The goal of this project is to characterize *Arabidopsis thaliana* m^6A methyl transferase (MTA) as a putative player in the miRNA biogenesis regulatory pathway.

Arabidopsis thaliana is a model plant that has been successfully used to understand various biological pathways thatdetermine plant development and health. These findings have also been shown to be true for many other crop plant species and thus have helped in improvement of the crop plants over the years. Many findings have also helped with human studies and have firmly established *Arabidopsis* as a robust model system to study basic cellular pathways.

Micro RNAs (miRNAs) are ~21nt long RNA molecules that specifically repress their target mRNAs. Over the years miRNAs, first studied in *Arabidopsis*, have been identified as important regulators of various metabolic pathways and their deregulation has been associated with direct effects on plant development and stress response. m^6A methylation is an important epigenetic mark that is known to influence messenger RNA (mRNA) levels in plants. While m^6A in animal systems has been shown to positively mark pri-miRNA for processing, **nothing is known regarding the role of m^6A in plant miRNA biogenesis. The goal of this project is to study the effects of m^6A methylation and MTA on plant miRNA biogenesis.**

Working towards this goal I tested miRNA levels in plants exhibiting low levels of MTA (*mta* line) and compared them to WT (control) miRNA levels. I found 37 miRNAs whose levels were changed in the mutant, 33 of which were downregulated. I also found that out of 60 pri-miRNAs tested 30 pri-miRNAs were upregulated in the mutant and 14 of them formed cognate pairs with downregulated miRNAs. This indicated that m^6A mark is playing a role in proper processing of pri-miRNA. I also found that MTA protein interacts with TOUGH (TGH) protein. TGH is a known player in miRNA biogenesis and this interaction is another indication of MTA's role in miRNA biogenesis. To study these effects in a comprehensive manner I will perform experiments like m^6A immunoprecipitation and RNA immunoprecipiataion to identify the pri-miRNAs/miRNAs which have this modification. I will also perform co-immunoprecipitation followed by mass spectrometry to identify new proteins that interact with MTA. To identify the miRNA genes (*MIR)* that are associated with MTA and TGH, I will also perform Chromatin Immunoprecipiataion followed by high throughput sequencing. The data obtained from all these experiments will be analysed to identify the role of m^6A methylation and its writer MTA in miRNA biogenesis.