

## Investigation of root exudation and phytotoxic potential of diverse *Sorghum* spp. through regulation of sorgoleone

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**Summary** Sorgoleones are a group of long chain benzoquinones specifically exuded in large quantities by the root hairs of *Sorghum* spp. Sorgoleones inhibit electron transport of higher plants and can completely inhibit both photosynthesis and respiration in sensitive seedlings. However, research on sorgoleone has focused solely on African *Sorghum* spp., including *S. bicolor* and *S. halepense*. Australia, by contrast, has 17 native *Sorghum* species which have not yet been examined with respect to their photosynthetic system, root architecture or metabolism. Eighteen *Sorghum* species were assembled and evaluated for sorgoleone biosynthesis, with an emphasis on pathway flux and gene regulation. This collection represents the majority of species in the genus, including 1, 4 and 13 species that are native to Asia, Africa and Australia, respectively. On average, *Sorghum* species of African, Asian or Australian origin produced approximately

1.79%, 0.68% and 1.66% root exudate of the fresh weight of living roots, respectively. Metabolic profiling of extracts enriched in exuded sorgoleones was performed using methanol root dips of 10-day-old seedling roots using UPLC coupled to time of flight mass spectrometry (UPLC/MS ESI QToF). Sorgoleones were positively identified by comparison to known standards. Exudates differed qualitatively with Asian and African *Sorghum* species yielding over 50-fold greater abundance of sorgoleone compared to Australian *Sorghum*. At this time, flux analysis of the biosynthetic pathways present in African, Asian and Australian genotypes is underway with specific focus on genes regulating biosynthesis and root architecture. Such studies will contribute to crop improvement and potentially weed suppression.

**Keywords** Australian native *Sorghum*, sorgoleone, allelopathy.