GenBank accession numbers for the *M. yongonense* strains identified in this study (FI-13004 and FI-13005) are KF224989–KF224999.

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DOI: http://dx.doi.org/10.3201/eid1911.130911

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Subcutaneous Infection with *Dirofilaria* spp. Nematode in Human, France

To the Editor: The article by Foissac et al. titled Subcutaneous infection with *Dirofilaria immitis* nematode in human, France (*1*) presents an interesting and challenging diagnostic dilemma. The paper described, but did not illustrate, the worm as having a strongly ridged external surface of the cuticle–a feature known not to exist on *Dirofilaria immitis*, the dog heartworm. However, molecular sequencing of the specimen demonstrated much closer similarity to *D. immitis* than to *D. repens*, the most common cause of zoonotic subcutaneous dirofilariasis infection in Europe.

Well-described morphologic features of parasites, including in tissue sections, have long been the standard for diagnosis. More recently, molecular diagnostics have helped in many of these difficult cases. However, in some cases, the morphology and molecular diagnosis are discordant. On the basis of the data in the article, the worm does not seem to represent *D. repens*. A more likely possibility is some other species for which no sequences are yet available for comparison. In such a worm, the regions sequenced must be similar to *D. immitis*, and distinct from *D. repens*, to achieve the observed results.

When one encounters a case such as this, where well-validated morphologic features (Figure) are contradictory to the molecular analysis, one must exercise caution in arriving at a final diagnosis. One disadvantage

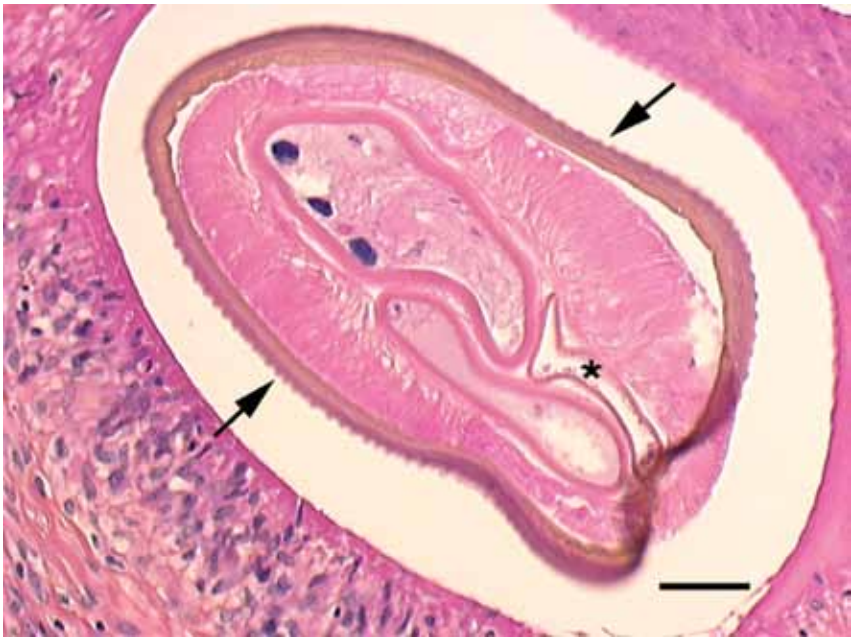

Figure. Cross-section of the filarial nematode seen in the subcutaneous nodule on the thigh of a woman in France. The features, as described in the original report (*1*), include prominent, longitudinal ridging of the cuticle (arrows), 2 reproductive tubes, and the intestine (asterisk). Scale bar indicates 50 μm. Image courtesy of Jean-Philippe Dales.

of morphologic and molecular diagnostics is an absence of information on poorly described and characterized pathogens or new pathogens that have yet to be identified. No good algorithm exists to resolve these conflicts other than to explore all possibilities. The diagnosis in the described case is probably best left as a *Dirofilaria* species of the *Dirofilaria* (*Nochtiella*) type, members of which exhibit marked cuticular ridging, and not *D.* (*Dirofilaria*) *immitis* type, members of which have as a feature an absence of cuticular ridging.

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DOI: http://dx.doi.org/10.3201/eid1911.130606

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In Response: We agree with Eberhard (*1*) that it is difficult to make a species identification when data derived from morphologic examinations do not correlate with those of molecular diagnostics. Errors may be the result of poor indexing of sequences deposited in sequence databases or inaccurate estimation of the degree of genomic polymorphisms within a species and between closely related species. On the other hand, a morphologic difference between 2 organisms, if it is associated with only 1 characteristic, should not be considered sufficient to classify them as 2 distinct species. Such a phenotypic variation may be the result of a single mutation or deletion. Consequently, the absence of a certain character does not exclude the categorization of an organism as a given species.

Molecular identification of the *Dirofilaria* spp. worm in our clinical case was made on the basis of 2 distinct sequences, each of which exhibited marked differences between *D. immitis* and *D. repens* (*2*). The first sequence targeted internal transcribed spacer regions of ribosomal genes and revealed up to 100% homology with *D. immitis* sequences from GenBank, whereas a maximum homology of 80% was observed with *D. repens* sequences from GenBank. The second sequence targeted the cytochrome oxidase 1 gene and showed 100% homology with *D. immitis*, whereas <90% homology was observed for *D. repens*. For both analyzed targets, GenBank contained several sequences for *D. immitis* and *D. repens* that were deposited by various investigators, and all sequences yielded consistent results. Therefore, there is no basis to suggest that the sequences deposited in GenBank were incorrect.

Nevertheless, we agree that an alternate hypothesis is possible. The worm reported in our article could conceivably belong to a species that differs slightly from both *D. immitis* and *D. repens*, displaying morphologic similarities with *D. repens* but being more closely associated with *D. immitis* at the genomic level.

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DOI: http://dx.doi.org/10.3201/eid1911.131176

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Cytomegaloviruses: From Molecular Pathogenesis to Intervention

Matthias J. Reddehase, editor (with the assistance of Niels A.W. Lemmermann)
Caister Academic Press, London, United Kingdom, 2013

ISBN: **978-1-908230-18-8**
Pages: 1,046; Price: **US $600**

Many health professionals rely on journal articles to keep up with advances in their field because textbooks are often 1–2 years out of date by the time they come to press, and are far more expensive than the occasional PDF downloaded from a university library Web site. This 2-volume text on cytomegalovirus (CMV) is costly and cites data from before 2012, but provides a solid foundation on which to apply new findings. Volume I is mainly focused on the basic science of and related animal experiments on CMV; volume II is aimed at the clinical reader, again with chapters on relevant animal model studies. Each chapter reads as a short review article, and is easily digestible. Many well-recognized experts in this field contributed content, which should be reassuring to the reader. The text and referencing style are easy to read and the figures and tables are illustrative and helpful. The volumes come in a compact size, making them convenient to carry, and also are downloadable as eBooks.

Volume I gives in-depth overviews of primate and murine CMVs, CMV metabolomics, miRNAs, and proteomics. Most of the chapters are dedicated to viral gene expression and function and virus interaction with human host cells, describing immune response, aspects of viral tropism, entry, pathogenesis, and latency. The terminology used in Volume I is specialized and may be difficult for readers who do not work in these fields.

Volume II covers essential clinical background: the epidemiology of CMV infections in pregnancy, CMV infections in solid and bone marrow transplants, CMV therapy and drug resistance, diagnostic methods, and vaccine development. Additional chapters describe the host immune response to CMV infection, and mechanisms of infection in specific targets, such as the placenta.

Chapters in both volumes are detailed and clearly written; the editors are to be commended on maintaining this standard. However, additional detail and discussion (i.e., pros and cons) about alternative targets for CMV PCR monitoring of transplant patients, such as pp65 antigen and pp67 mRNA versus DNA, would have been helpful. Also, an in-depth chapter on the characteristics of reinfecting or superinfecting strains of CMV in various clinical situations would be useful; such strains are frequently referred to without description throughout the clinical text. Perhaps one surprising omission on the clinical side is a chapter comparing and contrasting the various clinical guidelines for the treatment of CMV infections in transplant patients; this would highlight differences in how published data are interpreted.

Chapter II.23, Putative Disease Associations with Cytomegalovirus: a Critical Survey, explores the possible role of CMV as an etiologic agent for specific clinical syndromes, including glioblastomamultiforme, cardiovascular disease, and the role that CMV may play in immunosenescence. This makes fascinating and educational reading, especially in how the authors tease out the relevant (and irrelevant) evidence for and against these potential etiologic roles.

The price tag is considerable, although the 2 volumes can be purchased separately (http://www.horizonpress.com/hsp/supplementary/cmv2/cmv2-vol1-vol2.html). As a medical–clinical virologist, I find Volume II to be a useful reference text. Those working on the basic virology of CMV may consider Volume I a useful addition to their libraries. These volumes give comprehensive, yet succinct overviews of the current state of knowledge of many aspects of CMV and are detailed enough to satisfy most readers.

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DOI: http://dx.doi.org/10.3201/eid1911.131226

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