JANSSEN, GEERT[1]*, ROY MARTENS[2], REBECCA LARSON[2], MARIA NIHLGARD[1] and THOMAS KRAFT[1], [1]Syngenta Seeds, P.O. Box 302, 261 23 Landskrona, Sweden and [2]Syngenta Seeds, Inc., 1020 Sugarmill Road, Longmont, CO 80501. **Acceleration of *Rhizoctonia* resistance breeding.**

Rhizoctonia solani Kühn is one of the major sugar beet diseases and can cause severe yield losses due to root rot. Partial genetic resistance (tolerance) has been identified and is available in commercial varieties for effective control of the disease. Syngenta Seeds has developed several different molecular mapping populations to study the genetic inheritance of the disease resistance through a combination of phenotypic characterization and detailed genetic analysis. Phenotyping of relative resistance was performed using field observations performed in Longmont, Colorado, using artificial inoculation of the disease to obtain a severe and homogeneous infection level. Genetic analysis has revealed the presence of various quantitative trait loci (QTL's) spread over different linkage groups. QTL's were only partially overlapping between populations and years, indicating the complexity of the inheritance as well as confounding influence based on environmental variation. Molecular markers have been identified and implemented into the *Rhizoctonia* resistance programs within Syngenta Seeds to accelerate the breeding efforts towards higher yielding varieties maintaining the highest resistance levels possible.