Comparative repeat profiling of two closely related conifers (Larix decidua and Larix kaempferi) reveals high genome similarity with only few fast-evolving satellite DNAs

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• 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	12
Section: 2	INTRODUCTION	13
N/A	--- --- --- --- --- --- ---	0
N/A	--- --- --- --- --- --- ---	0
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Title   **Comparative repeat profiling of two closely related conifers (Larix decidua and Larix kaempferi) reveals high genome similarity with only few fast-evolving satellite DNAs**

S1 [001]   ABSTRACT

S1 [002]   In eukaryotic genomes, cycles of repeat expansion and removal lead to large-scale genomic changes and propel organisms forward in evolution.

> In eukaryotic genomes, ...
>
> ... cycles ...
>
> ... of repeat expansion ...
>
> ... and removal lead ...
>
> ... to large-scale genomic changes ...
>
> ... and propel organisms forward ...
>
> ... in evolution.

S1 [003]   However, in conifers, active repeat removal is thought to be limited, leading to expansions of their genomes, mostly exceeding 10 gigabasepairs.

> However, ...
>
> ... in conifers, ...
>
> ... active repeat removal is thought ...
>
> ... to be limited, ...
>
> ... leading ...
>
> ... to expansions ...
>
> ... of their genomes, ...
>
> ... mostly exceeding 10 gigabasepairs.

S1 [004]   As a result, conifer genomes are largely littered with fragmented and decayed repeats.

> As a result, ...
>
> ... conifer genomes are largely littered ...
>
> ... with fragmented ...
>
> ... and decayed repeats.

S1 [005]   Here, we aim to investigate how the repeat landscapes of two related conifers have diverged, given the conifers' accumulative genome evolution mode.

> Here, ...
>
> ... we aim ...
>
> ... to investigate how the repeat landscapes ...
>
> ... of two related conifers have diverged, ...
>
> ... given the conifers' accumulative genome evolution mode.

S1 [006]   For this, we applied low coverage sequencing and read clustering to the genomes of European and Japanese larch, Larix decidua (Lamb.) Carrière and Larix kaempferi (Mill.), that arose from a common ancestor, but are now geographically isolated.

For this, ...

... we applied low coverage sequencing ...

... and read clustering ...

... to the genomes ...

... of European ...

... and Japanese larch, ...

... Larix decidua ...

... (Lamb.) ...

... Carrière ...

... and Larix kaempferi ...

... (Mill.), ...

... that arose ...

... from a common ancestor, ...

... but are now geographically isolated.

S1 [007] We found that both Larix species harbored largely similar repeat landscapes, especially regarding the transposable element content.

We found ...

... that both Larix species harbored largely similar repeat landscapes, ...

... especially regarding the transposable element content.

S1 [008] To pin down possible genomic changes, we focused on the repeat class with the fastest sequence turnover: satellite DNAs (satDNAs).

To pin down possible genomic changes, ...

... we focused ...

... on the repeat class ...

... with the fastest sequence turnover: ...

... satellite DNAs ...

... (satDNAs).

S1 [009] Using comparative bioinformatics, Southern, and fluorescent in situ hybridization, we reveal the satDNAs' organizational patterns, their abundances, and chromosomal locations.

Using comparative bioinformatics, ...

... Southern, ...

... and fluorescent ...

... in situ hybridization, ...

... we reveal the satDNAs' organizational patterns, ...

... their abundances, ...

... and chromosomal locations.

S1 [010] Four out of the five identified satDNAs are widespread in the Larix genus, with two even present in the more distantly related Pseudotsuga and Abies genera.

Four out of the five identified satDNAs are widespread ...

... in the Larix genus, ...

... with two even present ...

... in the more distantly related Pseudotsuga ...

... and Abies genera.

S1 [011] Unexpectedly, the EulaSat3 family was restricted to L. decidua and absent from L. kaempferi, indicating its evolutionarily young age.

> Unexpectedly, ...
>
> ... the EulaSat3 family was restricted ...
>
> ... to L. decidua ...
>
> ... and absent ...
>
> ... from L. kaempferi, ...
>
> ... indicating its evolutionarily young age.

S1 [012] Taken together, our results exemplify how the accumulative genome evolution of conifers may limit the overall divergence of repeats after speciation, producing only few repeat-induced genomic novelties.

> Taken together, ...
>
> ... our results exemplify how the accumulative genome evolution ...
>
> ... of conifers ...
>
> ... may limit the overall divergence ...
>
> ... of repeats ...
>
> ... after speciation, ...
>
> ... producing ...
>
> ... only few repeat-induced genomic novelties.

S2 [013] INTRODUCTION

S2 [014] Ranging in size between 0.002 and nearly 150 Gb, eukaryotic genomes vary by several orders of magnitude (Hidalgo et al., 2017).

> Ranging ...
>
> ... in size ...
>
> ... between 0.002 ...
>
> ... and nearly 150 Gb, ...
>
> ... eukaryotic genomes vary ...
>
> ... by several orders ...
>
> ... of magnitude ...
>
> ... (Hidalgo et al., 2017).

S2 [015] Among those, conifer genomes are especially large with sizes up to 37 Gb (Ahuja and Neale, 2005).

> Among those, ...
>
> ... conifer genomes are especially large ...
>
> ... with sizes up to 37 Gb ...
>
> ... (Ahuja ...
>
> ... and Neale, 2005).

S2 [016] As new reference genome sequences are generated – among them conifers such as spruces, pines, and recently firs and larches – new insights into the composition of conifer genomes are brought forward (Nystedt et al., 2013; Wegrzyn et al., 2014; Stevens et al., 2016; Kuzmin et al., 2019; Mosca et al., 2019).

As new reference genome sequences are generated – ...

... among them conifers ...

... such as spruces, ...

... pines, ...

... and recently firs ...

... and larches – new insights ...

... into the composition ...

... of conifer genomes are brought forward ...

... (Nystedt et al., 2013; ...

... Wegrzyn et al., 2014; ...

... Stevens et al., 2016; ...

... Kuzmin et al., 2019; ...

... Mosca et al., 2019).

S2 [017] One of the main takeaways is that the steady accumulation of repeats is the main driver for conifer genome expansion, presumably due to limited elimination of transposable elements (TEs; Nystedt et al., 2013; Prunier et al., 2016).

One ...

... of the main takeaways is ...

... that the steady accumulation ...

... of repeats is the main driver ...

... for conifer genome expansion, ...

... presumably ...

... due to limited elimination ...

... of transposable elements ...

... (TEs; ...

... Nystedt et al., 2013; ...

... Prunier et al., 2016).

S2 [018] As the large conifer genomes have accumulated repeats over long periods of time with only slow removal and turnover of repetitive sequences, we wondered whether species-specific repeat profiles were able to evolve in closely related conifers.

As the large conifer genomes have accumulated repeats ...

... over long periods ...

... of time ...

... with only slow removal ...

... and turnover ...

... of repetitive sequences, ...

... we wondered ...

... whether species-specific repeat profiles were able ...

... to evolve ...

... in closely related conifers.

S2 [019] Regarding repetitive sequence classes, it is already hypothesized that TE families likely persist in conifers over long evolutionary timeframes (Zuccolo et al., 2015).

Regarding repetitive sequence classes, ...

... it is already hypothesized ...

... that TE families likely persist ...

... in conifers ...

... over long evolutionary timeframes ...

... (Zuccolo et al., 2015).

End of Sample Audit