Sex-linked genetic diversity originates from persistent sociocultural processes at microgeographic scales

Ning Ning Chung, Guy S. Jacobs, Herawati Sudoyo, Safarina G. Malik, Lock Yue Chew, J. Stephen Lansing and Murray P. Cox

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Revised submission: 25 July 2019
Final acceptance: 26 July 2019

Note: Reports are unedited and appear as submitted by the referee. The review history appears in chronological order.

Note: This manuscript was transferred from another Royal Society journal without peer review.
Recommendation?
Accept with minor revision (please list in comments)

Comments to the Author(s)
The authors present data of genetic variation which allow to test different models of socio-genetic interactions involving sex-biased migration, lineage-focused founder effects, and heritable social dominance. The subject is interesting and the data sound. Here are a few minor comments:
a) I always find weird that population geneticists keep using 'heterozygosity' for haploid loci.
b) the color coding in fig 2A (ie from 0 to 600 for matrilocal is not a density and the number should be explain in the figure legend, this applies to subsequent figures

c) p7 delta should be explained line 48 in addition to table 1. An explanation of the value chosen (0.06) is welcomed, a reference would be even better.
d) First occurrence of PE page 10, it would be nice to define.
e) Fig 6: I would like a discussion about the significance of the difference of 0.3 and 0.32 in the Timor founder model (and 0.51 and 0.53 in Slatkin's exact test)

Review form: Reviewer 2

Is the manuscript scientifically sound in its present form?
Yes

Are the interpretations and conclusions justified by the results?
Yes

Is the language acceptable?
Yes

Do you have any ethical concerns with this paper?
No

Have you any concerns about statistical analyses in this paper?
No

Recommendation?
Accept with minor revision (please list in comments)

Comments to the Author(s)
To the Authors:

In “Sex-linked genetic diversity originates from persistent sociocultural processes at microgeographic scales” Chung, Jacobs and colleagues analyse mtDNA (540bp) and Y chromosome (12 STRs + haplotype informative SNPs) for ~1,100 individuals from two Indonesian islands characterised by opposite societal systems. In doing so, they observe a marked opposite skewness in the observed heterozygosity (H) in matrilocal and patrilocal populations and used different simulation models to identify the best model explaining the observed heterozygosity. Testing the combination of i) post-marital movements, ii) social dominance and iii) founder-ideology patterns the authors found that a founder model with dominance can approximate the observed H pattern in the patrilocal Sumba,
while the same model with No dominance provides a better fit for the matrilocal Timor, although there is a limited power for the latter population.

The work is well conceived and written, and the methods are rigorous, although some clarifications and additional figures summarising the simulated model could help to raise the interest of the anthropologists' community. Overall, I would recommend the publication of the manuscript after some modifications (see comments to the author).

Here are more specific comments:

P2. Introduction: The introductory paragraph is too concise, and do not adequately summarise what is the actual state of the art in using genetics to characterise the impact of social strategies. Please consider to expand it.

P2, L8 : This sentence seems truncated, please consider to rephrase it.

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P2, L50. The term Heterozygosity usually refers to an individual rather than a population metric. Given that the work is expected to be of interest to the anthropologists’ community, I would consider adding a brief explanation. For the same reason, it would be very useful to include a figure summarising the simulated models.

Decision letter (RSOS-190733.R0)

17-Jul-2019

Dear Dr Cox

On behalf of the Editors, I am pleased to inform you that your Manuscript RSOS-190733 entitled "Sex-linked genetic diversity originates from persistent sociocultural processes at microgeographic scales" has been accepted for publication in Royal Society Open Science subject to minor revision in accordance with the referee suggestions. Please find the referees' comments at the end of this email.

Both reviewers are very positive about publication of the manuscript but they also suggest some minor revisions to your manuscript. Therefore, I invite you to respond to the comments and revise your manuscript.

• Ethics statement
If your study uses humans or animals please include details of the ethical approval received, including the name of the committee that granted approval. For human studies please also detail whether informed consent was obtained. For field studies on animals please include details of all permissions, licences and/or approvals granted to carry out the fieldwork.

• Data accessibility
It is a condition of publication that all supporting data are made available either as supplementary information or preferably in a suitable permanent repository. The data accessibility section should state where the article’s supporting data can be accessed. This section should also include details, where possible of where to access other relevant research materials.
such as statistical tools, protocols, software etc can be accessed. If the data has been deposited in an external repository this section should list the database, accession number and link to the DOI for all data from the article that has been made publicly available. Data sets that have been deposited in an external repository and have a DOI should also be appropriately cited in the manuscript and included in the reference list.

If you wish to submit your supporting data or code to Dryad (http://datadryad.org/), or modify your current submission to dryad, please use the following link: http://datadryad.org/submit?journalID=RSOS&manu=RSOS-190733

• Competing interests
Please declare any financial or non-financial competing interests, or state that you have no competing interests.

• Authors’ contributions
All submissions, other than those with a single author, must include an Authors’ Contributions section which individually lists the specific contribution of each author. The list of Authors should meet all of the following criteria; 1) substantial contributions to conception and design, or acquisition of data, or analysis and interpretation of data; 2) drafting the article or revising it critically for important intellectual content; and 3) final approval of the version to be published.

All contributors who do not meet all of these criteria should be included in the acknowledgements.

We suggest the following format:
AB carried out the molecular lab work, participated in data analysis, carried out sequence alignments, participated in the design of the study and drafted the manuscript; CD carried out the statistical analyses; EF collected field data; GH conceived of the study, designed the study, coordinated the study and helped draft the manuscript. All authors gave final approval for publication.

• Acknowledgements
Please acknowledge anyone who contributed to the study but did not meet the authorship criteria.

• Funding statement
Please list the source of funding for each author.

Please ensure you have prepared your revision in accordance with the guidance at https://royalsociety.org/journals/authors/author-guidelines/ -- please note that we cannot publish your manuscript without the end statements. We have included a screenshot example of the end statements for reference. If you feel that a given heading is not relevant to your paper, please nevertheless include the heading and explicitly state that it is not relevant to your work.

Because the schedule for publication is very tight, it is a condition of publication that you submit the revised version of your manuscript before 26-Jul-2019. Please note that the revision deadline will expire at 00.00am on this date. If you do not think you will be able to meet this date please let me know immediately.

To revise your manuscript, log into https://mc.manuscriptcentral.com/rsos and enter your Author Centre, where you will find your manuscript title listed under "Manuscripts with Decisions". Under "Actions," click on "Create a Revision." You will be unable to make your
revisions on the originally submitted version of the manuscript. Instead, revise your manuscript and upload a new version through your Author Centre.

When submitting your revised manuscript, you will be able to respond to the comments made by the referees and upload a file "Response to Referees" in "Section 6 - File Upload". You can use this to document any changes you make to the original manuscript. In order to expedite the processing of the revised manuscript, please be as specific as possible in your response to the referees. We strongly recommend uploading two versions of your revised manuscript:

1) Identifying all the changes that have been made (for instance, in coloured highlight, in bold text, or tracked changes);
2) A 'clean' version of the new manuscript that incorporates the changes made, but does not highlight them.

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2) A separate electronic file of each figure (EPS or print-quality PDF preferred (either format should be produced directly from original creation package), or original software format);
3) Included a 100 word media summary of your paper when requested at submission. Please ensure you have entered correct contact details (email, institution and telephone) in your user account;
4) Included the raw data to support the claims made in your paper. You can either include your data as electronic supplementary material or upload to a repository and include the relevant doi within your manuscript. Make sure it is clear in your data accessibility statement how the data can be accessed;
5) All supplementary materials accompanying an accepted article will be treated as in their final form. Note that the Royal Society will neither edit nor typeset supplementary material and it will be hosted as provided. Please ensure that the supplementary material includes the paper details where possible (authors, article title, journal name).

Supplementary files will be published alongside the paper on the journal website and posted on the online figshare repository (https://rs.figshare.com/). The heading and legend provided for each supplementary file during the submission process will be used to create the figshare page, so please ensure these are accurate and informative so that your files can be found in searches. Files on figshare will be made available approximately one week before the accompanying article so that the supplementary material can be attributed a unique DOI.

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Once again, thank you for submitting your manuscript to Royal Society Open Science and I look
Kind regards,

Lianne Parkhouse
Editorial Coordinator
Royal Society Open Science
openscience@royalsociety.org

on behalf of Dr Alecia Carter (Associate Editor) and Steve Brown (Subject Editor)
openscience@royalsociety.org

Reviewer comments to Author:

Reviewer: 1

Comments to the Author(s)
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d) First occurrence of PE page 10, it would be nice to define.
e) Fig 6: I would like a discussion about the significance of the difference of 0.3 and 0.32 in the Timor founder model (and 0.51 and 0.53 in Slatkin's exact test)

Reviewer: 2

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interest of the anthropologists’ community. Overall, I would recommend the publication of the manuscript after some modifications (see comments to the author).

Here are more specific comments:

P2. Introduction: The introductory paragraph is too concise, and do not adequately summarise what is the actual state of the art in using genetics to characterise the impact of social strategies. Please consider to expand it.

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P2, L12-14: The few works mentioned in this sentence should be cited.

P2, L50. The term Heterozygosity usually refers to an individual rather than a population metric. Given that the work is expected to be of interest to the anthropologists’ community, I would consider adding a brief explanation. For the same reason, it would be very useful to include a figure summarising the simulated models.

Author’s Response to Decision Letter for (RSOS-190733.R0)

See Appendix A.

Decision letter (RSOS-190733.R1)

26-Jul-2019

Dear Dr Cox,

I am pleased to inform you that your manuscript entitled "Sex-linked genetic diversity originates from persistent sociocultural processes at microgeographic scales" is now accepted for publication in Royal Society Open Science.

You can expect to receive a proof of your article in the near future. Please contact the editorial office (openscience_proofs@royalsociety.org and openscience@royalsociety.org) to let us know if you are likely to be away from e-mail contact. Due to rapid publication and an extremely tight schedule, if comments are not received, your paper may experience a delay in publication.

Royal Society Open Science operates under a continuous publication model (http://bit.ly/cpFAQ). Your article will be published straight into the next open issue and this will be the final version of the paper. As such, it can be cited immediately by other researchers. As the issue version of your paper will be the only version to be published I would advise you to check your proofs thoroughly as changes cannot be made once the paper is published.
On behalf of the Editors of Royal Society Open Science, we look forward to your continued contributions to the Journal.

Kind regards,

Lianne Parkhouse
Editorial Coordinator
Royal Society Open Science
openscience@royalsociety.org

on behalf of Dr Alecia Carter (Associate Editor) and Steve Brown (Subject Editor)
openscience@royalsociety.org

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Reply to Reviewers

We thank the editor and reviewers for reading our manuscript, and for their careful and thoughtful comments. We have made a number of changes to the manuscript to directly address the points they raise. These focus on two main areas. First, general improvements in readability, emphasizing points specifically noted by the reviewers. And second, clarifying questions about the form of the models. We believe that these changes address the points that the reviewers raised, and we are grateful for their help in making this work stronger.

Reviewer 1

The authors present data of genetic variation which allow to test different models of socio-genetic interactions involving sex-biased migration, lineage-focused founder effects, and heritable social dominance. The subject is interesting and the data sound.

Here are a few minor comments:

a) I always find weird that population geneticists keep using 'heterozygosity' for haploid loci.

*Although commonly used, we agree that ‘heterozygosity’ can be a confusing term in the context of haploid loci, especially for readers outside population genetics. To make the text more accessible, we now use the term ‘haplotype diversity’ in the text and figures instead.*

b) the color coding in fig 2A (ie from 0 to 600 for matrilocal is not a density and the number should be explain in the figure legend, this applies to subsequent figures.

*This is a good point. We now clarify in the figure legends what the contours mean. In short, contour lines are estimated based on $10^4$ data points simulated under the relevant model. The probability value for the contour line at a given location $(x, y)$, after being divided by the simulation size ($10^4$), thus gives the probability of a data point being found within the grid $(x–0.0025, y–0.0025, x+0.0025, y+0.0025)$.*

c) p7 delta should be explained line 48 in addition to table 1. An explanation of the value chosen (0.06) is welcomed, a reference would be even better.

*The meaning of $\delta$ – the fraction of the population that has a selective advantage over the nondominant population – is now given in the text, in addition to Table 1. We also provide a reference explaining the simulated value of 0.06.*

d) First occurrence of PE page 10, it would be nice to define.

*Yes! We thank the reviewer for noting this omission. The variable $P_E$ is now defined at first use in the text.*

e) Fig 6: I would like a discussion about the significance of the difference of 0.3 and 0.32 in the Timor founder model (and 0.51 and 0.53 in Slatkin’s exact test)

*We agree. We now explicitly discuss these differences (0.3 vs 0.32, and 0.51 vs 0.53), and emphasize that they are not significant. Note that this was our original interpretation; we are simply now making this point clearer in the text.*
Reviewer 2

In “Sex-linked genetic diversity originates from persistent sociocultural processes at microgeographic scales” Chung, Jacobs and colleagues analyse mtDNA (540bp) and Y chromosome (12 STRs + haplotype informative SNPs) for ~1,100 individuals from two Indonesian islands characterised by opposite societal systems. In doing so, they observe a marked opposite skewness in the observed heterozygosity (H) in matrilocal and patrilocal populations and used different simulation models to identify the best model explaining the observed heterozygosity. Testing the combination of i) post-marital movements, ii) social dominance and iii) founder-ideology patterns the authors found that a founder model with dominance can approximate the observed H pattern in the patrilocal Sumba, while the same model with No dominance provides a better fit for the matrilocal Timor, although there is a limited power for the latter population.

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Here are more specific comments:

P2. Introduction: The introductory paragraph is too concise, and do not adequately summarise what is the actual state of the art in using genetics to characterise the impact of social strategies. Please consider to expand it.

This is a good point. We have now expanded the Introduction to provide a lengthier summary of how genetics can be used to characterize social strategies. We have also added several new citations, which cover a broader range of publications across this subject area.

P2, L8 : This sentence seems truncated, please consider to rephrase it.

We have rephrased this sentence.

P2, L12-14: The few works mentioned in this sentence should be cited.

We have cited these publications. Note that this sentence differs slightly from the original version as part of the wider changes made to the Introduction as requested above.

P2, L50. The term Heterozygosity usually refers to an individual rather than a population metric. Given that the work is expected to be of interest to the anthropologists’ community, I would consider adding a brief explanation. For the same reason, it would be very useful to include a figure summarising the simulated models.

As noted above, the term ‘heterozygosity’ has been replaced by ‘haplotype diversity’ for improved readability.

We have also included a new figure (Figure 7), which gives a more general graphical overview of the simulated models, particularly for an anthropological audience.