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ABSTRACT BOOK

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smRNA in Gonad Development: A search for tiny regulators governing tight regulation during sex determination and gonad development in mice

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Molecular players of sex determination and gonad development in mice are very much known indeed. Antagonistic regulation among players of male and female pathways is the key to successful development of embryonic gonads in mammals. Nevertheless, role of smRNA-based regulation is still under investigation. To explore it further, we aimed to investigate the epitranscriptome of male and female mice embryonic gonads. Our sncRNAs-seq experiment followed by in-depth bioinformatics analysis of 11.5 to 13.5 dpc gonads identified multiple and unique miRNAs and piRNAs in a total of 9 intersex and intra-sex comparisons. Comparing male and female smRNA-seq data yielded 61, 74 and 72 differentially expressed (DE) miRNAs at 11.5, 12.5, and 13.5 dpc, respectively. Further, target prediction utilizing robust miRanda algorithm followed by overlap correlation analysis of sncRNA-seq and total RNA RNA-seq showed novel interactions such as male-specific miRNAs targeting female-specific genes like Fst, Rspo1, and female-specific miRNAs targeting male-specific genes like Sry, Fgf9, Ptgds. However, analysis with experimentally validated datasets has relatively fewer targets for all the stages. We also identified DE passenger strands, targeting key players viz. Fgf9, Rspo1, Foxl2. Furthermore, identification of upstream regulators (TFs) of DEmiRNAs provided evidence of the involvement of TFs in the upregulation of miRNAs during gonadogenesis. Interestingly, Sox9 is found to have a binding site on the promoter region of malespecific miR-199b, miR-6236, and miR-5121. Moreover, DE piRNAs targeting various genes were also predicted using piRNAdb with a prime focus on their origin and cluster formation. Akr1c13 was found as a target of male-specific piR-018417 at 11.5 dpc only. Therefore, our results provide evidence of tight regulation by tiny regulators through sncRNA-based gene silencing during sex determination and gonadogenesis. We are thankful to the UGC and CSIR for financial support.