

## Abstract

The size of the genome, in other words the content of DNA in the gametic cells of organisms, is expressed using the C-value indicating the number of nuclear base pairs in units of *Mpb* or the mass of DNA in units of *pg*. A simple method used, among other things, to determine the size of the genome is flow cytometry, which in recent years has been very popular, especially among botanists. The study of insects is lagging behind in regard to the number of described species of insect numbering more than one million in comparison to the number of species whose genome size is known (only a few hundred of them). This diploma thesis therefore aims to expand the dataset on the size of the genomes of representatives of the Polyneoptera group, to compare the data found within individual orders and to help understand the links of genome size to the evolution and ecology of insects.

This work provides genome size information for eighty species of insects of the Polyneoptera group. The results showed the largest insect genome measured so far - the locust *Dictyophorus griseus* (149.33 *pg*), whose genome size exceeds the previously published results by several times.

Key words: flow cytometry, genome size, c-value, Polyneoptera