Abstract for Docent lecture, Åsa Grimberg 2025-03-11

Plant breeding for future food: Genetic regulation of seed quality

Today we are dependent on a few major crops that form the basis for our food system which makes it vulnerable. Through plant breeding of underutilized crops, new high-yielding varieties with desired quality can be developed to diversify agriculture and increase food system resilience.

Seed development in plants is fundamental in determining seed quality traits in crops. This development is regulated by gene expression ‘programs’ that ensure the accumulation of starch, protein and oil as energy reserves in seed storage tissues. The stored carbon reserves are mobilized during germination, before the growing seedling itself is able to fuel further plant growth through photosynthesis. Different crops, but also different varieties of the same crop, contain varying proportions of these storage compounds in their seeds which determines the crops end-use. One reason for differences in seed nutrient composition between crops is due to different seed physiology, for example if the major storage tissue is made up of endosperm or embryo tissue. However, seed nutrient composition is also regulated by the partitioning of carbon between different storage compounds within the same type of storage tissue.

In this lecture I will talk about transcription factors -proteins that control the expression of genes in a specific tissue in an organism, leading to cells performing specialized functions. These proteins play an important regulatory role for seed development and accumulation of storage compounds, and are therefore of interest as candidate targets in plant breeding. Increased knowledge about the genetic regulation of seed development in crops can contribute to more precise breeding strategies aiming at improved seed quality. I will present results from research on the identification and characterization of genes encoding transcription factors of importance for seed nutrient composition in three diverse underutilized crops; the cereal oat (*Avena sativa*), the pseudocereal quinoa (*Chenopodium quinoa*), and the grain legume faba bean (*Vicia faba*). The results are based on complementary methods including chemical analysis, gene expression analysis, microscopy, X-ray tomography, phenotyping, genotyping, and genome-wide association studies, with plant material from both greenhouse and field experiments. Furthermore, results from studies of the genetic regulation of phenotypic diversity available in faba bean genetic resources will be presented in a wider perspective, covering both agronomic and seed quality traits.

The lecture will have a special focus on faba bean, which is a protein crop with high a potential for increased cultivation in the Nordic region and increased use in plant-based food. Such development can contribute to an increased self-sufficiency of plant proteins and to a more sustainable food system.

(Photos Åsa Grimberg)