



**BIOINFORMATICS 2016 SPRING SEMINAR SERIES**

Hosted by: Department of Computer and Information Sciences,  
Department of Electrical and Computer Engineering &  
Center for Bioinformatics and Computational Biology  
<http://bioinformatics.udel.edu/Seminars/Current>

**MONDAY, March 14, 2016**

**3:30pm**

**DBI Room 102**

**miTRATA: a web-based tool for  
microRNA Truncation and Tailing Analysis**

***Parth Patel***

***PhD Student; Bioinformatics and Systems Biology***

**ABSTRACT:** We describe miTRATA, the first web-based tool for microRNA Truncation and Tailing Analysis—the analysis of 3' modifications of microRNAs including the loss or gain of nucleotides relative to the canonical sequence. miTRATA is implemented in Python (version 3) and employs parallel processing modules to enhance its scalability when analyzing multiple small RNA (sRNA) sequencing datasets. It utilizes miRBase, currently version 21, as a source of known microRNAs for analysis. miTRATA notifies user(s) via email to download as well as visualize the results online. miTRATA's strengths lie in (i) its biologist-focused web interface, (ii) improved scalability via parallel processing and (iii) its uniqueness as a webtool to perform microRNA truncation and tailing analysis.

**Phased, secondary siRNAs in non-grass monocots**

***Atul Kakrana***

***PhD Student; Bioinformatics and Systems Biology***

**ABSTRACT:** Two male germline specific pathways, generating diverse and numerous “in-phase” 21-nt (pre-meiotic) and 24-nt (post-meiotic) siRNAs have been reported in maize and rice. These phased siRNAs show striking similarity to mammalian piRNAs in terms of their abundance, distribution, distinct stage, and timing of accumulation. Interestingly, the functions for both potentially-analogous, plant phasiRNA and mammalian piRNA pathways remain largely unknown. Since the original report of reproductive phasiRNAs in rice, no systematic study of their evolutionary origins have yet been reported; in this context, the meiotic phasiRNAs are particularly interesting, as they have only been described in grasses. To assess their origins, we investigated the presence of reproductive phasiRNA pathways in asparagus, a non-grass monocot that speciated ~63 mya. Our analyses reveal that the miRNA triggers for both classes of phasiRNAs are conserved and exhibit grass-like spatiotemporal expression. In addition, asparagus displays at-least 66 pre-meiotic and 65 meiotic phasiRNA loci. Though these numbers are significantly lower than those reported in grasses, these loci clearly demonstrate the presence of meiotic phasiRNA pathways outside of the grasses, extending the origin back in the monocots. Motivated by these results and with the aim of tracing the origins of the meiotic phasiRNAs, we extended our study to three additional species from the Liliales, the Asparagales and the Poales, spanning ~114 million years of monocot evolution. Our comparative analysis of reproductive phasiRNAs and their biogenesis components from these species is providing insights into the origins of the pathway for meiotic phasiRNA biogenesis seen in grasses.