**Figure A1** Geographic distribution of *Dendroctonus* lineages.

**Table A2** Background regions where pseudo-absences where generated when investigating niche divergence among *Dendroctonus* lineages.

**Figure A3** Principal component analysis of climatic data extracted from occurrences of *Dendroctonus rufipennis*, *D. pseudotsugae* and *D. brevicomis* lineages.

**Figure A4** Niche similarity and equivalency tests based on Schoener’s D index performed with the MaxEnt algorithm.

**Table A5** Boyce Index calculated for each model.

**Figure A6** Maps of climatic suitability predicted by MaxEnt models for *Dendroctonus* lineages.

**Figure A7** Maps of climatic suitability predicted by Boosted Regression Tree models for *Dendroctonus* lineages.

**Figure A8** Geographic representation of mismatches between classical species models and the aggregated predictions that combine the outputs of conspecific lineage models.
Figure A1: Pooled occurrences of *Dendroctonus* conspecific lineages

(a) *Dendroctonus valens*

(b) *Dendroctonus ponderosae*
(c) *Dendroctonus rufipennis*

(d) *Dendroctonus pseudotsugae*
(e) *Dendroctonus brevicomis*
Appendix 2. Background area where pseudo-absences were generated when investigating niche divergence among conspecific lineages.

(a) *Dendroctonus valens*

- Eastern lineage: Eastern America (latitude between 23°N and 72 °N/longitude between 95°W and 50°W)
- Western lineage: Western America (latitude between 30°N and 72 °N/longitude between 150°W and 92°W)
- Southern lineage: Mexico and Central America (latitude between 12°N and 30 °N/longitude between 150°W and 82°W)

(b) *Dendroctonus ponderosae*

Lineage monticola : Western America (latitude between 25°N and 72 °N/longitude between 115°W and 100°W)
lineage ponderosae : Western America (latitude between 30°N and 72 °N/longitude between 150°W and 110°W)

(c) *Dendroctonus rufipennis*

-lineage *P. glauca*: Northern America (latitude between 35°N and 72 °N/longitude between 150°W and 72°W)
-lineage *P. engelmannii*: North-Western America (latitude between 30°N and 55 °N/longitude between 150°W and 100°W)

(d) *Dendroctonus pseudotsugae*

-D. *p. pseudotsugae* : Western America (latitude between 30°N and 72 °N/longitude between 150°W and 92°W)
-D. *p. barragani* : Mexico and Central America (latitude between 17°N and 30 °N/longitude between 150°W and 82°W)

(e) *Dendroctonus brevicomis*

-lineage *P. p. scutulum*: Western America (latitude between 25°N and 72 °N/longitude between 114°W and 100°W)
-lineage *P. p. ponderosae*: Western America (latitude between 30°N and 72 °N/longitude between 150°W and 113°W)
Figure A3: Principal component analysis of climatic data extracted from occurrences of *Dendroctonus rufipennis*, *D. pseudotsugae* and *D. brevicomis* lineages

(a) *Dendroctonus rufipennis*

(b) *Dendroctonus pseudotsugae*
(c) Dendroctonus brevicomis
Figure A4: Niche similarity and equivalency tests based on Schoener’s D index performed with MaxEnt algorithm.

(a) *Dendroctonus valens*: lineage Eastern America vs lineage Western America
(b) *Dendroctonus valens:* lineage Eastern America vs southern lineage

**Equivalency**

- Frequency distribution with a peak around 0.90 to 0.95, with a p-value of 0.0198.

**Similarity 2→1**

- Frequency distribution with a peak around 0.6 to 0.65, with a p-value of 0.0198.

**Similarity 1→2**

- Frequency distribution with a peak around 0.4 to 0.5, with a p-value of 0.0396.
(c) *Dendroctonus valens*: lineage Western America vs southern lineage

<table>
<thead>
<tr>
<th>Similarity</th>
<th>Frequency</th>
<th>p.value</th>
</tr>
</thead>
<tbody>
<tr>
<td>2→1</td>
<td></td>
<td>0.0594</td>
</tr>
<tr>
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</table>

Equivalency

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<tr>
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Similarity 2→1

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Similarity 1→2

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<th>p.value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0.0198</td>
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</tbody>
</table>
(d) *Dendroctonus ponderosae*

**Equivalency**

- Frequency
  - Similarity: 2
    - p.value = 0.0198
  - Similarity: 1
    - p.value = 0.0198

**Similarity 2→1**

- Frequency
  - Similarity: 1
    - p.value = 0.0198

**Similarity 1→2**

- Frequency
  - Similarity: 2
    - p.value = 0.09901
(e) *Dendroctonus rufipennis*

**Equivalency**

- Frequency distribution for *D* values ranging from 0.70 to 0.95, with a p-value of 0.0198.

**Similarity 2→1**

- Frequency distribution for *D* values ranging from 0.0 to 0.8, with a p-value of 0.05941.

**Similarity 1→2**

- Frequency distribution for *D* values ranging from 0.0 to 0.7, with a p-value of 0.0198.
(f) *Dendroctonus pseudotsugae*

**Equivalency**

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<th>Frequency</th>
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<th>0.5</th>
<th>0.6</th>
<th>0.7</th>
<th>0.8</th>
<th>0.9</th>
<th>1.0</th>
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<tbody>
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$$p\text{.value} = 0.0198$$

**Similarity 2→1**

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<th>0.3</th>
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$$p\text{.value} = 0.0396$$

**Similarity 1→2**

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<th>0.2</th>
<th>0.3</th>
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<tbody>
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<td></td>
<td></td>
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</tbody>
</table>

$$p\text{.value} = 0.0396$$
(g) *Dendroctonus brevicomis*

**Equivalency**

- Frequency distribution
- p.value = 0.0198

**Similarity 2→1**

- Frequency distribution
- p.value = 0.05941

**Similarity 1→2**

- Frequency distribution
- p.value = 0.0198
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<th>Taxonomic entity</th>
<th>BRT</th>
<th>MaxEnt</th>
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<td>model2</td>
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<td>D. pseudotsugaes barragani</td>
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<tr>
<td>D. valens all lineages</td>
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<td>---------------------------------</td>
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<td>D. valens southern lineage</td>
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<td>0.623</td>
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</table>
Figure A6: Maps of climatic suitability predicted by MaxEnt lineage-based models for *Dendroctonus* species. Climatic suitability maps display the arithmetic mean of values of 10 replicates. We also represented a map displaying the frequency at which models (out of 10 replicates) predicted a presence when transformed into binary maps with the lowest presence threshold.

(a) *Dendroctonus valens*

**Climatic suitability**
Lowest presence threshold (LPT)
(b) *Dendroctonus ponderosae*

*Climatic suitability*

![Map showing climatic suitability for all lineages, lineage monticola, and lineage ponderosae.](image-url)
Lowest presence threshold (LPT)

- For all lineages:
- For lineage maticola:
- For lineage ponderosae:
(c) *Dendroctonus rufipennis*

Climatic suitability

![Map showing climatic suitability for all lineages, lineage *Picea glauca*, and lineage *Picea engelmannii*.](map-image)
Lowest presence threshold (LPT)

- **All lineages**
- **Lineage Picea glauca**
- **Lineage Picea engelmannii**

Predicted presence frequency scale:
- 1.0
- 0.8
- 0.6
- 0.4
- 0.2
- 0.0
(d) *Dendroctonus pseudotsugae*

*Climatic suitability*
Lowest presence threshold (LPT)

- **all lineages**
- **D. p. pseudotsugae**
- **D. p. barragani**
(e) *Dendroctonus brevicomis*

_Climatic suitability_
Lowest presence threshold (LPT)

[Map showing predicted presence frequency for various lineages of Pinus ponderosa across the world]
Figure A7: Maps of climatic suitability predicted by Boosted regression trees lineage-based models for *Dendroctonus* species (mean of 10 replicates).

(a) *Dendroctonus valens*

Climatic suitability
Lowest presence threshold (LPT)
(b) *Dendroctonus ponderosae*

*Climatic suitability*
Lowest presence threshold (LPT)
(c) *Dendroctonus rufipennis*

*Climatic suitability*
**Lowest presence threshold (LPT)**

- **Lowest presence threshold (LPT)**
- **predicted presence frequency**
  - all lineages
  - lineage *Picea glauca*
  - lineage *Picea engelmannii*
(d) *Dendroctonus pseudotsugae*

*Climatic suitability*
Lowest presence threshold (LPT)

- All lineages
- D. p. pseudotsugae
- D. p. barragani

The maps show the predicted presence frequency across the world, with different colors representing different frequencies.
(e) *Dendroctonus brevicomis*

*Climatic suitability*
Lowest presence threshold (LPT)

- All lineages
- Lineage Pinus ponderosa ponderosa
- Lineage Pinus ponderosa scopulorum
Figure A8: Maps showing the change in worldwide suitable climatic conditions when aggregating binary predictions of lineage-based models. These predictions were compared with the classical species-based models. These projections were obtained by assigning a presence to each pixel that was predicted as climatically suitable for at least one lineage. A pixel was considered as climatically suitable for one lineage if more than 50% of the IS-models (i.e., at least six out 10 models) predicted this pixel as suitable when implementing the lowest presence threshold (Pearson et al., 2007).

(a) *Dendroctonus valens*
(b) *Dendroctonus ponderosae*

MaxEnt

BRT

Legend:
- Green: presence for both projections
- Orange: presence for species-based model only
- Blue: presence when aggregating lineages-based model only
(c) *Dendroctonus pseudotsugae*

MaxEnt

BRT

- **presence for both projections**
- **presence for species-based model only**
- **presence when aggregating lineages-based model only**
(d) *Dendroctonus brevicomis*

MaxEnt

BRT

- presence for both projections
- presence for species-based model only
- presence when aggregating lineages-based model only