



Decision on your PeerJ submission: "An elucidation of the links between hormones, DNA methylation, the microbiome, and disease to restore homeostasis to each component through the genomic engineering of CRISPR microbes" (#2019:01:34525:0:2:REVIEW)

1 message

PeerJ <peer.review@peerj.com>
Reply-to: PeerJ <peer.review@peerj.com>
To: Tatiana Hillman <stemhill86@gmail.com>

Thu, Mar 14, 2019 at 10:47 AM

PeerJ

Dear Tatiana,

Thank you for your submission to PeerJ.

I am writing to inform you that your manuscript - [An elucidation of the links between hormones, DNA methylation, the microbiome, and disease to restore homeostasis to each component through the genomic engineering of CRISPR microbes](#) - has been rejected for publication.

Editor comments (Vladimir Uversky)

REJECT

As you can see, both reviewers have found numerous serious issues that preclude further consideration of your manuscript.

PeerJ Staff Note - this decision was reviewed and approved by Pedro Silva, a PeerJ Section Editor covering this Section

Reviewer 1 (Anonymous)

[Basic reporting](#)

This review fails to meet the basic requirements:

- 1. Sentences are copied directly from references - Line 34 and 35 from reference 4*
- 2. Within the first and second paragraphs, the author has paraphrased sections from reference 4 and 6 in a way that distorts the context and the meanings of those sections as they are presented in the original articles.*
- 3. This pattern repeats through out the manuscript making this a confusing read.*
- 4. The author needs to re-write this, have colleagues correct/offer suggestions before submitting for publication*

Thank you for your honest and detailed comments. I performed a test to check the manuscript for similarities and plagiarism. I have included the results from the test in the supplementary files. The test detected 1% of similarity. For the similar sentences, citations were included and provided at the end of those sentences. The pattern discussed of paraphrasing in the entire text was not detected by the test. The manuscript was rewritten and reorganized, and I have colleagues currently proofreading the manuscript.

Experimental design

Due to the confusing nature of the text, it is impossible to judge whether the methodology is sound.

I understand. I included a PRISMA diagram and a checklist to map my survey methodology for the manuscript.

Validity of the findings

The author suggests in the abstract that there is a link between hormones, DNA methylation and disease with the microbiome somehow contributing to the diagnosis. This seems like a huge leap and is not adequately addressed or proved in the text. Again, the confusing nature of the text, the mixed up paraphrasing from references and lack of organization make it difficult for the reader to follow the thought processes of the author.

I understand. I restructured the title, the abstract, and the paper to better explain the connection between hormones and DNA methylation. I chose not to focus a great deal on the link between all the four key terms of hormones, DNA methylation, disease, and the gut microbiome. Hormones are affected by DNA methylation frequency. I improved my description of hormones linked to DNA methylation. For

example, I described the hormone called progesterone increasing in expression with the downregulation of DNA methylation at its promoter site, which can cause breast cancer. I changed the central part of the paper to only explain and describe hormones, DNA methylation, and each component's link to disease as cancer. CRISPR-Cas9 was suggested as an effective method for restoring hormonal balance by modifying DNA methylation sites. A specific method from the Jaenisch lab of the Whitehead Institute engineered a form of CRISPR-Cas9 editing that added or deleted a methyl group, using mouse cells was discussed. I believe making hormones linked to DNA methylation the central idea of the manuscript can help alleviate the increased confusion.

Reviewer 2 (Anonymous)

Basic reporting

This manuscript by Hillman attempts to connect different processes (hormones, epigenetics, CRISPR, microbiome). However the paper as it stands is disjointed. The different concepts are often mixed throughout the text and numerous paragraphs are difficult to follow. In addition, the figures are borrowed from other previously published papers (I assume the author obtained permission to use these) as opposed to generating new ones for this review.

Thank you for your comments. I agree with your statement. Therefore, I included more support from the literature to explain the process or the feedback loop of hormones increasing with DNA methylation down regulation. CRISPR-cas9 is a new and promising method that can not only delete a DNA target site but it can add or remove methyl groups from DNA sites. This method is described in more detail in the new version of the manuscript. The paper was reorganized with more subsections of the body paragraphs. No figures were included in the new version of this manuscript resubmission.

Experimental design

-

Validity of the findings

-

Comments for the Author

-

With kind regards,

[Vladimir Uversky](#)

Academic Editor, PeerJ

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