Methylmercury cycling in wetlands managed for rice agriculture and wildlife: Implications for methylmercury production, transport, and bioaccumulation

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Extensive research on Hg has shown that wetland conditions promote microbial methylation of inorganic mercury into MeHg, primarily through the activity of sulfate- and iron-reducing bacteria. Agricultural wetlands, especially rice farms, are among the most abundant wetland ecosystems in temperate and tropical latitudes. In California, rice field acreage is greater than that of remaining natural wetlands. In 2007–8, a multidisciplinary study documented MeHg dynamics in seasonally flooded wetlands, specifically assessing the influence of agricultural management for white rice and wild rice production (shallow flooding, fertilizer addition, and high rates of carbon fixation). We focused the study on the Yolo Bypass Wildlife Area, one of several wetland regions of the California Central Valley where sediment Hg is elevated due to historic gold and mercury mining. Quantitative comparison of processes among different fields and between seasons showed that ecosystem components (water, soil, biota) were linked but that processes were temporally decoupled in seasonally flooded wetlands. Within-field hydrology (e.g. transpiration) strongly influenced water and sediment chemistry, with important variability between winter and summer flooding periods and between seasonally and permanently flooded wetlands. Other key findings [1, and references therein] were the significance of winter MeHg production and export, the dominant role of vegetation in MeHg cycling among components, and the elevation of MeHg bioaccumulation during periods of evapoconcentration. The data suggest that field management options may exist to reduce MeHg production (winter detrital management) or to promote MeHg degradation and storage (open-water cells), prior to MeHg export or biotic exposure.

[1] Windham-Myers *et al* (2014) *Sci. Tot. Environ.*