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Simple Way to Study Plant Ionomics : A Functional Tool of Genomics

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ABSTRACT

In the present era of omics/genomics, Ionomics is one of the major technology for the structural and functional genomics study. Natural variation in the regulation of the accumulation of mineral nutrients and trace elements in plant tissues is crucial to plant metabolism, development, and survival across different habitats. With the advancement in the field of genomic study the genomic level regulation of the ions in the plant system has been studied which pave the path for the discovery of the novel gene with its function. Studies of the genetic basis of natural variation in nutrient metabolism have been facilitated by the development of Ionomics. Ionomics is a functional genomics approach for the discovery of the genes and gene networks which regulate the elemental composition, ionome of an organism. The complete ionomic profiling of the plants are done by using a number of analytical tools like ICP-MS, ICP-OES, X-Ray crystallography, Neutron Activation Analysis (NAA) etc. All these analytical tools yields complete profile of the ions present in the plants. These data are stored in a database called PiiMS (Purdue Ionomics Information Management System). This huge data helps in the forward and reverse genetic approach for studying the structural and functional genomics of the particular organism. Studying genetic variation in elemental accumulation can provide major insights into how plants adapt to heterogeneity of soil types that comprise the natural landscape. Thus, Ionomics is a relatively inexpensive yet comprehensive physiological profiling technique, especially for research questions involving mineral nutrition, making it well suited for plant studies. Using the appropriate combinations of instrument, tissue and controls will enable researchers to harness the power of Ionomics for genetics, gene discovery and modelling.

Key words: *Functional genomics, Ionome, Ionomics, Database, QTL mapping.*

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INTRODUCTION

Plants being sessile in nature, take nutrients in the water soluble form as ions. Based on the plant requirement, nutrient ions are classified into 3 categories: 1) macronutrients, 2) micronutrients, 3) beneficial elements. Among 92 elements, 17 elements are found to be essential for all the plants. The elements required in large amount, i.e., >0.1% dry mass, are named as the macronutrients (C, H, O, N, S, P, Ca, Mg, K) and those which are required in very low amount, i.e., <0.01% of dry mass, are referred as the micronutrients (Ni, Mo, Cu, Zn, Mn, B, Fe and Cl) and beneficial elements (Na, Co, Al, Se, Si), which promote growth and may be essential to some plants. Moreover, the better growth and development of the plant depends upon the balanced supply of nutrients to the plants. With the advancement in the genomic study the genomic level regulation of the ions in the plant system has been studied which leads to discovery of the novel gene with its function[7].

Ionomics specifically focuses on the total ionome profile of an organism and how these ions are regulated in the organism's body for balanced metabolic process. Hence, ionomics is one of the most important and novel tool of the functional genomics. Ionome is defined as 'the mineral nutrient and trace element composition of an organism, representing the inorganic component of cellular and organismal systems'[13]. It is a dynamic network of elements that are controlled by the physiology and biochemistry of the plant, which are ultimately controlled by the genome, in response to the environment. Hence, the Ionomics is defined as the, "study of quantitative complement of low molecular weight molecules present in cells in a particular physiological and developmental state of the plant"[7].

History:

The idea of plant ionomics begins with the mixing of metabolomics and mineral nutrition (Robinson and Pauling-late 60s and early 70s). David *et al.*[4], included all the metals, metalloids, and non-metals present in an organism in the ionome. Salt[10] described the term 'plant ionome'.

Concept of the Ionome and Ionomics:

Ionome was defined as total mineral nutrient and trace elements found in an organism. This definition extended the metallome to include biologically significant nonmetals. The ionome also includes both non essential and essential elements. The concept of the ionome has been applied to *Saccharomyces cerevisae*; the mineral nutrient and trace element profile of 4385 mutant strains from the *Saccharomyces* Genome Deletion collection were recently quantified. The study in *S. cerevisae* represents the first full genome wide scan for genes involved in the regulation of the ionome in any organism[4].

The ionome term originally used to describe the global metabolite pools in *Escherichia coli* and *S. cerevisae* and has now been generalized to describe the "quantitative complement of all the low molecular weight molecules present in cells in a particular physiological or developmental state"[7]. Further drawing on these parallels with the metabolome and its study of metabolomics, the study of the ionome, called Ionomics, is defined as 'the quantitative and simultaneous measurement of elemental composition of living organisms and changes in this composition in response to physiological stimuli, developmental state, and genetic modifications'[4]. This definition captures and highlights several critical concepts in the study of the ionome.

Firstly, the study of the ionome is predicated on the fact that, it should provide a snapshot of particular functional status or physiological or disease state of complex biological organism; this information is held in both the quantitative and qualitative patterns of mineral nutrients and trace Secondly, the power of ionomics lies in its ability to precisely capture information about the functional state of an organism under different conditions[4]. These conditions may be driven by factors like genetic differences or developmental differences or by biotic or abiotic factors. The underlying cause of change in the ionome may be either indirect or direct.

Ionomics has the potential to provide a relatively high throughput and relatively low cost approach to not only the functional analysis of the genes and gene networks that directly control the ionome, but also to analysis of the more extended gene networks that control developmental and physiological processes that indirectly affect the ionome[6].

Analytical tools for Ionomics:

The analytical tools used are ICP-MS, ICP-OES, X-Ray crystallography, Neutron Activation Analysis etc. These data are stored in a database called PiiMS (Purdue Ionomics Information Management System). This data helps in the forward and reverse genetics approach for studying the structural and functional genomics of the particular organism[2].

Applications of Ionomics:

As defined, central theme of Ionomics is the study of changes in the ionome in response to "physiological stimuli, developmental state, and genetic modifications." In this context we discuss the application of Ionomics[13].

1. Studying genetic variation in elemental accumulation provide major insight into how plants adapt to heterogeneity of soil.
2. Identification of QTLs/genes or gene network that govern the elemental accumulation (Table1) and also correlation studies between the elements in the organisms.
3. Ionome as biomarkers - the study establishes the multivariable ionomic signatures of physiological states associated with mineral nutrient homeostasis.
4. Rapid characterization of plant mutants with an altered ion-profile can be done.
5. Phylogenetic analysis - We can use ionome profile for evolution pattern of organisms.
6. Functional genomics - Ionomics is called as the fourth pillar of the functional genomics.

Table 1: Mineral nutrient QTLs discovered in different crops

Sl No.	QTL for	Marker interval/Marker	Chromosome	Organism	Refference
1	Fe	Xwmc382-Xbarc124	2	Wheat	Vijay, *et al.,* (2009)
2	Zn	Xcfd31-Xcfa2049	7	Wheat	Vijay, *et al.,* (2009)
3	Mn	RM3475	1	Rice	Ana, et al., (2009)
4	P	umc59e	3	Maize	Domagoj, *et al.,* (2011)
5	Ca	e721b	8	Yellow monkey flower	Lowry, *et al.,* (2012)

CONCLUTION

The Ionomics is one of the pillar for the functional genomics, helps us to widen the area of functional genomics. It will help in the identification of the gene and the gene network and coordination among the different genes controlling different ion accumulation in the plant system. It also helps in better understanding of the relationship between the ions and identification of the gene and environment interaction at different stages of growth. Ionomics also helps in the marker assisted breeding of the plant with introgression of the gene into the other plant. In this way, the Ionomics helps in the nutrigenomics approach for production of the micronutrient rich food. Many of the ions are toxic for the plant as well as the human beings. Hence, by the knowledge of the genes that regulate the accumulation of the ions, we can manipulate the ionome profile of the plant system.

Thus, Ionomics is a relatively inexpensive yet comprehensive physiological profiling technique, especially for research questions involving mineral nutrition, making it well suited for plant studies. Using the appropriate combinations of instrument, tissue and controls will enable researchers to harness the power of Ionomics for genetics, gene discovery and modelling[11].

Future of Ionomics[8]

- Bioinformatics tools for analysis & data storage are lacking, hence we need to develop the tools
- Ionomics for MAS with introgression of gene can be done
- We can apply Ionomics in the field of Nutrigenomics
- Phylogenetic studies can be conducted using Ionomics analysis
- Transfer of QTLs which are responsible for specific elements across the species
- Regulation of toxic ions by manipulating ionome profile at genomic level
- We need Ionomic imaging for different plant tissues with high resolution for multiple elements
- Ionomics study should extend to more species
- Reduction of cost of technology
- The contention that quantitative profiles of biomolecules contain information about the physiological state of the organism has motivated a variety of high-throughput molecular profiling experiments. However, unbiased discovery and validation of biomolecular signatures from these experiments remains a challenge.

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