

Description for the general public

Seeds of legumes, including pea, are among the most important groups of foods consumed by both humans and animals. They constitute an important source of protein and are for meeting the dietary requirements for amino acids. What takes on additional importance are oligosaccharides of the raffinose family present in seeds (in large amounts), recently recognised as prebiotics, which stimulate the development of the health-promoting bacterial microflora in human intestines and in intestines of monogastric animals.

In recent years, intensive research has been conducted on creating the conditions to decrease the importation of protein (coming mainly from soybean seeds), by increasing the biological and utility value of plant protein from domestic raw materials. One of the most important domestic sources of protein are legumes, including peas. Pea seeds (containing from 20% to 22% of protein) constitute 60 % of legume seeds consumed in Poland. A significant problem in the cultivation of pea is the susceptibility of plants to drought stress, resulting in yield reduction. Determining the mechanisms governing the resistance of plants to drought has taken on particular importance in the light of the observed climatic changes – disturbances in precipitation distribution and intensity, in air temperatures, in soil water content and a serious lowering of groundwater levels.

The main objective of the project is to select metabolic markers of the resistance of pea vegetative tissues to drought stress. The research will allow the changes in metabolic profile of pea in response to drought to be determined, and to select the compounds which potentially accumulate in pea tissues during an early response to a decrease in soil moisture. Identification of such metabolites may prove to be a useful tool for the selection of new pea varieties with increased resistance to drought. The metabolomic research planned in the project will be performed using a modern analytical technique – gas chromatography coupled with mass spectrometry. This research will constitute an integral part of the rapidly developing post-genome sciences.