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Gene Expression in the Spermatogenically Inactive "Dark" and Maturing "Light" Testicular Tissues of the Prepubertal Colt

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In the testis of the 1.5-year-old horse, spermatogenesis initiates locally in grossly light, central areas that contrast with grossly dark, peripheral areas that are as yet inactive in spermatogenesis. Gene expression was compared between "light" and "dark" tissues of 1.5-year-old horse testes to identify mechanisms important to the initiation of spermatogenesis. Microarrays containing human cDNAs were used to assess expression levels of 9132 genes simultaneously in matched pairs of dark and light testis tissues from 3 prepubertal colts. In all 3 analyses, dysferlin (DYS), down-regulated in ovarian cancer 1 (DOC1), and Golgi apparatus protein 1 (GLG1) genes were preferentially expressed in dark tissues, while outer dense fiber of sperm tails (ODF2) and phosphodiesterase 3B (PDE3B) genes were more highly expressed in light testis tissue (>1.7 balanced difference value, Incyte GEM tools software). Expression levels of 88 additional genes appeared to be different between dark and light tissues in 2 of the 3 microarray analyses. The preferential expression of *DYS*, *DOC1*, *ODF2*, and *PDE3B* genes in dark or light testis tissues was confirmed on Northern blots and localized to cell types by in situ hybridization. Future studies to determine the role of genes regulated during the initiation of spermatogenesis may aid in elucidating molecular mechanisms during this critical time as well as in identifying new therapies for enhancing male fertility.

Key words: Gene regulation, testis, spermatogenesis, puberty

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