



University of Groningen

Erratum to

Vidalis, Amaryllis; Živković, Daniel; Wardenaar, René; Roquis, David; Tellier, Aurélien; Johannes, Frank

Published in:
Genome Biology

DOI:
[10.1186/s13059-017-1176-4](https://doi.org/10.1186/s13059-017-1176-4)

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2017

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):

Vidalis, A., Živković, D., Wardenaar, R., Roquis, D., Tellier, A., & Johannes, F. (2017). Erratum to: Methylome Evolution in plants. *Genome Biology*, 18(1), 1-3. [41]. <https://doi.org/10.1186/s13059-017-1176-4>

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

ERRATUM

Open Access



Erratum to: Methylome Evolution in plants

Amaryllis Vidalis^{1†}, Daniel Živković^{2†}, René Wardenaar³, David Roquis¹, Aurélien Tellier^{2*} and Frank Johannes^{1,4*}

Erratum

After publication of this article [1] we noticed that the centromere of Chromosome 3 was missing from Fig. 4a, and that the Fig. 4e y-axis should read 'CG meth. Div. W-Acc.'. The y-axis of the barplot in Fig. 5a should read 'Number of cytosines'. The corrected Figs. 4 and 5 are shown below.

Author details

¹Population Epigenetics and Epigenomics, Technical University of Munich, Liesel-Beckman-Str. 2, 85354 Freising, Germany. ²Population Genetics, Technical University of Munich, Liesel-Beckman-Str. 2, 85354 Freising, Germany. ³Groningen Bioinformatics Centre, University of Groningen, 9747 AG Groningen, The Netherlands. ⁴Institute for Advanced Study, Technical University of Munich, Lichtenbergstr. 2a, 85748 Garching, Germany.

Received: 19 February 2017 Accepted: 19 February 2017

Published online: 27 February 2017

Reference

1. Vidalis A, Živković D, Wardenaar R, Roquis D, Tellier A, Johannes F. Methylome evolution in plants. *Genome Biol.* 2016;17:264.

* Correspondence: tellier@wzsw.tum.de; frank@johanneslab.org

†Equal contributors

²Population Genetics, Technical University of Munich, Liesel-Beckman-Str. 2, 85354 Freising, Germany

¹Population Epigenetics and Epigenomics, Technical University of Munich, Liesel-Beckman-Str. 2, 85354 Freising, Germany



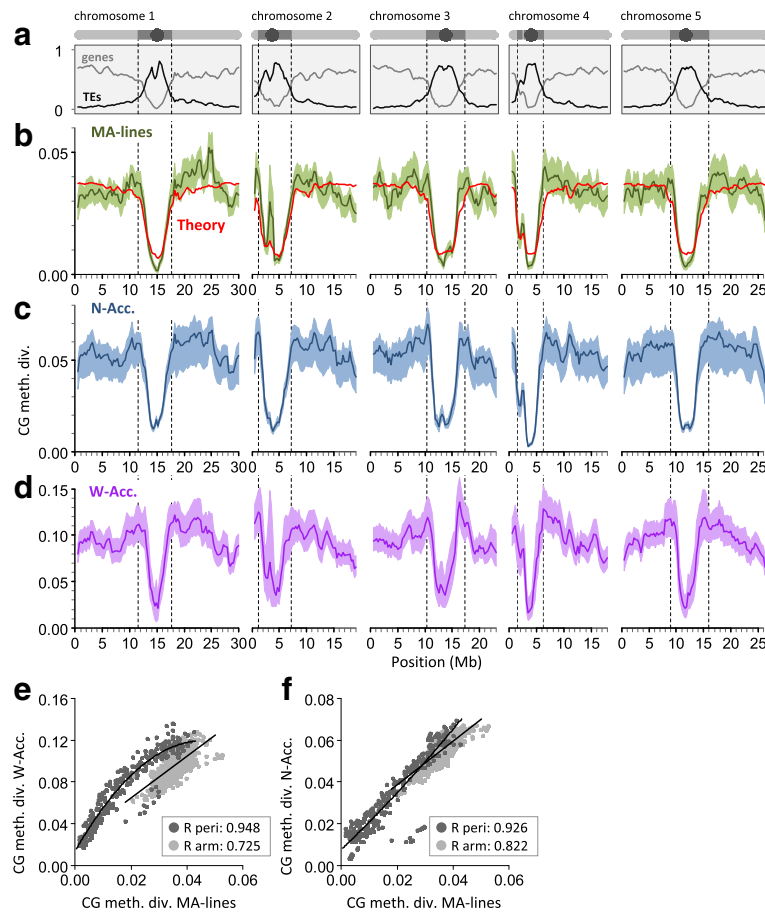


Fig. 4 **a** Gene (*light gray*) and transposable element (TE) (*dark gray*) densities along the *A. thaliana* genome (Columbia reference). A schematic representation of the five chromosomes is shown above (circle, centromere; *dark gray*, pericentromeric region; *light gray*, arm). **b** Annotation-specific CG epimutations produce distinct methylome diversity (CG meth. div.) patterns among mutation accumulation lines (MA-lines) that have diverged for merely 30 generations (average diversity was calculated in 1 Mb sliding windows, step size 100 kb). These diversity patterns can be predicted from annotation-specific estimates of epimutation rate and the density distribution of annotation units along the genome (*red theoretical line*). **c** CG methylome diversity (CG meth. div.) patterns among 13 North American accessions (N-Acc.) (after around 200 generations of divergence). **d** Methylome diversity patterns among 138 worldwide accessions (W-Acc.) (after several hundred thousand years of divergence). **e** CG methylome diversity patterns are significantly correlated between the MA-lines and the W-Acc., both in pericentromeric (*dark gray dots*) as well as in euchromatic chromosome arms (*light gray dots*). **f** These correlations are even stronger when MA-lines are compared to the N-Acc., suggesting that the accumulation of DNA sequence polymorphism has perturbed epimutation-induced methylome diversity patterns over time

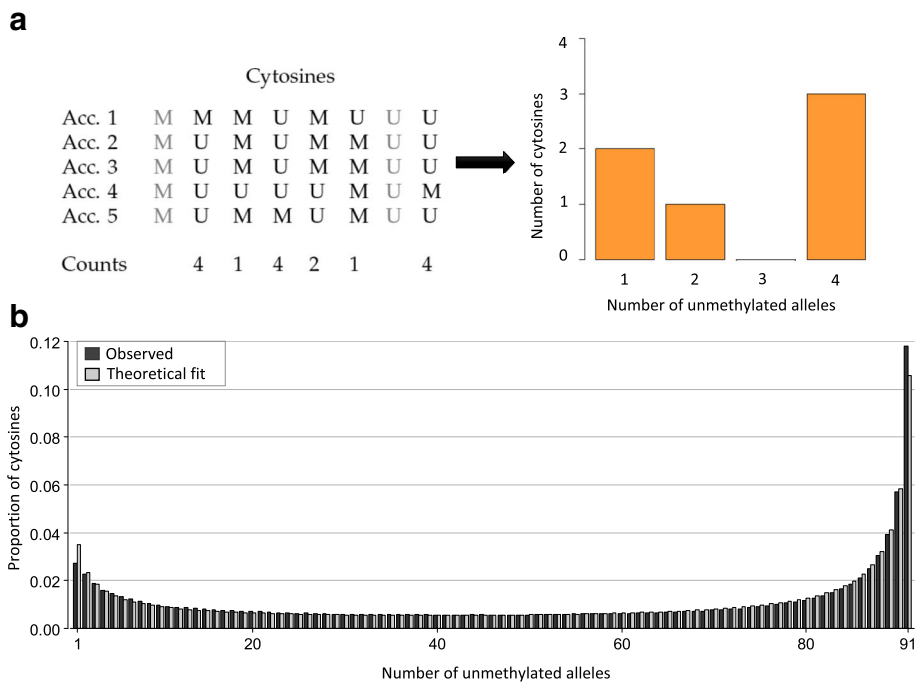


Fig. 5 a Simplification of the reconstruction of a methylation site frequency spectrum (mSFS). In this example, we consider a sample size of five accessions (Acc.), and eight sites among which two (in *gray*) are monomorphic and thus discarded for the mSFS. For each cytosine, each accession might exhibit a methylated (M) or an unmethylated (U) state. For the mSFS, counts are taken of the number of accessions that are unmethylated for that cytosine. These counts define discrete epiallelic classes (number of unmethylated alleles). **b** The observed frequencies of each epiallelic class is determined, in this case, from genic CG sites of 92 *A. thaliana* worldwide natural accessions (*red bars*), along with the maximum likelihood estimate based on the theoretical result of Charlesworth and Jain [123] (*pink bars*). The theoretical model (see Box 1) provides an accurate fit to the observed genic CG methylation diversity patterns, suggesting that CG epimutations are a major factor in shaping methylome diversity in natural populations of *A. thaliana* over evolutionary timescales