



**Ascaris: The Neglected Parasite: Chapter 11.
Decoding the Ascaris suum Genome using
Massively Parallel Sequencing and Advanced
Bioinformatic Methods - ... for Fundamental and
Applied Research**

Aaron R. Jex, Shiping Liu, Bo Li, Neil D. Young, Ross S. Hall, Yingrui Li, Peter Geldhof, Peter Nejsun, Paul W. Sternberg, Jun Wang, Huanming Yang, Robin B. Gasser

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Parasitic nematodes cause substantial morbidity and mortality in animals and people globally and major losses to food production annually. *Ascaris* is among the commonest geohelminths of swine and people worldwide, and causes major disease and socioeconomic losses, particularly in developing countries. The control of ascariasis has become a global health and welfare priority, but current treatment programs carry a significant risk of inducing anthelmintic resistance. Therefore, there is a need to work toward the sustainable control of *Ascaris*/ascariasis, built on a solid understanding of its molecular biology and genetics. Recently, we reported the 273 megabase (Mb) draft genome of *Ascaris suum* (sequenced from the reproductive tract of a single adult female worm) and explored transcription in different organs, stages, and both sexes of this nematode using advanced sequencing and computer technologies. We characterized key genes and biological pathways linked to the parasite's migration in the host, and its immunobiology, reproduction, and development. We also predicted and prioritized drug targets in *A. suum*, providing a basis for discovering new groups of nematocides. The present chapter provides an account of these recent advances, describes new methodologies established, and emphasizes prospects for profound investigations into the comparative genomics, genetics, evolution, immunobiology, epidemiology, and ecology of *Ascaris* from both pig and human hosts as well as for the development of new interventions against ascariasis and other helminthiases.

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