

Characterization of reproductive parameters from Pennsylvania bull elk (*Cervus canadensis*)

Luisa Ramírez-Agámez,^a Camilo Hernández-Aviles,^a Jeremiah Banfield,^b Michael O'Connor,^c Mariah Pearson,^a Sheila Spacek,^a Sheila Teague,^a Charles Love^a

^aCollege of Veterinary Medicine, Texas A&M University, College Station, TX; ^bPennsylvania Game Commission, Harrisburg, PA; ^cDepartment of Animal Science, Pennsylvania State University, University Park, PA

Pennsylvania (PA) elk (*Cervus canadensis*) are a population of free-ranging cervids that live in north central PA, and were initially reintroduced in 1913 as a measure to recover the elk population that was extirpated by uncontrolled hunting. Currently, the herd size of PA elk approaches ~ 1,400 individuals. During the 2019 calving season, a reduction in the number of calves was noticed. Gross anatomic inspection from the uteruses and ovaries harvested from selected cows revealed evidence suggestive of embryonic death whereas conventional sperm parameters (e.g. morphology, viability) analyzed from selected bulls were largely normal. This study was conducted to characterize certain sperm quality parameters from bulls (n = 24) harvested during the 2020 hunting season, to determine potential causes for reduced fertility. Testes and epididymides were harvested from hunted animals,

immediately cooled at 5 °C and shipped from PA to Texas within 24 hours. Upon arrival, each testis and epididymis were isolated and weighed. Tissue wedges were obtained from testes and fixed in Davidson's fixative. Each caudal epididymis was flushed with 5 ml of INRA-96® extender and total sperm numbers (TSN; 10⁹), total and progressive motility (TMOT, PMOT; %), curvilinear velocity (VCL; μm/s), plasma membrane/acrosomal intactness (VAI; %), DNA integrity (COMP_{act}; %), and sperm morphology (Normal; %) were determined by CASA, flow cytometry and DIC microscopy, respectively. Overall, the sperm quality was consistent with parameters from other species (e.g. stallion, bull; Table). The % (mean ± SD) of morphologically normal sperm was low due to the incidence of proximal, distal droplets (13 ± 11, 43 ± 21; respectively), and bent midpieces (14 ± 11). Surprisingly, the % COMP_{act} was high (mean ± SD 45 ± 17; range: 3 - 71). Spearman's correlation analysis revealed no linear relationship (p > 0.05 [positive or negative]) among testes and epididymides sizes, sperm morphology, or COMP_{act} values. At this point, it can be speculated that the observed values of COMP_{act} (susceptibility of DNA to denaturation) in the wild PA elk population may partially explain the reduced fertility recently observed. Further studies are warranted to confirm this hypothesis and to determine a potential cause for such increased values of sperm DNA damage in the absence of other sperm quality abnormalities.

Keywords: Pennsylvania elk, *Cervus canadensis*, sperm quality, fertility, DNA integrity

Table. Sperm quality parameters from 24 PA elks obtained after epididymal harvest

Parameter	Testis	Epid.	TSN	TMOT	PMOT	VCL	VAI	COMP _{act}	Normal
(Mean ± SD)	83 ± 21	21 ± 5	0.6 ± 1	55 ± 20	34 ± 15	162 ± 51	87 ± 6	45 ± 17	34 ± 14

Expression and abundance of prostaglandins in healthy and fibrotic mare endometrium

Michael Byron,^a Jennine Lection,^a Bettina Wagner,^b Andrew Miller,^c Tracey Chenier,^d Soon Hon Cheong,^a Mariana Diel de Amorim^a

^aDepartment of Clinical Sciences, ^bDepartment of Population Medicine and Diagnostic Sciences, ^cDepartment of Biomedical Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY; ^dDepartment of Population Medicine, Ontario Veterinary College, University of Guelph, Canada

Inflammation and fibrosis of the endometrium is a major cause of infertility in the mare. A better understanding of the mechanisms of degenerative diseases of the endometrium can help to improve diagnosis and clinical outcomes in the mare. Prostaglandins have a wide range of roles including in tissue remodeling, inflammation, and fibrosis in the endometrium. We hypothesized that expression of prostaglandin-related genes in the endometrium and abundance of prostaglandins in low-volume uterine lavage is different in healthy mares compared to mares diagnosed with fibrosed endometrium. Our objective was to discern any changes in prostaglandin abundance and

gene expression among healthy and fibrosed endometrium in order to better understand the mechanisms of endometrial inflammation and fibrosis. A total of 27 estrous mares were enrolled in this study. A uterine lavage using 250 ml of 0.9% NaCl solution was performed with a sterile bivona catheter, and the concentration of prostaglandins in the fluid was measured using enzyme-linked immunosorbent assays (ELISAs) for PGE₂ and PGF_{2α}. An endometrial biopsy was collected and sectioned in half. One half of the endometrial biopsy was fixed in 10% formalin, sectioned, stained with hematoxylin & eosin and graded according to the Kenney-Doig system by a board-certified pathologist; the second half was snap frozen in liquid nitrogen and stored at -80 °C until analysis. Mares were assigned to either the healthy group (n = 15) if the endometrial biopsy score was I or IIA, or to the fibrosed endometrium group (n = 12) if the endometrium biopsy score was IIB or III. Total RNA was extracted from endometrial biopsies and real-time PCR was performed to evaluate the relative abundance of the following genes: PTGES, PTGS2, PTGFR, PTGER2, PTGER4, CBR1, and SLCO2A1. Mean threshold cycle (Cq) was determined and then normalized to the reference gene (GAPDH) (ΔCT). Statistical analyses were performed with JMP® software using p < 0.05. Data were