Arginine methylation plays a critical role in bovine preimplantation development

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Protein arginine methyltransferase 1 (PRMT1) is a key enzyme responsible for catalyzing the asymmetric dimethylation of arginine residues on histone and non-histone proteins. The methylation of substrates occurs within glycine and arginine-rich domains, relying on the association of PRMT1 with co-regulators, which leads to crosstalk with other post-translational modifications on lysine (K) in histones. PRMT1 and asymmetric arginine dimethylation (me2a) are highly expressed in bovine oocytes and preimplantation embryos. To assess the role of PRMT1 in early development, we disrupted PRMT1-mediated arginine methylation with pharmacological methods in bovine embryos. When the inhibitors successfully reduce PRMT1-mediated H4R3me2a, we observed a significant reduction in the recruitment of the histone marks H3K27 trimethylation and a significant enhancement increase in the levels of H3K9 acetylation, suggesting an impact on chromatin dynamics through crosstalk. Of note, inhibition of PRMT1 also resulted in reduced expression of SOX2, a vital transcription factor for embryonic development. Despite blastocyst rates in bovine embryos being unaffected by PRMT1 inhibition, a notable decrease in the cell counts of total cells, inner cell mass (ICM) cells, and trophectoderm (TE) cells was observed. Furthermore, PRMT1 disruption also reduced depletion of glucose and pyruvate during the blastocyst stage, indicating altered metabolic activity in the presence of PRMT1 inhibitors. In summary, our findings reveal an important role of PRMT1 in orchestrating the intricate regulatory network governing the epigenetic landscape and gene expression profile of pre-implantation bovine embryos. The inhibition of PRMT1 activity not only disrupts histone modifications but also impacts transcription factor expression and metabolic processes, ultimately influencing embryonic cell fate determination and metabolic competence.