

Abstract

Agriculture has tended towards genetic monocultures over the past 100 years, despite benefits that have been noted for planting different species or different genotypes of the same species together. Along with this change has been the increasing reliance on chemical fertilizers. However, pollution from use of these fertilizers is a major environmental problem. Roots are the plant organ responsible for uptake of nutrients, and it has been noted their spatial configuration can have major impacts on a crops' abilities to acquire water and nutrients. Optimizing root system architecture through careful evaluation of different architectures and their effects on yield or other agronomic indexes is one method to increase yield while reducing nitrogen pollution caused by leaching pass the rooting zone of a crop stand. In conjunction, genetic mixtures of the same species composed of cultivars with contrasting root architectures is a promising method to increase overall stand efficiency. However, when sampling roots in these mixtures is is not possible to visually tell the roots apart. It is desirable to use a molecular method to quantify contributions of roots from each genotype to these samples.