



Worming



through



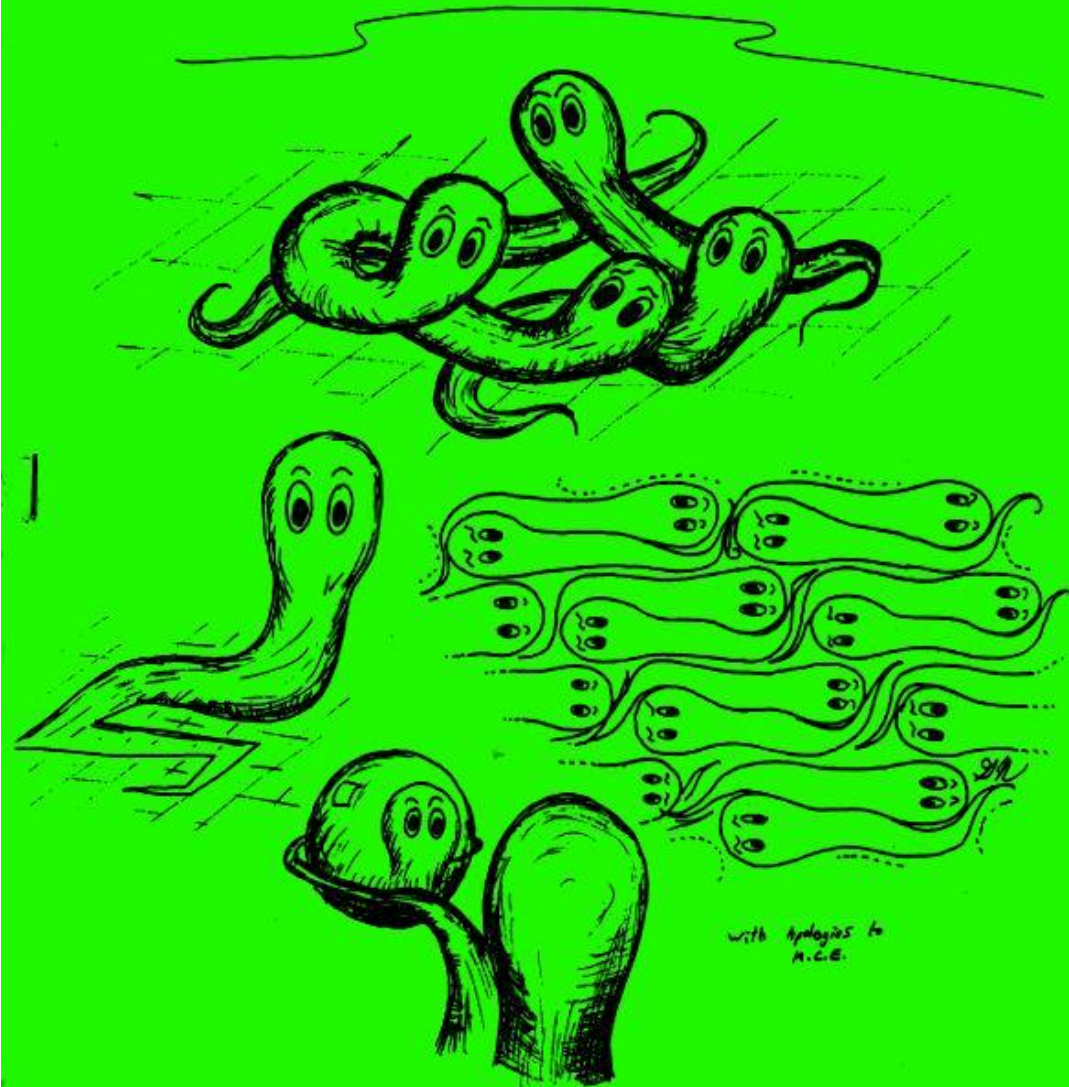
academic publishing



Jonathan Pettitt j.pettitt@abdn.ac.uk

[@genotripe](#) [@genotripe@mastodonapp.uk](#)

The Worm Breeders' Gazette



Volume 11 Number 3

These abstracts should not be cited in bibliographies. Material contained herein should be treated as personal communication and should be cited as such only with the consent of the author.

A Type IV Collage Gene in *Ascaris suum*

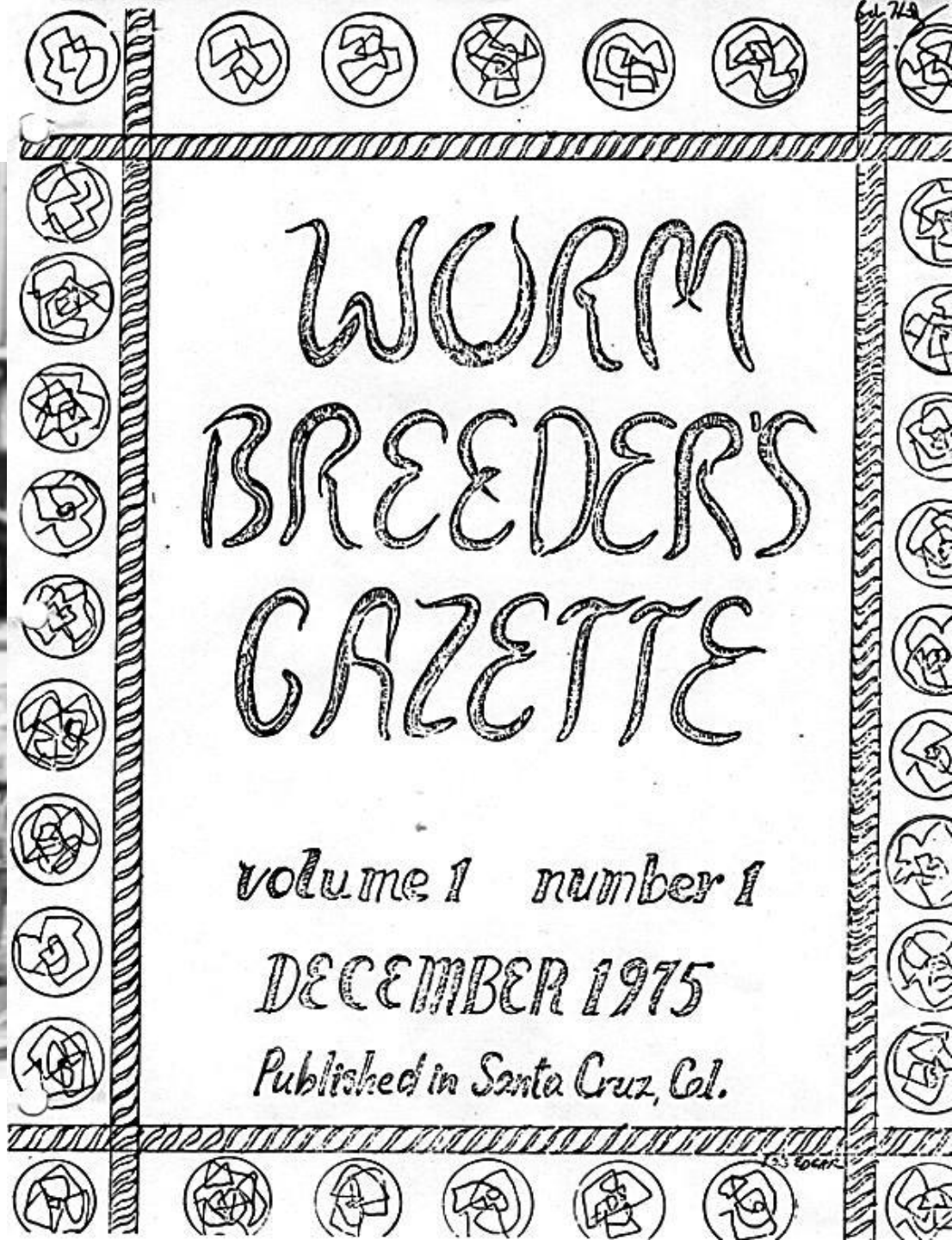
Jonathan Pettitt and Barry Kingston

We have begun an analysis of the organization, structure and expression of collagen genes in *Ascaris suum*. During the course of this work we have isolated a collagen containing clone (ucol-11) from a lambda genomic library of *Ascaris* DNA. Specific fragments obtained from this clone during sequence analysis were found to hybridize to a transcript of about 5.5 kb in several Northern blots of RNA derived from different *Ascaris* adult tissues and developmental stages. In order to further characterize the nature of the gene contained in the genomic clone, corresponding cDNA clones were isolated and sequence analysis of these revealed that the ucol-11 clone contained a type IV collagen gene. A comparison of the NC-1 domain amino acid sequence with that of type IV collagen genes in other organisms showed that the gene specifically encoded the alpha 2 chain of *Ascaris* type IV collagen.

Sequence analysis of the genomic clone revealed that although the gene constituted most of the insert, the clone did not contain the entire gene. We have found that the reason for this is in part a consequence of the presence of large introns in the gene. Such comparatively large introns have also been reported for two putative *Ascaris* cuticular collagen genes (Kingston et al), suggesting that *Ascaris* genes may generally have larger introns than those of *C. elegans*. However, the intron/exon borders of the *Ascaris* genes are very similar to the *C. elegans* consensus sequences for donor and acceptor splice sites.

So far we have determined the sequence of about 9 kb of the genomic clone and have identified 15 exons which range in size from approximately 150 to 450 bp. These are separated by introns whose sizes range from about 200 to 800 bp. Since the clone does not contain the entire sequence there are likely to be more exons in the complete gene. This organization is in contrast to the nine exons of the *Drosophila* alpha 1 chain gene, which are separated by relatively short introns, and the invertebrate genes, which although they have many exons, have much larger introns.

We are currently using a cDNA clone as a probe to study the expression of the type IV collagen gene during embryogenesis, using runoff transcription in nuclei isolated from specific cell stages in *Ascaris* embryos. There have been few studies of the synthesis of specific macromolecules in nematode embryos and we anticipate that because of the similarity between the embryonic lineages of different nematodes, the information gained from such studies on *Ascaris* embryos may also be applicable to *C. elegans*.



California Institute of Technology

<https://calisphere.org/item/c4cced272d3b60a35571f6cd7c308f2e/>

<http://wbg.wormbook.org/about/archives/>



bioRxiv

THE PREPRINT SERVER FOR BIOLOGY

[HOME](#) | [SUBMIT](#) | [FAQ](#) | [BLOG](#) | [ALERTS / RSS](#) | [ABOUT](#) | [CHANNELS](#)



[Advanced Search](#)

bioRxiv posts many COVID19-related papers. A reminder: they have not been formally peer-reviewed and should not guide health-related behavior or be reported in the press as conclusive.

[← Previous](#)

[Next →](#)

Posted May 27, 2019.

New Results

[Follow this preprint](#)

Deep evolutionary origin of nematode SL2 trans-splicing revealed by genome-wide analysis of the *Trichinella spiralis* transcriptome

[Marius Wenzel](#), [Christopher Johnston](#), [Berndt Müller](#), [Jonathan Pettitt](#), [Bernadette Connolly](#)

doi: <https://doi.org/10.1101/642082>

This article is a preprint and has not been certified by peer review [what does this mean?].

[Download PDF](#)

[Email](#)

[Print/Save Options](#)

[Share](#)

[Supplementary Material](#)

[Citation Tools](#)

[Revision Summary](#)

[Tweet](#)

μ P microPublication Biology

get your data out, be cited

Aims and Scope

microPublication is a new entrant to the emerging genre of rapidly-published research communications. Such journals aim to transform science publication by publishing single, validated results that include novel findings, negative and/or reproduced results, and results that are perceived to lack high impact. Each article of a *microPublication* journal is peer-reviewed, assigned a DOI, and published online as HTML and PDF. However, we differ from other journals in this space in one in one fundamental way: research results contained in the article are curated and, upon publication, deposited to and integrated in community-directed authoritative databases, e.g., WormBase, FlyBase, PomBase, ZFIN. As such, *microPublication* journals short circuit the publication-to-database process, placing new findings directly into information discovery spaces. Seamlessly and behind the scenes, *microPublication* turns the scientific publishing process into a curatorial one.



the
genetics society



Genes
& Development

Heredity

The official journal of the Genetics Society



November 2022 Vol 129 No 5
www.nature.com/hdy

SPRINGER NATURE





Publish and Perish

Bright Club

Thursday 8th December

7.30pm – 9.30pm

The Blue Lamp

121 Gallowgate, Aberdeen

Jonathan Pettitt

j.pettitt@abdn.ac.uk

[@genotripe](#)

[@genotripe@mastodonapp.uk](#)