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Project title:	Combining root architecture, root function and soil management to improve production efficiency and quality of apples
Project number:	CTP_FCR_2017_4
Project leader:	Richard J. Harrison, NIAB. Felicidad Fernández Fernández, NIAB EMR. Amanda Rasmussen, University of Nottingham. Nicola Harrison, AHDB.
Report:	Third year annual report, November 2020.
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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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CONTENTS

GROWER SUMMARY

Headline

The next step in identifying the genes for rootstock dwarfing has been achieved. The chromosomal regions containing the dwarfing genes have been narrowed down from 4.4Mb to 2.1Mb in chromosome 5 and from 5.8Mb to 1.8Mb in chromosome 11.

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 third year of this project, root bark development data revealed that all the rootstocks have a high root bark percentage at an early stage of development and this is decreasing as they develop. At the end of the first growing season, differences in root bark percentage between dwarfing and vigorous rootstocks start to appear but these differences are not fully expressed. All this information suggests that during the first growing season there are fundamental differentiation processes occurring which will lead to differences in root bark proportion. Therefore, more studies should be focused on this time frame to better understand these mechanisms.

The dwarfing markers previously developed were screened on rootstocks available in the breeding trials at NIAB EMR. New recombinants were detected and root segments were collected from all the trees at the end of the trials. Recombinants identified from these breeding trials allowed us to narrow down the genetic regions containing the dwarfing genes. The region located in chromosome 5 was narrowed down from 4.4Mb to 2.1Mb and the region located in chromosome 11 from 5.8Mb to 1.8Mb. Consequently, the number of genes contained in the dwarfing regions has dramatically decreased and this will facilitate the identification of potential genes controlling dwarfing. Currently, the rootstock breeding programme at NIAB EMR is using the markers developed in this project to help them with the rootstocks breeding selections. In addition, this dataset showed that the scion also has an impact on root bark percentage. Further investigations will be conducted to understand this intriguing interaction.

An experiment to assess the impact of dwarfing on root system architecture has been performed during 2020 using a mapping population from a cross of Golden Delicious and M9, which segregates for vigour. This will allow us to map important root traits such as rooting ability, root thickness and total root area and markers for these traits could be created.

Financial Benefits

The financial benefits cannot be quantified at present. However, this work will provide fundamental insights into the genetic basis of root system architecture in apple rootstocks, generating molecular markers 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.