

Correction

Correction: Serendipitous discovery of *Wolbachia* genomes in multiple *Drosophila* species

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After the publication of this work [1], other researchers independently discovered that some of the data deposited in the NCBI Trace Archive was labeled erroneously. In particular, the sequencing center responsible for two of the *Drosophila* genome projects (Agencourt Biosciences) mistakenly deposited 20,000 sequences from *D. ananassae* and labeled them as *D. mojavensis*. The center recently corrected the mistake by removing the mislabeled sequences from the Trace Archive. We then searched through the newly updated *D. mojavensis* sequences for the 114 *Wolbachia* sequences that we had originally reported, and found that all had been removed. Thus our article should be corrected to report that new *Wolbachia* genome sequences were discovered in *D. ananassae* and *D. simulans*, but not in *D. mojavensis*.

While searching the Trace Archive to verify this correction, however, one of us (S.L.S.) found that the traces for a new fly sequencing project, that of *D. willistoni*, had just been deposited. On searching the *D. willistoni* traces, a substantial

Wolbachia infection in this species was discovered and 2,291 sequences belonging to *Wolbachia* were found. They were assembled into 485 contigs using the comparative assembler AMOS-Cmp [2] and the methods described in [1]. These sequences and assemblies are freely available for download from [3].

Acknowledgements

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References

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2. Pop M, Phillippy A, Delcher AL, Salzberg SL: **Comparative genome assembly.** *Brief Bioinform* 2004, **5**:237-248.
3. ***D. willistoni* sequences and assemblies** [<ftp://ftp.cbcb.umd.edu/pub/salzberg>]