



## Correction to: Neighbourhood effects modify deer herbivory on tree seedlings

Jan Holík<sup>1,2</sup> · David Janík<sup>1</sup> · Libor Hort<sup>1</sup> · Dušan Adam<sup>1</sup>

Published online: 9 February 2021

© Springer-Verlag GmbH Germany, part of Springer Nature 2021

**Correction to: European Journal of Forest Research**  
<https://doi.org/10.1007/s10342-020-01339-8>

In the original publication of the article, Fig. 2 was published incorrectly. The correct Fig. 2 is given in this correction.

The original article has been corrected.

**Publisher's Note** Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

---

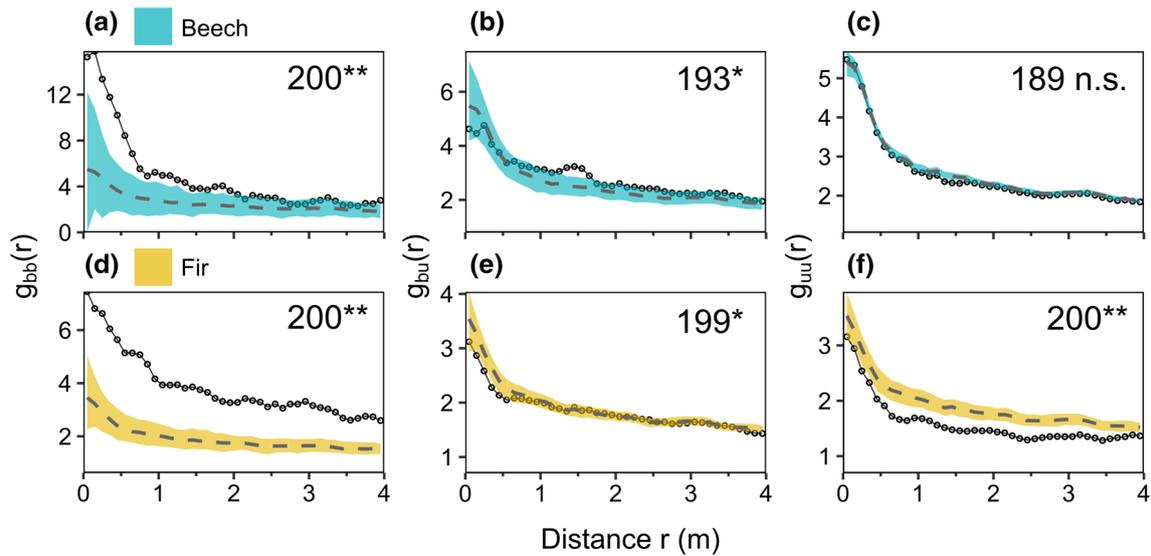
The original article can be found online at <https://doi.org/10.1007/s10342-020-01339-8>.

---

✉ Jan Holík  
xholik4@gmail.com

<sup>1</sup> Department of Forest Ecology, The Silva Tarouca Research, Institute for Landscape and Ornamental Gardening, Brno, Czech Republic

<sup>2</sup> Department of Silviculture, Faculty of Forestry and Wood Technology, Mendel University in Brno, Brno, Czech Republic



**Fig. 2** The results of pair correlation functions to detect potential departures from the random labelling null model in beech (a–c) and fir seedlings (d–f). Summary statistics examine the spatial relationships of browsed seedlings (a, d), browsed and unbrowsed seedlings (b, e) and unbrowsed seedlings (c, f). The values above/below the simulation envelopes indicate the clustering/hyperdispersion of browsed seedlings ( $g_{bb}$ ), clustering/hyperdispersion of unbrowsed seedlings ( $g_{uu}$ ) and aggregation/segregation of browsed

and unbrowsed seedlings ( $g_{bu}$ ). The random labelling null here represents an assumption that deer browsing is a spatially random process unrelated to the distance to seedling neighbours. The 95% simulation envelopes were constructed at a given scale as the fifth largest and fifth smallest value of 199 Monte Carlo simulations. The numbers in each subplot denote the rank of a goodness-of-fit test. Significant departures are indicated by \*\* and \* for  $p$  values < 0.01 and < 0.05, respectively