# Genomic architecture and evolutionary dynamics of a social niche polymorphism in the California harvester ant, Pogonomyrmex californicus

## What is the Manuscript Microscope Sentence Audit?

The Manuscript Microscope Sentence Audit is a research paper introspection system that parses the text of your manuscript into minimal sentence components for faster, more accurate, enhanced proofreading.

# Why use a Sentence Audit to proofread your manuscript?

- Accelerated Proofreading: Examine long technical texts in a fraction of the usual time.
- Superior Proofreading: Detect subtle errors that are invisible to traditional methods.
- Focused Proofreading: Inspect each individual sentence component in isolation.
- Reliable Proofreading: Ensure every single word of your manuscript is correct.
- Easier Proofreading: Take the hardship out of crafting academic papers.

Bonus 1: Improved Productivity: Rapidly refine rough drafts to polished papers.
Bonus 2: Improved Authorship: Cultivate a clear, concise, consistent, writing style.
Bonus 3: Improved Reputation: Become known for rigorously precise publications.

Manuscript Source: https://www.biorxiv.org/content/10.1101/2021.03.21.436260v1

Manuscript Authors: Mohammed Errbii, Ulrich R. Ernst, Aparna Lajmi, Jürgen Gadau & Lukas

Schrader

Audit Date: 31/03/21 Audit Identifier: J8GCR1H590G0CQO Code Version: 3.6

### **Features of the Sentence Audit:**

The Sentence Audit combines two complementary proofreading approaches:

- 1. Each sentence of your text is parsed and displayed in isolation for focused inspection.
- 2. Each individual sentence is further parsed into Minimal Sentence Components for a deeper review of the clarity, composition and consistency of the language you used.

The Minimal Sentence Components shown are the smallest coherent elements of each sentence of your text as derived from it's conjunctions, prepositions and selected punctuation symbols (i.e. commas, semicolons, round and square brackets).

The combined approaches ensure easier, faster, more effective proofreading.

### **Comments and Caveats:**

- The sentence parsing is achieved using a prototype natural language processing pipeline written in Python and may include occasional errors in sentence segmentation.
- Depending on the source of the input text, the Sentence Audit may contain occasional html artefacts that are parsed as sentences (E.g. "Download figure. Open in new tab").
- Always consult the original research paper as the true reference source for the text.

### **Contact Information:**

To get a Manuscript Microscope Sentence Audit of any other research paper, simply forward any copy of the text to John.James@OxfordResearchServices.com.

All queries, feedback or suggestions are also very welcome.

# **Research Paper Sections:**

The sections of the research paper input text parsed in this audit.

Section No.	Headings	Sentences
Section: 1	Abstract	9
Section: 2	Introduction	18
N/A		0

Genomic architecture and evolutionary dynamics of a social niche polymorphism in the California harvester ant, Pogonomyrmex californicus

# S1 [001] Abstract

**S1 [002]** The societies of social insects are highly variable, including variation in the number of reproductives in a colony.

The societies ...
... of social insects are highly variable, ...
... including variation ...
... in the number ...
... of reproductives ...
... in a colony.

**S1 [003]** In the California harvester ant, Pogonomyrmex californicus (Buckley 1867), colonies are commonly founded by a single queen (haplometrosis, primary monogyny).

In the California harvester ant, ...
... Pogonomyrmex californicus ...
... (Buckley 1867), ...
... colonies are commonly founded ...
... by a single queen ...
... (haplometrosis, ...
... primary monogyny).

**S1 [004]** However, in some populations in California (USA), two or more queens cooperate in colony founding (pleometrosis) and continue to share a nest over several years (primary polygyny).

```
However, ...
... in some populations ...
... in California ...
... (USA), ...
... two ...
... or more queens cooperate ...
... in colony founding ...
... (pleometrosis) ...
... and continue ...
... to share a nest ...
... over several years ...
... (primary polygyny).
```

**S1 [005]** Here, we use population genomics and linkage mapping to study the evolutionary dynamics and genetic architecture of this social niche polymorphism.

```
Here, ...
... we use population genomics ...
... and linkage mapping ...
```

```
... to study the evolutionary dynamics ...... and genetic architecture ...... of this social niche polymorphism.
```

**S1 [006]** Our analyses show that both populations underwent consecutive bottlenecks over the last 100,000 generations, particularly decreasing population size in the P-population and that the two populations diverged until 1,000 generations ago, after which gene flow increased again and we found signs of recent genetic admixture between the two populations.

Our analyses show ...
... that both populations underwent consecutive bottlenecks ...
... over the last 100,000 generations, ...
... particularly decreasing population size ...
... in the P-population ...
... and that the two populations diverged until 1,000 generations ago, ...
... after which gene flow increased again ...
... and we found signs ...
... of recent genetic admixture ...
... between the two populations.

**S1 [007]** We further uncover an 8 Mb non-recombining region segregating with the observed social niche polymorphism, showing characteristics of a supergene comparable to the ones underlying social niche polymorphism in other ant species.

We further uncover an 8 Mb non-recombining region segregating ...
... with the observed social niche polymorphism, ...
... showing characteristics ...
... of a supergene comparable ...
... to the ones underlying social niche polymorphism ...
... in other ant species.

**S1 [008]** In addition, 57 genes in five genomic regions outside the supergene show signatures of a selective sweep in the P-population, some of which are differentially expressed between haplo- and pleometrotic queens during colony founding.

```
In addition, ...
... 57 genes ...
... in five genomic regions outside the supergene show signatures ...
... of a selective sweep ...
... in the P-population, ...
... some of which are differentially expressed ...
... between haplo- ...
... and pleometrotic queens ...
... during colony founding.
```

**S1 [009]** Our findings expose the social niche polymorphism in P. californicus as a polygenic trait involving a supergene.

```
Our findings expose the social niche polymorphism ... ... in P. californicus ... ... as a polygenic trait ... ... involving a supergene.
```

# S2 [010] Introduction

**S2 [011]** An important component of the social organization of eusocial species is the number of reproductive individuals (Wilson 1971; Hölldobler and Wilson 1977; Boomsma et al. 2014).

```
An important component ...
... of the social organization ...
... of eusocial species is the number ...
... of reproductive individuals ...
... (Wilson 1971; ...
... Hölldobler ...
... and Wilson 1977; ...
... Boomsma et al. 2014).
```

**S2** [012] This number is usually described as fixed for a given species with insignificant variations.

```
This number is usually described ...
... as fixed ...
... for a given species ...
... with insignificant variations.
```

S2 [013] However, with the advent of genetic marker systems it became clear that many species show a range of social organization related to queen number both in terms of their species range (e.g. Formica exsecta (Seppä et al. 2004), Solenopsis invicta (Ross et al. 2007), Messor pergandei (Helms et al. 2013), Pogonomyrmex californicus (Overson et al. 2016)) and colony stage (secondary polygyny or monogyny) (Boomsma et al. 2014).

```
However, ...
... with the advent ...
... of genetic marker systems it became clear ...
... that many species show a range ...
... of social organization related ...
... to queen number both ...
... in terms ...
... of their species range ...
... (e.g. Formica exsecta ...
... (Seppä et al. 2004), ...
... Solenopsis invicta ...
... (Ross et al. 2007), ...
... Messor pergandei ...
... (Helms et al. 2013), ...
... Pogonomyrmex californicus ...
... (Overson et al. 2016)) ...
... and colony stage ...
... (secondary polygyny ...
... or monogyny) ...
... (Boomsma et al. 2014).
```

**S2 [014]** This variation can be considered as specializations to different social niches, i.e. "the set of social environments in which the focal individual has non-zero inclusive fitness" (Saltz et al. 2016).

```
This variation can be considered ...
... as specializations ...
... to different social niches, ...
... i.e. "the set ...
... of social environments ...
... in which the focal individual has non-zero inclusive fitness" ...
... (Saltz et al. 2016).
```

**S2 [015]** For example, if queens become tolerant towards co-founding queen(s), a novel social niche can be established (pleometrosis = multiple queens found a colony together) that is distinct from the original niche (haplometrosis = queens found a colony alone), where queens kill potential co-foundresses either immediately or after the first workers emerge (Bernasconi and Strassmann 1999; Overson et al. 2014; Overson et al. 2016).

```
For example, ...
... if queens become tolerant towards co-founding queen(s), ...
... a novel social niche can be established ...
... (pleometrosis = multiple queens found a colony together) ...
... that is distinct ...
... from the original niche ...
... (haplometrosis = queens found a colony alone), ...
... where queens kill potential co-foundresses either immediately ...
... or after the first workers emerge ...
... (Bernasconi ...
... and Strassmann 1999; ...
... Overson et al. 2014; ...
... Overson et al. 2016).
```

**S2 [016]** Species that show intraspecific social niche variation are ideal to study the genetic architecture and evolutionary dynamics underlying such transitions.

```
Species ...
... that show intraspecific social niche variation are ideal ...
... to study the genetic architecture ...
... and evolutionary dynamics underlying ...
... such transitions.
```

**S2 [017]** For example, recent population genomic studies in Solenopsis fire ants (Ross et al. 2007; Yan et al. 2020) and Formica wood ants (Purcell et al. 2014; Brelsford et al. 2020) have provided significant insights into the origin, evolution, and geographic distribution of social niche variation (monogyny vs polygyny) in ants.

```
For example, ...
... recent population genomic studies ...
... in Solenopsis fire ants ...
... (Ross et al. 2007; ...
... Yan et al. 2020) ...
... and Formica wood ants ...
... (Purcell et al. 2014; ...
... Brelsford et al. 2020) ...
```

# **End of Sample Audit**

This is a truncated Manuscript Microscope Sample Audit.

To get the full audit of this text (or any other research paper), forward a copy of the research paper to John James at John.James@OxfordResearchServices.com