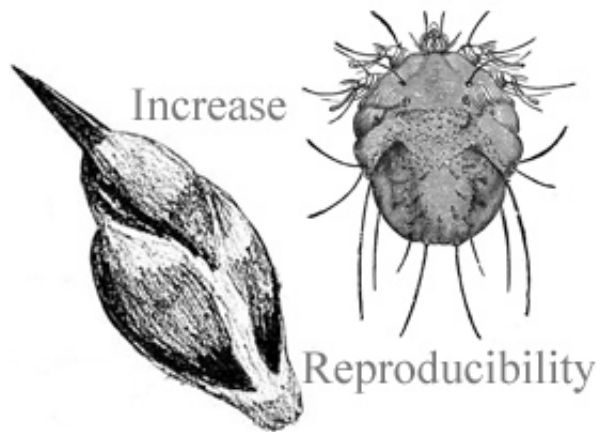


We've got tapeworms and scabies! And reproducible research

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Parasite research publication in *GigaScience* improves research reproducibility by creating citable methods 'recipes' from protocols.io. Credit: Adapted from *Schistocephalus Solidus* Life Cycle from Lukas Schärer by Claus Wedekind. Adapted from *Sarcoptes scabiei*s from Popular Science Monthly in public domain.

Two new research papers on scabies and tapeworms published today in the Open Access journal *GigaScience* also include a collaboration with protocols.io. This collaboration showcases a new way to share scientific methods that allows scientists to better repeat and build on these complicated studies on difficult-to-study parasites. It also highlights a new means of writing all research papers with citable methods that can be updated over time. Keeping work clear, consistent, and current.

Parasitology remains a complex field given the often extreme differences between parasites, which all fall under the umbrella definition of an organism that lives in or on another organism (host) and derives nutrients at the host's expense. Published today in the Open Access journal *GigaScience*, are articles on two parasitic organisms, scabies and the tapeworm, *Schistocephalus solidus*. Not only are both papers in parasitology, but the way in which these studies are presented includes a unique means for reporting the Methods that serves to improve reproducibility. Here the authors take advantage of the open access repository of [scientific methods](#) and a collaborative protocol-centered platform, protocols.io. New mechanisms for presenting scientific research are a must to improve reusability of scientific information.

Currently, the most common way of presenting methods in articles is in extremely brief paragraphs or as supplemental downloadable PDF files. The result is often incomplete or non-discoverable methodology: a serious problem given methodology is key for scientists to properly build on scientific discovery. The parasitology articles published today are the first two studies to showcase the seamless integration into the manuscript submission and publication process of clear, detailed, and complete methodology descriptions. The protocols.io platform enables researchers to submit their methods in a standard format, with no space limitations, that can be directly linked to any article simply through a citable link. These can also be searched online, and best yet, can be versioned allowing for adaptations for future work. Not only does this allow the research community easy access to detailed methods, it also means authors don't have to continually rewrite methods for every paper that uses them. They can simply cite and credit the 'recipe' in protocols.io.

It seems fitting that the complexity of making scientific reporting reproducible is demonstrated in papers that capture the complexity of parasitic organisms, and, in these cases, parasites that require many

different complicated experimental steps and unusual computational pipelines to study them.

In the first study, researchers from the Walter and Eliza Hall Institute of Medical Research and 4 other Australian institutions studied the genome of the human scabies parasite collected from remote disadvantaged and indigenous communities in Northern Australia, where up to 25% of adults and 50% of children acquire scabies infections each year. Scabies infections are linked to bacterial skin infections and rheumatic fever. As a consequence of this, children with scabies do less well, and this is a contributing factor to indigenous Australians having significantly reduced life expectancy and among the highest rates of rheumatic heart disease in the world.

Until now studying this species has been challenging. Being fractions of a millimeter in size, the researchers needed to collect, per sample, about 1000 mites to obtain enough DNA for next generation sequencing. In addition to the complications of collecting and pooling the mites, their tiny size also meant they had to deal with contamination from the mite's gut contents. All of these variables can create difficulty in clearly describing how conclusions are derived and how the research can be built on. The lead author Anthony Papenfuss, discussing the challenges of communicating this work, stated: "Writing clear and accurate descriptions of the wet lab and bioinformatics methods is a challenge at the best of times. It is especially hard when the design is complex and requires iterative exploratory analysis using multiple tools. It necessitates great care and time consuming refinement of the text. I think documenting the methods using protocols.io will make this much easier."

In the second paper, researchers from the Institut de Biologie Intégrative et des Systèmes and University of 22 Leicester studied the molecular biology of the parasitic tapeworm *Schistocephalus solidus*. Despite *S. solidus* serving as an emblematic study system in parasitology with two

centuries of research, it has an extremely complicated life-cycle with multiple developmental states and host species (parasitizing crustaceans, fish and birds). As a consequence, while there is much known about its morphology and physiology, identifying which genes are used at each stage of infection, has been comparatively lacking. The work here includes recreating the different host conditions and collecting living worms from the different life cycles to collect RNA and producing a transcriptome gene catalogue. First author François-Olivier Hébert explained: "Describing such a long process of field sampling, experimental infections in the lab using multiple hosts and, of course, the complementary bioinformatic analyses, was one of the greatest challenges in this paper". With the new integrated data and method publishing pipeline aiding this, the authors added: "We were able to achieve that by making all of our homemade scripts, programs and datasets freely available to the public through *GigaScience*, GigaDB and protocols.io. They represent essential complementary platforms that allowed us to respect our vision of a reproducible science".

More information: Mofiz E. et al., Genomic resources and draft reference assemblies of the human and porcine scabies mites, *Sarcoptes scabiei* var. *hominis* and var. *suis*. *GigaScience*. 2016. [DOI: 10.1186/s13742-016-0129-2](https://doi.org/10.1186/s13742-016-0129-2)

Mofiz, E; Holt, D; Seemann, T; Currie, B, J; Fischer, K; Papenfuss, A, T (2016): Draft genome assembly using parasitic mite population NGS DNA sample from mites extracted from host wound environment. Protocols.io. dx.doi.org/10.17504/protocols.io.exwbfpe

Hebert FO. et al., Reference transcriptome for the parasite *Schistocephalus solidus*: insights into the molecular evolution of parasitism. *GigaScience*. 2016. [DOI: 10.1186/s13742-016-0128-3](https://doi.org/10.1186/s13742-016-0128-3)

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dx.doi.org/10.17504/protocols.io.ew9bfh6

Provided by GigaScience

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