This research project will be focused on detailed characterization and comparison of *Arabidopsis* thaliana *ch1* mutants (chlorophyll *b*-less mutants) with corresponding ecotypes, commonly used in laboratories as background lines, on a chloroplast level.

For years plants have been extensively studied regarding morphological and phenological differences between altitudinal and geographic races or ecotypes. Arabidopsis thaliana plant, a genetic model species, inhabits a wide range of climates across its native Eurasian range. Therefore Arabidopsis ecotypes are known for their remarkable adaptability and a huge diversity of forms. As a genetic model species, Arabidopsis thaliana has become a useful tool in developing genetic resources (e.g. knockout mutants, transgenic overexpression lines) to elucidate the architecture of developmental and physiological pathways underlying ecologically important traits. Still, not enough attention has been paid to the specific adaptation mechanism detectable at chloroplast level that we could observe among Arabidopsis ecotypes. In comparison with corresponding mutants lacking chlorophyll b (chl), we could try to characterize and detect changes that occur in the composition of the photosynthetic apparatus. Therefore we will characterize and compare performance and spectral properties of the photosynthetic apparatus combined with lipid and protein composition and biophysical properties of thylakoid membranes in selected Arabidopsis ch1 mutants and corresponding control plants: Arabidopsis ecotypes. Also, high light (HL) and low light (LL) conditions will be applied as a stress factor. The purpose of this procedure is to "capture" the changes in thylakoid membranes between analyzed plants providing information about their adaptation mechanism.

We hope that the realization of these project will gain attention and broaden the available knowledge in the literature about the reasons for differences occurring between analyzed plants on the chloroplast level, which arise from their possible compensation mechanism.