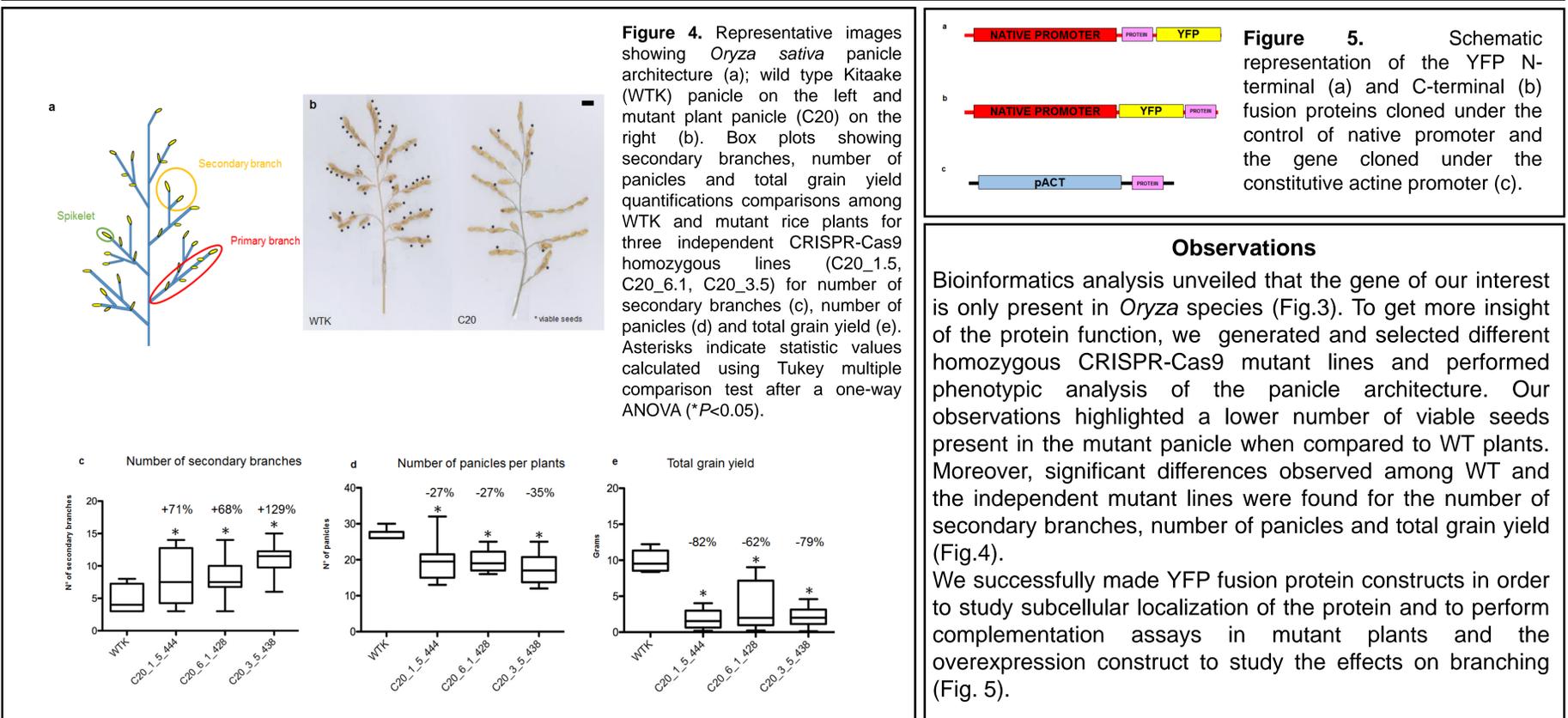
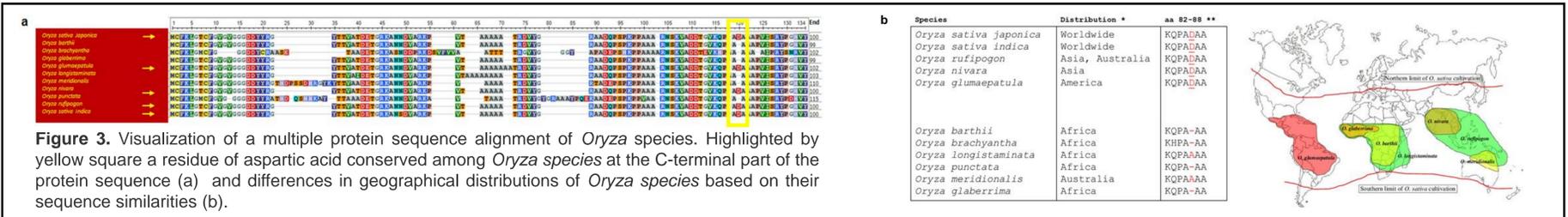
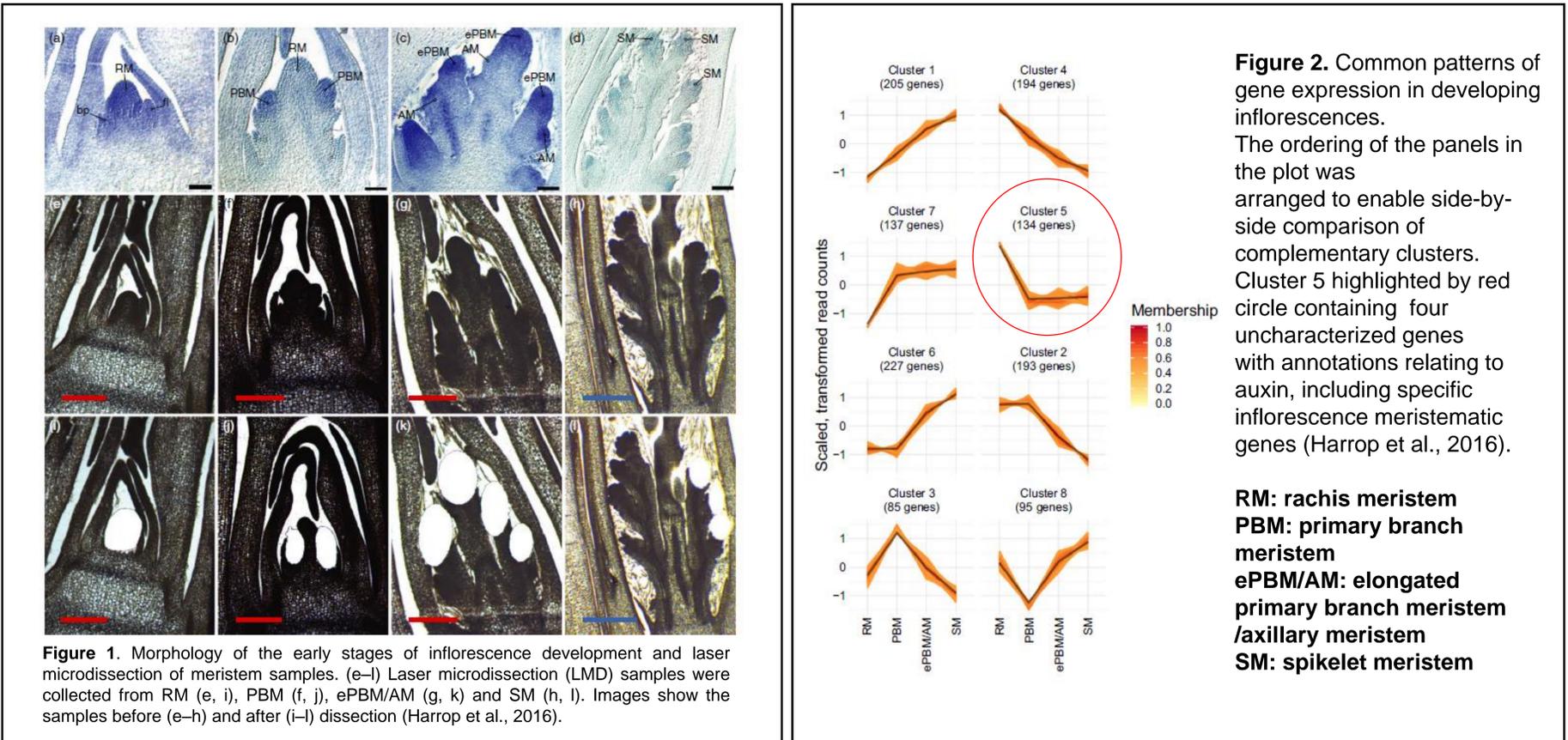


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In rice, panicle size and architecture are considered critical key targets for the breeding programs to improve grain yield potential of the plant. The inflorescence architecture depends on the activity of many genes acting in different reproductive meristem types. Especially primary and secondary branch meristem activities directly affect the complexity of branching, and therefore the number of seeds that will develop on the panicle (Ikeda et al., 2004; 2013). Here, we report an initial study of an uncharacterized gene previously identified by a rice reproductive meristems specific transcriptome analysis using laser microdissection microscopy (Harrop et al., 2016). Interestingly, our initial studies reveal that this gene is present only in *Oryza* species and encoding a protein of just 100 amino acids. To address the biological role of this protein, we successfully generated homozygous CRISPR-Cas9 mutant plants and performed preliminary phenotypic analysis on the panicle structure. Our findings show that loss of function of the gene affects panicle architecture suggesting that this *Oryza* specific gene may have evolved to determine rice specific panicle characteristics.



## CONCLUSIONS AND FUTURE PERSPECTIVES

Our preliminary results suggest the hypothetical function of the protein as positive regulator of panicle architecture, potentially contributing to grain yield of the rice plant. Concomitantly, subcellular localization will be crucial step for protein detection in its native form and to further understand its various roles inside the cell. Future experimental plan will involve the identification of putative interactors of the protein to better characterize the genetic pathways and its involvement in rice panicle architecture determination.