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Wheat (*Triticum aestivum*) L. is one of the world's most important crops. The introduction of dwarfing genes has resulted in high yielding modern varieties. Microbes are known to be highly important for plant growth and health, and offer potential to aid in the sustainable intensification of agriculture, yet little is known about how plant breeding has affected the plant root microbiome structure and function. The main goal of this work was to study rhizosphere bacterial communities from thirty hexaploid wheat varieties grown under field conditions ranging in chronology from Chidham White Chaff, a long straw variety from 1790, to Crusoe, a short straw variety from 2012. Plants were sampled, rhizosphere soil DNA extracted and a fragment of the 16S rRNA gene subjected to Illumina amplicon sequencing. Plant growth parameters were measured from wheat grown in pots under glasshouse conditions and root exudate profiles were obtained for two contrasting varieties using HPLC. Principal coordinates analysis (PCoA) showed that the tall and short cultivars generally separate and analysis of root exudation profiles revealed differences between the varieties, concerning phenolic compounds. Taken together, these preliminary results suggest that the dwarfing of wheat varieties has resulted in changes to root architecture, composition of root exudates and has also influenced the plant root microbiome structure, the significance of this is as yet unknown.

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