Evaluation of One-Step versus Multi-Step Partition Modeling Approaches for Relating Selenium Concentrations in Surface Water and Fish

David K. DeForest,[1] Kevin V. Brix,[2,3] William J. Adams[4]

[1] Windward Environmental, Seattle, Washington
[2] EcoTox, Key Biscayne, Florida
[3] University of Miami, RSMAS, Miami, Florida
[4] Rio Tinto, Lake Point, Utah

For many bioaccumulative chemicals for which trophic transfer is the dominant exposure pathway, the concentration of a chemical in an organism's tissue may be a better indicator of potential toxicity than the concentration of the chemical in the external environment (e.g., surface water). However, in order to develop water quality criteria or guidelines for such chemicals, it is necessary to relate a tissue-based toxicity threshold to a water-based concentration. One example is selenium, an essential element that exists in inorganic and organic forms, with toxicity primarily manifested in aquatic systems via the transfer of organic selenium to oviparous vertebrates (e.g., fish, birds). The bioaccumulation potential of selenium is highly dependent on site-specific biogeochemistry. Mechanistic selenium bioaccumulation models have so far proven to require significant amounts of data and have not been validated for a range of sites. Rather, selenium partitioning modeling approaches based on empirical data have shown more promise. These partitioning models simply rely on coefficients that relate selenium concentrations between two media. In a one-step approach, the selenium concentration in fish or bird tissue (eggs) is related directly to co-located water selenium concentrations. In a multi-step approach, selenium partitioning coefficients are derived for each general step in the food chain: a K_d to describe selenium partitioning from water to the base of the food chain and trophic transfer factors (TTFs) to describe the transfer of selenium between trophic levels. The selenium K_d may vary by 1 to 2 orders of magnitude between sites, while TTFs are much less variable between taxa (often varying by a factor of < 2). Accordingly, the selenium K_d is the most critical variable in deriving site-specific selenium criteria or in deriving generic screening criteria. The site-specific selenium K_d is implicitly accounted for in a one-step partitioning model and is an explicit variable in a multi-step partitioning model. Overall, information provided by both one-step and multi-step modeling approaches is useful for developing generic screening criteria. However, for site-specific criteria development, the one-step modeling approach is more desirable because it includes empirical measurements of selenium in the critical target tissue (or surrogate tissue) and eliminates the uncertainty in accounting for the site-specific food chain structure.