## Metabolic profiling for benzoxazinoids in weed-suppressive and early vigour wheat genotypes

James Mwendwa<sup>\*1</sup>, Paul Weston<sup>2</sup>, Inge Fomsgaard<sup>3</sup>, Bente Laursen<sup>3</sup>, William Brown<sup>2</sup>, Hanwen Wu<sup>4</sup>, Jane Quinn<sup>2</sup>, Razia Shaik<sup>2</sup>, Jeffrey Weidenhamer<sup>5</sup>, and Leslie Weston<sup>2</sup>

<sup>1</sup>Graham Centre for Agricultural Innovation – Charles Sturt University, Wagga Wagga, New South Wales 2678, Australia, Australia

<sup>2</sup>Graham Centre for Agricultural Innovation – Charles Sturt University, Wagga Wagga, New South Wales 2678, Australia

<sup>3</sup>Department of Agroecology – Aarhus University, Forsøgsvej 1, DK-4200 Slagelse, Denmark

<sup>4</sup>Department of Primary Industries, Plant Biosecurity – Wagga Wagga, New South Wales 2650, Australia

<sup>5</sup>Department of Chemistry, Geology and Physics – Ashland University, Ashland, Ohio 44805, United States

## Abstract

Replicated and randomised wheat (Triticum aestivum L.) cultivar trials were conducted in moderate to low rainfall zones at Wagga Wagga and Condobolin NSW, respectively in 2014 to 2016. At each experimental site, crop and/or weed growth were monitored at selected growth stages including tillering, vegetative, grain filling, harvest and after crop harvest. In addition, shoots, roots, rhizoplane and bulk rhizosphere soil samples were collected. All shoot and root samples were extracted in methanol using Buchi automated high pressure extractor, while soil samples were extracted using a rotary shaker. Extracts were profiled for unique secondary plant products acting as allelochemicals for weed suppression, specifically benzoxazinoids (BXs), using liquid chromatograph coupled to a triple quadrupole mass spectrometer (UPLC-MS QQQ). In addition, non-targeted metabolomics analysis was performed to evaluate relative abundance of diverse metabolites using a quadrupole time-of-flight mass spectrometry (UPLC-MS QToF) platform. Metabolic profiling of wheat shoots, roots, and soils resulted in detection of up to 14 BXs including BX glycosides and other metabolites of interest. Both qualitative and quantitative differences in BXs were observed and were cultivar-, growth stage- and location-dependent. Plant part and rhizosphere location (distance from root) also impacted BX concentration. The distribution of the secondary metabolites in wheat cultivar tissues suggest differential production of some key bioactive metabolites. Further metabolic profiling provided crucial information regarding crop metabolism, as well as the biosynthesis and release of metabolites associated with weed suppression in currently available commercial wheat cultivars, in contrast to weed suppressive rye (Secale cereale L.) and heritage wheat cultivars such as Federation, known for their potent ability to suppress weeds. This presentation will focus on the results of three years of field experimentation at two locations and predict which cultivars are best-suited for weed suppressive properties due to canopy architecture and allelopathic traits while maintaining high yield potential.

<sup>\*</sup>Speaker

 ${\bf Keywords:} \ {\bf Weed \ suppression, \ metabolomics, \ residue, \ competition, \ resource \ allocation.}$