Functional trait differences between native and alien plant species in local communities of different habitat types

Jan Divíšek[1,2], Milan Chytrý [1], Brian Beckage[3], Nicholas J. Gotelli [4], Zdeňka Lososová [1], Petr Pyšek[5,6], David M. Richardson[7] & Jane Molofsky[3]

[1] Department of Botany and Zoology, Masaryk University, Brno, CZ; [2] Department of Geography, , Masaryk University, Brno, CZ; [3] Department of Plant Biology, University of Vermont, Burlington, USA; [4] Department of Biology, University of Vermont, Burlington, USA; [5] Department of Invasion Ecology, The Czech Academy of Sciences, Průhonice, CZ; [6] Department of Ecology, Charles University, Praha, CZ; [7] Centre for Invasion Biology, Stellenbosch University, Matieland, ZA
e-mail: divisekjan@sci.muni.cz

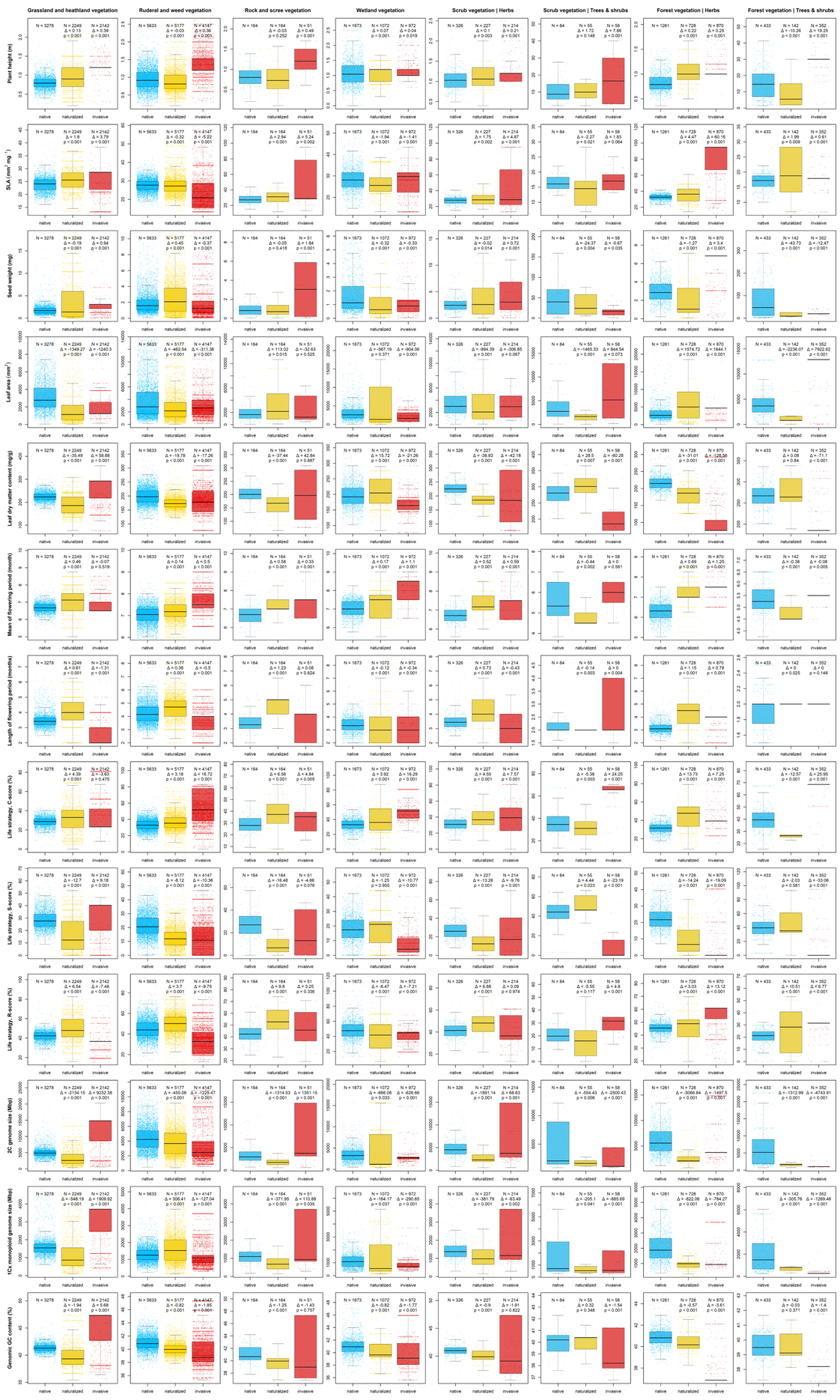
Questions & hypotheses

There is an ongoing debate on how alien plant species become integrated into native communities and what makes them invasive. We hypothesize that alien species integrate themselves into the margin of the trait distribution, i.e. their trait values are considerably different from the mean value for the native community. If so, alien species are probably filling empty niches in the community. An alternative hypothesis would be that alien species integrate themselves near the mean of the trait distribution, i.e. their trait values do not differ considerably from the mean trait value of native species. If so, alien species may be converging on optimal trait values for a habitat, possibly suggesting that resource limitation is not important. In this case, coexistence of native and non-native species may be possible in spite of high niche overlap.

Data

- 24 918 vegetation plot records of six main habitat types of the Czech Republic
- 1398 native species, 309 aliens (259 non-invasive naturalized, 50 invasive species)
- 13 functional traits for each species (missing trait values were imputed based on relationship with other traits and species phylogenetic relatedness)

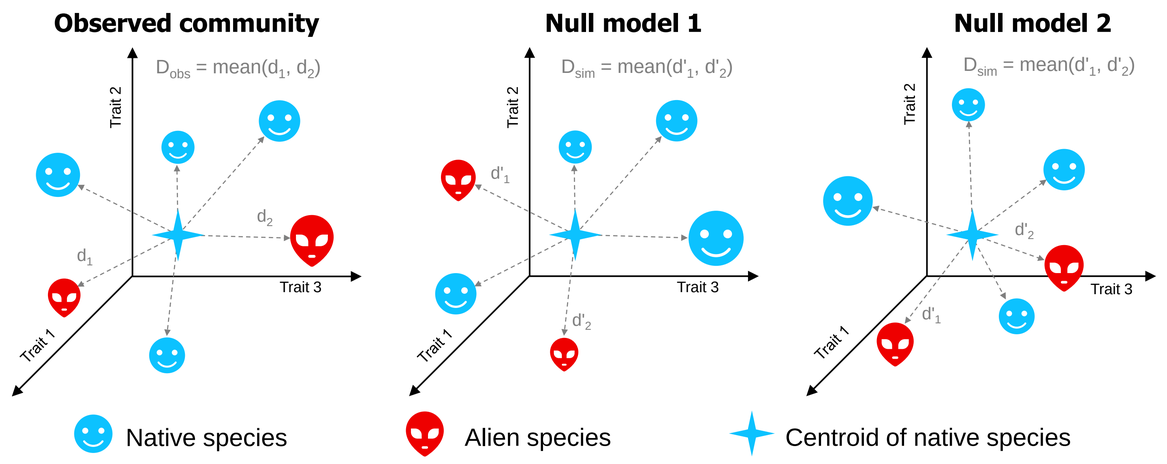
Mean traits of native and alien species in vegetation plots recorded in six habitat types



↑ Fig. 1 Traits of native (blue), non-invasive naturalized (yellow) and invasive species (red) in vegetation plots recorded in six major habitats of the Czech Republic. Jittered points represent mean traits of species recorded in each vegetation plot. N is the number of plots containing i) native and any alien species, ii) native and non-invasive naturalized species, and iii) native and invasive species. Δ is the median of the within-plot differences between the mean traits of alien (either non-invasive naturalized or invasive) and native species. p is the statistical significance of the difference between the mean traits of native and alien species in each plot resulting from paired Wilcoxon test.

Analyses

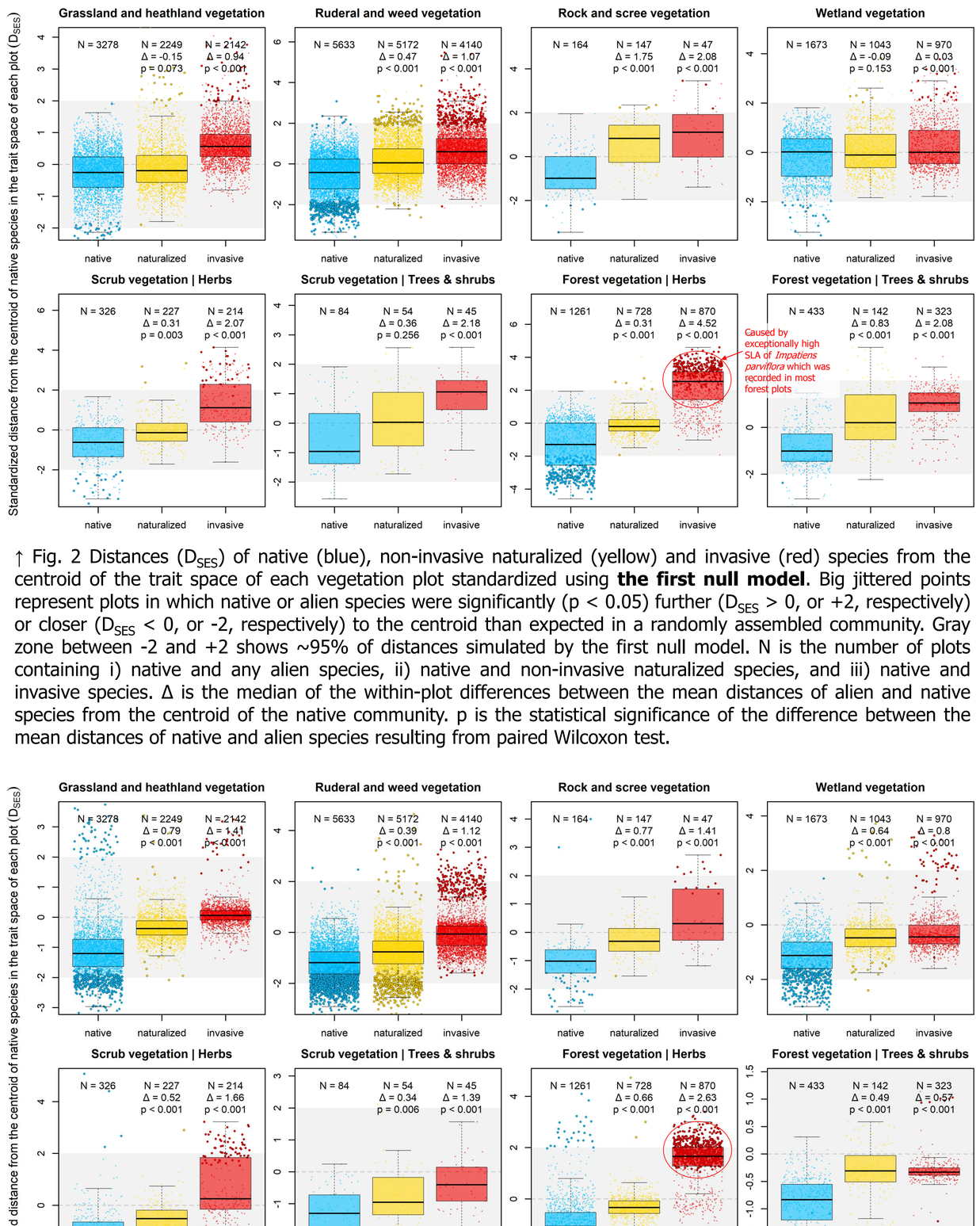
For each vegetation plot, we calculated the mean distance of native and alien (either non-invasive naturalized or invasive) species from the centroid of native species (average native species) in the multivariate trait space (D_{SES}). Each dimension of this trait space was defined by one trait. We standardized observed mean distances using two null models. In the first null model, we simply shuffled (1000×) species-status labels within each vegetation plot, while in the second null model, we randomly sampled (1000×) trait values from the habitat species pool, but only from the corresponding life forms.



$$D_{SES} = \frac{D_{obs} - mean(D_{sim1} \dots D_{sim1000})}{SD(D_{sim1} \dots D_{sim1000})}$$

Results

Standardized distances from the centroid of native species in the trait space of each plot



↑ Fig. 2 Distances (D_{SES}) of native (blue), non-invasive naturalized (yellow) and invasive (red) species from the centroid of the trait space of each vegetation plot standardized using **the first null model**. Big jittered points represent plots in which native or alien species were significantly ($p < 0.05$) further ($D_{SES} > 0$, or +2, respectively) or closer ($D_{SES} < 0$, or -2, respectively) to the centroid than expected in a randomly assembled community. Gray zone between -2 and +2 shows ~95% of distances simulated by the first null model. N is the number of plots containing i) native and any alien species, ii) native and non-invasive naturalized species, and iii) native and invasive species. Δ is the median of the within-plot differences between the mean distances of alien and native species from the centroid of the native community. p is the statistical significance of the difference between the mean distances of native and alien species resulting from paired Wilcoxon test.

↑ Fig. 3 Distances (D_{SES}) of native (blue), non-invasive naturalized (yellow) and invasive (red) species from the centroid of the trait space of each vegetation plot standardized using **the second null model**. For details, see Fig. 2.

Conclusions

In each habitat, alien species are on average further than native species from the center of the trait space of native community in each plot, indicating their functional dissimilarity with average native species. This dissimilarity was more pronounced for invasive than for non-invasive naturalized species. However, in most vegetation plots, alien species do not differ from the native-community average more than would be expected in a randomly assembled community (D_{SES} between -2 and +2). We thus conclude that especially invasive species occupy the edge of the trait space of each vegetation plot.