



PROJECT TITLE: Delineating the complex omics network associated with adaptive response of rice (*Oryza sativa*) to fluoride toxicity

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PROJECT SUMMARY:

Rice is one of the commonly consumed cereals for more than half of the world's population. However, recent reports have shown that fluoride content is gradually increasing in many rice varieties owing to excessive usage of ground water and phosphate fertilizers. Excessive bioaccumulation of F inhibits plant growth by reducing hormone signalling, preventing polyamine biosynthesis and affecting photosynthesis. Therefore, it is essential to develop fluoride tolerance rice genotypes to reduce the fluoride toxicity in plants as well as humans. To date, there is no perfect strategy for control or amelioration of F toxicity in rice because the mechanism underlying F accumulation and subsequent biochemical changes is not clear yet. Transcript profiling in *Camellia sinensis* post treatment with F has established the expression of a few genes related to plant metabolism, hormone biosynthesis and transcription factors. Likewise, differential regulation of defense signaling pathways has been reported in aromatic and non-aromatic rice towards fluoride. Nevertheless, the genetic networks associated with fluoride accumulation and tolerance in rice is still poorly understood mainly due to lack of more comprehensive genome sequence knowledge. The high-throughput Omics platforms have emerged as powerful and cost-efficient tools for decoding gene expression, biochemical regulation and physiological response during stress conditions in plants. Therefore, a genome wide characterization of coding transcripts, proteins and non-coding RNA network in rice with differential sensitivity to fluoride toxicity is highly necessary to establish their role in ameliorating fluoride toxicity in this agriculturally significant crop.