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Higher and more variable methylmercury biomagnification factors for floodplain than the contiguous river (South River, Virginia USA)

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ABSTRACT

Extending previous trophic transfer studies of the mercury-contaminated South River watershed, predictive models were built for mercury biomagnification in floodplain food webs at two more locations (North Park and Grand Cavern). Four of five models built to date based on methylmercury and $\delta^{15}N$ met the *a priori* requirement for useful prediction (prediction $r^2 \approx 0.80$). An additional factor included in models was organism thermoregulatory strategy (poikilothermy or homeothermy). The methylmercury food web biomagnification factors (FWMFs, fold increase per trophic level) for the North Park and Grand Cavern locations were 17.4 (95% CI of 9.5–31.6) and 6.2 (95% CI of 3.5–11.0) respectively. FWMF calculated in 2009 were 9.3 (95% CI of 5.4–16.2) for the Augusta Forestry Center and 25.1 (95% CI of 12.6–50.1) for Grottoes Town Park. The overall South River floodplain FWMF generated by meta-analysis of the four locations was 12.4 (95% CI of 6.8–22.3). These results supported previous findings that the South River floodplain food webs had higher biomagnification factors than the contiguous aquatic food web (4.6, 95% CI of 3.6–5.7). Floodplain FWMFs were also more variable than those of the river.

1. Introduction

Mercury, specifically methylmercury, can be elevated in some species due to biomagnification. Consequently, an ecosystem with modestly elevated mercury concentrations in soils or sediments might still have high body burdens of mercury in apex predators (dos Santos et al., 2006; Macedo-Sousa et al., 2009). This being the case, effective natural resource management and decision making requires tools for predicting mercury concentrations in apex predators via biomagnification (Tom et al., 2010).

Mercury biomagnification is influenced by community structure (Chasar et al., 2009), food source (Gorski et al., 2003; Chételat et al., 2011), food chain length (Cabana et al., 1994), trophic position (Newman et al., 2011) and other factors; however, trophic position is the most widely studied of these factors. Trophic position is commonly characterized with stable nitrogen isotope quotients ($\delta^{15}N$). Mercury biomagnification models have been produced for diverse aquatic food webs based on $\delta^{15}N$ (Campbell et al., 2008; Chasar et al., 2009; Tom et al., 2010). Far fewer have been produced for terrestrial food webs (Gaines et al., 2002; Choy et al., 2010; Newman et al., 2011) despite suggestions from recent studies that members of terrestrial food webs might experience similar or even higher mercury exposure (e.g., Cristol et al., 2008).

This study extended previous trophic transfer studies of a mercury-contaminated reach of the South River (Virginia USA). In a 2007 sampling of aquatic organisms at six locations along a river reach extending downriver 23 miles from the historic site of release, Tom et al. (2010) found that a $\delta^{15}N$ based trophic transfer model could predict methylmercury concentrations in members of aquatic food webs. The methylmercury food web biomagnification factor (FWMF) calculated from that model was 4.6 fold increase per trophic level (TL) (95% CI of 3.6–5.8) assuming that $\delta^{15}N$ increased 3.4‰ per TL (Newman et al., 2011; Chasar et al., 2009). Because several studies (Brasso and Cristol, 2008; Cristol et al., 2008) suggested that wildlife on the South River floodplain might be experiencing harmful mercury exposure, mercury biomagnification in two terrestrial locations on the South River floodplain, Augusta Forestry Center (AFC, Crimora, VA, 11.8 river miles (RM) below historic point of input) and Grottoes Town Park (GTP, Grottoes, VA, RM=22.4), was studied in 2009 (Newman et al., 2011). The 2009 floodplain study built models for each site, reinforcing the findings of the previous aquatic study that a $\delta^{15}N$–based model had better predictive capability for methylmercury concentration than for total mercury, and that the FWMFs from these floodplain locations (9.3, 95% CI of 5.4–16.2 and 25.1, 95% CI of 12.6–50.1 for AFC and GTP respectively) were

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higher than that of the contiguous aquatic food webs. Models for more floodplain locations were deemed necessary due to the material difference between floodplain and aquatic food webs, and the large difference between the two modeled floodplain sites. In May 2010, two more floodplain locations were studied (1) to assess whether the floodplain food webs had consistently higher FWMF than the contiguous aquatic food webs; and (2) to explore factors that might produce the differences observed among floodplain locations.

2. Materials and methods

2.1. Sampling

Two locations (AFC and GTP) were sampled during the summer of 2009 and another two were sampled in the same 23 mile river reach (North Park (NP, RM=2.0, about 10 acres) and Grand Cavern (GC, RM=20.0, about 30 acres)) during the first two weeks of May 2010. General sampling locations related to recent terrestrial studies can be found in Brasso and Cristol (2008). These two locations were added to collect samples between the historic point source and AFC, and between AFC and GTP, so that the four locations were relatively evenly distributed along the 23 mile river reach. Also, the locations selected were based on accessibility and coordination with another South River bird study. In each location, three sites were randomly selected within 50 m of the river bank. Terrestrial invertebrates were collected using either pitfall traps or sweep net. Samples from each site were pooled together for each species to form one replicate with at least two individuals (for invertebrates) in each pooled sample based on their sizes and availability. Triplicate samples were collected whenever possible. Mice and voles were captured by baited snap trap. Unfortunately, only a few small mammals were caught during the sampling period, so only three deer mice in NP, two pine voles in GC and one deer mouse in GC were available for analysis. Birds were captured using mist nets in each site. Again, the number of replicates depended largely on the availability of each species. Triplicate samples of emergent aquatic insects and crayfish were collected along the river bank. More details about sampling procedures can be found in Tom et al. (2010) and Newman et al. (2011). Species sampled in these two locations were shown in Table 1.

Table 1
Organisms from the two floodplain locations in South River watershed (VA, USA).

Locations	Common name	Latin name	Sample type	Symbol
Abiotic				
NP, GC	Soil			A
NP, GC	Leaf litter			B
Aquatic emergent insect				
NP, GC	Mayfly	*Ephemeroptera*	Adult—whole body	C
NP, GC	Midge	*Diptera*	Adult—whole body	D
NP, GC	Caddisfly	*Trichoptera*	Adult—whole body	E
Aquatic invertebrate				
NP, GC	Crayfish	*Astacoidea*	Whole body	F
Plant				
NP, GC	Grass	*Festuca elatior*	Green tissue	G
NP, GC	Honey suckle	*Lonicera japonica*	Green tissue	H
NP, GC	Violet	*Viola striata*	Green tissue	I
Detritivore				
NP, GC	Earthworm	*Lumbricus rubellus*	Whole body	J
NP, GC	Isopod	*Microcerberidae*	Whole body	K
NP	Slug	*Prophysaon dubium*	Whole body	L
Insect				
NP, GC	Ladybug	*Harmonia axyridis*	Adult—whole body	M
GC	Ground beetle	*Harpalus pensylvanicus*	Adult—whole body	N
GC	Caterpillar	*Lepidoptera*	Whole body	O
NP, GC	Eastern tent caterpillar	*Malacosoma americanum*	Whole body	P
NP	Asiatic garden beetle	*Maladera castanea*	Adult—whole body	Q
NP, GC	Common black ground beetle	*Pterostichus melanarius*	Adult—whole body	R
GC	Sawflies	*Tenthredinidae*	Larvae—whole body	S
Spider				
NP, GC	Wolf spider	*Lycosidae*	Whole body	T
Small mammal				
GC	Pine vole	*Microtus pinetorum*	Liver, muscle	U1,U2
NP, GC	Deer mouse	*Peromyscus maniculatus*	Liver, muscle	V1, V2
Bird				
NP, GC	Eastern tufted titmouse	*Baeolophus bicolor*	Blood, feather	BA1, BA2
NP, GC	Northern cardinal	*Cardinalis cardinalis*	Blood, feather	BB1, BB2
GC	Eastern wood-pewee	*Contopus virens*	Blood, feather	BC1, BC2
NP	Gray catbird	*Dumetella carolinensis*	Blood, feather	BD1, BD2
GC	Wood thrush	*Hylocichla mustelina*	Blood, feather	BE1, BE2
NP, GC	Eastern song sparrow	*Melospiza melodia*	Blood, feather	BF1, BF2
GC	Great crested flycatcher	*Myiarchus crinitus*	Blood, feather	BG1, BG2
NP, GC	Eastern screech-owl	*Otus asio*	Blood, feather	BH1, BH2
NP, GC	Downy woodpecker	*Picoides pubescens*	Blood, feather	BI1, BI2
GC	Scarlet tanager	*Piranga olivacea*	Blood, feather	BJ1, BJ2
GC	Eastern phoebe	*Sayornis phoebe*	Blood, feather	BK1, BK2
GC	White-breasted nuthatch	*Sitta carolinensis*	Blood, feather	BL1, BL2
GC	American goldfinch	*Spinus tristis*	Blood, feather	BM1, BM2
NP, GC	American robin	*Turdus migratorius*	Blood, feather	BN1, BN2
NP, GC	Carolina wren	*Thryothorus ludovicianus*	Blood, feather	BO1, BO2
GC	Red-eyed vireo	*Vireo olivaceus*	Blood, feather	BP1, BP2
GC	Mourning dove	*Zenaida macroura*	Blood, feather	BQ1, BQ2