Polymorphic responses of Medicago truncatula accessions to potassium deprivation

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Potassium (K⁺) supply for crops is becoming an emerging issue in agriculture due to the constant increase of K⁺-deprived soils.¹ Because this cation is involved in many growth and developmental processes,²,³ plants evolved various strategies to cope with K⁺ deprivation, including developmental adjustments, the expression of high-affinity transporters, and associations with beneficial microbes.⁴,⁶ Exploring natural variation of low K⁺ responses will help to understand, manage and possibly optimize these strategies for sustainable agricultural practices.⁶ Legumes are important crops for food and feed due to their high protein content, but also due to their ability to enrich soils with nitrogen. Studies investigating the adaptation of legumes to K⁺ deficient conditions are still limited. Also, although well characterized in Arabidopsis, the developmental adaptations to K⁺ deprivation and the genotypic variations of these responses are still unknown in legumes.⁵,⁷,¹⁰ In a recent study, we started filling this gap by describing for the first time the physiological and transcriptional adaptations of the model legume  Medicago truncatula  Jemalong A17 to long-term K⁺ deprivation, and by evaluating how the arbuscular mycorrhizal symbiosis modulates these responses.¹¹

In this report, we describe the shoot and root development of two genetically different accessions of  M. truncatula and quantified the production of reactive oxygen species (ROS) by their roots in response to short-term K⁺ deprivation. Jemalong A17 and Tunisian Tn11.1 accessions were acid-scarified, surface sterilized and grown on K⁺-sufficient (3.75 mM) or K⁺-free (0.00 mM) solid Long Ashton medium for 2 weeks. Shoot and root fresh weights, and the number of lateral roots were determined for each accession (Fig. 1). Both accessions displayed a significant reduction of shoot fresh weight under K⁺-free condition (Fig. 1A). However, only Tn11.1 displayed a root phenotype to short-term K⁺ deprivation: a reduced root fresh weight (Fig. 1B), and a higher number of lateral roots per plant were observed at low K⁺ (Fig. 1C). ROS production was also examined in roots using carboxy-H₂DFFDA as described in García et al.¹¹ Both accessions produced significantly more ROS when K⁺ was removed from the medium (Fig. 2).

These data revealed that A17 and Tn11.1 did not respond similarly to K⁺ deprivation. Indeed, Tn11.1 plants were able to modify their root architecture much more rapidly than A17 to cope efficiently with K⁺ deprivation, particularly by increasing the number of lateral roots. Interestingly, Tn11.1 belongs to a Tunisian population of  M. truncatula well adapted to saline soils.¹² This trait could explain why Tn11.1 adapted faster to K⁺ stress in our experiment. Indeed, because K⁺ and sodium (Na⁺) ions are physicochemically very similar, low K⁺ availability often enhances the uptake of Na⁺ by roots.¹³ Although Na⁺ can be moderately taken up by plants, it rapidly reaches toxic levels and inhibits enzymatic reactions that normally require K⁺, resulting in deleterious and irreversible effects.¹⁴ As a consequence, it is likely that the better tolerance of Tn11.1 to elevated Na⁺ conditions might offer a more efficient and rapid adaptation to K⁺ deprivation than with A17. It is also worth mentioning that the weight of A17 roots did not change during this short period of complete K⁺ removal, whereas we observed a reduction of root biomass when plants were grown for 6-weeks under the low K⁺ regime.¹¹ Although it is very hard to compare both experiments due to important technical differences, the developmental effect of K⁺ deprivation on A17 roots might be detectable only after a more prolonged stress period.

SHORT COMMUNICATION

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suggesting a slower adaptive behavior of this accession than Tn11.1 to K⁺ deprivation again.

Describing these polymorphic responses to K⁺ deprivation between two genetically distinct *Medicago truncatula* accessions paves the way for developing genome-wide association studies involving larger populations. Linking these phenotypical traits to genetic variations will help to decipher the molecular responses of *M. truncatula* to low K⁺ condition, and optimize the varietal selection of legumes to face with nutrient limitations.

Moreover, investigating the impact of arbuscular mycorrhizal symbiosis on physiological and transcriptional responses to K⁺ deprivation in various *M. truncatula* accessions will allow understanding how the genetic background of the host affects the mycorrhiza-dependent K⁺ acquisition. These studies might also be accompanied by computational cell biology simulations of the arbuscular mycorrhizal system to pinpoint the contributions of the different entities.

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No potential conflicts of interest were disclosed.

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