Phytate degradation by different phosphatase enzymes: Contrasting kinetics, isomer compositions, decay rates, pathways, and isotope effects

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Phytate (IP_6) is often the most common organic phosphorus compound in soils and sediments. Understanding the fate of inositol phosphate (IP_x) isomers in the environment in terms of their composition and concentration and assessing their relative resistance (or preference) against degradation is essential to estimate their potential role on resupplying inorganic P (P_i) and impacting water quality. Furthermore, distinction made among the suites IP_x compounds produced and degradation pathways generated allows potential identification of active phosphohydrolase enzymes in the environment. We sought to identify distinction among the suites IP_x compounds produced and degradation pathways generated by different enzymes. Particularly, we analyzed IP_6 degradation by four different phosphohydrolase enzymes (phytase from wheat and *Aspergillus niger* and acid phosphatase from wheat germ and potato) with particular focus on degradation pathways, isomer kinetic decay rate, and isotope effect during degradation using a combination of HPIC, NMR, stable isotopes, and process-based modeling techniques. Our results show that all enzymes generate largely distinct sets of isomers and have both major and minor degradation pathways. The process-based model and Bayesian inverse modeling allowed to determine the decay kinetics parameters of phytate and the generated isomers and well captured the trend and magnitude of the measured concentrations for each IP_x isomer. Furthermore, oxygen isotope ratios ($\delta^{18}O_P$) of released P_i enabled to identify isotopically identical phosphate moieties in phytate. We conclude that distinctly different fractionation factors, degradation pathways, and kinetic decay rate coefficients among enzymes studied could lead to potential discrimination of phytate sources and the presence of active enzymes in the environment.