

## ERRATUM

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# Erratum to: The whole genome sequence of the Mediterranean fruit fly, *Ceratitis capitata* (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species

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## Erratum

After publication of our recent article [1] we noticed that Monica Munoz-Torres had been omitted from the author list. We have now added her, and the updated Funding and Authors' contributions sections are below.

### Funding

Support of this project was provided by the U.S. Department of Agriculture (USDA), Agricultural Research Service (ARS), Animal and Plant Health Inspection Service (APHIS), and National Institute of Food and Agriculture (NIFA)-Biotechnology Risk Assessment Grants Program (grant #2011-39211-30769 to AMH) for funding the initial phase of this project, and to the National Institutes of Health (NIH)-National Human Genome Research Institute (NHGRI) for funding the medfly genome sequencing, assembly and Maker 2.0 automated annotation as part of the i5K 30 genome pilot project (grant #U54 HG003273 to RAG). The NIH Intramural Research Program, National Library of Medicine funded the NCBI Gnomon annotation and the USDA-National Agricultural Library (NAL) provided support for the WebApollo curation website, with support for manual curation training (to MM-T) provided by NIGMS (grant #5R01GM080203),

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### Authors' contributions

AMH and SR conceived of and directed the project whose management was assisted by MFS, AP, and RAG. LMG reared the inbred ISPR lines and extracted genomic DNA and RNA that was used for library construction, sequencing, assembly and Maker annotations at HGSC by SR, SD, SLL, HC, HVD, HD, YH, JQ, SCM, DSTH, KCW, DMM and RAG. Additional community RNA-Seq analysis was performed by GO, IC, and EAW; JAMg annotations were performed by AP and Gnomon (NCBI) annotations were directed by TDM that were provided for manual annotation at the USDA-NAL WebApollo

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site managed by MP, and CC, with curation assistance and training by MM-T; AD, JHW, AP, TDM, GT and KB identified and analyzed bacterial sequence contaminants; SG and SBS performed orthology and phylogeny analysis; AMH, AZ, and PH-C made scaffold map assignments; GT and KB performed symbiont horizontal gene transfer analysis; PS, PA, PWA and AMH analyzed transposable elements; GGe, DK, MDP, ISV, and AGH manually annotated and analyzed microRNAs; LMG, FS, GS, PS, MM, ARM, and GGa manually annotated and analyzed odorant binding protein, odorant receptor, and seminal fluid protein genes; SDG and HMR manually annotated and analyzed gustatory and ionotropic receptor genes; MF and JWJ manually annotated and analyzed opsin genes; AJR, AER, JPC and JBB manually annotated and analyzed aquaporin and cuticle protein genes; PK, MR and KM manually annotated and analyzed immunity-related genes; PC, FO, PH-C, MG-G, EU and AG-A manually annotated and analyzed toxin metabolism and insecticide resistance genes (P450s, carboxylesterases, GSTs, cysLGICs and sodium channels); MS and GS manually annotated and analyzed sex determination genes; and MFS and AMH manually annotated and analyzed programmed cell death genes. All authors read and approved the final manuscript.

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