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Understanding the regulatory network landscape of naive and primed states of human pluripotency

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Insight into the key genes of pluripotency and their interrelationships is necessary for understanding the underlying mechanism of pluripotency in human and hence their successful application in regenerative medicine. Moreover pluripotent stem cells (PSCs) have been observed to occur in two distinct states — naive state and primed state. Both naive and primed state PSCs can give rise to tissues of all the three germ layers in vitro but differ in their potential to generate germline chimera in vivo. Understanding the molecular mechanisms that govern these two states of pluripotency in human can open a plethora of opportunities for studying early embryonic development and in biomedical applications. Weighted gene co-expression network analysis (WGCNA) method was used to identify the key molecular makers and their interactions that define the two distinct pluripotency states. Signed hybrid network was reconstructed from transcriptomic data (RNA-seq) of naive and primed state pluripotent samples. Our analysis revealed two sets of genes that are involved in the establishment and maintenance of naive and primed states. The naive state genes were associated with metabolic processes while primed state genes were associated with systems development. We further filtered these lists to identify the intra-modular hubs and the hub transcription factors (TFs) for each state. We finally reported a list of 52 and 33 TFs as the set of core TFs that are responsible for the induction and maintenance of naive and primed states of pluripotency in human, respectively. Among these, the newly reported TFs were ZNF275, ZNF232, SP4, and MSANTD3 which warrants further experimental validation.

Biography

Anup Som has completed his PhD in Computational Biology from Jadavpur University (worked at Indian Association for the Cultivation of Science (IACS), Kolkata) and postdoctoral studies from Washignton State University (USA), Arizona State University (USA), University of Houston (USA), and University of Rostock (Germany). He is Assistant Professor of Bioinformatics at University of Allahabad. He has published more than 32 papers in reputed journals and serving as an assiciate editor and editorial board member of repute. His research interest includes networks and systems biology, computational cancer biology and stem cell bioinformatics

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