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Temporal genetic patterns of root growth in Brassica napus L

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The root system is a vital plant component for nutrient and water acquisition and is targeted to enhance plant productivity. Genetic dissection of the root system generally focuses on a single stage, but roots grow continuously during plant development. To reveal the temporal genetic patterns of root development, we measured nine root-related traits in a rapeseed recombinant inbred line population at six continuous stages during vegetative growth using a modified hydroponic system with low-cost and high-efficiency features that could synchronize plant growth under controlled conditions. Phenotypic correlation and growth dynamic analysis suggested the existence of two types of genetic factors ("persistent" and "stage-specific") that control root development. Dynamic (unconditional and conditional) quantitative trait loci (QTL) mapping detected 28 stage-specific and 23 persistent QTLs related to root growth. Among them, 13 early stage-specific, 19 persistent and 8 later stage-specific QTLs were detected at 7 DAS (days after sowing), 16 DAS and 5 EL (expanding leaf stage), respectively, providing efficient and adaptable stages for QTL identification. The effective prediction of biomass accumulation using root morphological traits (up to 96.6% or 92.64% at a specific stage or the final stage, respectively) verified that root growth allocation with maximum root uptake area facilitated biomass accumulation. Furthermore, marker-assistant selection, which combined the "persistent" and "stage-specific" QTLs, proved their effectiveness for root improvement with an excellent uptake area. Our results highlight the potential of high-throughput and precise phenotyping to assess the dynamic genetics of root growth and provide new insights into ideotype root system-based biomass breeding.