



# 73rd CRC Seminar

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Dr. Brian Waters of University of Nebraska-Lincoln, is the speaker of 73<sup>rd</sup> CRC seminar. Dr. Brian works on iron, an essential mineral element in plant and human. He is an expert in iron transport and translocation in plant. Recently his group has taken a transcriptional profiling approach in different accessions of Arabidopsis to find the difference in “ironomes” in different accessions. Based on the transcriptional profiling data, they propose that iron and copper homeostasis are tightly linked across biology. Dr. Brian will introduce the data and discuss on yet unidentified potential regulators of copper or iron uptake carriers in plant.

**"Copper and iron deficiencies interact to increase uptake of both metals".**

時間：2012年12月4日（水）16:40～18:00

場所：総合教育研究棟（生命系）1階 遠隔講義室

Iron (Fe) is an essential mineral element for plants and humans. Understanding regulation of plant Fe uptake and transport is crucial to improve the Fe nutritional quality of plant-based foods (biofortification) and to improve agricultural production. Fe uptake and transport genes (among others) have altered expression when plants experience Fe deficiency. Transcriptional profiling indicated substantial natural variation in Fe deficiency responses, shown by differences in ‘ironomes’ between different accessions. Iron and copper (Cu) homeostasis are tightly linked across biology. Here, a model is presented and tested, which states that plants accumulate additional Cu when they are Fe deficient, in order to facilitate replacement of Fe containing proteins with Cu containing proteins. Arabidopsis mutants were used to test whether this Cu accumulation requires the primary Fe uptake system. The *Cucumis melo* Fe uptake mutant C940-fe was used to test whether Cu deficiency stimulated Fe uptake. Increased accumulation of Cu or Fe was stimulated by deficiency of the other metal. Neither Cu nor Fe uptake depended on the currently known primary Cu or Fe uptake systems, as indicated by analysis of mutants, suggesting that additional uptake genes are yet to be identified.

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