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Comparative Genomic and Transcriptomic Analyses of Functionally Characterized Arabidopsis IncRNAs Reveals Conservation in Unexpected Places

Full Paper (https://pag.confex.com/pag/xxvii/recordingredirect.cgi/oid/Recording3683/paper37313_1.pdf)

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Body

Long non-coding RNAs (IncRNAs) are a functionally diverse and yet poorly defined transcriptional unit. Thanks to high throughput next-generation sequencing technologies, it is now clear that eukaryotic transcriptomes are teeming with IncRNAs. Despite this abundance, it is quite difficult to infer function, particularly in plant systems where there are few functionally described IncRNAs to serve as archetypes. Here we apply a comparative genomic and transcriptomic strategy to examine the functional conservation and diversification of four functionally characterized Arabidopsis IncRNAs: *APOLO*, *DRIR*, *ELENA*, and *HID1*. Each of these IncRNAs exhibit different levels of sequence and transcriptional conservation across the plant lineage. Of the four, *HID1* is the most sequence conserved, yet displays a remarkably different transcriptional profile and appears to function in different regulatory pathways across examined angiosperms. In the case of *APOLO*, a positionally conserved but highly sequence divergent IncRNA is found across Brassicaceae, suggesting transcription and small RNA recruitment is more important than sequence conservation at this locus. In sum, these data highlight the ways in which function influences evolution of IncRNA loci, as well as the benefits of guilt-by-association techniques for inferring novel IncRNA function.

Sessions



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Places Sunday, Jan 13 2:50 PM Town and Country, Royal Palm Salon 3-4 (/pag_2019/event/7983b3ea7b95e59e4bf47ab04f1182b1)