THE EFFECT OF INSECT-VIRUS INTERACTIONS ON THE WHEAT METABOLOME UNDER INCREASING ATMOSPHERIC CARBON DIOXIDE.

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Rising CO\textsubscript{2} associated with climate change may affect the interactions between plants, pathogens and their vectors. Although plant response to elevated CO\textsubscript{2} (eCO\textsubscript{2}) has been well studied, little is understood about the interactions between plants, insects and pathogens under simulated future climates. Subsequently, there is a lack of knowledge on how the plant metabolome will respond to future atmospheric changes.

The effect of eCO\textsubscript{2} on wheat production in Australia is being investigated at the Australian Grains Free-Air CO\textsubscript{2} Enrichment (AG FACE) research facility in Horsham, Victoria. Additionally, controlled environment growth chambers are being used to study the effect of eCO\textsubscript{2} on the feeding behaviour of the aphid Rhopalosiphum padi and its ability to acquire and transmit Barley yellow dwarf virus (BYDV). A significant decrease in the fecundity of \textit{R. padi} as well as changes to its feeding patterns have been observed when the aphids are reared on wheat grown under eCO\textsubscript{2}, potentially indicating changes in the nutritional quality of the wheat or the production of molecules that are inhibitory to aphid reproduction.

Understanding the link between wheat chemistry and aphid infestation under future climate scenarios will ensure better preparedness for pest and diseases occurrences. Further to this, chemical changes identified to have a negative association with the insect's fecundity and development may be exploited in future breeding lines. An initial metabolomics study has investigated the effect of virus infection on the wheat plant metabolome under both eCO\textsubscript{2} (550ppm) and ambient atmospheric levels 385ppm). LCMS profiling will be detailed as will statistical analysis highlighting metabolites changing to infected and uninfected wheat, under elevated and ambient CO\textsubscript{2}.

THE BIOLOGICAL INTERPRETATION OF METABOLOMIC DATA CAN BE MISLED BY THE EXTRACTION METHOD USED

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The field of metabolomics is getting more and more popular and a wide range of different sample preparation procedures are in use by different laboratories. Chemical extraction methods using one or more organic solvents as the extraction agent are the most commonly used approach to extract intracellular metabolites and generate metabolite profiles. Metabolite profiles are the scaffold supporting the biological interpretation in metabolomics. Therefore, we aimed to address the following fundamental question: can we obtain similar metabolomic results and, consequently, reach the same biological interpretation by using different protocols for extraction of intracellular metabolites? We have used four different methods for extraction of intracellular metabolites using four different microbial cell types (Gram negative bacterium, Gram positive bacterium, yeast, and a filamentous fungus). All the samples were identical. After extraction and GC-MS analysis of metabolites, we did not only detect different numbers of compounds depending on the extraction method used and regardless of the cell type tested, but we also obtained distinct metabolite levels for the compounds commonly detected by all methods (p-value < 0.001). These differences between methods resulted in contradictory biological interpretation regarding the activity of different metabolic pathways. Therefore, our results show that different solvent-based extraction methods can yield significantly different metabolite profiles, which impact substantially in the biological interpretation of metabolomics data. Thus, development of alternative extraction protocols and, most importantly, standardization of sample preparation methods for metabolomics should be seriously pursued by the scientific community.