February 2013: BSP Journal Club
J.R. Stothard, Liverpool School of Tropical Medicine

Dynamics of parasite distributions: modern analytical approaches
Parasitology (2012), **139** (issue 14), 1813-1974.
Editors Sarah Randolph & Les Chappell

Today, can a single paper ever entirely define a new field of research? Perhaps not, but sixty years ago, it clearly could. With their deliberate understatement, Watson and Crick's terse note in *Nature* on "*Molecular structure of nucleic acids"*, they wrote '*It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic materials*' which opened the door for modern molecular genetics, and with it the subsequent technology of polymerase chain reaction (PCR). By matching theory with evidence, the seeds were also sown of the importance of modelling and the power of a reductionist approach. With creative intellects and trial-and-error approaches (i.e., model testing), these rather innocuous organic compounds were woven together within an elegant double helix model proposed, later astonishing the world how much biological information it could contain with a simple genetic code, as was later revealed. Thus the balance between simplicity and complexity was firmly struck; it then appeared that knowing the 'essence' of something was all that was needed.

In our evolving world where complexity begets complexity, can a 'single' theory ever account for important biological processes that play out in the life and death events of disease dynamics? Clearly not, thus no single paper can now define a discipline whereas a 'clutch' of papers perhaps can. The Special Issue of *Parasitology* entitled "**Dynamics of parasite distributions: modern analytical approaches**", goes a long way to do this. What is more remarkable is that, as parasitologists, we are often looking for new ways to better reveal the adaptations of our chosen parasites and pathogens. So we strive to understand their evolutionary advantage that has led them to colonise successfully their chosen habitats, albeit within definitive or intermediate hosts, vectors thereof or whilst during their environmental stages. The breadth of this special issue, as edited by Sarah Randolph, is very significant. Changes in human behaviour and lifestyles, e-technologies for disease reporting, spatial and theoretical epidemiological frameworks and evolutionary phylogenetics are all brought together convincingly. What is more, and I think is the testimony to multi-disciplinary research, is that without knowledge of the 'one' the knowledge of the 'other' is conceptually flawed; are the global patterns of a parasite, for example, best explained by local ecological and environmental processes in recent time or rather by deeper evolutionary processes (and accidental biogeographically events) that have shaped their phenotypes and genotypes – or are both equally intertwined? Questions could include why are tsetse flies still only found in the Old World – what has stopped their spread? Related themes are developed in the paper by Serge Moran on "*Phylogeography helps with investigating the building of human parasite communities*".

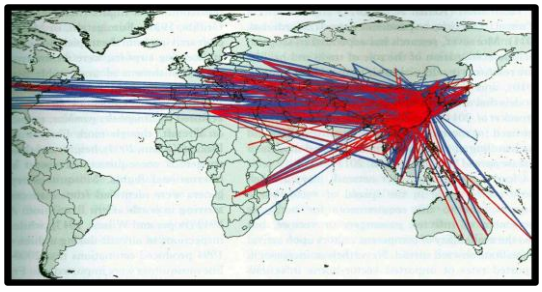

Figure 1. Flight connections to and from China in 2010 and 2011, taken from Tatem *et al.* in "*Air travel and vector-borne disease movement*."

In the modern world, old biogeographical rules of population isolation, fragmentation and evolutionary separation perhaps no longer apply and as shown in figure 1, there are novel opportunities for rapid global dispersal. The rapid movement of people by air travel is thus the problem and the answer leading to the changing picture in the global epidemiology of malaria and chikungunya, as discussed by Tatem *et al.*; even in the news just this morning, a newly discovered type of coronovirus, thought to have evolved and spread from Saudi Arabia, is making

news in the UK. Two infected cases (a father with a travel history and son who had not) are hospitalised in Birmingham with respiratory disease. As a corollary, with evermore connections and networks being formed with better communications, transportation and financial 'incentives', is it a surprise that 'horse' meat enters into our UK-consumption chain in processed food, and with it perhaps another new epidemiological opportunity? It is simply good evolutionary luck that all of these slaughtered animals were prion free, or were they? With the public health finger of suspicion being raised towards other cryptic health threats, e.g. occurrence of phenylbutazone, there is no room for complacency but where is the balance between simplicity or complexity here? The real failing is perhaps the break-down of the general surveillance and reporting system to pre-empt such illicit practices before becoming widespread; they should have seen it coming if only there were 'eyes'.

As some of the BSP membership are also health professionals, we often wonder how could, or should, a disease or food surveillance system react to such changes that happen so quickly and then respond to these in real-time settings with joined-up preventative actions? Answers to this can be found in part in the article by Chunara *et al.* and they advance a novel e-tracking system that could potentially respond much quicker than existing health system alternatives, figure 2.

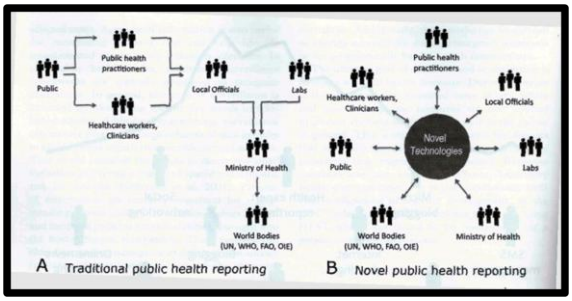

Figure 2. Flow of information in a public health system, taken from Chunara *et al.* in "*New technologies for reporting real-time emergent infections*."

The danger here, however, is the old computer-user adage GIGO – Garbage In Garbage Out – so there needs to be an appropriate filtering system to weed out irrelevant reporting whilst ensuring data retained have 'high' information content. Please excuse my mixed metaphors, for it is like sorting the meat (horse) from the bones (beef). The major benefit perhaps of the approach that Chunara *et al.* propose is in its scalability in geographical coverage. In Africa, services are presently rather thinly spread on the ground and need bolstering. Nonetheless, these technologies have to be judged in their longer-term capacity to '*support*' and not '*parallelise*' health systems.

A decade after the death of Francis Crick, I am sure Crick would have been very interested to learn of the response efforts of the Food Standards Agency with PCR-methods. As former admiralty man developing acoustic mines in WWII, Crick was no stranger to the need of rapid technological progress but with his interests in acoustics, he would have also been interested in the paper of Morgan *et al.* who reveal the importance of the phylogeography of vampire bats in the spread of diseases they carry. Such bats use a variety of auditory cues to seek out preferred feeding hosts, figure 3, unlike humans, however, they are not at all choosy upon feeding on horses.

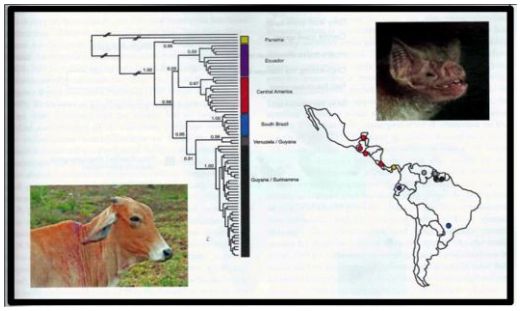

Figure 3. Phylogenetic pattern and distribution of sampling of the common vampire bat *Desmondus rotundus*, taken from Morgan *et al.* in "*Parasite epidemiology in a changing world: can molecular phylogeny help us tell the wood from the tree?"*

So to close, the debate between scientific simplicity versus complexity continues and may even lead to future BSP journal clubs with multiple rather than single papers? Good grief(!), far too much work for those who might wish to contribute, so I hope not. But on this special occasion of the publication of a rather ground-breaking special issue, defining a new field of multi-disciplinary research, we should embrace complexity (along with multiple papers) and not reject it.

Further reviews of articles within this special issue of Parasitology can be found at:
http://blog.journals.cambridge.org/2012/12/where-are-parasites-going-next-can-we-pre-empt-and-halt-them-with-a-mobile-phone/