**Spatial and Temporal Patterns in Distemper Virus Cases Reported to SCWDS 1975-2013**

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**Introduction**

Canine distemper is an important infectious disease that affects many mammal species. The causative agent, canine distemper virus (CDV) is an enveloped, single stranded, negative sense RNA virus in the *Morbillivirus* family. Transmitted via the respiratory route, CDV is highly infectious (Deem et al 2000). There is evidence of CDV infection in all terrestrial carnivores families and some marine carnivore families (Deem et al 2000). Morbidity and mortality varies depending on the species but closely resembles rabies in wild carnivores (Hoff and Bigler 1974). The Mustelidae family is among the species with the highest fatality rate, while the domestic dog can be a asymptomatic carrier (Deem et al 2000). CDV has been detected in wild animal species such as the African lion and Amur tigers and has been responsible for substantial population declines of the animals during outbreaks (Roelke-Parker et al 1996, Seimon et al 2013).

**Canine Distemper Virus In the U.S.**

First seen in domestic dogs in the late 1970’s, CDV spread through the population rapidly (Alison et al 2013). CDV is seen most commonly in domestic cats and dogs but frequent cross species transmission does occur in non-domestic carnivores (Allison et al 2013 and Greene and Appel 1990). Severity in domestic dogs depends on the animals’ immune status and age in addition to strain virulence (Beineke et al 2015). In the U.S. raccoons (*Procyon lotor*), foxes (*Vulpes vulpes* and *Urocyon cinereoargenteus*), coyotes (*Canis latrans*), wolves (*Canis lupus*) , skunks (*Mephitis mephitis*), badgers (*Taxidea taxus*), mink (*Mustela vison*) and ferrets (*mustelidae spp.*) are among the species susceptible to CDV infection (Williams et al 1988 and Kapil et al 2008). In domestic ferrets mortality rates can reach 100%. CDV has been responsible for population declines of endangered mustelids like the black-footed ferret. CDV is also endemic in the eastern U.S. raccoon population. Raccoons are thought to be a reservoir for other wild animals and domestic dogs as well as other species of carnivores (Alison et al 2013, Mitchel et al 1997 and Roscoe 1993). CDV has been found to be persisting in areas like Yellow Stone national park, which has a diverse carnivore population. Multiple outbreaks have occurred in the wolf, coyote and cougar populations (Almberg et al 2009 and Almberg et al 2010).

Although raccoons are thought to be a major reservoir for CDV, little research has been done to identify the disease dynamics within this population. Available data is sparse, dated and focuses on individual states and discrete sites. The use of past and current presence only cases allows for spatio-temporal analysis of the CDV in the southeastern United States. The objective of this study was to identify spatial and temporal patters in distemper virus cases reported to the Southeastern Cooperative Wildlife Disease Study from 1975 to 2013.

**3. Methods**

Data was recorded from Canine distemper positive cases submitted to SCWDS between 1975 and 2013. Cases were identified as CDV by fluorescent antibody testing and/or histologic diagnosis of characteristic lesions. Species, date of submission, county of origin, and sex were noted.

Data was first analyzed using ArcGIS. Cases were pinpointed on a map of each state by county and longitude and latitude coordinates were taken from the center of each county. States with more than 2 cases in given month were considered an outbreak.

Cases were also analyzed by month, year and by species to tease out any temporal patterns.

* Habitat classification: Permeable surfaces
* Land cover
* Ripley’s K (spatial patterns)

**4. Results**

**Number of cases total: 702 submissions**

**Total number of states: 13 states**

**Which states:**

**Species breakdown (positive submission) over time:**

**Raccoons (N=462)**

**Grey fox (N=211)**

**Red fox (N=3)**

**Coyote (N=7)**

**Striped skunk (N= 130)**

**Bear (N=1)**

**Spatiotemporal patterns**

**GA raccoons:**

**Total patterns of submissions temporal:**

**Total patterns of submissions spatial:**

**Number of species submitted/temporal pattern (year submissions)**

**Season**

**Spatial spread patterns**

**Within Georgia**

**Overall southeast (not enough data)**

A total number of 702 positive cases were submitted from 13 states over the 38-year period. Positive cases were comprised of raccoons (n=462), gray foxes (n=211), striped skunks (n=13), coyotes (n=7), red foxes (n=3), gray wolves (n=3) and a black bear.

Cases were submitted from the following states: Alabama, Arkansas, Florida, Georgia, Kansas, Kentucky, Louisiana, Maryland, Mississippi, Missouri, North Carolina, Pennsylvania, South Carolina, Tennessee, Virginia and West Virginia.

The largest number of cases were submitted in 1988 (n=85) and consisted mostly of raccoons (n=65).

Patterns among submitted cases show a seasonal relationship with submitted cases. The greatest number of cases per year are seen in March and the lowest number in September. Data was de-trended to remove seasonality. Data reveal that a boon in cases start with gray foxes with raccoons occurring in the same month or following one month behind.

**5. Discussion**

* Initial introduction into wild carnivores in the U.S. in 1960’s was through grey foxes and subsequent spread to raccoons. (Hoff and Bigler 1974).
* Primary mode of infection is inhalation, suggesting habitat overlap and contact. (Hoff and Bigler 1974).
* Outbreaks appear to being during breeding seasons in both foxes and raccoons.
* Contact structure of a raccoon population can significantly impact disease transmission (Reynolds et al 2015)
* Rabies spreads for quickly in raccoons when introduced during the breeding season. (Reynolds et al 2015)
* Raccoon contact networks change depending on the season (breeding vs. non breeding) (Reynolds et al 2015)
* Outbreak in Berlin, German appears to have originated in foxes (Renteria-solis et al 2014)
* Gray foxes and raccoons in Tennessee (Nov. 2013 – Aug. 2014) were infected frequently (Pope et al 2016)
* Passive surveillance only captures animals showing clinical signs. Does not account for asymptomatic cases (Pope et al 2016)
* Populations sizes of each species vs. number of submitted cases