

glucose, along with rate of digestion using alpha-amylase as a digestive enzyme. It was found that the simple sugars rise linearly with the ripening stage due to degradation of starch and cell wall materials. Starch in raw banana is less rapidly hydrolysed compared to starch in partially ripened banana suggesting structural changes in starch during ripening. To add value to visually blemished or other waste from banana cultivation, pasta was made from the raw banana flour and investigated for its nutritional and structural aspects. It was found that the banana flour pasta was less susceptible to alpha-amylase digestion compared to the control, a conventional wheat (durum) flour pasta, suggesting the potential of the banana flour pasta as a gluten free and less glycemic alternative to conventional pasta. The structure of green banana pasta, inner and outer surfaces were observed under confocal laser scanning microscopy and the viscosity of flour mixtures was measured by rapid viscoanalysis. The digestibility of pasta was found to be related to not only the properties of the starch granules but also the protein network as the matrix. The effects of gums and proteins on pasta formation and digestibility are further discussed.

[P138] Mango Genomics

Theme: 4. Science Driven Solutions

Natalie Dillon^{1*}, David Kuhn², David Innes¹, Ian Bally¹, Rajeev Varshney³

1 Department of Agriculture and Fisheries, Queensland, Australia

2 USDA-ARS, Subtropical Horticultural Research Station, Florida, USA

3 ICRISAT, Hyderabad, India

Mango (*Mangifera indica*) is regarded among the five most important fruit commodities traded worldwide, along with bananas, apples, grapes and oranges, with over 40M tonnes produced annually worldwide. The genus *Mangifera* is believed to contain up to 70 species, with origins in the North-Eastern Indian subcontinent and South East Asia. Despite this, there is a relatively poor understanding of the pedigree, genetic relatedness and the history of domestication of many *M. indica* cultivars and related species worldwide. The development of molecular tools for mango is extremely limited, thus its genes, genetics and genomics remain largely unidentified. Whole genome sequencing and the development of genetic maps of these species are important components in marker assisted breeding and genetic improvement. An international genomics program is being undertaken to build these genetic resources including the development of large numbers of single nucleotide polymorphism (SNP) molecular genetic markers, the development of a genetic map for mango, association of phenotypic traits to the genetic map to identify useful individual markers for breeding, assessment of the genetic diversity in mango germplasm collections, and sequencing, assembly and annotation of the mango genome. These genetic resources will facilitate identification of genetic components with useful agronomic traits for breeding material. The goal of whole genome sequencing of mango is accelerated progress in the breeding of mango cultivars with improved agronomic traits (eg reduced vigour, disease resistance, fruit colour) that could not be accomplished by traditional methods.

[P139] Estimating phosphorus intake from faeces in cattle grazing tropical pastures

Theme: 4. Science Driven Solutions

Rob Dixon^{1*}, David Reid², David Coates³