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## Abstract Booklet

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## Poster Session 1

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#7: Thi Thanh Mai Nguyen

### Correlation between key transcription factors controlling lignin biosynthesis and the lignification pattern within an elongating stem internode of *Setaria*.

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Lignocellulosic biomass from C<sub>4</sub> bioenergy crops, predominantly grasses, has emerged as a potential source of renewable energy. Foxtail millet (*Setaria italica*) and its wild ancestor, green foxtail (*Setaria viridis*), have been proposed as novel model species for undertaking functional genomics of C<sub>4</sub> grasses. Lignin, a principal component of plant biomass, poses a significant challenge to enzymatic digestibility during the process of biofuel production. The RNA-Seq investigation of the fifth elongating stem internode of *S. viridis* has revealed a cohort of regulatory genes likely to be involved in controlling lignin biosynthesis, with the most highly upregulated transcription factors (TFs) belonging to the MYB and NAC domain gene families. In particular, *MYB42*, *MYB59-like*, *NAC73* and *NAC63* were expressed most highly in the transitional (TZ) and maturation zones (MZ) of the elongating internode where lignin deposition occurs. Confirmation of the expression profile of the candidate TFs was sought in *S. italica*, with five accessions exhibiting a similar phenotype but predicted to possess differences in cell wall (CW) lignin content, selected for histological examination of stem anatomy and lignin content analysis. The correlation between TF expression profile measured by quantitative RT-PCR, lignification pattern within the stem CW and total lignin content will be reported.