



Peer Community In...

Denis Bourguet

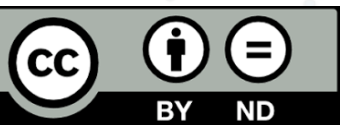
Benoit Facon

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**A free recommendation process of preprints based
on peer reviews**



PCI

The aim of PCI

Communities of researchers handling the **evaluation** of (through peer review) and **recommending preprints** in their scientific field.

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etc ...

PCI Ecology

PCI Evolutionary Biology

PCI Genomics

PCI Microbiology

etc..

PCI

The aim of PCI

- 15 PCI (15 thematic PCIs + PCI RR)
- preprint based
- free, diamond OA, CC-BY, Plan S compatible
- transparent evaluation if accepted
- all PCIs welcome reproductions, preregistrations,
- PCI RR dedicated to registered reports

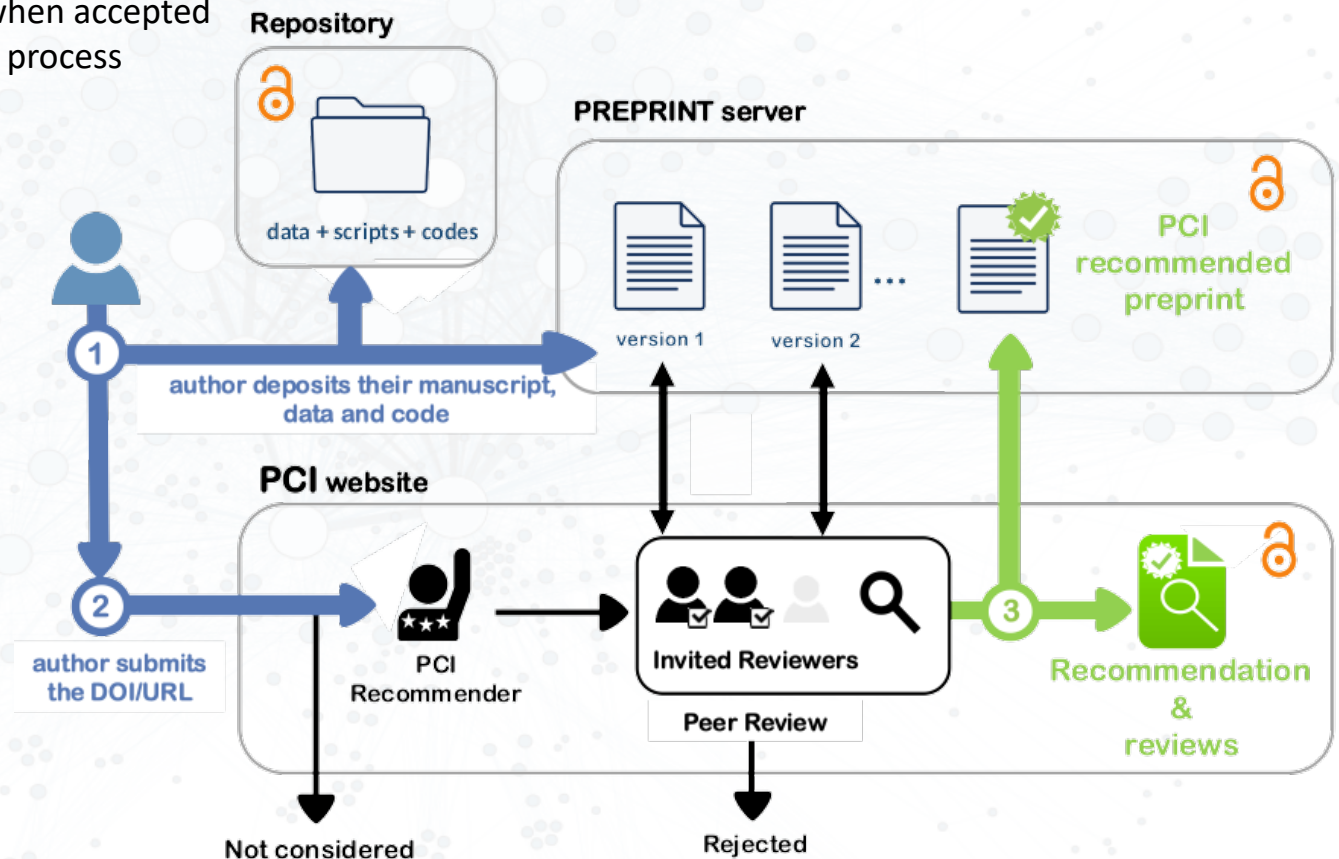
A complex network diagram with numerous nodes of varying sizes (small dots, medium circles, and large white circles) connected by thin, light blue lines. The nodes are distributed across the slide, with a higher density in the center and some clusters on the periphery. The overall effect is a sense of interconnectedness and data flow.

How does it work?

How does it work

in all PCIs: Classic evaluation but

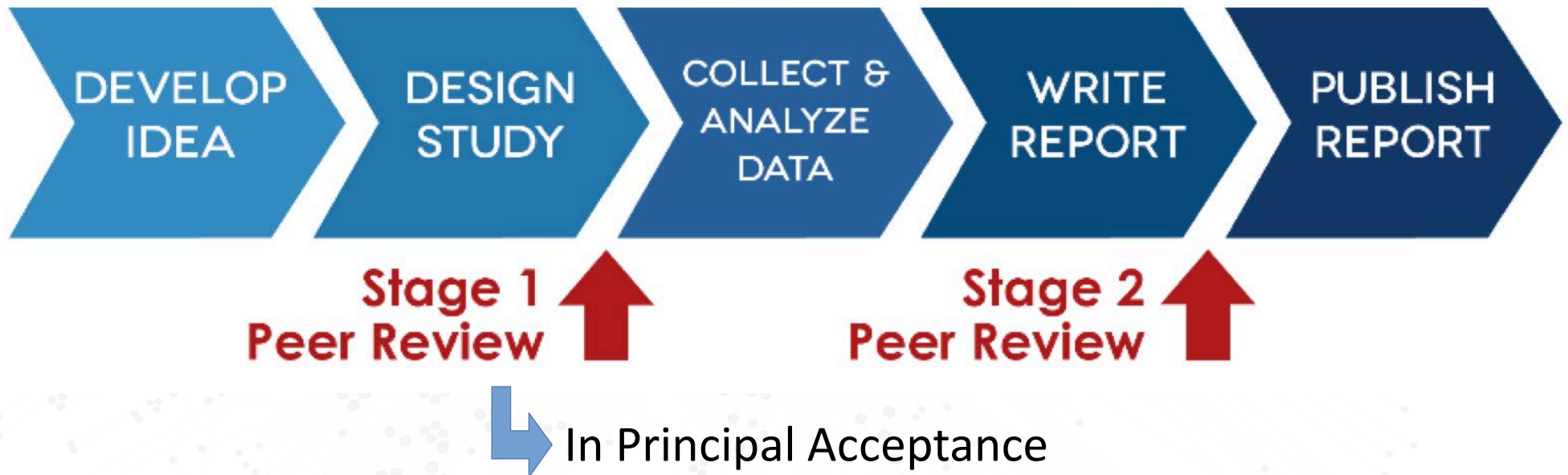
- preprint based
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- publication of recommendation when accepted
- publication of the whole editorial process
- the preprint is not published
- badge of the preprint




How does it work

PCI RR: Not classic! 2 stage peer-reviews





- 1st stage peer review on ideas, hypotheses, methodology, when still possible to change
- In Principal acceptance (IPA)
- 2nd stage PR to check if all went ok



PCI-recommended preprint

 **Peer Community In**
Evolutionary Biology

RESEARCH ARTICLE

 Open Access
 Open Data
 Open Code
 Open Peer-Review

Transposable Elements are an evolutionary force shaping genomic plasticity in the parthenogenetic root-knot nematode *Meloidogyne incognita*

Djampa KL Kozłowski¹, Rahim Hassanaly-Goulamhoussen¹, Martine Da Rocha¹, Georgios D Koutsovoulos¹, Marc Bailly-Bechet^{1*}, Etienne GJ Danchin^{1*}.

¹ Université Côte d'Azur, INRAE, CNRS, ISA – Sophia Antipolis, France
* equal contribution

This article has been peer-reviewed and recommended by
Peer Community in Evolutionary Biology
<https://doi.org/10.24072/pci.evolbiol.100106>


ABSTRACT
Despite reproducing without sexual recombination, the root-knot nematode *Meloidogyne incognita* is adaptive and versatile. Indeed, this species displays a global distribution, is able to parasitize a large range of plants and can overcome plant resistance in a few generations. The mechanisms underlying this adaptability without sex remain poorly known and only low variation at the single nucleotide polymorphism level have been observed so far across different geographical isolates with distinct ranges of compatible hosts. Hence, other mechanisms than the accumulation of point mutations are probably involved in the genomic dynamics and plasticity necessary for adaptability. Transposable elements (TEs), by their repetitive nature and mobility, can passively and actively impact the genome dynamics. This is particularly expected in polyploid hybrid genomes such as the one of *M. incognita*. Here, we have annotated the TE content of *M. incognita*, analyzed the statistical properties of this TE content, and used population genomics approach to estimate the mobility of these TEs across 12 geographical isolates, presenting phenotypic variations. The TE content is more abundant in DNA transposons and the distribution of TE copies identity to their consensus sequence suggests they have been at least recently active. We have identified loci in the genome where the frequencies of presence of a TE showed variations across the different isolates. Compared to the *M. incognita* reference genome, we detected the insertion of some TEs either within genic regions or in the upstream regulatory regions. These predicted TE insertions might thus have a functional impact. We validated by PCR the insertion of some of these TEs, confirming TE movements probably play a role in the genome plasticity with possible functional impacts.



Keywords: transposons, genomic plasticity, evolution, agricultural pest, parthenogenesis, hybridization


Posted: 03 Aug 2020
Recommender: Inés Alvarez
Reviewers: Daniel Vitales and two anonymous reviewers
Correspondence: etienne.danchin@unice.fr, djampa.kozlowski@unice.fr

PEER COMMUNITY IN EVOLUTIONARY BIOLOGY 1

Recommendation text

 **Recommendation**


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Comparative genomics in the chestnut blight fungus *Cryphonectria parasitica* reveals large chromosomal rearrangements and a stable genome organization

Sebastien Duplessis based on reviews by Benjamin Schwessinger and 1 anonymous reviewer


A recommendation of:



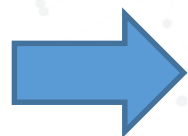
Chromosomal rearrangements with stable repertoires of genes and transposable elements in an invasive forest-pathogenic fungus

Arthur Demene, Benoit Laurent, Sandrine Cros-Arteil, Christophe Boury, Cyril Dutech (2022), *bioRxiv*, 2021.03.09.434572, ver.6 peer-reviewed and recommended by Peer Community in Genomics <https://doi.org/10.1101/2021.03.09.434572>

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Data used for results ✓
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Evolutionary Biology

Relaxation of purifying selection suggests low effective population size in eusocial Hymenoptera and solitary pollinating bees

Weyna, Arthur; Romiguier, Jonathan^{1,2} &

10.24072/pcjournal.3 - Peer Community Journal, Volume 1 (2021), article no. e2.

With one of the highest number of parasite, eusocial and pollinator species among all insect orders, Hymenoptera features a great diversity of specific lifestyles. At the population genetic level, such life-history strategies are expected to decrease effective population size and efficiency of purifying selection. In this study, we tested this hypothesis by estimating the relative rate of non-synonymous substitution in 169 species to investigate the variation in natural selection efficiency throughout the hymenopteran tree of life. We found no effect of parasitism or body size, but show that relaxed selection is associated with eusociality, suggesting that the division of reproductive labour decreases effective population size in ants, bees and wasps. Unexpectedly, the effect of eusociality is marginal compared to a striking and widespread relaxation of selection in both social and non social bees, which indicates that these keystone pollinator species generally features low effective population sizes. This widespread pattern suggests specific constraints in pollinating bees potentially linked to limited resource and high parental investment. The particularly high load of deleterious mutations we report in the genome of these crucial ecosystem engineer species also raises

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Section: Ecology

RESEARCH ARTICLE

Published
2022-01-19

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Youssooupha Niang, Mamoudou

Diallo, Arame Ndiaye, Philippe

Gauthier, Marion Borderon, Laurent

Granjon, Carine Brouat and Karine

Berthier (2022) Interplay between

historical and current features of the

cityscape in shaping the genetic

structure of the house mouse (*Mus*

musculus domesticus) in Dakar

(Senegal, West Africa), Peer

Community Journal, 2: e11.

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Peer-review

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recommended by

PCI Ecology

<https://doi.org/10.24072/pci.ecology.100044>

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Interplay between historical and current features of the cityscape in shaping the genetic structure of the house mouse (*Mus musculus domesticus*) in Dakar (Senegal, West Africa)

Claire Stragier¹, Sylvain Piry², Anne Loiseau², Mamadou Kane¹, Aliou Sow¹, Youssooupha Niang¹, Mamoudou Diallo¹, Arame Ndiaye¹, Philippe Gauthier², Marion Borderon³, Laurent Granjon², Carine Brouat^{4,5,6}, and Karine Berthier^{4,6,7}

Volume 2 (2022), article e11

<https://doi.org/10.24072/pcjournal.85>

Abstract

Population genetic approaches may be used to investigate dispersal patterns of species living in highly urbanized environment in order to improve management strategies for biodiversity conservation or pest control. However, in such environment, population genetic structure may reflect both current features of the cityscape and urbanization history. This can be especially relevant when focusing on exotic commensal rodents that have been introduced in numerous primary colonial European settlements. Accounting for spatial and temporal cityscape heterogeneity to determine how past and recent demographic events may interplay to shape current population genetic structure of synanthropic rodents may provide useful insights to manage their populations. In this study, we addressed these issues by focusing on the house mouse, *Mus musculus domesticus*, in Dakar, Senegal, where the species may have been introduced as soon as Europeans settled in the middle of the nineteenth century. We examined genetic variation at one mitochondrial locus and 15 nuclear microsatellite markers from individuals sampled in 14 sampling sites representing different stages of urbanization history and different socio-economic environments in Dakar. We used various approaches, including model-based genetic clustering and model-free smoothing of pairwise genetic estimates. We further linked observed spatial genetic patterns to historical and current features of Dakar cityscape using random forest and Bayesian conditional autoregressive models. Results are consistent with an introduction of the house mouse at colonial time and the current genetic structure exhibits a gradient-like pattern reflecting the historical process of spatially continuous expansion of the city from the first European settlement. The genetic patterns further suggest that population dynamics of the house mouse is also driven by the spatial heterogeneity of the current cityscape, including socio-economics features, that translate in habitat quality. Our results highlight the potential importance of accounting for past demographic events to understand spatial genetic patterns of non-native invasive commensal rodents in highly urbanized environment.

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PCI in figures



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