# P-16 Effect of Androgen on the Expression of Hox Genes in Mouse Epididymis

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**Objectives:** Hox genes play a role in the patterning and segment identity along the anterior/posterior (A/P) axis of the embryo. In mammals, 39 Hox genes are distributed along four clusters designated Hox A, B, C and D. The epididymis can be distinguished by their morphology as well as by their different patterns of gene and protein expression. These region specific patterns may reflect epididymal function that are crucial for sperm maturation and storage. To elucidate the role of androgen in the segmentation of epididymis, changes in the expression of Hox genes following orchidectomy (ORX) was examined in mice.

**Methods:** Adult male mice were subjected to ORX. After recovery, to allow clearance of circulating androgen following ORX or sham, mice were rested for two weeks, and then subjected to subcutaneous injections of 5α-dihydrotestosterone (DHT) at 3 mg/kg (for 7 days) dissolved in sesame oil (n = 5 for each treatment). Immunohistochemical localization of Hox proteins in caput, corpus, and cauda epididymis was conducted together with optimized RT-PCR analysis of Hox mRNA in epididymis.

**Results:** Hoxa-9, -10, -11, Hoxd-9, -10 were detected in all three regions of epididymis. Hoxa-11 mRNA level in corpus epididymis was significantly higher compared with other regions. In caput epididymis, Hoxa-10 mRNA level was increased until puberty and then decreased. Following exposure to 5α-DHT (3 mg/kg), Hoxa-9 mRNA level increased a little in caput epididymis. In cauda epididymis, Hoxa-11 and Hoxd-9 mRNA level increased by 5α-DHT.

**Conclusion:** Hox mRNA was differentially expressed among the three different region of mouse epididymis. Epididymal expression of Hoxa-9, Hoxa-11 and Hoxd-9 increased 5α-DHT in ORX mice, suggesting that 5α-DHT may regulate segmentation in epididymis and thus sperm maturation and storage in epididymis.