

**PROCEEDINGS OF THE  
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Presque Isle State Park

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## **ORAL PRESENTATIONS:**

In order of presentation.\* Designates presenter.

### **Water Level Fluctuations in Presque Isle Bay, Erie, PA, and the Ponds of Presque Isle and Implications for Water Quality**

**Shawn Kiskadden\*,  
Gannon University**

**Rick Diz,  
Gannon University**

While the Great Lakes do not experience astronomical tides, water levels are constantly changing and are affected in the long term by variations in the hydrology of the watershed, and in the short term by wind events which produce seiche effects. Seiches are the oscillations of the water surface from one end of a basin to the other due to the effect of the wind. These events are well studied in Lake Erie (the Lake) and the other Great Lakes (Treibitz, 2006). However, no such studies have been reported on water level fluctuations in Presque Isle Bay (the Erie, PA, harbor). Presque Isle Bay (the Bay), with a volume of about 52.6 million cubic meters (~13,900 million gallons), is connected to Lake Erie by a narrow channel, through which essentially all of the water exchange with Lake Erie occurs. In the long run, water level in PIB is determined by hydrologic factors. In the short run, water level is largely determined by flow in or out through the channel and any internal seiche effect due to wind. Water level of the interior ponds (Ponds) of the Presque Isle peninsula may also be influenced by water level changes in the Lake and the Bay.

NOAA operates a water level monitoring station at the entrance to the channel which records the level of Lake Erie. Water level data loggers were installed by the authors at several locations on the Bay and selected Ponds. Data loggers were synchronized to universal time and set to store data points at the same time interval (0.1 hrs) as the NOAA monitoring station. Early analysis of the data has indicated that while the Bay is influenced by changes in the Lake's water level, the Bay has its cycle of water level fluctuations. The magnitude of changes in the Bay's water level at a given site often exceeds the magnitude of changes in the Lake's water level at the channel entrance, apparently due to the Bay's own seiche behavior. The interior ponds of Presque Isle exhibit individual fluctuation patterns as a function of their hydrologic connections to the Bay and Lake.

Water level fluctuations may contribute to changes in water quality in the ponds due to a pumping of groundwater up and down through the pond sediments over long periods of time. The water of the Bay is diluted by inflowing Lake water, with a shortening of the hydraulic residence time (HRT) of Bay water. Estimates will be given for the Bay's HRT due to this mixing phenomenon. Since water quality in the Bay is of great interest to local environmental groups and government agencies, this new understanding of water level fluctuations and its effect on water quality will be of considerable value to decision makers.

## **Brown Bullhead Study Update**

**James L. Grazio\*,  
Great Lakes Biologist, Office of the Great Lakes,  
Pennsylvania Department of Environmental Protection.**

Located in the northwest corner of Pennsylvania on the southern shore of Lake Erie, Presque Isle Bay is a 3718 acre (1505 hectare) natural embayment formed by a 7 mile long (11.3 km) recurved sand spit. Over 80% of the bay's watershed is comprised of urban and industrial land uses in the City of Erie and its outlying townships. As a relatively closed system with a hydraulic detention time of almost 2.5 years, Presque Isle Bay tends to act as a natural "settling basin" for sediment entering its waters. Given the urban nature of the majority of the watershed, much of this sediment is contaminated with heavy metals and various organic compounds. Presque Isle Bay was designated as the 43<sup>rd</sup> Great Lakes Area of Concern by the US Department of State in 1991. In response, the Pennsylvania Department of Environmental Protection (PADEP) examined over 3100 brown bullhead catfish from the bay. Histopathology confirmed an external tumor rate of 64% and a liver tumor rate of 22%. This striking tumor rate was thought to be causally related to contaminants in the sediment.

Perhaps not surprisingly, these changes corresponded to dramatic improvements in the health of the Bay's brown bullhead population. Longitudinal monitoring of these bottom-feeding fish has shown that between 1992 and 1999, the frequency of external tumors has declined from 64% to 17%, and the frequency of liver tumors has declined from 22% to 0%.

Brown bullhead monitoring has continued annually in Presque Isle Bay since Presque Isle Bay was declared to be in a "Recovery Stage" in December 2002. Bullhead are collected and examined for grossly observable external lesions, and a subsample of fish are necropsied for histopathological analysis. In addition, PADEP initiated a study in 2002 to determine the background (reference) incidence rate of brown bullhead lesions in inland Pennsylvania lakes and elsewhere in Lake Erie. The results of this work will be used to support the development of appropriate delisting targets for the "Fish Tumors or Other Deformities" Beneficial Use Impairment in the bay.

Several additional lines of research have recently been initiated to better understand the environmental biology and ethology of the Bay's brown bullhead population. This research includes genetic studies to understand the role that hybridization may play in the etiology of the bullhead tumors and the extent to which bullhead geneflow occurs to areas outside of the bay, investigations of role of parasites and viruses in tumor causation, and a radiotelemetry study to track migration and sediment exposure patterns of the bay's brown bullhead.

An overview of the brown bullhead study will be presented, with an emphasis on recent studies and results to date.

## **An Analysis of Brown Bullhead Tumor Data from Presque Isle Bay and Lake Erie**

**Michael A. Rutter\*, Mathematics Department  
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Brown bullhead (*Ameiurus nebulosus*) were sampled in Presque Isle Bay (Erie, PA), a Lake Erie area of concern, from 1999 to 2005. Sampled bullheads were examined for skin and mouth tumors, and in selected fish, examined for liver tumors and aged using otoliths. A Bayesian statistical model was used to estimate tumor incidence rates as a function of length, weight, and/or age. First, the best predictors of liver or skin tumor incidence rates were determined using logistic regression. Multiple sampling locations around Lake Erie were a possible source of increased variation in the data and this was accounted for by including sampling location and date as a random effect in the model. Once the best model is found, liver and skin tumor incidence rates in Presque Isle Bay can be compared to the lowest rates, or baseline rates, found in sites around Lake Erie. From these results, the probability of the tumor incidence rates in Presque Isle Bay being higher than the baseline Lake Erie rates can be calculated.

## **Breeding Parameters and Population Structure of Two State Threatened Darter Species *Etheostoma camurum* and *E. tippecanoe*.**

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Little is known about the breeding parameters and population structure of two Pennsylvania darters, the bluebreast darter, *Etheostoma camurum*, and the Tippecanoe darter, *E. tippecanoe*. Both are Pennsylvania state threatened species, and they are considered threatened or endangered in several other states throughout their range. Although some limited breeding information is available from populations in other states, the timing and duration of spawning has not been documented for Pennsylvania populations. Both species occupied disjunct riffle habitats in the Allegheny River system, with stable populations in French Creek. We have found an additional population for these species about 110 miles downstream in Deer Creek, Harmar, PA. Through weekly catch-and-release sampling of this population, we have identified the peak breeding times and the duration of the breeding season for the Deer Creek populations of these two species. Observations of population peaks and mark-recapture studies indicate possible seasonal migrations into spawning areas. Collections from multiple sites throughout the Allegheny Basin, and genetic analysis indicate a metapopulation structure, possibly spreading from source population(s) in the Allegheny River to sink populations or seasonal breeding habitats in suitable tributaries. Population structure will be useful to conservation efforts by identifying breeding populations with the greatest genetic variation. Breeding times will be a useful guide for ecologically responsible development of riparian areas, assisting with avoiding disturbances to important spawning areas during the breeding season.

## **Potential Control of the Invasive Round Goby Fish Using Pheromones**

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The success of the invasive fish, the round goby, may be due in part to its pheromonal communication between males and females during reproduction. We hypothesize that reproductive males (RM) secrete pheromones into the water that attract conspecific females to the nests but deters conspecific males. Our histological and biochemical studies showed that specialized glandular tissue in the testes of the round goby produce androgen steroids, two of which (11-oxo-etiocholanolone (ETIO) and 11-oxo-ETIO-sulfate) are novel compounds in teleosts. Our behavioural experiments showed that ripe females exposed to odours of RM spent more time near the odour source ( $P < 0.05$ ), exhibited elevated swimming velocities ( $P < 0.05$ ), and directed movement to the odour source when compared with responses to control water. When the response of females were tested against blends of synthesized steroids found in male round goby gonads, there was an overall significant difference between treatment and control ( $P < 0.003$ ), but no difference in response between reproductive (ripe) and non-reproductive females. Moreover, different blends of steroids (free vs. more soluble conjugated steroids) did not elicit differences in behavioural responses by females. Although males in other gobiids illicit aggressive displays when exposed to conspecific male odour, this was not the evident in the round goby.

## **Determining Species Identity and Size of Fragmented Zebra Mussels (*Dreissena polymorpha*) and Quagga Mussels (*Dreissena bugensis*) from Presque Isle Bay, Lake Erie**

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Gannon University**

Size-selective predation likely plays an important role in the population dynamics of zebra mussels (*Dreissena polymorpha*) and quagga mussels (*D. bugensis*). Determining species identity and the size of consumed dreissenids can be problematic because their shells are often fragmented by predators. A consistent relationship between valve length and the length of the shell's internal septum has been previously used to estimate the size of fragmented dreissenids recovered from predators. However, determining species identity of fragmented dreissenids remains a problem. In the current study, regression analyses revealed highly significant relationships between valve length and septum length in zebra mussels and quagga mussels collected from Presque Isle Bay, Lake Erie. The regression equations of valve length on septum length did not significantly differ between the two species in either their slopes or y-intercepts, suggesting that valve lengths of fragmented dreissenids recovered from predators at this site can be calculated by a single equation. We also investigated the relationship between septum width and septum length in both species and found that the septa of quagga mussels are relatively wider than those of zebra mussels. The septum width:septum length ratio may therefore prove useful in determining species identity of fragmented dreissenids recovered from predators. However, this relationship should be investigated on a location by location basis because dreissenid morphology is known to vary among study sites.

## **A Study of Shrew Diversity at Erie Bluffs State Park**

**Mark E. Peterson\*, Biology Department  
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**Steven J. Ropski, Biology Department  
Gannon University**

From April 2005 to October 2005, a census of the shrew population at Erie Bluffs State Park was conducted. The three habitats emphasized were bluff, wet woodlands, and Duck Run, and Kirkland Pitfall Arrays were used. Air temperature and moon phases were examined to see if they had any effect on capture success. When the last quarter moon phase was present, there were three shrews captured. When the waxing crescent moon phase was present, there were two shrews captured. When the first quarter, waxing gibbous, or waning gibbous moon phases were present, there was one shrew captured in each phase. In over 525 trap-nights, eight shrews were captured: six ( 4 *Sorex cinereus* and 2 *Blarina brevicauda*) in the bluff area and one in each the wet woods area (1 *S. cinereus*) and Duck Run area (1 *S. cinereus*). The shrews captured were not threatened or endangered and represent the expected species. These results will help the park staff develop an appropriate management plan for the newest Pennsylvania state park.



## **Rethinking the Role of Lake Agassiz Overflow in the Early Great Lakes**

**Andy Breckenridge\*, Department of Geology,  
Mercyhurst College**

Oxygen isotopic records from benthic ostracodes in sediment cores from Lakes Michigan, Huron, and Erie have been used to reconstruct the paleohydrology of the early Great Lakes. Recent analyses from Lake Superior yield oxygen isotopic values from 10,500 to 9,000 cal yr BP between  $-18$  and  $-22$ ‰ PDB. In great contrast, coeval records from Huron and Michigan are characterized by extreme  $\delta^{18}\text{O}$  variations, ranging from values reflecting a source that is primarily glacial in origin ( $\sim -20$ ‰ PDB) to much higher values characteristic of a regional meteoric source ( $\sim -5$ ‰ PDB). Re-evaluated age models from Huron and Michigan yield a more consistent oxygen isotope stratigraphy than previously recognized. The most striking feature is a negative isotopic excursion between 9,400 and 9,000 cal yr BP. In Huron, this negative excursion was formerly ascribed to the Late Stanley lowstand, and in Michigan the event was attributed to Lake Agassiz overflow. Catastrophic flooding from Lake Agassiz is not ruled out, but I attribute this excursion to the switching of Lake Superior overflow from a previously undocumented northern outlet back to Lake Huron. Quantifying freshwater fluxes for this system remains difficult because Lake Superior's benthic ostracodes may not faithfully record the average isotopic composition of surface water.

## **Identification and Enumeration of Bacteria and Viruses in Beach Water**

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This summer, there have been over 40 Presque Isle State Park beach closures due to high levels of aquatic bacteria. Similar problems were reported nationwide in 2006. This alarmingly high incidence of beach water contamination has caused great concern for public welfare, providing an impetus for the development of rapid and thorough methods for identifying disease causing microbes in recreational waters.

To address this concern, we are utilizing molecular approaches to measure bacterial and viral levels in water. For bacteria, common DNA extraction procedures are coupled with real-time PCR to quantitatively measure DNA content, and hence abundance of bacteria, in water sample. To track viral abundance, a multi-filtration unit is utilized to capture viruses on a grid where they are then illuminated and counted using epifluorescence microscopy. Both techniques allow for a greater repertoire of microorganisms to be identified compared to current protocols, and can be completed in two hours time, a dramatic reduction compared to the current EPA approved protocol that requires twenty-four hours for testing bacterial levels.

Our work indicates that there is both temporal and spatial variability in the relative abundance and distribution of both bacteria and viruses in the different Presque Isle Beach waters tested. Our current effort is focused on expanding this study to monitor sites believed to be possible sources of non-point pollution and to determine whether the source of microbial pollution are from human or non-human origin.

## **Modeling to Predict *Escherichia coli* at Presque Isle Beach 2 in Erie, Pennsylvania**

**Theodore F. Buckwalter, U.S. Geological Survey,  
Pittsburgh, Pennsylvania**

**Tammy M. Zimmerman, U.S. Geological Survey,  
New Cumberland, Pennsylvania**

**Scott White, Erie County Department of Health,  
Erie, Pennsylvania**

The use of *E. coli* as an indicator of recreational water quality has been largely effective in determining when fecal contamination is present; however, there are drawbacks with using it as the *only* indicator. Concentrations of *E. coli* may change significantly between the time of sample collection and the reporting of results (anywhere from 18-24 hours). A more rapid method that some managers of recreational waters have adopted is the use of water-quality and environmental variables as surrogates for fecal-indicator bacteria that include, for example, precipitation, wind speed and direction, streamflow, and turbidity to predict, or forecast, when concentrations of fecal-indicator bacteria will exceed recreational standards. These emerging techniques may supplement the use of *E. coli* as an indicator of fecal contamination.

The U.S. Geological Survey (USGS), in cooperation with the Erie County Health Department (ECHD), studied the use of water-quality and environmental variables in beach-specific predictive models as surrogates for *E. coli* in forecasting the bacteriological health of Presque Isle Beach 2 in Erie, Pa. The study was based on *E. coli* concentrations and other water-quality and environmental data collected at Presque Isle Beach 2 during the 2004 and 2005 recreational seasons. All variables statistically related to *E. coli* concentrations were included in the initial regression analyses, and after several iterations, only those explanatory variables that made the models significantly better at predicting *E. coli* concentrations were included in the final models.

Models were developed for the 2004 data, the 2005 data, and the combined 2004-2005 dataset. Combining the 2004 and 2005 data yielded a significantly better model for predicting *E. coli* exceedance probabilities that included the explanatory variables turbidity log, rain weight, wave height (calculated), and wind direction.

## **Using Non-invasive Techniques to Determine Mercury Levels in Snapping Turtle (*Chelydra serpentina serpentina*) Tissues**

**Jeanette L. Schnars\***  
**Penn State University**

Mercury has long been a concern in the aquatic life of the Great Lakes region. Regular monitoring usually results in the euthanization of those individuals sampled. In this study I test a non-invasive technique to determine mercury levels in various snapping turtle tissues. Adult turtles were sampled from various waters in Erie County. Individuals were euthanized and muscle, adipose, liver, and claw samples were collected. Mercury was found to concentrate itself in the liver and claw tissues and was undetectable in muscle and fat tissues at 0.300 ppm. Larger turtles were found to carry high mercury levels in liver tissues (0.300 - 4.670 ppm). Although there was not a significant regression, claw samples can provide some indication of mercury concentration in the liver tissue. Such a technique may be useful in other turtle species with threatened or endangered populations.

## **Poster Sessions:**

Alphabetical by author's last name. \* Designates presenter.

### **Completed Mitochondrial Genome of Canada goose (*Branta canadensis*) and a Comparison to White Fronted Goose (*Anser albifrons*).**

**Robert S. Disantis\***  
**Joshua C. Snyder,**  
**Craig Andrew Mackaness**  
**Megan R. Sopher**  
**Adam R. Snider**  
**Jonathan P. Huber**  
**Edward J. Disantis,**  
**Andrew J. Senecal,**  
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**Page E. Tobelmann,**  
**Natalie M. Hecht,**  
**Patrick M. Barry,**  
**Matthew D. Show,**  
**Leanne Hubiak Speering,**  
**Joe R. Sanchez,**  
**Frederic J. Brenner,**  
**Durwood B. Ray,**

The *Branta canadensis* (Canada goose) has several classical morphologically defined subspecies within the common North American waterfowl. We have sequenced the entire 16,760 bp mitochondrial genome of the Canada goose (accession number: NC 007011) and compared it to the only other known entire mitochondrial DNA (mtDNA) goose genome of the *Anser albifrons* (white-fronted goose) (accession number: NC 004539). Mitochondrial DNA was isolated by Perfectprep Plasmid Mini Spin Columns (Eppendorf) from Canada goose liver. Polymerase chain reaction (PCR) was performed utilizing primers that we derived from the previously published mtDNA of the white fronted goose. PCR products were evaluated by gel electrophoresis. Cycle sequencing reactions were prepared in triplicate for both heavy and light DNA strand and sequenced utilizing our ABI 310 Genetic Analyzer. Our contig was compiled using Lasergene sequence analysis software (DNASTAR, Inc) from 220 sequences for both heavy and light strands. Our GCC-A haplotype showed regions of significant variation in lengths among the coding (Canada goose +5 bp) and non-coding regions (Canada goose +18 bp) of the mitochondrial genomes of these two species. This difference in length (23 bp) occurs due to a +20 bp non-coding D-loop region and several intergenic spacers of varying length within the Canada goose coding region. Namely: a) between the NADH1 and the tRNA-ile genes (+9bp) b) between the NADH2 and the tRNA-Trp genes (+1bp) and c) between the NADH5 and the Cytochrome b genes (-8bp), partially accounting for the observed variation. The overall homology between the two species is 91.9% (1363/16,760), the non-coding region is 76.0% (286/1,194) and the coding regions is 93.1% (1077/15,566). Detailed comparisons of the protein sequences are tabulated. Characterizing the genetic sequence and differences of mtDNA, wildlife biologists will be able to genetically define and monitor migration, breeding, feeding patterns as well as accurately classifying various geese species.

## Repellent for Zebra Mussels

**Jill Flanagan, Biology Department,  
Edinboro University**

Lake Erie hosts a variety of indigenous and non-indigenous species. A non-indigenous species introduced to the great lakes was the zebra mussel (*Dreissena polymorpha*). The striped pattern the shell of the zebra mussel distinguishes the zebra mussel from other bivalve mollusks. The non-indigenous species of mollusk the zebra mussel has gained notoriety for causing chaos to the great lakes ecosystems and industry operations along the great lakes. The zebra mussel presents a variety of concerns for both naturalists and industry. Studies conducted by Sea Grant focus on the filtration capabilities of the zebra mussel. In a study of zebra mussel filtration Sea Grant discovered the capacity of zebra mussel filtration; "Experts estimate that Lake Erie's zebra mussel population filters the entire volume of the lake's western basin once a week (Sea Grant 2003)." The effect of over filtration of the lake increases the population of bottom dwelling algae. The increase of bottom dwelling algae reduces the amount of dissolved oxygen in the water. Naturalists have concerns of the zebra mussel populations penetrating creek ecosystems. Zebra mussel populations in creek ecosystems could detrimentally affect native mussel populations, such as the northern riffle shell (*Epioblasma torulosa rangiana*). The zebra mussel competes with indigenous filter feeding species for food sources. The information gathered by naturalists on zebra mussels provides industry with knowledge of the zebra mussel. Zebra mussel attachment to intake pipes, traveling screens in water treatment plants, piers, docks and ships leaves industry grappling with effective methods to combat zebra mussel infestations. The expenditures of industries along the great lakes incur for the containment and removal of zebra mussels approximate into millions of dollars. In a study of socio-economic cost of zebra mussel management "140 facilities report monitoring and control of zebra mussels cost 60.2 million dollars during 1989-1994(Hushak 1993)." Industries work toward discovering techniques for zebra mussel repulsion.

## **The Comparative Distribution and Abundance of Species of Fleshy Fungi on Presque Isle State Park, Erie PA, from 1990 to 1995 and 2005-2006.**

**Larry P. Gauriloff\*, Biology Department  
Mercyhurst College**

**Patricia R. Flanagan, Department of Biology,  
Mercyhurst College**

Surveys to collect and identify the variety of species of fleshy fungi that occur on Presque Isle State Park in Erie, PA, were conducted from 1990 to 1995. This collection period formed the basis of a baseline study to determine the number, occurrence and distribution of fungal species as well as their relative abundance during different seasons of the year on the park. A second survey was begun in 2004 and continues to date to reevaluate the species present ten years later and any changes in the number, occurrence and distribution that was observed in the 1990's. In the 1990's, 146 species of basidiomycetous fungi were documented to occur in different locations and at different times throughout the year. So far during the current survey, we have documented 143 species of basidiomycetous fungi from the seven primary survey areas on the park that were established during the baseline study. These data are currently being compared for discrepancies in species occurrence and distribution between the 1990's survey and the current survey. Data will be presented showing the distribution and abundance of each species in the seven areas into which the park was divided for survey and resurvey purposes. An effort is also being made to freeze-dry as many different specimens for a collection of species for storage and future use at The Tom Ridge Center at Presque Isle. On going surveys include the quantification of the fleshy ascomycetous fungi and the distribution and occurrence of aquatic fungi of the Chytridiomycetes, Oomycetes, and Hyphochytridiomycetes in the park's waterways and soils.

# Mitochondrial DNA Sequence Variations in Partial Sequences of the D-loop Region in Northern Bobwhite, Chukar Partridge, Ruffed Grouse and Ring-Necked Pheasant

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Frederic J. Brenner, Biology Department,  
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As part of an ongoing study of wildlife genetics, we have sequenced 413 bp of the non-coding d-loop region of the mitochondrial genome of the northern bobwhite (*Colinus virginianus*), chukar partridge (*Alectoris chukar*), ruffed grouse (*Bonasa umbellus*) and ring-necked pheasant (*Phasianus colchicus*) for genetic comparison. Mitochondrial DNA (mtDNA) was prepared by Perfectprep Plasmid Mini Spin Columns (Eppendorf) from liver samples harvested in western Pennsylvania. Polymerase Chain Reaction (PCR) was employed to amplify the mtDNA d-loop using a consensus primer set we designed from previously published sequences of the mtDNA d-loop of five different gallinaceous birds. The same primer set was used to amplify the 413 bp sequence from each bird. PCR products were evaluated by slab gel electrophoresis and purified using the QIAquick PCR purification Kit (Qiagen) spin column. Cycle sequencing reactions with BigDye Terminator Chemistry were run in triplicate for each DNA strand and purified to remove dye terminators by DyeEx Spin Kit (Qiagen). The samples were then sequenced using our ABI single capillary Prism 310 Genetic Analyzer. Our 1110 BP contig was compiled using Lasergene sequence analysis software (DNASTAR, Inc) and “blasted” into the NCBI Genbank.

	% Homology			
	Northern Bobwhite	Chukar Partridge	Ruffed Grouse	Ring-necked Pheasant
Northern Bobwhite	1.000	0.882	0.867	0.879
Chukar Partridge	0.882	1.000	0.952	0.952
Ruffed Grouse	0.867	0.952	1.000	0.956
Ring-necked Pheasant	0.879	0.952	0.956	1.000

Northern bobwhite mtDNA d-loop sequences have not previously been reported. Although in the same family (Phasianidae) as the ring-necked pheasant and the chukar partridge, the northern bobwhite exhibited less homology when compared to the other three species. These data suggest that there exists genetic relationship between these species that is not accounted for by the use of current classifications and known native ranges. Characterizing the genetic sequences and differences within the mitochondrial genome, wildlife biologist will be able to define genetic difference among gallinaceous species.



## **Mitochondrial DNA Sequence Variations in Partial Sequences of *Odocoileus virginianus* (White Tail Deer) mtDNA d-loop**

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**Frederic J. Brenner, Biology Department  
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A concern in white deer management is that larger, older deer are preventing the younger from breeding, thereby limiting gene pool. Our intention is to use mitochondrial DNA (for maternal) and nuclear genetic sequences (for maternal and paternal) to trace breeding history within deer populations. Mitochondrial DNA (mtDNA) was prepared by Perfectprep Plasmid Mini Spin Columns (Eppendorf) from *Odocoileus virginianus* fetal liver harvested in western Pennsylvania. Polymerase Chain Reaction (PCR) was employed to amplify the mtDNA d-loop using primers we designed from a previously published sequence of mtDNA d-loop from another white tail deer specimen. PCR products were evaluated by slab gel electrophoresis and purified using the QIAquick PCR purification Kit (Qiagen) spin column. Cycle sequencing reactions with BigDye Terminator Chemistry were run in triplicate for each DNA strand and purified to remove dye terminators by DyeEx Spin Kit (Qiagen). The samples were then sequenced using our ABI single capillary Prism 310 Genetic Analyzer. Our 1110 BP contig was compiled using Lasergene sequence analysis software (DNASTAR, Inc) and “blasted” into the NCBI Genbank. Our GCC-A haplotype showed a 96% homology (948/974) with clone POB133, accession number AF 318096 (Illinois) and isolate WHITETAILEA, accession number AF 016978 (Alberta, Canada) as well as 96% homology (942/972) with clone RAN22, accession number AF 318100 (Illinois). Our data shows Western Pennsylvania’s *Odocoileus virginianus* haplotype GCC-A is a distinct haplotype. This technique and our future technology development for nuclear DNA markers will allow us to evaluate maternal inheritance and paternal inheritance within a specific herd of deer. In addition, we believe this new mtDNA haplotype is the first White Tailed Deer to be sequenced in the Northeastern United States.

**Breeding History Determination By Sequencing  
D-loop, Cox I, tRNA-Ser, tRNA-Asp and Cox II genes in  
*Branta bernicla*, *Branta canadensis*, and *Anser albifrons***

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Defining the genetic sequence of mitochondrial DNA (mtDNA), wildlife biologists will be able to genetically define and monitor migration, breeding, and feeding patterns of various geese species. We have sequenced 330 bp of the D-loop and 1,433 bp within a central region of the coding region of a brant (*Branta bernicla*) from Chesapeake, Virginia, and compared them to a Canada goose (*Branta canadensis*) from Western Pennsylvania and a white fronted goose (*Anser albifrons*) from Sweden. Total DNA was collected from liver tissue onto FTA cards (Whatman) and discs punched from the cards were used for Polymerase Chain Reaction (PCR) for amplifying the D-loop region. Mitochondrial DNA for amplifying the coding regions was prepared by Perfectprep Plasmid Mini Spin Columns (Eppendorf) from brant liver. PCR primers we designed previously for our sequencing of the genome of a Canada goose haplotype GCC-A were used. PCR products were evaluated by gel electrophoresis and cycle sequencing reactions were run (in triplicate for each DNA strand) and sequenced in our ABI 310 Genetic Analyzer. Contigs were compiled using Lasergene sequence analysis software (DNASTAR, Inc) and “blasted” into the NCBI Genbank. Our 330 bp mtDNA D-loop non-coding region contig showed a homology of 88.2% with Canada goose. White fronted goose (in a different genera) shows a homology of 81.5 % with Canada goose. Our 1,433 sequenced bps included three separate contigs in the coding region. They show a homology with the Canada goose of 94.5% (451/477) in contig 1, 95.7% (551/576) in contig 2, and 93.9% (358/380) in contig 3. White fronted goose sequences show a homology with the Canada goose of 92.4% (441/477) in contig 1, 93.9% (541/576) in contig 2, and 92.4% (351/380) in contig 3. These 1,433 sequenced bps constituted portions of the COXI, tRNA-Ser, tRNA-Asp, and COXII genes. We are continuing to analyze the other portions of the mtDNA of the brant in order to better compare the genotypes of these three species.