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A novel system for controlled phenotyping of drought stress tolerance in oilseed rape

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Introduction

Current expansion of oilseed rape production into Eastern European regions with low rainfall, coupled with the increasing occurrence of extreme climatic events – including drought – due to global climate change, confront breeders with the emerging problem of selecting for adaptation to water stressor drought conditions. In the past conventional pot trials were often used to compare plant performance under water-stress and non-stress conditions, however results of such trials could rarely be correlated to the performance of plants under natural field conditions. One logical explanation for this is the strong restriction of root growth, a key factor in water stress tolerance, in pot trials. On the other hand, trials in rainout shelters are more similar to field conditions, however it can be very difficult to accurately control the exact quantity of water available to the plant roots.

Methods and Materials

In an effort to obtain detailed data about water stress tolerance under controlled conditions that nevertheless as closely as possible resemble a field situation, we are testing a large-scale container system in which plants are grown in a rain-out shelter in 120 litre, 90 cm deep containers (Figure 1). The containers are filled with 50 cm of sandy subsoil and 40 cm of sandy topsoil from a water stress-prone field location. Five plants from each genotype are sown per container at field-sowing densities with three repetitions for each genotype and treatment. By weighing the containers regularly with a hydraulic measuring system (Figure 2) it is possible to exactly control the water capacity (WC) of the soil. Data will be collected on chlorophyll content, leaf water content, relative plant height, pod and seed production, seed quality and straw dry biomass under water stress compared to non-stress treatments More detailed data will be collected from the middle plants in each container with regard to exact yield components (e.g. seeds and pods per main raceme and side-branches, seeds per pod, whole-plant yield), oil content and seed composition.

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Figure 1. Container system for detailed phenotyping of drought stress reactions in oilseed rape shortly before flowering (above) and at the beginning of flowering (below). Five plants per container are sown at field-sowing density in 90cm deep natural soil profiles.

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In a preliminary study, 20 diverse winter oilseed varieties that show strong differences in their reactions to drought stress in the field are being phenotyped in the containers under two different water regimes (60% WC control, 30% WC stress variant, stress applied at beginning of flowering). The same genotypes are being simultaneously grown in field trials at seven different drought-stress locations, including 5 sites with the possibility to run repetitions with varying degrees of irrigation.

Figure 2. Hydraulic lifting and weighing system with inbuilt scales for exact control of water capacity in the 90cm deep containers. At 80% WC each container weighs around 180kg, while the 30% WC treatment containers weigh around 15 kg less. A foot pump is used to lift the containers off the ground and simultaneously weight them without moving them form their position in the trial.



On the one hand the data collected will be used to select extreme genotypes for comprehensive analysis of root physiology and its association to drought tolerance in oilseed rape. On the other hand, through detailed phenotyping of morphological and physiological traits in the container trial, we hope to identify simple indicator traits correlated to field performance that can be used to select for improved water stress tolerance in winter oilseed rape.

Outlook

Indicator traits for drought stress reactions will be used for detailed phenotyping within a large *B. napus* diversity set under irrigated and non-irrigated conditions. Using genome-wide SNP data gathered with a new Illumina Brassica SNP array, we will perform genome-wide association studies to identify markers and potential candidate genes associated with improved drought stress tolerance. After validation these can then be implemented into breeding programs to improve oilseed rape yields under drought conditions. The contained system we developed in this work will be an important tool for exact phenotyping of drought stress reactions in roots, leaves, seeds and oil content.

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