



Project title: Combining root architecture, root function and soil management to improve production efficiency and quality of apples

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Location of project: NIAB EMR

Industry Representative: NA

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The results and conclusions in this report are based on an investigation conducted over a one-year period. The conditions under which the experiments were carried out and the results have been reported in detail and with accuracy. However, because of the biological nature of the work it must be borne in mind that different circumstances and conditions could produce different results. Therefore, care must be taken with interpretation of the results, especially if they are used as the basis for commercial product recommendations.

AUTHENTICATION

We declare that this work was done under our supervision according to the procedures described herein and that the report represents a true and accurate record of the results obtained.

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GROWER SUMMARY

Headline

A total of 142 recombinant genotypes were identified across seven rootstock populations which segregate for vigour. These recombinant individuals will be fundamental for narrowing down the genomic regions responsible for dwarfing.

Background

Most of the temperate tree fruit crops grown in commercial production are grafted onto rootstocks selected for specific traits such as growth control, early fruit production, precocity, pest and disease resistance, soil anchorage and cold hardiness. Rootstocks are an essential component of successful tree fruit production, conferring productivity through altering the floral and vegetative balance. Growth-controlling rootstocks produce compact trees and have facilitated the transition of low-yielding traditional orchards to high-density modern orchards. However, breeding dwarfing rootstocks is difficult since the dwarfing effect is usually lost over generations, therefore new molecular markers strongly linked to rootstock-induced dwarfing are essential to hasten rootstock breeding.

Root bark is described as all tissues outside the cambium layer and a high proportion of root bark in the root of an apple rootstock has been associated with rootstock-induced dwarfing. A Quantitative Trait Loci (QTL) map for root bark ratio identified three regions in the genome controlling the root bark. Two of these regions colocalise with areas previously linked with dwarfing although the genes controlling this complex mechanism have not yet been discovered.

Recent studies at NIAB EMR have identified different types of root system architecture (RSA) associated with commercial rootstocks utilised in apple orchards, indicating a relationship between dwarfing and RSA. However, RSA is poorly understood, despite the importance of RSA for optimising both productivity and resilience, as global challenges drive the need for more efficient and resilient crop production.

The overall aim of this project is to assess the effect of dwarfing on RSA and ultimately to assess the impact of dwarfing-associated roots on nitrogen uptake efficiency.

This work will generate molecular markers for dwarfing and root traits which will assist the rootstock breeding programmes. Furthermore, understanding the movement of nitrogen in apple rootstock will allow us to advise growers on sensible fertilization protocols. Additionally, this research could have a significant impact for other high value perennial crops including pear, cherry and apricot.

Summary

In the second year of this project, molecular markers spanning the root bark QTL regions, a proxy for dwarfing, have been identified. These markers have been screened in 871 individuals from seven rootstock populations which segregate for vigour. Fifty-five recombinants in the region on chromosome 5 and eighty-seven recombinants in the region on chromosome 11 have been identified. These recombinants will be essential to narrow down the genetic regions and identify potential genes controlling this complex mechanism. The root bark measurements to complete the fine mapping of these regions will be taken in December 2019.

In addition, a root structure analysis is being carried out to understand the root bark development in commercial rootstocks with different levels of dwarfing and also to further understand the link between root bark percentage and dwarfing.

A rootstock population from a Golden Delicious x M9 cross has been established in the field and trees have been prepared as stoolbeds for propagation. A linkage map using nearly 9000 markers has also been generated for this population. The stoolbeds will help us to propagate interesting genotypes and together with the linkage map will allow us to study the effect of dwarfing in root system architecture. This experiment will take place during 2020.

Financial Benefits

The financial benefits cannot be quantified at present since this report summarises the work carried out in the first two years of a four-years project. However, this work will provide fundamental insights into the genetic basis of root system architecture in apple rootstocks, generating molecular marker for dwarfing and root traits. These markers can then be deployed into breeding programmes to aid the generation of new and improved rootstocks to benefit the industry.

Action Points

There are no grower action points at this early stage of the project