

The genome of the fire ant *Solenopsis invicta*

Yannick Wurm^{a, b, 1}, John Wang^{a, c}, Oksana Riba-Grognuz^{a, b}, Miguel Corona^a, Sanne Nygaard^d, Brendan G. Hunt^e, Krista K. Ingram^f, Laurent Falquet^b, Mingkwan Nipitwattanaphon^a, Dietrich Gotzek^g, Michiel B. Dijkstra^a, Jan Oettler^h, Fabien Comtesse^a, Cheng-Jen Shihⁱ, Wen-Jer Wuⁱ, Chin-Cheng Yangⁱ, Jerome Thomas^j, Emmanuel Beaudoin^j, Sylvain Pradervand^j, Volker Flegel^b, Erin D. Cook^e, Roberto Fabbretti^b, Heinz Stockinger^b, Li Long^b, William G. Farmerie^k, Jane Oakey^l, Jacobus J. Boomsma^d, Pekka Pamilo^m, Soojin V. Yi^e, Jürgen Heinze^h, Michael A. D. Goodisman^e, Laurent Farinelliⁿ, Keith Harshman^j, Nicolas Hulo^o, Lorenzo Cerutti^o, Ioannis Xenarios^{b, o, 2}, DeWayne Shoemaker^{p, 2}, and Laurent Keller^{a, 2}

- Author Affiliations

^aDepartment of Ecology and Evolution, University of Lausanne, 1015 Lausanne, Switzerland;

^bVital-IT Group, Swiss Institute of Bioinformatics, 1015 Lausanne, Switzerland;

^cBiodiversity Research Center, Academia Sinica, Nangang Taipei 115, Taiwan;

^dCentre for Social Evolution, Department of Biology, University of Copenhagen, 2100 Copenhagen, Denmark;

^eGeorgia Institute of Technology, School of Biology, Atlanta, GA 30332-0230;

^fDepartment of Biology, Colgate University, Hamilton, NY 13346;

^gDepartment of Entomology, National Museum of Natural History, Smithsonian Institution, Washington, DC 20013-7012;

^hBiologie I, Universität Regensburg, 93040 Regensburg, Germany;

ⁱDepartment of Entomology, National Taiwan University, Taipei 10617, Taiwan;

^jLausanne Genomic Technologies Facility, University of Lausanne, 1015 Lausanne, Switzerland;

^kInterdisciplinary Center for Biotechnology Research, University of Florida, Gainesville, FL 32610;

^lBiosecurity Queensland, Brisbane QLD 4108, Queensland, Australia;

^mDepartment of Biosciences, University of Helsinki, 00014, Helsinki, Finland;

ⁿFasteris SA, 1228 Plan-les-Ouates, Switzerland;

^oSwiss Institute of Bioinformatics, 1211 Geneva, Switzerland; and

^pUS Department of Agriculture Agricultural Research Service, Center for Medical, Agricultural, and Veterinary Entomology, Gainesville, FL 32608

Edited* by Gene E. Robinson, University of Illinois at Urbana-Champaign, Urbana, IL, and approved November 8, 2010 (received for review July 6, 2010)

*I.X., D.S., and L.K. contributed equally to this work.

Abstract

Ants have evolved very complex societies and are key ecosystem members. Some ants, such as the fire ant *Solenopsis invicta*, are also major pests. Here, we present a draft genome of *S. invicta*, assembled from Roche 454 and Illumina sequencing reads obtained from a focal haploid male and his brothers. We used comparative genomic methods to obtain insight into the unique features of the *S. invicta* genome. For example, we found that this genome harbors four adjacent copies of vitellogenin. A phylogenetic analysis revealed that an ancestral vitellogenin gene first underwent a duplication that was followed by possibly independent duplications of each of the daughter vitellogenins. The vitellogenin genes have undergone subfunctionalization with queen- and worker-specific expression, possibly reflecting differential selection acting on the queen and worker castes. Additionally, we identified more than 400 putative olfactory receptors of which at least 297 are intact. This represents the largest repertoire reported so far in insects. *S. invicta* also harbors an expansion of a specific family of lipid-processing genes, two putative orthologs to the *transformer/feminizer* sex differentiation gene, a functional DNA methylation system, and a single putative telomerase ortholog. EST data indicate that this *S. invicta* telomerase ortholog has at least four spliceforms that differ in their use of two sets of mutually exclusive exons. Some of these and other unique aspects of the fire ant genome are likely linked to the complex social behavior of this species.

[social insect](#)[caste differences](#)[nonmodel organism](#)[de novo genome assembly](#)

Footnotes

¹To whom correspondence should be addressed. E-mail: yannick.wurm@unil.ch.

Author contributions: Y.W., J.W., O.R.-G., M.C., S.N., B.G.H., M.A.D.G., L. Farinelli, N.H., L.C., I.X., D.S., and L.K. designed research; Y.W., J.W., O.R.-G., M.C., S.N., B.G.H., L. Falquet, F.C., E.D.C., L. Farinelli, N.H., L.C., and I.X. performed research; Y.W., J.W., O.R.-G., M.C., S.N., B.G.H., K.K.I., L. Falquet, M.N., M.B.D., J. Oettler, C.-J.S., W.-J.W., C.-C.Y., J.T., E.B., S.P., V.F., R.F., H.S., L.L., W.G.F., J. Oakey, J.J.B., P.P., S.V.Y., J.H., M.A.D.G., L. Farinelli, K.H., N.H., L.C., I.X., D.S., and L.K. contributed new reagents/analytic tools; Y.W., J.W., O.R.-G., M.C., S.N., B.G.H., K.K.I., L. Falquet, D.G., N.H., L.C., and I.X. analyzed data; and Y.W., O.R.-G., M.C., S.N., B.G.H., K.K.I., N.H., L.C., D.S., and L.K. wrote the paper.

The authors declare no conflict of interest.

Data deposition: The sequences reported in this paper have been deposited at the National Center for Biotechnology Information under Genome Project ID 49629.

↵*This Direct Submission article had a prearranged editor.

This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1009690108/-/DCSupplemental.
