

Legumes belong to the *Leguminosae* family, which consists of approximately 18000 species. They have the ability to symbiotically fix nitrogen from the air. That is why their cultivation is beneficial for soil fertility and allows to reduce need of the mineral nitrogen fertilizers. Legumes provide over one third of the human protein intake worldwide. They are also an important source of animal feed. The pea (*Pisum sativum* L.) is one of the most widely grown legume on the world. In Poland the acreage of pea cultivation is 12 thousand hectares. Pea seeds are rich in protein (23-25%), starch (50%), soluble sugars (5%), fiber, vitamins and minerals.

Despite its advantages, pea is not a popular crop among farmers in Poland. The reason for that is high yielding instability.

Pea is

very susceptible to lodging – phenomenon which occurs when plant stem bends near the ground surface which leads to the collapse of the whole canopy. Because of lodging huge crop areas may lie down on the ground. It makes the harvest more difficult and enhances the microclimate for fungal diseases development. As a result the yield is lower and its quality is worse. Losses caused by lodging may reach even 70%.

Unfortunately there are no totally lodging resistant pea cultivars. Genetic background of this trait is not known. Lodging resistance

is a composed trait. It is controlled by multiple genes and strongly affected by the environmental conditions. Research on pea showed that more resistant to lodging are plants with more stiff stem and higher amount of lignin and cellulose in stem. Research on *Medicago truncatula* - model plant for legumes, allowed to identify genes associated with lignin and cellulose content in the stem. Those genes encodes enzymes which are responsible for lignin and cellulose biosynthesis. It was presented that lower genes expression makes plants more flabby.

The aim of this project is to analyze the expression of chosen genes, associated with cell wall biosynthesis in pea cultivars, which

differ in stem stiffness, lodging resistance and lignin content. A hypothesis was made that expression of the cell wall genes is correlated with the observed phenotypic traits of pea. The proposed project involves some basic research. Identification of orthologs of *Medicago truncatula* genes in pea genome will be necessary. This will allow gene expression analysis in pea stems. Additionally lignin content analysis in pea stems is planned to confirm molecular analysis results.

The proposed research will give us a new insight into genetic background of the observed traits. The confirmation that gene expression level is correlated with lignin content, stem stiffness and lodging will allow further investigations to identify molecular markers for lodging resistance. Molecular markers are a very useful tool for breeders of new, improved cultivars. Marker assisted selection makes breeding process much easier and faster.