Regulation of xylem formation in lateral roots

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Transport of water and nutrients is critical for complex higher organisms. Like human beings have blood vessels, higher plant has a vascular system to transport these vital molecules. Xylem, which is an essential part of plant vasculature, is responsible for water conduction. There are two types of xylems in plants, protoxylem and metaxylem. To ensure water and nutrient transport, the two types of xylem in root are arranged intricately. In primary roots of model plant *Arabidopsis thaliana*, xylem pattern is governed by a group of genes named "*HD-ZIP III*". High *HD-ZIP III* level promotes metaxylem formation, whereas low *HD-ZIP III* level helps protoxylem formation.

In primary root of Arabidopsis, *HD-ZIP III* level can be controlled by microRNA165/166 (miR165/166). These microRNAs bind to HD-ZIP III messenger RNAs and helps to degrade mRNA, thus repressing *HD-ZIP III* function. So far, impacts of miR165/166 and HD-ZIP III on xylem patterning were mostly studied in primary root; and the roles of these important factors in lateral root are poorly known. Notably, the primary root meristem, which is responsible for primary root growth, is part of the embryo and did not differentiate before; whereas lateral root meristem are derived from mature tissues that have undergone differentiation. Given that the initiation of lateral root is different from that of primary root, miR165/166 and *HD-ZIP III* might have some unexpected functions in lateral roots.

To determine their effects in lateral root, we checked their expression using green fluorescence protein as a reporter. miR165/166 was expressed both in primary root and lateral root. Then, if miR165/166 functions in lateral root, alteration of its activity would lead to changes in xylem patterns. Here, we showed that elevated miR165/166 level promoted protoxylem formation in primary root and lateral root. *HD-ZIP III* expression that was not controlled by miR165/166, in other words, loss of apparent miR165/166 activity caused promoted metaxylem formation throughout the root. In addition, protein that represses miR165/166 functions was also likely to play a role. To sum up, miR165/166 could influence xylem patterning not only in primary root, but also in lateral root; and it is likely that it functions by regulating *HD-ZIP III* activity.

Despite the similarities mentioned above, xylem changes in primary root and lateral root also exhibited differences. Hence, there might be some unshared regulation mechanisms between primary and lateral roots. This project demonstrated that miR165/166 and *HD-ZIP III* are important for xylem development in lateral root. To show the overall picture of this regulation pathway, further analysis of miR165/166 and *HD-ZIP III* activity in lateral root is required.

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