Summary

Brassica species are of great importance for human food and animal feed supply. *Brassica napus* occupies the second position among the oilseed crops behind soybean. *Brassica oleracea* includes numerous species of vegetables. Salinity is one of the abiotic stresses that adversely affect the productivity of these crops globally. Salinity tolerance varies along the plant ontogeny, meaning that it is stage-related, species-specific and organ-specific. In comparison to our knowledge about the genetic properties of seed glucosinolates (GSL), our knowledge about the genetic control of leaf GSL is rather limited.

The objectives of this project are: (1) to study the effect of salinity on two stages of plant growth, namely seed germination and the young plant stage, and to map QTL (Quantitative Trait Loci) that control salt tolerance in both growth stages in doubled-haploid (DH) mapping populations of *B. napus* and *B. oleracea*, (2) to examine the variation in leaf GSL content and the impact of salinity on GSL, and to map the QTL that control GSL variation under control and salt stress.

The effect of salinity on seed germination was investigated in three double haploid (DH) populations, two *B. napus* populations and one *B. oleracea* population. The first two were derived from Alesi × H30 and from Mansholts × Samourai, respectively. The *B. oleracea* population was derived by crossing a DH rapid cycling TO1000DH3 (TO) line and a DH broccoli line Early Big (EB). 138 DH lines for each population were tested either for germination experiments or for the greenhouse experiments. The frame work maps that were used for QTL mapping compromised 188, 208 and 128 markers Alesi × H30, Mansholts × Samourai and TO × EB, respectively.

The salt treatments were 200 mM NaCl for the *B. napus* populations and 100 mM NaCl for the *B. oleracea* population. Ten seeds from each DH line were sown in nine cm Petri dishes on filter paper moistened with five ml tap water for control and five ml solution of the corresponding salt concentrations. The Petri dishes were incubated at 20°C in the dark. The number of germinated seeds was counted daily. The results revealed that salt stress significantly reduced seed germination and slowed down the germination rate. Nevertheless, several DH lines showed a better performance than the parent, with a high germination percentage and high germination pace (germination rate) in all populations. Several QTL were mapped for all the studied traits in all populations. A number of these QTL control the variation in these traits under both control and salt stress conditions, while others control the trait variations under either the control or salt stress.

The influence of salinity on plant growth at the young plant stage was evaluated in the *B. napus* DH population Mansholts × Samourai and the *B. oleracea* population TO × EB. The DH lines of each population and their parents were tested in pot experiments in the greenhouse under semi-controlled conditions in two replicates. The salt treatments were 200 mM NaCl for the *B. napus* populations and 100 mM NaCl for the *B. oleracea* population. A number of traits, i.e. fresh weight (FW), dry weight (DW), chlorophyll content (SAPD), relative water content (RWC), sodium content (Na^+ mg/ g DM), potassium content (K^+ mg/ g DM), and sodium potassium ratio (Na^+/ K^+), were scored. The salt stress started on 21 days after sowing (das) for two weeks, the experiments were terminated on 35 das.

A significant variation was observed in all traits in both populations. In both populations salinity reduced plant growth, where a reduction in FW and DW was very large, while RWC showed a weak reduction. In both populations, the remaining parameters exhibited an increase under salt stress; the exception was K^+ in the *B. oleracea* population. SPAD values showed an increase. Similarly, Na^+ mg/ g DM and Na^+/ K^+ exhibited a very large increase. Unexpectedly, K^+ increased in the *B. napus* DH population. Oppositely, the K^+ content decreased in *B. oleracea* population. Maintenance of high K^+ concentration under salt stress is one of the salt tolerance characteristics. These findings supporting the preceding results that revealed *B. napus* was more salt tolerant than *B. oleracea*.

In both populations, several QTL were mapped under control and salt stress. In the *B. napus* DH population, a number of QTL hotspots were mapped on different linkage groups (LGs). The largest hotspot was localized on LG C3. Likewise, in the *B. oleracea* population, QTL hotspots were detected on LG C3, where many traits cluster together. In other words, one genomic region harbors gene(s), which regulate(s) the variation of more than one trait under both control and salt stress conditions. The variation in these traits might be controlled by the pleiotropic effect of one gene or by different genes controlling their variation independently. The genomic regions, where QTL for more than one trait were mapped, are of great importance because more than one trait can be improved jointly.

Leaf GSL variation was investigated under the same growth conditions in both *B. napus* and *B. oleracea* DH populations. In both populations, the parental lines varied largely in their GSL profiles and contents. In the *B. napus* population, Mansholts exhibited high GSL content under control and salt stress conditions compared with Samourai. The two parents performed differently under salt stress, Mansholts revealed an increase, while Samourai exhibited a reduction in the total GSL content. In the *B. oleracea* population, the parental line TO showed higher GSL content than the parent EB. In both DH populations, all components revealed a decline under salt stress, except RAA and GBC in the *B. napus* population and GBC in the *B. oleracea* population. Because of their antioxidant properties, the increase in RAA and GBC might serve to detoxify the effects of ROS, which are produced as a consequence of salt stress. Several QTL were mapped under control and salt stress. Noteworthy, in the *B. napus* mapping population, QTL hotspots were mapped where QTL had been mapped earlier for seed GSL. This was clear, especially on LG A9 and LG C2. In the *B. oleracea* mapping population, QTL hotspots were localized on LG C9 and LG C7. The clustering of these QTL in both populations was logical because occasionally they were QTL for GSL components of the same class.

No consistency was found between the QTL controlling seed germination under salt stress and the QTL that control the trait variations at the young plant stage. These results suggest that different mechanisms control salt tolerance throughout the plant life cycle. By combining QTL for salt tolerance of different developmental stages a good adaptation to salt stress can be achieved