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Global changes in transcriptome regulation in post-meiotic spermatids

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The male germ cell undergoes a proliferative step of amplification of the cell number, a meiotic step that reduces the genome to haploid, and a morphological differentiation stage to form spermatozoa. Although each phase requires a dynamic repertoire of functional factors, transcription is not always active in spermatogenesis, being characterized by a mitotic phase in spermatogonia, a meiotic phase in pachytene spermatocytes and a post-meiotic phase in round spermatids. We have performed deep-sequencing analysis of the transcriptome of purified populations of pachytene spermatocytes and round spermatids. We generated strend-specific RNAseq data for polyadenylated RNAs, resulting in >100 million 100bp mapped reads for each sample. Comparison of the spermatid versus spermatocytes transcriptome revealed 5508 up regulated and 7218 down-regulated genes in post-meiotic germ cells. Cell cycle and splicing were the most significantly up regulated pathways in post-meiotic versus meiotic cells. As for the splicing, 3278 exons in 2185 genes were differentially regulated in spermatids and spermatocytes. The most represented classes were alternative first exons, intron retention, alternative last exons and exon cassettes. These changes were accompanied by changes in the expression of key splicing factors, like the overall down regulation of the serine-arginine rich (SR) family, involved in positive regulation of constitutive and alternative splicing events. Our results indicate that male germ cells extensively modify the pattern of gene expression during the meiotic divisions and identify key molecular players involved in this transition. The global reduction in the SR protein family, known positive regulators of splicing events, may drive the extensive changes in alternative splicing observed between meiotic and post-meiotic germ cells.

Keywords

Spermatogenesis, meiosis, spermatocytes, spermatids, transcriptome, splicing, splicing factors.