**A critical realist return to natural science: The case of biting midges and their symbiotic bacteria**

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**Abstract**

A case study is provided of the investigation of biting flying insects that are vectors for some infectious diseases in animals and humans. This is offered as an insider account from the author and it traces the challenges and messiness of doing research in practice. The account illuminates a range of matters that can be understood productively, using critical realism as a meta-theoretical resource. These include the challenges for a neophyte researcher joining a pre-exiting ongoing line of scientific inquiry, dealing with existing fallible knowledge, working between open systems in the field and the closed system of the laboratory and the necessity of working in interdisciplinary networks. These are discussed in order to highlight the antecedent condition of possibility for the research reported and its implications for human and animal health.

Keywords: vector-borne diseases; autoethnography; symbionts

**Introduction**

The impact of critical realism on social science is now well recognised but its’ influence is reported less often in the natural science literature. Roy Bhaskar took an early interest in the theory and practice of natural science (Bhaskar, 1975) but by the end of his life he recognised this uneven development to date (see Bhaskar 2016, 210). This article returns to his early interest and reports a specific piece of work from within natural science and is divided into two parts.

In the first there is a personal account from the author. It reports on the content and process of investigating biting flying insects and their role in infection transmission. This is an inherently complex topic and one of serious concern to both human and veterinary medicine. Flying insects are the vectors of a range of diseases affecting people and animals (e.g. dengue fever and malaria). The fact that these small animals fly means they have significance beyond local outbreaks of disease.

Their importance for global health means that their recent vigorous investigation necessitates the inter-disciplinary contribution of a number of scientists. This topic-focussed research community is beginning to recognise the generative mechanisms of infection transmission that are specific to both insect (vector) and host species. However, in some cases they seem to be common across species. For this reason, the consideration, for example, of the pathogenic role of the micro-physiology of a mosquito species might be usefully compared and contrasted with that of a biting midge species.

With this background in mind, this paper reports a research project attempting to understand the fine detail of how biting midge symbiotic bacteria (symbionts) can affect the ability of a vector to spread disease. In the first section, a first person account is offered, with the researcher starting with a relatively blank sheet of exploring biting midges and their symbionts, when joining an ongoing field of inquiry. For accessibility, technical language, as well as a summary of the area and its significance, is described for those outside of the disciplines noted above.

The second part of the paper focuses on a range of matters more generally within critical realism and applied to the case study. These are related to the messy fallibilism and uncertainties of doing most serious research, working between the open system of field work and the technologically rich, but closed, system of the laboratory, as well as the challenges of communicating in interdisciplinary research networks (Bhaskar, Danemark and Price, 2018; Danermark, 2019).

**Starting context of the study**

Vector-borne diseases are infections transmitted by blood-feeding invertebrates. The most well-known examples of these infections are pathogens spread by mosquitoes, although tick, sand fly and midge-borne diseases are also of importance (Gubler 2009). For example, *Anopheles* and *Aedes* mosquito species transmit malaria and flaviviruses (e.g. dengue, Zika and chikungunya viruses), causing hundreds of thousands of human deaths every year (World Health Organisation 2019). Vector-borne diseases are also of importance in the veterinary world including pathogens such as tick-borne *Babesia* sp*.* (babesiosis in several mammals and birds) and mosquito transmitted *Dirofilaria immitis* (heartworm in dogs and cats).

*Control of vector-borne diseases*

Traditional vector control approaches have relied heavily upon the removal of breeding sites and the use of insecticides (Flores and O’Neill 2018). However, these are proving insufficient to cope with human population density increases, resulting from urbanisation, particularly in tropical regions (Pang, Mak, and Gubler 2017). Additionally, meteorological factors can influence the reproduction and survival of vectors meaning that climatic variables can influence the range of the vector’s impact (Takken and Knols 2007). Approximately a third of emerging diseases are deemed to be vector-borne (Jones et al. 2008), suggesting that new health interventions are of pressing need.

One vector control approach aims to reduce insect population numbers. Population suppression approaches include sterile insect technique (SIT) where male vectors are sterilised via irradiation or chemical treatment. As a consequence, females fail to produce offspring after mating (Lees et al. 2015). Another approach is the release of genetically modified insects, which leads to early mortality when a lethal gene is switched on in the wild (Phuc et al. 2007). The shortcomings of these approaches include the limited epidemiological evidence available to suggest effectiveness, the reduced competitive fitness of laboratory-reared mosquitoes compared to their wild counterparts (particularly irradiated insects), and the negative public perception of releasing genetically modified insects into nature (Flores and O’Neill 2018). An approach which aims to overcome some of these obstacles is the use of symbionts (symbiotic bacteria residing within the body or cells of insect hosts).

Symbiont protection of insects was first observed in *Drosophila* fruit fliesinfected naturally with the bacteria *Wolbachia*, which were protected against fungal and viral pathogens (Teixeira, Ferreira, and Ashburner 2008; Panteleev et al. 2007). Further experimental work demonstrated the ability to introduce sustained infections of mosquito species with *Wolbachia* leading to a blocking effect of several viruses of human importance (van den Hurk et al. 2012). Importantly as symbionts are often transmitted maternally, this allows for the spread of this virus-blocking effect through vector populations, although the exact mechanisms of how symbionts confer this protection is unclear[[1]](#endnote-1).

Encouragingly, the results of releasing symbiont-infected mosquitoes into the wild indicate a viable method to control these viruses. For example, since the 2017 release of *Wolbachia*-infected *Aedes aegypti* mosquitoes in Malaysia, there has been a decrease in dengue fever incidence near release sites (Nazni et al. 2019). Importantly, as symbionts are naturally occurring and ubiquitous, public acceptance of these *Wolbachia-*based initiatives may be seen as more acceptable than other genetic modification interventions. Despite these promising field advancements, symbionts are often a neglected factor in non-mosquito-borne disease dynamics.

*Culicoides biting midges and their symbionts*

Turning to the specific study for this paper, it entailed the examination of *Culicoides* biting midges. These are blood-feeding flies which spread numerous pathogens including bluetongue and Schmallenberg viruses (BTV and SBV). BTV results in lameness and mouth lesions of ruminants. It caused serious economic and animal health damage to the European livestock industry during the last major outbreak in 2006 (Wilson and Mellor, 2009). SBV can lead to severe and fatal congenital malformations along with stillbirths and abortion in sheep.

Apart from the economic and animal health implications of these veterinary viruses, the human pathogenic oropouche virus, observed in the Americas (during the 1950s), also makes these vectors of human health significance (Anderson *et al.*, 1961). Indeed, a recent review (Sick et al. 2019) suggests *Culicoides* are possibly a neglected vector of human diseases, with the lack of information deriving from a bias towards surveillance of mosquitoes. So far, control interventions of midge-borne viruses rely primarily on vaccination. However, the various circulating strains (BTV) and unpredictable emergence (SBV) of these viruses has led to the pressing need for novel control interventions, such as the use of symbionts in their blocking role. This prompted the research describe below, which describes the investigation of midges and their symbionts. For stylistic purposes, the author will now switch to the first person tense.

**Autoethnographic account**

The study began with my appointment as a doctoral training fellow[[2]](#endnote-2). I had just completed my training as veterinary practitioner, which had included an intercalated master’s degree in infectious disease and epidemiology. The latter involved a small research project which examined *Wolbachia*. This provided some legitimacy for my application for a funded fellowship focussing on symbionts. The original structure of the project was determined by a study (see below) from the research group I was joining in my host university. The initial title of my project was “The Role of Symbiotic Bacteria in Vectors of Schmallenberg and Bluetongue Viruses”[[3]](#endnote-3).

*The early challenge of inheriting flawed data*

Previous studies of *Culicoides* had described the presence of the symbiont *Cardinium*. However, a suitable system to study *Cardinium*-midge interactions did not exist. This was due to difficulties in initiating laboratory-based experiments involving *Cardinium* infected midges. Before overcoming this hindrance, I first had to identify a suitable “candidate” midge species, which could be used to study interactions between the symbiont and insects. Recent work by a master’s student, in my local research group, described the presence of *Cardinium* in two UK midge species of vector importance (*Culicoides pulicaris* and *Culicoides punctatus*). Therefore, as my work was also based in the UK, I set upon clarifying the feasibility of using these two species as model organisms to continue future work looking into interactions between the insect host and its symbiont. I looked to build upon the work of the master’s student and their findings.

An ideal midge-*Cardinium* system for investigation would involve the use of a *Culicoides* species which:

1. Contains *Cardinium* at intermediate prevalence. i.e. populations containing a mixture of individuals where the symbiont is present or absent. This allows for natural negative controls (symbiont absent) to be used in experiments investigating potential effects of the bacteria on the midge[[4]](#endnote-4).
2. Is present at high levels in field populations. This allows for readily available material to bring into a laboratory for scrutiny.
3. Is known as a vector species, as not all *Culicoides* species are thought to be epidemiologically significant.

Thus, during the initial proposal for my project, the plan was to use *C. pulicaris*, because work by the master’s student suggested the above criteria fitted this species. The other vector species found to be infected with *Cardinium* (*C. punctatus*), however, is less common and the symbiont was present at nearly 100% prevalence, suggesting an inadequate system for investigation.

As the midge season in the UK generally lasts between May and September, and my project began in October, fresh *C. pulicaris* samples for study were not immediately available to me. I decided then, as a baseline for further work, to “simply” replicate the study by the master’s student. This would have validated the *Cardinium* screening method to be used when material became available to me next season. This building of the baseline was possible as the materials (e.g. DNA extracts of specimens) used in the recently inherited study were still readily available in my laboratory. However, during repeated and failed efforts on my part to validate the original findings noted above, I concluded that *cross-contamination of DNA extracts had occurred in the earlier study*.

At this point, it is necessary to explain some technicalities about my discovery of contamination of the samples. An important part of midge research is the accurate taxonomic identification of species of interest, with genetic markers deemed the gold standard for such classification. When amplifying a commonly used genetic marker (*COI* gene) I found conflicting results using two separate methods. For the “*C. pulicaris*” DNA extracts which were positive for *Cardinium* in the original study, the *COI* gene suggested both *C. pulicaris* and *C. punctatus* as the designated species. However, this was not plausible because each individual DNA extract was supposed to be aligned to an individual midge. Overall, this indicated to me that cross-contamination of DNA extracts between *Cardinium* positive *C. punctatus* and *C. pulicaris* negative DNA extractions had occurred in the original study. Further work assessing fresh *C. pulicaris*, undertaken by myself and others (Pagès et al. 2017), failed to detect *Cardinium* and suggests symbiont infection is not common in this species and likely has little biological significance.

*Challenges of redirected work*

As most of my intended project was based on the assumed validity of the (flawed) work inherited, plans for the project now required re-evaluation. Fortunately, a colleague who was tasked with studying the genome (the entire genetic material of an organism) of *Cardinium* serendipitously identified another symbiont, R*ickettsia*, which was the first finding of its kind in midges. This now formed a new basis of work for the project.

Through an extensive search for *Culicoides* harbouring *Rickettsia*, I found approximately a third of all species contained this newly found symbiont (Pilgrim et al. 2017). However, most midge species carried *Rickettsia* at nearly 100% prevalence, meaning that antibiotic curing would be necessary to achieve negative controls for experiments. Additionally, at this point, none of the *Rickettsia*-containing species had been successfully colonised and maintained (the importance of lab-rearing midges was noted above and returned to below), adding to the complexity of furthering this body of work.

While I was considering the problem of finding a practicable midge-*Rickettsia* system to work with, I was speculating about the potential significance of the bacterium by exploring tissue-specific infections. For example, infection of *Rickettsia* in salivary glands has previously been reported for blood and sap-sucking insects, which indicates the transmission of the bacterium to animals and plants, respectively. Thus, I set about investigating the presence of *Rickettsia* in various tissues of several developmental life stages in the species *Culicoides impunctatus*.

*C. impunctatus* is prevalent across Northern Europe but it is most abundant in the Highlands of Scotland. Here they are a biting nuisance with “midge attacks” accounting for a significant economic impact, with losses in the Scottish tourist and forestry industries (Hendry and Godwin 1988). Most biting midges require a blood meal to reproduce (anautogeny). However, *C. impunctatus* are able to reproduce a single time only in the absence of a blood meal (autogeny). This means that large numbers can develop even where animal/human blood hosts are not available (Boorman and Goodard 1970). I read that *Rickettsia* presence in booklice is necessary for egg development (Perotti et al. 2006), and so it was possible that *C. impunctatus* *Rickettsia* could be assisting in autogeny. This might offer the prospect of offering *Rickettsia* as a target for population suppression in the future.

To take stock for the reader at this point, in order for me now to investigate the possibilities emerging, after the false start of my project it was necessary to examine the species of interest in its natural habitat. In simple terms, this required me travelling to Scotland during midge season to get bitten. This was in the knowledge that the individuals biting me would produce eggs (and subsequently larvae/pupae) to analyse back in the laboratory.

There were several difficulties in attaining specimens for this study. First, the climatic conditions of the field site at the time of collections in Scotland was unusually dry. I surmised at the time this was due to the desiccation of breeding sites leading to lower than expected numbers. Secondly, visits to the Scottish site of necessity were short, this was because I needed to get back to the laboratory (in Liverpool) within a short time frame. That time pressure came from my need to analyse the samples as quickly as possible; blood-fed midges will lay eggs approximately after 5-9 days.

Some previous studies of *C. impunctatus* had utilised field laboratories. However, in my case, the original proposal for my project did not anticipate the necessity for such a facility. Moreover, once the midges had been transported back to the laboratory, I still faced the challenge of rearing them from egg-larva-pupa-adult (to assess *Rickettsia* presence in different life stages). I wanted to cultivate a live and complete life cycle in laboratory conditions, which based on previous literature I knew would be challenging (Carpenter 2001).

In comparison to mosquitoes and other flies, lab cultivation of midges is difficult, in part due to problems in optimising larval rearing environments. Although I was able to rear midges to pupa, this was only a small percentage of starting material. Most of the insects died during larval development. At this point, I recognised the challenges involved in moving between the open system of the field and the closed system of the laboratory. The latter clearly was not providing the complex and not fully understood sustaining system of the midge’s natural habitat.

Despite these hurdles, I was able to collect enough material to study *Rickettisa* in multiple life stages of *C. impunctatus* back in the laboratory (Pilgrim et al. 2020). I found *Rickettsia* present in the ovaries suggesting both maternal transmission and effects on egg development could be occurring. I also found the connective tissues surrounding the ovaries to be infected with *Rickettsia.* This indicated a possible route for how the symbiont enters developing eggs. Additionally, I found infections in the fat body (an organ analogous to our livers) of *C. impunctatus*. As BTV replicates in the fat body before travelling to the salivary glands, this indicated to me that possible interactions (like those observed in *Wolbachia* and mosquitoes) could be occurring in midges in *Rickettsia*. A study occurring at the same time described *Rickettsia* infection of *C. sonorensis* (Möhlmann 2019), a vector species of North America, which is already colonised and is used as a gold standard for infection experiments. Thus, by the end of the funded project a model species to test *Rickettsia*-effects on midge-borne viruses was now available and I could complete and submit my PhD thesis.

**Reflections on the study**

Some of the reflections I now summarise occurred during the research project but I opted not to report them, or only fleetingly, in my thesis. Others have come to mind after the PhD was completed. I developed the strong impression that typically biological scientists take political and social matters as givens and tend to discuss them little in their daily work. The focus is very much on methodological rigour and empirical detachment combining to provide a habitual confidence in researches of all grades, while they have an occasionally anxious eye on competing and emerging literature in a field of inquiry. In addition there is a routine scanning for funding opportunities for the next project after the current one is completed. Matters such as benefit to health or human welfare are taken for granted, as are the general market position of ideas in the biotech industry or for state and other research funders. I return to these points at the end.

To go beyond those norms of daily discourse in my research network and laboratory colleagues, I want to focus now on three main themes that will resonate for critical realists but which are also anticipated and illuminated by critical realism as a meta-theoretical resource. These include: the necessity and ambiguous character of interdisciplinarity; the risks of relying on pre-existing fallible knowledge; the dilemmas of moving to and fro between closed and open systems (the lab and field); and joining science as an ongoing social activity as a junior researcher.

When I entered the world of biting insects, it soon became apparent to me that research questions pertaining to vectors of disease were in the process of being answered by researchers from varying backgrounds. These included: epidemiologists, microbiologists, ecologists, virologists, climatologists and computer programmers. This interdisciplinary effort allows for specific questions to be answered due to specialised skills necessitated by each individual discipline.

For example, the effects that fluctuating temperature has on the ability of a mosquito to survive and/or transmit a virus can be examined in a laboratory setting by an ecologist/microbiologist. However, it is through the expertise of a climate scientist, that a model can be created to extrapolate these findings to map and predict vector risk globally (c.f. Price, 2019). Although this is an obvious example of how specific skill sets can combine to answer a complex question, what surprised me was the implicit and latent abilities of researchers, including myself, which also allowed for problem solving.

My veterinary degree focussed on the applied end of animal health in order to become a competent junior practitioner. By contrast, the project I was assigned to during my doctoral studies was largely shrouded in the disciplines of ecology, evolutionary biology and entomology. I knew little about these bodies of knowledge. Despite this ignorance, while I was investigating *Rickettsia* presence in various *C. impunctatus* tissues (see above), I noticed two focal points of infection in the ovaries and gut.

Having mused about the potential connection between these two strongly infected areas, I remembered from my veterinary training that a ligament exists in animals suspending the ovaries to the body wall, which prevents twisting and tissue damage. I soon discovered insects also have a similar protective structure. Through a focused attention on this ligament under the microscope (previously uncharacterised in midges) I found that it was connected to the focal point of infection at the gut, leading to a possible explanation for why these two areas were infected. Thus, a memory from my earlier training of surgery (spaying cats and dogs) led to a tenuous connection that the suspensory ligament of the ovary could be biologically significant for symbiont delivery to ovaries (Pilgrim et al. 2020).

I soon realised the importance of the collaborative nature of science when my project became unstuck early on. With the plans for my initially intended project now obsolete, it was a colleague working on the same area (but a different research question) which led to the discovery of *Rickettsia* in midges and allowed me to pivot my research. Scientists work in teams and networks (with brilliant autonomous hero innovators rarely existing) and I had soon learned the positive aspects of this in my research group. These included a shared enthusiasm for a shared venture and a generous willingness to think about individual problems in regular team meetings (see Rowe, 2008). However, the efficiency of communication to maximise group efficiency I noticed was variable. Moreover, the doctoral system of the necessary *individualism* (to become a “candidate” who has to personally “defend” their thesis in their *viva voce*) can at times create loneliness and uncertainty.

For example, I had a discussion with a fellow PhD student, who was having trouble with getting an experiment to work. It became clear that they had not attempted to discuss the matter with someone with more experience in their lab. This seemed to be from a reticence borne of embarrassment. They were an intelligent and committed student of science but their efforts alone were not sufficient for a functional experiment. To mitigate these risks, as a I noted above, within the culture of life science research group meetings are encouraged and well received by colleagues of all grades. However, this does not inevitably lead to all problems being aired by participants, with equal confidence. Individuals in their particular projects might opt to struggle on privately.

A significant private moment during my work project was the discovery of flawed work undertaken by a previous researcher in the same research group. Although this caused me *angst* at a personal level, it exemplified the messy fallibilism of research. It prompted me to read around the challenge at the time. I found that despite the reported detailed methodologies in papers, natural science has a “reproducibility” or “replicability” challenge (Baker and Penny 2016). To further mitigate the problem of replicability, some journals are now requesting all raw data and analysis to be included in published papers for transparency[[5]](#endnote-5). Despite this, when replicability is unsuccessful, it may be unclear wherein the process the problem might lie.

When I failed to reproduce the initial study on which my project was to be based, this could have been due to my lack of experience in the lab or the deterioration of the samples’ quality during storage. The alternative explanation was the failure of the original study. This could be unintentional (methodological or analytical error) or intentional (falsified data). In the case of my account documented above, it was clear a methodological error had occurred; namely, the inappropriate storage of DNA extracts, such that cross contamination of samples had occurred. Regardless of intent, flawed studies can take a long time to acknowledge and it is likely that many are not acknowledged at all.

My account here is unusual because, unlike most researchers attempting to reproduce a study at a distance of time and place, I had fortuitous access to the raw data *and* materials used in the original recent study. Again, this demonstrates the importance of understanding science in a social context and the complex contingencies involved in human activity; human systems themselves are open systems, with stable and unpredictable elements. The clarification of what had occurred in the original study was only possible through me tracing the master’s student to provide me with their lab book. This was linked to the storage of their original DNA extracts in the same lab I was working (allowing my access) and local knowledge of the whereabouts of the departed researcher. In many other situations the elucidation of the original process through retrodiction would have been extremely difficult or even impossible.

Another observation from my account above is the problem of directing research between the field and laboratory (an open and closed system). An open system is broadly defined as a system which has external interactions. In contrast, a closed system is isolated from its environment. The laboratory is designed to furnish methodological control but a price is paid, which in simple terms might involve us getting it “wrong” about our findings for practical human relevance. This insight stimulated the emergence of General Systems Theory during the 1920s from laboratory scientists, who grasped the problems of understanding the open system of the real world (Weiss, 1969; von Bertalanffy, 1968).

To elaborate, my field work studying *C. impunctatus* involved collecting numbers of insects, the success of which was determined by several fluctuating and often immeasurable external variables *independent of my research skills.* In contrast, the maintenance of a laboratory colony of midges undergoes a predictable repeated number of methodological steps and will often give the same predicted results (i.e. if successful the emergence of multiple midge adults every three weeks).

The climatic variables which led to problems in collecting materials included unexpected dry weather and sporadic windy days, which were both suboptimal for collections of large insect numbers. In addition, the limitations of relying on unpredictable short-term weather conditions was exacerbated by the UK midge season only lasting a few months of the year, meaning repeated field trips were limited during the year.

The closed system of rearing *C. impunctatus* in a laboratory environment posed another set of a problems. Attempts to mimic the environment to allow for successful cultivation of *C. impunctatus* can lead to inherent problems in the task of data collection. Without altering components of the midges’ natural environment, it is difficult to measure the detailed processes underlying midge biology. In this case, allowing for the rearing of larvae in their natural soil habitat in the laboratory obscured my observation of important behaviours (e.g. feeding habits and movement) as well as development (e.g. metamorphosis).

Therefore, a separate system, *which was very much detached from the midges’ natural environment*, was used (transparent agar plates) to monitor development and life stages needed for further analysis. Other colleagues and I in this field are faced with uncertain trade-offs. For example, simplifying the natural larval habitat in order to observe the insects accurately may be misleading, as their behaviour and development may then be an artefact of the closed system of the laboratory[[6]](#endnote-6).

Working at the boundary then between open and closed systems illuminated for me the overlap in practice between natural and social science. In the former, the critical realist logic to describe the typical practice of laboratory researchers is the DREIC sequence (Description, Retroduction, Elimination, Identification, Correction). In the case of social science this related but more elaborated sequence is RRREIC (Resolution, Redescription, Retrodiction, Elimination, Identification, Correction). The uncertainties I experienced as a result of inheriting flawed data meant that I did not start with a straightforward empirical description. I had to abandon the first impression and re-imagine (i.e. redescribe) my starting point. The range of speculations about *particular* retroductions, both in relation to infection routes in the microscopic midge anatomy and physiology, and the many uncertainties of the conditions operating in the natural field habitat, meant that retrodiction was a necessary overall framework for weighing up plausible options and the relevant generative mechanisms possibly operating. Whether it was the ambiguities of the links between the gut and the ovaries or the complexity of their naturally sustaining habitat, I was constantly pondering what was going on.

Finally I return to science as an ongoing social activity. To repeat a point made earlier about the context of my study, I was not an autonomous neophyte researcher simply pursuing a project that appealed to my imagination. Instead, the epistemological agenda which had been set by a community of scholars investigating insects pre-existed and was independent of my interest. This community of researchers furnished me with an existing body of knowledge related to vector-borne diseases to situate the starting point for my research project. Implicitly I was also joining a group that had specific value-led assumptions (which I already shared). These referred to the broad direction of learning to reduce or eliminate animal and human disease. At this point the relationship between natural ontology and social ontology (or natural necessity and scientific knowledge) becomes relevant.

Before our species existed the mechanisms of interest about vectors and their relationship with the pathogens they contain were simply there (and would be there after the Anthropocene). Mammals and birds would be affected by them, whether or not this eventuality is of any interest to humans. The survival of these pathogens would be a function of the vectors capacity to feed upon targeted hosts. Both the insect and microbe would still accumulate genetic mutations, contributing to the ongoing process of natural selection. This process of evolution and all of its effects on the natural world would still be occurring without humans to witness it.

Current witnessing involves humans making value judgements about disease and pathology. Scientific activity is directed *inter alia* at infectious diseases, and its character and scale is one manifestation of “why things matter to people” (Sayer 2011). In this case, vector-borne diseases matter for two main reasons. First they are one source of suffering and early death in humans and other species. Second, the impairments accruing from that impact have social and economic implications.

Parents to be do not want foetuses affected by the Zika virus. The Scottish tourist industry would prefer not to have swarms of midges in the summer. Farmers want to avoid diseases affecting their cows and sheep. The biotech industry profits from technical interventions produced by science in this field. From insect repellents and insecticide treated nets to genetic engineering and vaccines, profits are awaiting. And even if that industry were to be socialized, rather than profit-driven, it would still be directed at the protection of human and animal welfare.

**Conclusion**

I have offered a case study of an exercise in natural rather than social science for consideration by those with an interest in critical realism. This has required me to explain for an interdisciplinary readership the technical details of working within biological research directed at mitigating the impact of some forms of infectious disease. In particular my focus has been on the messy fallibilism of knowledge production in a form of inquiry often culturally assumed to be working with clear empirical descriptions, guided by simple neat methodologies, which are amenable to certainties in the laboratory. The reality in practice for researchers is somewhat different.

I have also highlighted the difficulties of positioning the individualistic ethos of doctoral research for junior scientists, within the typical scenario of research networks constituted by those from a wide range of disciplinary backgrounds. By the end I concluded that, within biological science we find a blurred boundary between the sequential logic of natural science (DREIC) and the more complex elaborated version of social science (RRREIC). The shared ontology of open systems drives that blurring.

Finally I offered some reflections on the social and economic linkages that can be traced in the ongoing social activity of science, which is being constantly joined by new investigators. In this particular case, tiny flying insects have many implications for human and animal health and shape the emergence of products in the biotech industry.

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**Declaration of interest**

The author declares no conflicts of interest.

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1. Hypotheses for symbiont-conferred blocking include the competition for resources between pathogen and symbiont, as well as increased immune-sensitivity due to symbiont presence. [↑](#endnote-ref-1)
2. A Biotechnology and Biological Sciences Research Council Doctoral Training Program award [↑](#endnote-ref-2)
3. Title was later changed to “The prevalence of endosymbiotic bacteria in Culicoides biting midges and the distribution of Torix group Rickettsia”. Thesis available at: https://livrepository.liverpool.ac.uk/3075607/1/200597841\_Feb2020.pdf [↑](#endnote-ref-3)
4. If a symbiont is at high prevalence in a population, it is possible to “cure” the insect of its symbiont using antibiotics but this can lead to confounding of studies as perceived direct (toxic) effects of the antibiotics cannot be distinguished easily from the indirect effects of eliminating the bacteria. [↑](#endnote-ref-4)
5. Examples of these journals include Scientific Data (Nature) and GigaScience (BMC Biology). [↑](#endnote-ref-5)
6. Cannibalism of larvae were observed on my agar plates but it is uncertain if this was an artefact of the artificial environment they are reared in, which likely provided an unpalatable food source compared to diets otherwise available in the wild. [↑](#endnote-ref-6)