***Multi-omic correlations for the elongating rice internode suggests multiple regulatory mechanisms for cell wall synthesis.***

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The developmental gradient of the elongating internode of grass stems offers an elegant system for studying cell wall synthesis and regulation. We present multi-omics data for eight asymmetric segments (S1-S8) of the developing rice internode-II to reveal potential regulatory mechanisms for rice cell wall biosynthesis. Lignin and hydroxycinnamic acids vary from the internode base (S1) to the upper internode segments (S8). Principal component analysis confirms the unique gene and protein expression profiles of the segments in which cell division (S1) and elongation (S2) cluster, followed by a gradual transition to maturation (S3-S8). DNA methylation results highlight glycosyl hydrolases, involved in cell wall remodeling as being positively regulated by methylation, contrary to expectations. Protein-to-transcript abundance correlations show good agreement (Pearson Correlation Coefficient, median = 0.6), with notable cell wall-related exceptions. Further, phosphoproteome analysis reveals novel phosphorylation of lignin biosynthesis enzymes and BAHD acyl-CoA acyltransferases that add phenylpropanoid pathway-derived hydroxycinnamic acids to lignin and xylan. Network analysis identifies kinases that potentially phosphorylate cell wall-related enzymes. The transcript data also reveal a set of LncRNAs belonging to the natural antisense transcript (NATs) category. Functional enrichment of the rice locus IDs putatively targeted by these NATs reveals a cluster of serine-threonine protein kinases, including many wall-associated kinases potentially regulated by LncRNAs. This study will lead to greater control over grass cell wall development, improving grass agronomic and biorefining properties.