

ANALYSIS OF SEMINAL ROOT ARCHITECTURE IN DURUM WHEAT- *THINOPYRUM PONTICUM* RECOMBINANT LINES

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To meet the numerous challenges that wheat breeding is facing today, such as climate changes and rise in global food demand, a promising approach consists of widening the crop genetic basis by resorting to alien genes from wild wheat relatives. In fact, recent progress in chromosome engineering, through which alien chromosome segments can be transferred to wheat chromosomes, enables targeting of even complex traits, such as those underlying root system architecture, that are of great importance for yield performance of crop species. Previous studies on three durum wheat-*Thinopyrum ponticum* near-isogenic recombinant lines (NIRLs), containing 23, 28 and 40% of their distal 7AL arm replaced by corresponding (homoeologous) portions of the alien 7AgL arm, had indicated the presence of yield-contributing QTL for grain and above-ground biomass in defined 7AgL segments introgressed into the NIRLs. In the present study, root architecture and root and shoot biomass of the same NIRLs were evaluated. The study was conducted under controlled conditions by using two different micro-methods, i.e. paper no-roll (PNR) and rhizotrons (RHZ). In both experiments, seminal root and shoot traits were investigated, including spread of root angle, root diameter, as well as root and shoot length and biomass. In replicated experiments, 60 and 30 seedlings for each NIRL (homozygous 7AgL carriers and non-carriers, respectively) were analysed with the paper no-roll method, and 16 and 8 seedlings/NIRL with rhizotrons, respectively.

The results obtained from both methods showed that presence of 7AgL portions significantly enhanced several root traits involved in yield performance, abiotic stress resistance and nutrient uptake in the three NIRLs compared to their controls lacking any 7AgL segment. In particular, presence of the 5% 7AgL segment differentiating the NIRL with 28% 7AgL from that with 23% 7AgL, determined a significant increase in most of the analysed traits, such as spread of root angle (+17% and +37% with PNR and RHZ, respectively), average root diameter (+14% and +30%), root biomass (+31% and +38%) and average root length (+16%, both PNR and RHZ). The same analyses showed the 23%-long most distal 7AgL segment to be associated with a significant increase of root to shoot dry weight ratio (+18%). Thus, the results obtained allow to functionally dissect the 40% 7AgL spanning the alien content of the three NIRLs, and hence to associate the genetic control of several root traits to defined 7AgL portions.

Overall, it seems plausible to hypothesize that the observed increase in grain yield and above-ground biomass can be at least partly related to the positive characteristics of root architecture and biomass conferred by the presence of 7AgL genes/QTL.