MORPHOMETRICAL ANALYSIS OF THE BIOLOGICAL INVASION

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INTRODUCTION

Biological invasions along with climate change present a major biodiversity problem worldwide in recent years. During the process of introduction to the new environment, organisms try to settle in by creating several phenotypes. Invasions are often linked with organisms capable of exhibiting a large phenotypic nature plasticity, such as thrips [1]. Many species of thrips pose a real threat to agro-cultural commodities [2]. The invasion process is related to adaptation to new conditions, with the phenotype changes and the phenotypic plasticity itself functions as a certain compensatory mechanism in a changing environment [3]. The model species *Hercinothrips femoralis* (Reuter, 1891) is a species easily distributable by humans [4] and is able to take up rapidly in a new environment, making it a potential threat to greenhouse plants in our conditions. Knowing the invasion process could help in the reconstruction of the timeline of introduction and attachment of a non-native species. Change in the morphology of the species in the process of invasion in the sense the possibility of using this data in a kind of "reverse-reconstruction of the invasion" is therefore one of the basic goals of this work.

MATERIAL AND METHODS

The experimental population was kept under laboratory conditions in boxes on a cucumber according to the method applied in the DeFraaf & Wood research [5]. Two lines (L1, L2) were bred, and within them four generations to simulate 2 types of invasion process. The founding generation of G0 came from stable ecological conditions in both lines. In the first model line, the next generations (G1 - G4) were kept in stable environmental conditions, but the food supply was changed (from honeydew to cucumber). The next three generations within the second line were maintained in unstable conditions (temperature, humidity, change of food). Individuals of all generations of both lines were prepared according to standard methods [6,7] and measured using a LEICA DM1000 microscope. Four morphometric features were measured: wing length, body length, ovipositor length and pronotum width. For each measured character of each bred line (L1, L2) we used the descriptive statistics and statistical tests performed in the R software program (Shapiro-Wilk test, ANOVA, Tuckey post-hoc test, Kruskal-Wallis test, Dunn post-hoc test, and linear regression).

RESULTS

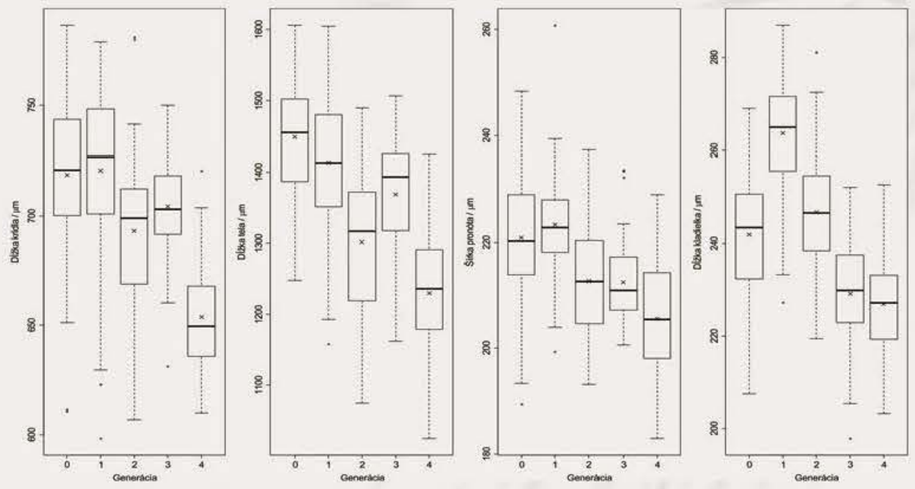

FIG. 1. Sizes of measured characters of individuals from the L1 line. From left G1-G4, wing length, body, pronoum width, ovipositor length.

The effect of food change on the size of measured characteristics proved to be significant in the L1 line (food change) ($p < 0.01$). Characters differed from each other intergenerationally. For each selected trait, we observed a declining trend for all generations (Fig. 1). Thus, a decrease in body characteristics can be observed after changing food source.

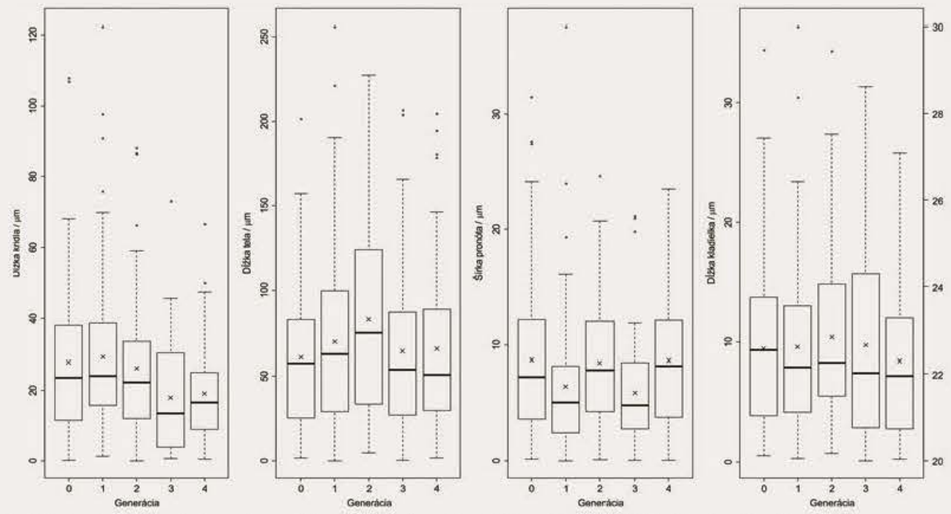

FIG. 2. Sizes of measured characters of individuals from the L2 line. From left G1-G4, wing length, body, pronoum width, ovipositor lenght.

The effect of food change showed no general trend when comparing the mean variance. Body size in generation G2 increased and showed the most visible changes, i.e. the highest variability. Although we can observe an "explosion of the phenotype" in the G2 generation, the differences in the other traits do not change significantly (Fig. 2).

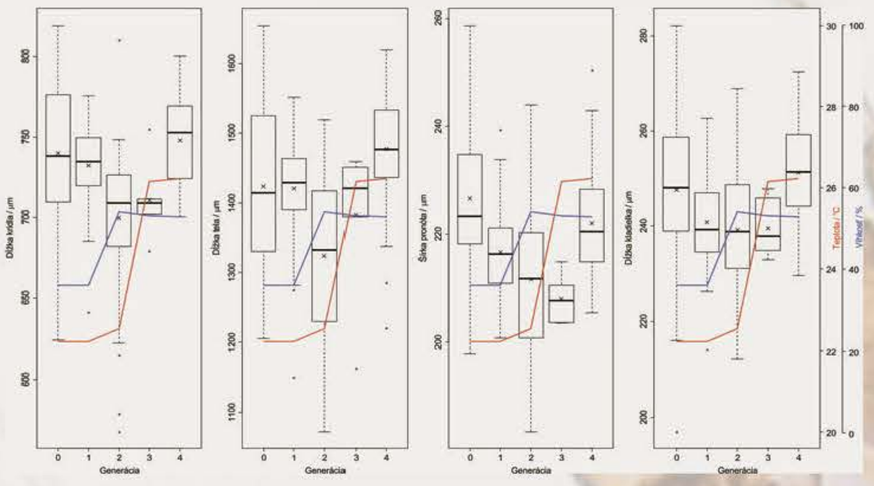

FIG. 3. Sizes of measured characters of individuals from line L2. The red line shows the temperature, the blue line the humidity. From left G1-G4, wing length, body, pronoun width, ovipositor lenght.

The effect of changes in environmental conditions on the size of morphometric measurements proved to be significant between L2 generations ($p < 0.01$). The changing features reflected the change in temperature and the changing humidity (Fig. 3).

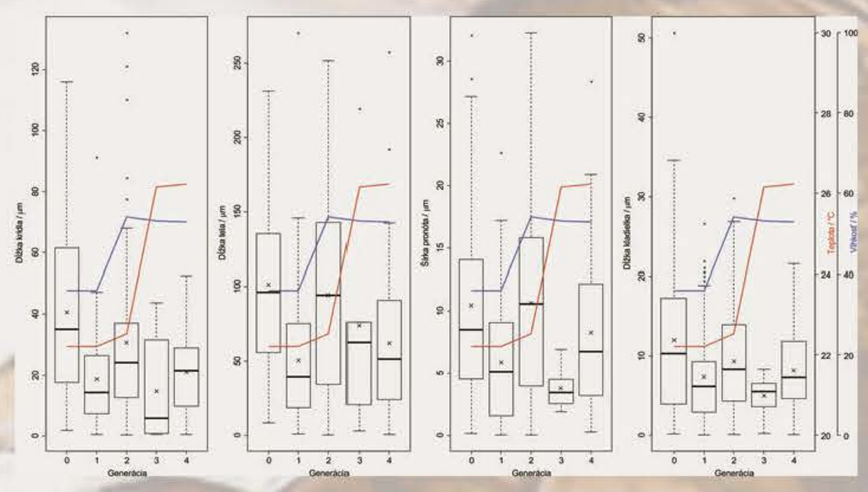

FIG. 4. Sizes of measured characters of individuals from line L2. The red line shows the temperature, the blue line the humidity.

The variations of characteristics in Line 2 do not change significantly due to the change in environmental conditions, no significant trend was shown and the changes are significant in only two characters (wing length and pronation width) ($p < 0.01$). The changes do not reflect the conditions of the laboratory, do not show trendiness (Fig. 4) and may be related to the reduction of air humidity, which is indicated by a blue line in the figure.

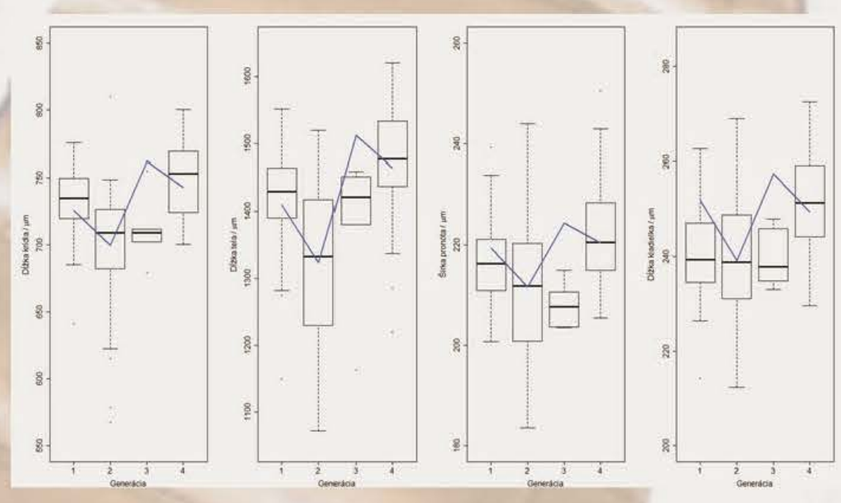

FIG.3. Graphs show a regression model in the form of box plots, with a predicted model (blue line). From left G1-G4, wing length, body, pronotum width, ovipositor length.

Linear regression showed a moderate effect of environmental variables. The regression underlines that although a change in food has a "shrinking" effect on individuals, the effect of temperature is significantly higher. The blue line shows the predicted model, reflecting real morphometric data of generations G1, G2, G4.

CONCLUSION

The results of our research have shown that any change in environmental conditions, such as food source, temperature, humidity or photoperiod affect the phenotype of the model species differently. A clear trend of changes is only shown in size, and the possibility of retrospective reconstruction of the invasion in *H. femoralis* therefore remains the subject of our research. Any change in the environmental factor (temperature, sunlight, food) can therefore affect the growth of the organism, reproduction, and development of the individual or affect the final size of selected measured features [8,9], which was confirmed by our results.

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