



## Corrigendum: Chromatin structure influences rate and spectrum of spontaneous mutations in *Neurospora crassa*

Mariana Villalba de la Peña, Pauliina A.M. Summanen, Martta Liukkonen, et al.

*Genome Res.* 2023 33: 836-837

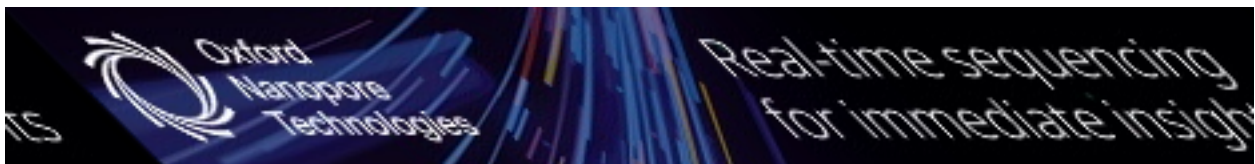
Access the most recent version at doi:[10.1101/gr.278126.123](https://doi.org/10.1101/gr.278126.123)

---

**Open Access** Freely available online through the *Genome Research* Open Access option.

**License**

**Email Alerting Service** Receive free email alerts when new articles cite this article - sign up in the box at the top right corner of the article or [click here](#).



---

To subscribe to *Genome Research* go to:  
<https://genome.cshlp.org/subscriptions>

---

Published by Cold Spring Harbor Laboratory Press

Corrigendum

Genome Research 33: 599–611 (2023)

Corrigendum: Chromatin structure influences rate and spectrum of spontaneous mutations in *Neurospora crassa*

Mariana Villalba de la Peña, Pauliina A.M. Summanen, Martta Liukkonen, and Ilkka Kronholm

The authors would like to correct formula S14 and the calculation error of the mutation rate during sexual reproduction. In this study, the authors reanalyzed the data collected by Wang et al. (2020) for mutations induced during the sexual cycle and, in error, divided the Poisson rate parameter by the number of tetrads, which had already been factored into the original data set. Subsequently, the authors reported a lower mutation rate than the original study.

The corrected equation for mutation rate has been updated in the [Supplemental Information](#) file:

$$\mu = \frac{\exp(\bar{\alpha})}{N}$$

where  $N$  is the number of called nucleotides and  $\bar{\alpha}$  is the average intercept from the Poisson model. The corrected mutation rates for the sexual cycle are shown below. The corrected estimates are much closer to the original estimate of  $3.34 \times 10^{-6}$  mutations / bp / sexual generation over the whole genome reported by Wang et al. (2020). Thus, there is no major discrepancy between this and the original estimate; the mutation rate in euchromatic regions during sexual reproduction seems to be very high in *N. crassa*.

| Corrected mutation rates during sexual reproduction in <i>N. crassa</i> , for different regions in the genome |                                     |
|---------------------------------------------------------------------------------------------------------------|-------------------------------------|
| Region                                                                                                        | Rate (mutations/meiosis/bp)         |
| Euchromatic                                                                                                   | $7.15 [3.85, 10.72] \times 10^{-7}$ |
| H3K9me3                                                                                                       | $1.68 [0.075, 5.09] \times 10^{-5}$ |

The corrected values have been updated in the main text as follows:

Results, final subsection:

“Based on our analysis, the mutation rate during meiosis in euchromatin was  $7.15 [3.85, 10.72] \times 10^{-7}$  mutations/meiosis/bp and was  $1.68 [0.075, 5.09] \times 10^{-5}$  in H3K9me3 domains. The mutation rate was substantially higher during meiosis than mitosis, as observed by Wang et al. (2020).”

Discussion, second paragraph:

“For euchromatic regions, our analysis supports a higher mutation rate during meiosis than in mitosis. We also observed that the spectrum of mutations was different in meiosis, but notably, there was no difference in C:G → T:A transitions in euchromatin. Moreover, because gene density is much higher in euchromatic regions, the action of RIP likely does not result in a high genetic load, but increased meiotic mutation rate in euchromatin may do so.”

This error does not affect the main results, which reported the mutation rate during asexual propagation. Moreover, ratios and relative rates concerning mutation rates during sexual reproduction are unaffected as well.

The authors thank Laurence Hurst, Sihai Yang, and Long Wang for bringing this matter to their attention and apologize for any confusion this may have caused.

In addition, the cited reference has exactly 10 authors, so “et al.” has been removed from the full reference, as shown below:

## Reference

Wang L, Sun Y, Sun X, Yu L, Xue L, He Z, Huang J, Tian D, Hurst LD, Yang S. 2020. Repeat-induced point mutation in *Neurospora crassa* causes the highest known mutation rate and mutational burden of any cellular life. *Genome Biol* **21**: 142. doi:10.1186/s13059-020-02060-w

doi: 10.1101/gr.278126.123