).

209 There was a notably strong indication of research interests in arboviruses, mainly
210 affecting humans but also livestock pathogens as well. These research interests and
211 activities are likely due to the emergence and importance of arboviruses such as
212 chikungunya, Zika, Schmallenberg and bluetongue [2, 55, 61-63]. Given the
213 historically important role of malaria research also in Europe, the overall importance

214 in the vector field is not surprising. Of note was the impact of tick-borne pathogens
215 in the category “Other” and this is worth mentioning especially with the impact of
216 Lyme disease across Europe and North America [64] and surge in interest in
217 Crimean-Congo hemorrhagic fever virus [65, 66].

218

219 **Table 2. Pathogens relevant to the survey participants.** Numbers of responses are
220 indicated as Major or Minor depending on pathogen category listed, or in the
221 category “Other” which incorporates other pathogens not specifically listed
222 (selection of responses shown).

Pathogen Category	Major	Minor
Arboviruses, human	96	40
Arboviruses, livestock	44	45
<i>Plasmodium spec.</i>	66	31
Other	68	28
Pathogens mentioned under “Other” (selection of most mentioned): <i>Leishmania</i> (15), trypanosomes (8), tick-borne pathogens (23).		

223

224 To describe their activities in more detail, we collected further data on the research
225 areas of interest to the survey participants (Table 3). In general vector biology
226 describes the research of over half of the participants, however this is a very broad
227 term. Vector ecology, behavior and control were also commonly reported. Of note,
228 genetic modification and vector immunity remain relatively small fields despite
229 important advances in these areas. Interest may increase with better tools and
230 access to new resources such as strains and facilities. The survey data showed that
231 studies of pathogens either directly or within the context of host-pathogen or
232 vector-pathogen interactions are a key area of research. This needs to be

233 emphasized as it integrates disciplines such as virology, parasitology, cell biology,
 234 microbiology and genetics into the vector field. Similarly, surveillance, diagnostics
 235 and epidemiology were important areas and this (alongside vector control, behavior
 236 and ecology) was an indication of the applied character of many activities in the field
 237 of vector-borne diseases.

238

239 **Table 3. Details of research areas relevant to survey participants.** Numbers of
 240 responses are shown by research area, or in the category “Other” which
 241 incorporates fields not specifically listed (selection of responses shown).

Research area	Response counts	Research area	Response counts
Vector biology	119	Host-pathogen interactions	102
Vector genetics/genomics	68	Vector-pathogen interactions	116
Vector immunity	32	Epidemiology	99
Vector behavior	77	Surveillance	96
Vector ecology	117	Diagnostics	69
Vector control	98	Other	29
Genetically modified arthropods	20	Other: evolution/population genetics, insecticide etc. (few precise indications given).	
Pathogen biology	88		
Genetically modified pathogens	28		

242

243 **Assessment of currently available facilities**

244 Knowledge of availability and/or ease of access to research infrastructures is a key
 245 factor in future planning of research activities. Survey participants were therefore
 246 asked to indicate their current organization’s current capabilities. As shown in Table
 247 4, survey participants indicated a certain level of capacity to provide vectors but also
 248 material across the community. Moreover facilities for biosafety level (BSL) 2 and 3

249 experiments with vectors, animals and pathogens are available in several places. The
250 concept of Research Infrastructure can be extended to reagent provision and has
251 been successfully established by FP7 Infravec and the European Virus Archive
252 (<http://www.european-virus-archive.com>). This indicates an existing infrastructure
253 base that can be developed and made available for research on vectors and
254 pathogens on a wider basis (for example those who do not have immediate access to
255 BSL 3 level insectaries but would require experiments to be carried out in such
256 facilities) through communities such as INFRAVEC-2.

257

258 **Table 4. Research infrastructures and resources available to survey participants.**

259 Various types of structures relevant to vector and pathogen research are indicated.

Available facilities and resources	Response counts
Furnish vectors to external users	74
Furnish BSL2/BSL3 infected vectors/extracts to external users	32
BSL2 containment: arthropod infections	91
BSL3 containment: arthropod infections	60
Pathogen work in cell culture	128
BSL2 or BSL3 containment: small animal work	83
BSL2 or BSL3 containment: large animal work	27

260

261 **Assessment of infrastructure and service requirements**

262 When survey participants were asked to indicate how many had requested access to
263 insectaries at BSL2 or 3 in other institutions, in total 62 positive responses were
264 received. However out of these, 18 responses indicated that access could not be
265 granted in a timely manner. This suggests that inability to consistently access secure
266 insectary facilities comprises a systematic weakness that impedes research on
267 vector-pathogen interactions and may also explain the weaker interest in vector
268 immunity studies, for example. The relevant secure insectary facilities exist in Europe

269 (Table 4), and thus a mutualized network of insectaries at BSL2 and 3 could resolve
270 access limitations and promote elevated levels of vector research under BSL2 and 3
271 conditions.

272

273 Access needs, or provision of infected vectors or extracts from infected vectors were
274 assessed and participants were asked to indicate which pathogens or
275 facilities/services would be of interest in the context of INRFAVEC-2 where these are
276 free of cost (or the requirement for collaboration) for the end user (Table 5).
277 Although the questions below were originally aimed at potential European users all
278 answers were taken into account. Survey data show that in particular services and
279 structures for arbovirus research would likely generate strong demand. Again this
280 may be due to the surge in research in this field described above. Similarly, BSL2 and
281 3 studies on infected vectors and insecticides as well as behavior scored highly.
282 Regarding technologies novel for the field, functional siRNA screens and imaging of
283 vectors did not score particularly high but this demand may increase in the future,
284 particularly if facilities were available for access.

285

286 **Table 5. Infrastructure services (vector infection and vector-pathogen interactions)**
287 **for the vector research community.** Survey participants responded whether the
288 services listed here (vector infection and vector-pathogen interactions) to study
289 vector infections and vector-pathogen interactions, would be of use if offered free of
290 cost. Response counts are grouped into Likely, Not likely or Possible use of the
291 infrastructure/service.

292

Infrastructure/service: Vector infection and vector-pathogen interactions	Likely	Not likely	Possible
Arboviruses	90	46	31
<i>Plasmodium falciparum</i>	36	77	33
Infected vector & insecticide studies	83	38	50
Behavioral studies with infected vectors	64	50	42
<i>In vivo</i> imaging with infected vectors	48	58	41
Functional siRNA screens of vector cells	35	68	36
Other needs	21	39	15
Category "Other needs" included various <i>Plasmodium</i> species, <i>Leishmania</i> , tsetse flies etc.			

293

294 Vector genetics and genomics (see www.vectorbase.org, [36]) but also studies of
 295 vector microbiomes (given their influence on mosquito infection with arboviruses
 296 and parasites [44-46, 67]) are expanding fields. These research areas have strongly
 297 benefited from high-throughput sequencing techniques and bioinformatics. Survey
 298 participants were enthusiastic about developing insect vector-oriented
 299 infrastructures, services and expertise in high throughput genomics and
 300 bioinformatics, especially transcriptional profiling and genome and population
 301 analysis (Table 6).

302

303 **Table 6. Infrastructure services (vector genomics and bioinformatics) for the vector**
 304 **research community.** Survey participants responded whether the services listed
 305 here (vector genomics and bioinformatics), would be of use if offered free of cost.
 306 Response counts are grouped into Likely, Not likely or Possible use of the
 307 infrastructure/service.

Infrastructure/service: Vector genomics and bioinformatics	Likely	Not likely	Possible
Transcriptional profiling	75	42	53
Genome or population analysis	72	43	54
Bacterial microbiome profiling	45	63	41
Population or focused SNP genotyping	39	63	48
Other needs	10	41	8
Category "Other needs" included proteomics, metabolomics.			

308

309 The era of genomics has brought about much needed information on vector
310 genomes (see for example [68-70]). Genetic manipulation of genomes in basic
311 biological studies of gene/sequence structure and function, and applications based
312 on genome manipulation (see for example [71-73]) are useful tools to maximize the
313 value of this information, and for example CRISPR/Cas9-mediated genome
314 manipulation is an important technical advance also for the vector field [74, 75]. We
315 therefore asked survey participants about their interest in applying genome editing
316 technologies within their work. As shown in Table 7, there was particularly strong
317 interest in genetic manipulation of aedine mosquitoes. *Culicoides* midges seemed at
318 present a less popular subject, probably at least in part because the community is
319 small as mentioned above, as well as that the technologies have not yet been
320 applied to this system or general issues with establishing colonies of important
321 midge vector species. Among the category "Other", ticks stood out.

322

323

324

325 **Table 7. Infrastructure services (vector genome editing) for the vector research**
326 **community.** Survey participants responded whether vector genome editing would
327 be of use if offered free of cost. Response counts are grouped into Likely, Not likely
328 or Possible use of the infrastructure/service.

Infrastructure/service: Vector genome editing	Likely	Not likely	Possible
<i>Anopheles spec.</i>	35	71	44
<i>Aedes spec.</i>	60	60	33
<i>Culicoides spec.</i>	20	85	17
Other	27	53	7
"Other" included ticks (17), phlebotomines (5), <i>Culex spec.</i> and tsetse flies (both 4).			

329
330 Studies on vectors (infected, uninfected or genetically modified) often include
331 components that analyze behavior and ecology. A further section of this survey
332 therefore focused on a number of specific potential requirements in this area. As
333 indicated in Table 8, the interest to work in field sites in endemic countries if access
334 could be provided, as well as standardized behavioral assays and bioassays for
335 vectors generated strong positive responses. This suggested a need for these in the
336 vector research community. Positive responses for large cage studies (controlled
337 indoors or semi-controlled outdoors) were also strong considering that such
338 applications are very specialized, and the facilities are rare. However, this illustrates
339 the potential contribution of a Research Infrastructure project, because community
340 mutualization of rare infrastructures can allow access to state of the art facilities for
341 researchers with occasional needs. In the future, the possibility to access such
342 facilities may become stronger as more genetically modified vectors will be assessed
343 in pre-release assays. Few positive responses for electrophysiology experiments

344 were obtained, suggesting that there is no major need for additional facilities
345 beyond what is already in place.

346

347 **Table 8. Infrastructure services (vector ecology and behavior) for the vector**
348 **research community.** Survey participants responded whether specific services or
349 infrastructures to study vector ecology and behavior, would be of use if offered free
350 of cost. Response counts are grouped into Likely, Not likely or Possible use of the
351 infrastructure/service.

Infrastructure/service: Vector ecology and behavior	Likely	Not likely	Possible
Facilitated work at endemic country field sites	96	39	43
Electrophysiology	14	99	23
Standardized vector behavioral assays & bioassays	65	52	52
Large cage studies (controlled large indoor insectary)	64	61	46
Large cage studies (semi-controlled outdoor large cages)	46	77	40
Other needs	7	44	3
Very few responses to "Other needs" given, for example cage trials in Europe.			

352

353 Survey participants were also asked about their requirements for more specific
354 vector-related data and research resources such as reference genomes, specific cell
355 lines and mosquito strains (Table 9). Results indicated that in particular, a bank of
356 standard vector colonies would be of interest to the community. Easily accessible
357 quality-controlled vector colonies available from a European repository could be an
358 important influence promoting comparability and reproducibility of experimental

359 infection and other results across laboratories. Similarly vector systematics and
360 collections generated high interest. However, the practices of systematics may be at
361 a juncture, because the technological capacity will soon be available to whole-
362 genome sequence large numbers of unidentified individuals of a putative vector
363 clade, and cluster them bioinformatically to determine phylogenetic relatedness.
364 These results will need to be compared to existing collections, including voucher
365 specimens. Perhaps surprisingly, new reference and cloned vector cell lines did not
366 score highly but these may be of interest to smaller research areas such as virologists
367 who carry out particular types of studies. Cell lines may be of less interest in malaria
368 vector research where the biology is not consistent with simple cell models of
369 *Plasmodium*-mosquito interaction. Despite high interest in *Wolbachia* to block
370 pathogen transmission [51], generation of novel trans-infected vector strains was
371 also not a priority. Finally, a small number of responses under “Other needs”
372 mentioned the importance of training.

373

374 **Table 9. Infrastructure services (vector biology resources) for the vector research**
375 **community.** Survey participants responded whether specific resources for vector
376 biology, would be of use if offered free of cost. Response counts are grouped into
377 Likely, Not likely or Possible use of the infrastructure/service.

378

379

380

381

382

Infrastructure/service: Vector biology resources	Likely	Not likely	Possible
Bank of standard vector reference strains (genome & RNA sequenced)	85	34	54
Colonization of novel vector strains & species	76	45	53
Production of new reference vector cell lines (genome & RNA sequenced)	38	74	38
Production of cloned vector cell lines	39	75	37
Production of microbiome-free mosquitoes	28	82	40
<i>Wolbachia</i> -transinfected vector strains	23	76	52
Vector systematics and collections	62	52	55
Other needs	5	44	3
Very few responses to “Other needs” given, mainly mentioning training needs.			

383

384 Our survey specifically addressed training needs, community networking and
 385 communication. As shown in Table 10, all suggestions - training in vector BSL2 and 3
 386 methods, training in bioinformatics and genomics and scientific communication by
 387 conferencing - were positively received by the survey participants. Clearly these are
 388 areas of need that should be developed as a real requirement within the vector
 389 research field.

390

391

392

393

394 **Table 10. Infrastructure services (training and networking activities) for the vector**
395 **research community.** Survey participants responded whether specific services or
396 infrastructures in the areas of training and networking activities, would be of use if
397 offered free of cost. Response counts are grouped into Likely, Not likely or Possible
398 use of the infrastructure/service.
399

Infrastructure/service: Training and networking activities	Likely	Not likely	Possible
Training in BSL2 and 3 vector infection and study techniques	96	30	51
Training in bioinformatics and genomic analysis	107	25	53
Conferencing	102	16	59
Other needs	8	32	7
Very few responses to "Other needs" given; one example: training of field workers and students in field identification.			

400
401 Survey participants were also asked to give their opinions in a text field on research
402 priorities for vector biology over the next 5-10 years. Answers varied but some key
403 areas were identified: 1) Vector interactions with hosts and pathogens, including
404 vector competence and transmission; 2) Insecticide resistance and novel
405 insecticides; 3) Ecology and behavior, including of infected vectors, introduction of
406 vectors etc.; 4) Vector control, novel control measures and surveillance; 5) Vaccines,
407 including anti-vector vaccines; 6) Modelling; 7) Vector genomics/genetics and
408 bioinformatics. Although no survey can be complete, the data presented here yields
409 a valuable picture of the needs and requirements in disease vector biology,
410 especially of European scientists. We thus expect this study to be relevant to

411 stakeholders such as governments, research councils and organizations but also
412 researchers as priorities for future activities such as those planned by INFRAVEC-2
413 are determined.

414

415 **Acknowledgments**

416 We acknowledge the assistance of Sarah J. Plowman of the UK BBSRC for advice in
417 survey design, and survey participants.

418

419 **References**

- 420 1. Weaver SC, Lecuit M. Chikungunya virus and the global spread of a mosquito-
421 borne disease. *N Engl J Med.* 2015;372(13):1231-9. doi: 10.1056/NEJMra1406035.
422 PubMed PMID: 25806915.
- 423 2. Gatherer D, Kohl A. Zika virus: a previously slow pandemic spreads rapidly
424 through the Americas. *J Gen Virol.* 2015. doi: 10.1099/jgv.0.000381. PubMed PMID:
425 26684466.
- 426 3. Guzman MG, Harris E. Dengue. *Lancet.* 2014;385:453-65. doi: 10.1016/S0140-
427 6736(14)60572-9. PubMed PMID: 25230594.
- 428 4. Miller LH, Ackerman HC, Su XZ, Wellems TE. Malaria biology and disease
429 pathogenesis: insights for new treatments. *Nat Med.* 2013;19(2):156-67. doi:
430 10.1038/nm.3073. PubMed PMID: 23389616.
- 431 5. Halbroth BR, Draper SJ. Recent developments in malaria vaccinology. *Adv*
432 *Parasitol.* 2015;88:1-49. doi: 10.1016/bs.apar.2015.03.001. PubMed PMID:
433 25911364.
- 434 6. Hoffman SL, Vekemans J, Richie TL, Duffy PE. The march toward malaria
435 vaccines. *Vaccine.* 2015;33 Suppl 4:D13-23. doi: 10.1016/j.vaccine.2015.07.091.
436 PubMed PMID: 26324116.
- 437 7. Thomas SJ, Rothman AL. Trials and tribulations on the path to developing a
438 dengue vaccine. *Vaccine.* 2015;33 Suppl 4:D24-31. doi:
439 10.1016/j.vaccine.2015.05.095. PubMed PMID: 26122583.
- 440 8. Schwartz LM, Halloran ME, Durbin AP, Longini IM, Jr. The dengue vaccine
441 pipeline: Implications for the future of dengue control. *Vaccine.* 2015;33(29):3293-8.
442 doi: 10.1016/j.vaccine.2015.05.010. PubMed PMID: 25989449; PubMed Central
443 PMCID: PMC4470297.
- 444 9. Neafsey DE, Juraska M, Bedford T, Benkeser D, Valim C, Griggs A, et al.
445 Genetic Diversity and Protective Efficacy of the RTS,S/AS01 Malaria Vaccine. *N Engl J*
446 *Med.* 2015;373(21):2025-37. doi: 10.1056/NEJMoa1505819. PubMed PMID:
447 26488565.

- 448 10. Newby G, Hwang J, Koita K, Chen I, Greenwood B, von Seidlein L, et al.
449 Review of mass drug administration for malaria and its operational challenges. *Am J*
450 *Trop Med Hyg.* 2015;93(1):125-34. doi: 10.4269/ajtmh.14-0254. PubMed PMID:
451 26013371; PubMed Central PMCID: PMC4497884.
- 452 11. Wells TN, Hooft van Huijsduijnen R, Van Voorhis WC. Malaria medicines: a
453 glass half full? *Nat Rev Drug Discov.* 2015;14(6):424-42. doi: 10.1038/nrd4573.
454 PubMed PMID: 26000721.
- 455 12. Sinha S, Medhi B, Sehgal R. Challenges of drug-resistant malaria. *Parasite.*
456 2014;21:61. doi: 10.1051/parasite/2014059. PubMed PMID: 25402734; PubMed
457 Central PMCID: PMC4234044.
- 458 13. Lim SP, Noble CG, Shi PY. The dengue virus NS5 protein as a target for drug
459 discovery. *Antiviral Res.* 2015;119:57-67. doi: 10.1016/j.antiviral.2015.04.010.
460 PubMed PMID: 25912817.
- 461 14. Chen YL, Yokokawa F, Shi PY. The search for nucleoside/nucleotide analog
462 inhibitors of dengue virus. *Antiviral Res.* 2015;122:12-9. doi:
463 10.1016/j.antiviral.2015.07.010. PubMed PMID: 26241002.
- 464 15. Lim SP, Wang QY, Noble CG, Chen YL, Dong H, Zou B, et al. Ten years of
465 dengue drug discovery: progress and prospects. *Antiviral Res.* 2013;100(2):500-19.
466 doi: 10.1016/j.antiviral.2013.09.013. PubMed PMID: 24076358.
- 467 16. Xie X, Zou J, Wang QY, Shi PY. Targeting dengue virus NS4B protein for drug
468 discovery. *Antiviral Res.* 2015;118:39-45. doi: 10.1016/j.antiviral.2015.03.007.
469 PubMed PMID: 25796970.
- 470 17. Ahola T, Courderc T, Ng LF, Hallengard D, Powers A, Lecuit M, et al.
471 Therapeutics and vaccines against chikungunya virus. *Vector Borne Zoonotic Dis.*
472 2015;15(4):250-7. doi: 10.1089/vbz.2014.1681. PubMed PMID: 25897811.
- 473 18. Kortekaas J. One Health approach to Rift Valley fever vaccine development.
474 *Antiviral Res.* 2014;106:24-32. doi: 10.1016/j.antiviral.2014.03.008. PubMed PMID:
475 24681125.
- 476 19. Mansfield KL, Banyard AC, McElhinney L, Johnson N, Horton DL, Hernandez-
477 Triana LM, et al. Rift Valley fever virus: A review of diagnosis and vaccination, and
478 implications for emergence in Europe. *Vaccine.* 2015;33(42):5520-31. doi:
479 10.1016/j.vaccine.2015.08.020. PubMed PMID: 26296499.
- 480 20. Ocampo CB, Mina NJ, Carabali M, Alexander N, Osorio L. Reduction in dengue
481 cases observed during mass control of *Aedes (Stegomyia)* in street catch basins in an
482 endemic urban area in Colombia. *Acta Trop.* 2014;132:15-22. doi:
483 10.1016/j.actatropica.2013.12.019. PubMed PMID: 24388794; PubMed Central
484 PMCID: PMC4654410.
- 485 21. Abad-Franch F, Zamora-Perea E, Ferraz G, Padilla-Torres SD, Luz SL.
486 Mosquito-disseminated pyriproxyfen yields high breeding-site coverage and boosts
487 juvenile mosquito mortality at the neighborhood scale. *PLoS Negl Trop Dis.*
488 2015;9(4):e0003702. doi: 10.1371/journal.pntd.0003702. PubMed PMID: 25849040;
489 PubMed Central PMCID: PMC4388722.
- 490 22. Harris C, Kihonda J, Lwetoijera D, Dongus S, Devine G, Majambere S. A simple
491 and efficient tool for trapping gravid *Anopheles* at breeding sites. *Parasit Vectors.*
492 2011;4:125. doi: 10.1186/1756-3305-4-125. PubMed PMID: 21722391; PubMed
493 Central PMCID: PMC3141746.

- 494 23. Salem OA, Khadijetou ML, Moina MH, Lassana K, Sebastien B, Ousmane F, et
495 al. Characterization of anopheline (Diptera: Culicidae) larval habitats in Nouakchott,
496 Mauritania. *J Vector Borne Dis.* 2013;50(4):302-6. PubMed PMID: 24499854.
- 497 24. Helinski ME, Nuwa A, Protopopoff N, Feldman M, Ojuka P, Oguttu DW, et al.
498 Entomological surveillance following a long-lasting insecticidal net universal
499 coverage campaign in Midwestern Uganda. *Parasit Vectors.* 2015;8:458. doi:
500 10.1186/s13071-015-1060-6. PubMed PMID: 26382583; PubMed Central PMCID:
501 PMCPMC4574096.
- 502 25. Kawada H, Dida GO, Ohashi K, Kawashima E, Sonye G, Njenga SM, et al. A
503 small-scale field trial of pyriproxyfen-impregnated bed nets against pyrethroid-
504 resistant *Anopheles gambiae* s.s. in western Kenya. *PLoS One.* 2014;9(10):e1111195.
505 doi: 10.1371/journal.pone.01111195. PubMed PMID: 25333785; PubMed Central
506 PMCID: PMCPMC4205095.
- 507 26. Sokhna C, Ndiath MO, Rogier C. The changes in mosquito vector behaviour
508 and the emerging resistance to insecticides will challenge the decline of malaria. *Clin*
509 *Microbiol Infect.* 2013;19(10):902-7. doi: 10.1111/1469-0691.12314. PubMed PMID:
510 23910459.
- 511 27. Gurtler RE, Garelli FM, Coto HD. Effects of a five-year citywide intervention
512 program to control *Aedes aegypti* and prevent dengue outbreaks in northern
513 Argentina. *PLoS Negl Trop Dis.* 2009;3(4):e427. doi: 10.1371/journal.pntd.0000427.
514 PubMed PMID: 19399168; PubMed Central PMCID: PMCPMC2669131.
- 515 28. Padilla-Torres SD, Ferraz G, Luz SL, Zamora-Perea E, Abad-Franch F. Modeling
516 dengue vector dynamics under imperfect detection: three years of site-occupancy by
517 *Aedes aegypti* and *Aedes albopictus* in urban Amazonia. *PLoS One.*
518 2013;8(3):e58420. doi: 10.1371/journal.pone.0058420. PubMed PMID: 23472194;
519 PubMed Central PMCID: PMCPMC3589427.
- 520 29. Norris LC, Main BJ, Lee Y, Collier TC, Fofana A, Cornel AJ, et al. Adaptive
521 introgression in an African malaria mosquito coincident with the increased usage of
522 insecticide-treated bed nets. *Proc Natl Acad Sci U S A.* 2015;112(3):815-20. doi:
523 10.1073/pnas.1418892112. PubMed PMID: 25561525; PubMed Central PMCID:
524 PMCPMC4311837.
- 525 30. Yewhalaw D, Asale A, Tushune K, Getachew Y, Duchateau L, Speybroeck N.
526 Bio-efficacy of selected long-lasting insecticidal nets against pyrethroid resistant
527 *Anopheles arabiensis* from South-Western Ethiopia. *Parasit Vectors.* 2012;5:159. doi:
528 10.1186/1756-3305-5-159. PubMed PMID: 22871143; PubMed Central PMCID:
529 PMCPMC3485103.
- 530 31. Ngufor C, N'Guessan R, Fagbohoun J, Subramaniam K, Odjo A, Fongnikin A, et
531 al. Insecticide resistance profile of *Anopheles gambiae* from a phase II field station in
532 Cove, southern Benin: implications for the evaluation of novel vector control
533 products. *Malar J.* 2015;14(1):464. doi: 10.1186/s12936-015-0981-z. PubMed PMID:
534 26581678; PubMed Central PMCID: PMCPMC4652434.
- 535 32. Sande S, Zimba M, Chinwada P, Masendu HT, Mazando S, Makuwaza A. The
536 emergence of insecticide resistance in the major malaria vector *Anopheles funestus*
537 (Diptera: Culicidae) from sentinel sites in Mutare and Mutasa Districts, Zimbabwe.
538 *Malar J.* 2015;14(1):466. doi: 10.1186/s12936-015-0993-8. PubMed PMID:
539 26589891; PubMed Central PMCID: PMCPMC4654866.

- 540 33. Djogbenou LS, Assogba B, Essandoh J, Constant EA, Makoutode M, Akogbeto
541 M, et al. Estimation of allele-specific Ace-1 duplication in insecticide-resistant
542 Anopheles mosquitoes from West Africa. *Malar J.* 2015;14(1):507. doi:
543 10.1186/s12936-015-1026-3. PubMed PMID: 26682913; PubMed Central PMCID:
544 PMC4683970.
- 545 34. Alout H, Labbe P, Berthomieu A, Makoundou P, Fort P, Pasteur N, et al. High
546 chlorpyrifos resistance in *Culex pipiens* mosquitoes: strong synergy between
547 resistance genes. *Heredity (Edinb).* 2015. doi: 10.1038/hdy.2015.92. PubMed PMID:
548 26463842.
- 549 35. Misra BR, Gore M. Malathion Resistance Status and Mutations in
550 Acetylcholinesterase Gene (Ace) in Japanese Encephalitis and Filariasis Vectors from
551 Endemic Area in India. *J Med Entomol.* 2015;52(3):442-6. doi: 10.1093/jme/tjv015.
552 PubMed PMID: 26334819.
- 553 36. Giraldo-Calderon GI, Emrich SJ, MacCallum RM, Maslen G, Dialynas E, Topalis
554 P, et al. VectorBase: an updated bioinformatics resource for invertebrate vectors and
555 other organisms related with human diseases. *Nucleic Acids Res.* 2015;43(Database
556 issue):D707-13. doi: 10.1093/nar/gku1117. PubMed PMID: 25510499; PubMed
557 Central PMCID: PMC4383932.
- 558 37. Kean J, Rainey SM, McFarlane M, Donald CL, Schnettler E, Kohl A, et al.
559 Fighting Arbovirus Transmission: Natural and Engineered Control of Vector
560 Competence in *Aedes* Mosquitoes. *Insects.* 2015;6(1):236-78. doi:
561 10.3390/insects6010236. PubMed PMID: 26463078; PubMed Central PMCID:
562 PMC4553541.
- 563 38. Fraser MJ, Jr. Insect transgenesis: current applications and future prospects.
564 *Annu Rev Entomol.* 2012;57:267-89. doi: 10.1146/annurev.ento.54.110807.090545.
565 PubMed PMID: 22149266.
- 566 39. Nolan T, Papathanos P, Windbichler N, Magnusson K, Benton J, Catteruccia F,
567 et al. Developing transgenic *Anopheles* mosquitoes for the sterile insect technique.
568 *Genetica.* 2011;139(1):33-9. doi: 10.1007/s10709-010-9482-8. PubMed PMID:
569 20821345.
- 570 40. Alphey L. Genetic control of mosquitoes. *Annu Rev Entomol.* 2014;59:205-24.
571 Epub 2013/10/29. doi: 10.1146/annurev-ento-011613-162002. PubMed PMID:
572 24160434.
- 573 41. Alphey N, Bonsall MB. Interplay of population genetics and dynamics in the
574 genetic control of mosquitoes. *J R Soc Interface.* 2014;11(93):20131071. Epub
575 2014/02/14. doi: 10.1098/rsif.2013.1071
576 rsif.2013.1071 [pii]. PubMed PMID: 24522781; PubMed Central PMCID:
577 PMC3928937.
- 578 42. Franz AW, Clem RJ, Passarelli AL. Novel Genetic and Molecular Tools for the
579 Investigation and Control of Dengue Virus Transmission by Mosquitoes. *Curr Trop
580 Med Rep.* 2014;1(1):21-31. doi: 10.1007/s40475-013-0007-2. PubMed PMID:
581 24693489; PubMed Central PMCID: PMC43969738.
- 582 43. Alphey L, McKemey A, Nimmo D, Neira Oviedo M, Lacroix R, Matzen K, et al.
583 Genetic control of *Aedes* mosquitoes. *Pathog Glob Health.* 2013;107(4):170-9. Epub
584 2013/07/03. doi: 10.1179/2047773213Y.0000000095. PubMed PMID: 23816508.

- 585 44. Hegde S, Rasgon JL, Hughes GL. The microbiome modulates arbovirus
586 transmission in mosquitoes. *Curr Opin Virol.* 2015;15:97-102. doi:
587 10.1016/j.coviro.2015.08.011. PubMed PMID: 26363996.
- 588 45. Clayton AM, Dong Y, Dimopoulos G. The Anopheles innate immune system in
589 the defense against malaria infection. *Journal of innate immunity.* 2014;6(2):169-81.
590 doi: 10.1159/000353602. PubMed PMID: 23988482; PubMed Central PMCID:
591 PMCPMC3939431.
- 592 46. Jupatanakul N, Sim S, Dimopoulos G. The insect microbiome modulates
593 vector competence for arboviruses. *Viruses.* 2014;6(11):4294-313. doi:
594 10.3390/v6114294. PubMed PMID: 25393895; PubMed Central PMCID:
595 PMCPMC4246223.
- 596 47. Bolling BG, Olea-Popelka FJ, Eisen L, Moore CG, Blair CD. Transmission
597 dynamics of an insect-specific flavivirus in a naturally infected *Culex pipiens*
598 laboratory colony and effects of co-infection on vector competence for West Nile
599 virus. *Virology.* 2012;427(2):90-7. doi: 10.1016/j.virol.2012.02.016. PubMed PMID:
600 22425062; PubMed Central PMCID: PMCPMC3329802.
- 601 48. Mosimann AL, Bordignon J, Mazzarotto GC, Motta MC, Hoffmann F, Santos
602 CN. Genetic and biological characterization of a dengue virus isolate that affects
603 dengue virus infection. *Mem Inst Oswaldo Cruz.* 2011;106(3):285-92. PubMed PMID:
604 21655815.
- 605 49. Rainey SM, Shah P, Kohl A, Dietrich I. Understanding the Wolbachia-mediated
606 inhibition of arboviruses in mosquitoes: progress and challenges. *J Gen Virol.*
607 2014;95(Pt 3):517-30. Epub 2013/12/18. doi: 10.1099/vir.0.057422-0
608 vir.0.057422-0 [pii]. PubMed PMID: 24343914.
- 609 50. Iturbe-Ormaetxe I, Walker T, SL ON. Wolbachia and the biological control of
610 mosquito-borne disease. *EMBO Rep.* 2011;12(6):508-18. Epub 2011/05/07. doi:
611 embor201184 [pii]
612 10.1038/embor.2011.84. PubMed PMID: 21546911.
- 613 51. Johnson KN. The Impact of Wolbachia on Virus Infection in Mosquitoes.
614 *Viruses.* 2015;7(11):5705-17. doi: 10.3390/v7112903. PubMed PMID: 26556361;
615 PubMed Central PMCID: PMCPMC4664976.
- 616 52. Lambrechts L, Ferguson NM, Harris E, Holmes EC, McGraw EA, O'Neill SL, et
617 al. Assessing the epidemiological effect of wolbachia for dengue control. *Lancet*
618 *Infect Dis.* 2015;15(7):862-6. doi: 10.1016/S1473-3099(15)00091-2. PubMed PMID:
619 26051887.
- 620 53. http://ec.europa.eu/research/infrastructures/index_en.cfm.
- 621 54. Angelini R, Finarelli AC, Angelini P, Po C, Petropulacos K, Macini P, et al. An
622 outbreak of chikungunya fever in the province of Ravenna, Italy. *Euro Surveill.*
623 2007;12(9):E070906 1. Epub 2007/09/29. doi: 2260 [pii]. PubMed PMID: 17900424.
- 624 55. Burt FJ, Rolph MS, Rulli NE, Mahalingam S, Heise MT. Chikungunya: a re-
625 emerging virus. *Lancet.* 2012;379(9816):662-71. Epub 2011/11/22. doi: S0140-
626 6736(11)60281-X [pii]
627 10.1016/S0140-6736(11)60281-X. PubMed PMID: 22100854.
- 628 56. Coffey LL, Failloux AB, Weaver SC. Chikungunya virus-vector interactions.
629 *Viruses.* 2014;6(11):4628-63. doi: 10.3390/v6114628. PubMed PMID: 25421891;
630 PubMed Central PMCID: PMC4246241.

- 631 57. Weaver SC, Forrester NL. Chikungunya: Evolutionary history and recent
632 epidemic spread. *Antiviral Res.* 2015;120:32-9. doi: 10.1016/j.antiviral.2015.04.016.
633 PubMed PMID: 25979669.
- 634 58. Lambrechts L, Scott TW, Gubler DJ. Consequences of the expanding global
635 distribution of *Aedes albopictus* for dengue virus transmission. *PLoS Negl Trop Dis.*
636 2010;4(5):e646. doi: 10.1371/journal.pntd.0000646. PubMed PMID: 20520794;
637 PubMed Central PMCID: PMC2876112.
- 638 59. Paupy C, Delatte H, Bagny L, Corbel V, Fontenille D. *Aedes albopictus*, an
639 arbovirus vector: From the darkness to the light. *Microbes Infect.* 2009. Epub
640 2009/05/20. doi: S1286-4579(09)00105-1 [pii]
641 10.1016/j.micinf.2009.05.005. PubMed PMID: 19450706.
- 642 60. Kraemer MU, Sinka ME, Duda KA, Mylne AQ, Shearer FM, Barker CM, et al.
643 The global distribution of the arbovirus vectors *Aedes aegypti* and *Ae. albopictus*.
644 *Elife.* 2015;4:e08347. doi: 10.7554/eLife.08347. PubMed PMID: 26126267; PubMed
645 Central PMCID: PMCPMC4493616.
- 646 61. Beer M, Conraths FJ, van der Poel WH. 'Schmallenberg virus'--a novel
647 orthobunyavirus emerging in Europe. *Epidemiol Infect.* 2013;141(1):1-8. Epub
648 2012/10/11. doi: 10.1017/S0950268812002245
649 S0950268812002245 [pii]. PubMed PMID: 23046921.
- 650 62. Powers AM. Risks to the Americas Associated with the Continued Expansion
651 of Chikungunya Virus. *J Gen Virol.* 2014. doi: 10.1099/vir.0.070136-0. PubMed PMID:
652 25239764.
- 653 63. Carpenter S, Wilson A, Mellor PS. Culicoides and the emergence of
654 bluetongue virus in northern Europe. *Trends Microbiol.* 2009;17(4):172-8. Epub
655 2009/03/21. doi: S0966-842X(09)00040-7 [pii]
656 10.1016/j.tim.2009.01.001. PubMed PMID: 19299131.
- 657 64. Schotthoefler AM, Frost HM. Ecology and Epidemiology of Lyme Borreliosis.
658 *Clinics in laboratory medicine.* 2015;35(4):723-43. doi: 10.1016/j.cll.2015.08.003.
659 PubMed PMID: 26593254.
- 660 65. Ergonul O. Crimean-Congo hemorrhagic fever virus: new outbreaks, new
661 discoveries. *Curr Opin Virol.* 2012;2(2):215-20. Epub 2012/04/10. doi:
662 10.1016/j.coviro.2012.03.001
663 S1879-6257(12)00044-2 [pii]. PubMed PMID: 22482717.
- 664 66. Papa A, Mirazimi A, Koksai I, Estrada-Pena A, Feldmann H. Recent advances in
665 research on Crimean-Congo hemorrhagic fever. *J Clin Virol.* 2015;64:137-43. doi:
666 10.1016/j.jcv.2014.08.029. PubMed PMID: 25453328; PubMed Central PMCID:
667 PMCPMC4346445.
- 668 67. Cirimotich CM, Ramirez JL, Dimopoulos G. Native microbiota shape insect
669 vector competence for human pathogens. *Cell Host Microbe.* 2011;10(4):307-10. doi:
670 10.1016/j.chom.2011.09.006. PubMed PMID: 22018231; PubMed Central PMCID:
671 PMCPMC3462649.
- 672 68. Arensburger P, Megy K, Waterhouse RM, Abrudan J, Amedeo P, Antelo B, et
673 al. Sequencing of *Culex quinquefasciatus* establishes a platform for mosquito
674 comparative genomics. *Science.* 2010;330(6000):86-8. Epub 2010/10/12. doi:
675 330/6000/86 [pii]
676 10.1126/science.1191864. PubMed PMID: 20929810.

- 677 69. Nene V, Wortman JR, Lawson D, Haas B, Kodira C, Tu ZJ, et al. Genome
678 sequence of *Aedes aegypti*, a major arbovirus vector. *Science*. 2007;316(5832):1718-
679 23. PubMed PMID: 17510324.
- 680 70. Holt RA, Subramanian GM, Halpern A, Sutton GG, Charlab R, Nusskern DR, et
681 al. The genome sequence of the malaria mosquito *Anopheles gambiae*. *Science*.
682 2002;298(5591):129-49. PubMed PMID: 12364791.
- 683 71. Dong Y, Das S, Cirimotich C, Souza-Neto JA, McLean KJ, Dimopoulos G.
684 Engineered *Anopheles* immunity to *Plasmodium* infection. *PLoS Pathog*.
685 2011;7(12):e1002458. Epub 2012/01/05. doi: 10.1371/journal.ppat.1002458
686 PPATHOGENS-D-11-01314 [pii]. PubMed PMID: 22216006; PubMed Central PMCID:
687 PMC3245315.
- 688 72. Isaacs AT, Li F, Jasinskiene N, Chen X, Nirmala X, Marinotti O, et al.
689 Engineered resistance to *Plasmodium falciparum* development in transgenic
690 *Anopheles stephensi*. *PLoS Pathog*. 2011;7(4):e1002017. Epub 2011/05/03. doi:
691 10.1371/journal.ppat.1002017. PubMed PMID: 21533066; PubMed Central PMCID:
692 PMC3080844.
- 693 73. Carvalho DO, McKemey AR, Garziera L, Lacroix R, Donnelly CA, Alphey L, et al.
694 Suppression of a Field Population of *Aedes aegypti* in Brazil by Sustained Release of
695 Transgenic Male Mosquitoes. *PLoS Negl Trop Dis*. 2015;9(7):e0003864. doi:
696 10.1371/journal.pntd.0003864. PubMed PMID: 26135160; PubMed Central PMCID:
697 PMC4489809.
- 698 74. Hammond A, Galizi R, Kyrou K, Simoni A, Siniscalchi C, Katsanos D, et al. A
699 CRISPR-Cas9 gene drive system targeting female reproduction in the malaria
700 mosquito vector *Anopheles gambiae*. *Nat Biotechnol*. 2016;34(1):78-83. doi:
701 10.1038/nbt.3439. PubMed PMID: 26641531.
- 702 75. Gantz VM, Jasinskiene N, Tatarenkova O, Fazekas A, Macias VM, Bier E, et al.
703 Highly efficient Cas9-mediated gene drive for population modification of the malaria
704 vector mosquito *Anopheles stephensi*. *Proc Natl Acad Sci U S A*. 2015;112(49):E6736-
705 43. doi: 10.1073/pnas.1521077112. PubMed PMID: 26598698; PubMed Central
706 PMCID: PMC4679060.
- 707

708 **Supporting information legends**

709 **S1 Table.** The INFRAVEC-2 Survey Questionnaire, as sent out to participants. A brief
710 description of the INFRAVEC-2 community is given, and the aims of the
711 questionnaire explained.

712 **S2 Table.** Responses to the INFRAVEC-2 and participation numbers by country, split
713 by continent.

Supporting information S1 Table.

The INFRAVEC-2 Survey Questionnaire, as sent out to participants. A brief description of the INFRAVEC-2 community is given, and the aims of the questionnaire explained.

HORIZON 2020 INFRAVEC-2 Questionnaire

Introduction

A consortium of European institutions based in the former FP7/INFRAVEC project is responding to the new H2020 call “Integrating Activities for Advanced Communities” of the European Research Infrastructures (RI) Programme under the item “Research Infrastructures for the control of vector-borne diseases”. The primary purpose of an “integrated infrastructure” is to provide the EU scientific community with access to its network of RI facilities and services, without charge to the end user, at the state-of-the art premises of participating institutions. Access to the specialized RI enables European researchers and SME to carry out experiments beyond their current capacities.

Building upon the major achievements of FP7/INFRAVEC in forging a European Starting Community of insect vector RI, we worked with EC representatives to generate the current H2020 call for an Advanced Community (AC). With strong commitment obtained from collaborating institutions hosting top-level specialized EU facilities for vector-borne disease (including Institut Pasteur FR, Imperial College UK, Centre de Recerca en Sanitat Animal (IRTA-CReSA) ES, Wageningen University NL, University of Glasgow UK, Institut de Recherche pour le Développement (IRD)-Montpellier FR, Polo d'Innovazione di Genomica, Genetica e Biologia (Polo GGB) IT, Pirbright Institute UK, Max-Planck-Institut für Infektionsbiologie DE, Radboud University Medical Center NL, and EMBL European Bioinformatics Institute DE), the group, chaired by K. Vernick (Institut Pasteur), has been invited to organize the AC.

The RI consortium will provide enabling infrastructures and support for research on disease vectors and their pathogens. We have listed possible RI and services within the following questionnaire, and we would like to solicit as wide as possible feedback from potential users in order to understand the major needs of the vector biology community. Your particular requirements and feedback will have strong impact on how the project will be structured, as this “integrated infrastructure” needs to be tightly tailored to, and inspired by real community needs. Please, take a minute to fill in a short questionnaire (~15 min) that will help us mobilize necessary resources for the future of our community.

Please feel free to forward this email to relevant colleagues. The primary target audience is EU insect vector researchers and SME, but we welcome replies from outside the EU as well. All individual replies and identity information will be kept confidential. Questions can be addressed to email: infravec-survey@pasteur.fr

Please complete this form as soon as you can. The survey will close November 25th 2015.

Thank you for your collaboration.

Q1. Please provide your name and contact details.

Title

.....

First name

.....

Last name

.....

Position

.....

Organization

.....

Country

.....

Email (optional)

Providing an email address is optional, but will permit us to keep you informed about the consortium; contact information will not be shared with other parties.

.....

Q2. Please identify the arthropod vectors and/or vector borne pathogens that you research

Select all that apply

	MAJOR	Minor
Aedes	<input type="checkbox"/>	<input type="checkbox"/>
Culex	<input type="checkbox"/>	<input type="checkbox"/>
Anopheles	<input type="checkbox"/>	<input type="checkbox"/>
Culicoides	<input type="checkbox"/>	<input type="checkbox"/>
Ticks	<input type="checkbox"/>	<input type="checkbox"/>
Other	<input type="checkbox"/>	<input type="checkbox"/>

If other other area

Please specify below

.....

Select all that apply

	MAJOR	minor
Arboviruses (human)	<input type="checkbox"/>	<input type="checkbox"/>
Arboviruses (livestock)	<input type="checkbox"/>	<input type="checkbox"/>
Plasmodium	<input type="checkbox"/>	<input type="checkbox"/>
Other	<input type="checkbox"/>	<input type="checkbox"/>

If other other area

Please specify below

Q3. Please select the most relevant areas that describe your research interests from the list below

Select all that apply

- Vector biology
- Vector genetics/genomics
- Vector immunity
- Vector behavior
- Vector ecology
- Vector control
- Genetically modified arthropods

- Pathogen biology
- Genetically modified pathogens

- Host-pathogen interactions
- Vector-pathogen interactions
- Epidemiology
- Surveillance
- Diagnostics
- Other

If other

Please specify below

Q4. Does your organization have infrastructure facilities described by the list below?

Select all that apply

- To rear arthropod vectors
- To furnish vectors as a provider to external users
- To infect arthropods in BSL-2 containment
- To infect arthropods in BSL-3 containment
- To work with pathogens using in vitro cell cultures
- To infect small animals under BSL-2 or 3 containment
- To infect large animals under BSL-2 or 3 containment
- To furnish BSL-2 or -3 infected vectors or extracts to external users

Q5. Have you ever tried to access BSL-2 or 3 vector research facilities based at organizations other than your own?

- Yes
- No
- Not applicable

a. If yes, did the facility have sufficient capacity to accommodate your request in a timely manner?

- Yes
- No

Q6. Which infrastructure services offered to European users would you be likely to use, with user access costs paid by a Horizon 2020 Research Infrastructure consortium (i.e., at no charge to the end-user). Items provided as user access or custom service, which does not require scientific collaboration with the providing facility.

a. VECTOR INFECTION AND VECTOR-PATHOGEN INTERACTIONS. Access to BSL-2 or 3 secure insectary facilities for infection of vectors, or provision of infected vectors or extracts custom-generated by such a facility. Vectors infected by the following pathogens, and for the following research purposes (select all that apply).

	Likely	Possible	Not likely
1. Arboviruses	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
2. Plasmodium falciparum	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
3. Infected vectors and insecticide studies	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
4. Behavioral studies with infected vectors (e.g., odorant/host choice)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
5. In vivo imaging of infected vectors (e.g., confocal, spinning disk)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
6. siRNA functional screening of vector cell lines	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
7. Other needs	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

If other needs--please specify below

.....

.....

.....

.....

.....

Q6. Which infrastructure services offered to European users would you be likely to use, with user access costs paid by a Horizon 2020 Research Infrastructure consortium (i.e., at no charge to the end-user). Items provided as user access or custom service, which does not require scientific collaboration with the providing facility.

b. VECTOR GENOMICS AND BIOINFORMATICS. High-throughput genomic services. If desired, with upstream bioinformatic design advice and downstream bioinformatic analysis (select all that apply)

	Likely	Possible	Not likely
1. Transcriptional profiling by Illumina RNA-seq	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
2. Genome or population analysis by Illumina DNA sequencing	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
3. Bacterial microbiome profiling by 16S rRNA amplicon deep sequencing	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
4. Population or focused SNPgenotyping (e.g., Sequenom)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
5. Other needs	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

If other needs--please specify below

.....

.....

.....

.....

.....

Q6. Which infrastructure services offered to European users would you be likely to use, with user access costs paid by a Horizon 2020 Research Infrastructure consortium (i.e., at no charge to the end-user). Items provided as user access or custom service, which does not require scientific collaboration with the providing facility.

c. VECTOR GENOME EDITING. Provision of custom genetic modification of your requested target gene or sequence using CRISPR or other technology in vectors (select all that apply). Could also include phenotyping the mutation effect by pathogen challenge under (a) above.

	Likely	Possible	Not likely
1. Anopheles	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
2. Aedes	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
3. Culicoides	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
4. Other needs	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

If other needs--please specify below

.....
.....
.....
.....
.....

Q6. Which infrastructure services offered to European users would you be likely to use, with user access costs paid by a Horizon 2020 Research Infrastructure consortium (i.e., at no charge to the end-user). Items provided as user access or custom service, which does not require scientific collaboration with the providing facility.

d. VECTOR ECOLOGY AND BEHAVIOR. Provision of access to facilities or custom-performed assays (select all that apply). Could also include pathogen infection of vectors under (a) above.

	Likely	Possible	Not likely
1. Facilitated work at endemic country field sites, Africa, Asia, S. America (population & epidemiology studies)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
2. Electrophysiology / EAG	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
3. Standardized vector behavioral tests & bioassays (e.g. odorant, host choice)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
4a. Large-cage studies (e.g. behavior, fitness, reproduction, test of modified genetic strains) in completely controlled indoor large insectary	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
4b. Large-cage studies (e.g. behavior, fitness, reproduction, test of modified genetic strains) in semi-controlled outdoor large cages (Africa)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
5. Other needs	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

If other needs--please specify below

.....
.....
.....
.....
.....

Q6. Which infrastructure services offered to European users would you be likely to use, with user access costs paid by a Horizon 2020 Research Infrastructure consortium (i.e., at no charge to the end-user). Items provided as user access or custom service, which does not require scientific collaboration with the providing facility.

e. VECTOR BIOLOGY RESOURCES. Provision of vector research resources by request (select all that apply).

	Likely	Possible	Not likely
1. Bank of standard vector reference strains (genome & RNA sequenced)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
2. Colonization of novel vector strains and species	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
3. Production of new reference vector cell lines (genome & RNA sequenced)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
4. Production of cloned vector cell lines	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
5. Production of microbiome-free mosquitoes	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
6. Wolbachia transfected vector strains	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
7. Vector systematics and collections	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
8. Other needs	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

If other needs--please specify below

.....

.....

.....

.....

.....

Q6. Which infrastructure services offered to European users would you be likely to use, with user access costs paid by a Horizon 2020 Research Infrastructure consortium (i.e., at no charge to the end-user). Items provided as user access or custom service, which does not require scientific collaboration with the providing facility.

f. TRAINING AND NETWORKING ACTIVITIES. Promotion of expertise using standardized, comparable practices, scientific exchange.

	Likely	Possible	Not likely
1. Training in BSL-2 and 3 vector infection and study techniques	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
2. Training in bioinformatics and genomic analysis	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
3. Conferencing	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
4. Other needs	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

If other needs--please specify below

.....

.....

.....

.....

.....

Q7. In your opinion, what are the top research priorities (up to 5) in vector biology and/or vector borne disease that need to be addressed in the next 5-10 yrs in the European research context?

1.

.....

.....

.....

.....

.....

2.

.....

.....

.....

.....

.....

3.

4.

5.

Thank you for participating!

Please use the space provided below to send us any additional feedback on this survey.

Supporting Information S2 Table

Responses to the INFRAVEC-2 and participation numbers by country, split by continent.

	Participants/country
Europe	
Albania	2
Austria	2
Belgium	4
Bosnia-Herzegovina	1
Bulgaria	2
Croatia	1
Czech Republic	3
Denmark	1
Estonia	2
Finland	1
France	56
Germany	11
Greece	3
Hungary	1
Italy	15
Kosovo	1
Latvia	1
Luxembourg	2
Moldova	1
Macedonia	2
Montenegro	1
Portugal	8
Romania	2
Serbia	4
Slovakia	2
Slovenia	2
Spain	15
Sweden	4
Switzerland	3
The Netherlands	4
UK	28
Asia	
Armenia	1
Burkina Faso	2
Cambodia	1
Israel	2
Palestine	2
Singapore	1
Turkey	3
Africa	
Algeria	1
Cameroon	1
Egypt	1
Morocco	2
South Africa	1

Australia	
Australia	1
North America	
USA	7