REVIEW ON INOMICS

ABSTRACT

Ionomics is a high-throughput elemental profiling technique used to investigate the molecular mechanisms driving the composition of minerals, nutrients, and trace elements in living things. The discovery of the gene networks that regulate the ionome has advanced significantly since the ionomics idea was first proposed more than 11 years ago. In this update, we provide a summary of the ionomics approach's ten-year progress, which includes studying natural ionomic variation and forward genetics-based gene identification. We also go over how ionomics might be used to study how ionomic alleles work ecologically in terms of environmental adaption.

Keywords: Ionomics, Minerals, Nutrients, Metabolics

INTRODUCTION

"The composition of minerals, nutrients, and trace elements in an organism, and the inorganic part of cellular and organismal systems" is the definition of the ionome. (Salt and others, 2008). Significant advancements have been achieved in the field of ionomics, which combines genetics and high-throughput elemental profiling to uncover the genes that control the ionome, since the concept of the ionome was initially presented more than 11 years ago (Lahner et al., 2003). (Danku et al., 2013).

IMPROTANTEVENTS IN IONOMICS

Combining metabolomics and mineral nutrition is where the concept of plant ionomics originates. It all began with the belief held by Robinson and Pauling in the late 1960s and early 1970s that an organism's metabolite profile is a rich source of information and a representation of its physiological state. Since the 19th century, when it was first recognized as a scientific field, significant progress has been achieved in characterizing and comprehending the fundamental biology of nutrient ion homeostasis in plants (Marschner 2011). The early theories of Robinson and Pauling on metabolomics may be correlated with mineral ions since a number of trustworthy technologies have been created to concurrently analyze the metabolites and

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mineral nutrition components of living beings. This marked the beginning of Ion is a reflection of an organism's physiological state.

The basic biology of nutrient ion homeostasis has been described and understood with amazing advancement in the notion of the ionome. With the aid of bioinformatics and other genetic tools, such as sequenced genomes, DNA microarrays, and others, ionomics is now growing stronger every day [12-16]. For the first time, the ionome of Lahner et al. (2003) contained every metal, metalloid, and non-metal found in an organism. The term "plant ionome," coined by Salt and colleagues in 2008, refers to the entire concentration (i.e., all forms) of specific elements in a plant tissue sample. It offers both quantitative and qualitative data regarding the state of a cell, tissue, or organism's functionality. Research on the relationships between While research on the genome, transcriptome, metabolome, proteome, and metabolome (Leonhardt et al., 2004; Fiehn et al., 2000; Koller et al., 2002) is ongoing, research on the ionome is only getting started (Fleet et al., 2011).

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IDENTIFICATION OF IONOMIC GENES BY FORWARD GENETICS

Lahner et al. conducted a methodical screen for mutants with altered leaf ionomic profiles (2003). From a screen of 4747 M2 fast neutron (FN) mutant plants, 338 putative mutants with changes in the leaf accumulation of single or multiple elements were found in this proof-of-concept screen. After rescreening all M3 families, 51 of these 338 suspected mutations were shown to be real. A similar extensive ionomic screen of 2000 mutagenized M2 Lotus japonica plants was carried out by Chen et al. (2009). To enable the collection and examination of thousands of plant samples, plants must be regularly cultivated in various experimental blocks (such as plant culture trays) over the course of several months in this kind of extensive studies. Notably, the ionome can change at different growth rates as well.

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In the FN-mutated Arabidopsis thaliana screen, each plant growth tray contained the wild type and the known ionomic mutant frd3 as controls. The plants were taken when they were five weeks old. According to several studies (Rogers and Guerinot, 2002; Green and Rogers, 2004; Durrett et al., 2007; Roschztardtz et al., 2011; Pineau et al., 2012), the citrate transporter encoded by FRD3 is crucial to the Fe deficient response. A mutation in FRD3 causes an excess of certain metals, such as Mn and Co, to accumulate in leaves (Delhaize, 1996). Using the leaf ionome as the phenotype, hierarchical clustering of 44 verified FN mutants (Lahner et al., 2003) shows that mutant grouping is typically independent of the plant cultivation tray or the soil batch. Additionally, frd3 cultivated in various growing trays and soil.

RECENT ADVANCES IN PLANT IONOMIC TECHNIQUES

The previously described element estimate techniques are not capable of studying the effects of any changes at the cellular or subcellular level in plants and their environment because they are based on either electronic or nuclear properties. In fact, some of the methods employed today to prepare samples for research on variations in elemental composition interfere so much that they upset the internal elemental profile of the cell [17,18]. To comprehend the process and regulation of ion homeostasis, which involves the movement and storage of a specific ion at the cellular and subcellular levels, new study is nevertheless required.

In this situation, synchrotron-based X-ray fluorescence microscopy (SXRF) will be perfect for providing fundamental answers about metal abundance and could be a very helpful technology for gathering spatially resolved data metal homeostasis in plants, including the types of membranes and cellular compartments involved in the uptake, transportation, and storage of these ions within a cell, among other details. Additionally, Fahrni (2007) gives information regarding the function of responsible transport systems and how they affect the element(s)' bioavailability.

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SXRF is a multi-elemental method that gathers data on several metals at once without altering the sample's initial state. With this approach, sample preservation and sectioning are typically not required. It provides simultaneous quantitative imaging of a greater number of elements in a non-destructive manner without requiring invasive sample preparation. This technique requires high-energy, focused X-rays produced at synchrotron facilities in order to photograph an element in a range of tissues, from moist roots to dried seed (Yang et al. 2012). The inner shell electrons are excited by an X-ray beam, which finally produces detectable X-ray fluorescence. This method enables multielement analysis since each element has a distinct fluorescence spectra (Qin et al. 2011). Using SXRF, Yang et al. (2012) investigated the distribution of Ca in various seed tissues and cells, realizing the potential use of SXRF in spatial resolution of components at the cellular and subcellular levels from newly harvested, thoroughly hydrated, or ideally living tissue.

TECHNOLOGY USED IN PLANT ELEMENT PROFILING

Plant ionomics necessitates measuring the elements and ion content of the entire plant, tissue, and even individual cells. Numerous cutting-edge technologies and equipment are involved, ranging from specialized instruments to sample preparation techniques. These could change based on the variables to be assessed, sample size availability, sample throughput, dynamic quantification range, sensitivity, accuracy, and dependability. These instrumental methods used an atom's property to detect things. Certain elements are based on their electrical properties, while others are based on their nuclear properties. All methods are categorized intotwo groups based on data from the literature:

(i) methods based on elemental electronic characteristics, such as X-ray fluorescence spectroscopy (XRF), Ion beam analysis (IBA), and atmospheric absorption spectrometry (AAS).

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Techniques based on the nuclear characteristics of elements: inductively coupled plasma spectroscopy

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(ii) Analysis of neutron activation (NAA)

USES OF PLANT IONOMICS

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Ionomics is utilized to find potential transporter genes and validate their functionalities in order to comprehend the mechanism of mineral transport in plants. Utilising high-throughput elemental analysis technology in conjunction with genetic and bioinformatics techniques is necessary. Plant physiological status is assessed, and this technique identifies biomarkers (ionome profiles) for each status (Baxter 2009). Phylogenetic study of plant species is another application for ionomic data (White et al. 2012). Here, we've discussed a few ionomics applications for researching plant mineral transport and storage.

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• QTL and gene identification

• Gene(s) functional validation

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CONCLUSIONS AND PERSPECTIVES

Over the past ten years, ionomics has become a potent technique for accurately identifying the genes and gene networks that regulate the homeostasis of minerals, nutrients, and trace elements. For this kind of achievement, high-throughput elemental profiling analytical techniques have to be quickly integrated with contemporary molecular genetics. Gene to function (and publication) can still take a while, but the molecular, cellular, and physiological roles of genes found using this method are beginning to be unravelled. Furthermore, ionomics has improved our knowledge of the locus governing spontaneous ionomic variation. If allelic variants of ionomic loci exist, their ecological roles are still mainly unclear. Following the publication of the 1307 A. thaliana accessions RegMap panel (Horton et al., 2012), It is now possible to investigate the potential ecological functions of ionomic loci across the genome thanks to the combination of both regional and species-wide collections, accurate information on the collection site of each accession, and the growing availability of whole-genome sequences of over 1000 accessions (http://1001genomes. org/). These potential are giving rise to a field of study that could be called "landscape ionomics," which will necessitate the integration of population genomics, ionomics, and field-based ecological investigations.

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REFERENCES

1. Baxter IR, Vitek O, Lahner B, Muthukumar B, Borghi M, Morrissey J, Guerinot ML, Salt DE (2008) The leaf ionome as a multivariable system to detect a plant's physiological status. Proc Natl Acad Sci USA. 105:12081–12086

2. Blake L, Goulding KWT (2002) Effects of atmospheric deposition, soil pH and acidification on heavy metal contents in soils and vegetation of semi-natural ecosystems at Rothamsted Experimental Station, UK. Plant Soil 240:235–251

3. Blake L, Goulding KWT, Mott CJB, Johnston AE (1999) Changes in soil chemistry accompanying acidification over more than 100 years under woodland and grass at Rothamsted Experimental Station, UK. Eur J Soil Sci 50:401–412

4. Chao D-Y, Gable K, Chen M, Baxter I, Dietrich CR, Cahoon EB, Guerinot ML, Lahner B, Lü S, Markham JE, Morrissey J, Han G, Gupta SD, Harmon JM, Jaworski JG, Dunn TM, Salt DE (2011) Sphingolipids in the root play an important role in sregulating the leaf ionome in Arabidopsis thaliana. Plant Cell 23:1061–1081. doi:10.1105/tpc.110.079095

5. Chen Z, Watanabe T, Shinano T, Okazaki K, Osaki M (2009) Rapid characterization of plant mutants with an altered ionprofile: a case study using Lotus japonicus. New Phytol 181:795–801

6. Cheng Y, Ishimoto K, Kuriyama Y, Osaki M, Ezawa T (2013) Ninety-year-, but not single, application of phosphorus fertilizer has a major impact on arbuscular mycorrhizal fungal communities. Plant Soil 365:397–407

7. DePaula FCF, Mozeto AA (2001) Biogeochemical evolution of trace elements in a pristine watershed in the Brazilian southeastern coastal region. Appl Geochem 16:1139–1151

8. Lahner B, Gong J, Mahmoudian M, Smith EL, Abid KB, Rogers EE, Guerinot ML, Harper JF, Ward JM, McIntyre L, Schroeder JI, Salt DE (2003) Genomic scale profiling of nutrient and trace elements in Arabidopsis thaliana. Nat Biotechnol 21:1215–1221

9. Li BY, Zhou DM, Cang L, Zhang HL, Fan XH, Qin SW (2007) Soil micronutrient availability to crops as affected by long-term inorganic and organic fertilizer applications. Soil Till Res 96:166–173
10. Liu A, Hamel C, Hamilton RI, Ma BL, Smith DL (2000) Acquisition of Cu, Zn, Mn and Fe by mycorrhizal maize (Zea mays L.) grown in soil at different P and micronutrient levels. Mycorrhiza 9:331–336

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11. Liu Y, Mi G, Chen F, Zhang J, Zhang F (2004) Rhizosphere effect and root growth of two maize (Zea mays L.) genotypes with contrasting P efficiency at low P availability. Plant Sci 167:217–223

12. Singh A, Jaiswal A, Singh A, Tomar RS, Kumar A. Plant ionomics: Toward high-throughput nutrient profiling. InPlant Nutrition and Food Security in the Era of Climate Change 2022 Jan 1 (pp. 227-254). Academic Press.
13. Zhang Y, Xu Y, Zheng L. Disease ionomics: understanding the role of ions in complex disease. International Journal of Molecular Sciences. 2020 Nov 17;21(22):8646.
14. Huang XY, Salt DE. Plant ionomics: from elemental profiling to environmental adaptation. Molecular plant. 2016 Jun 6;9(6):787-97.
15. Pita-Barbosa A, Ricachenevsky FK, Flis PM. One “OMICS” to integrate them all: ionomics as a result of plant genetics, physiology and evolution. Theoretical and Experimental Plant Physiology. 2019 Mar 15;31(1):71-89.
16. Mann A, Singh S, Kumar A, Kumar S, Kumar B. Plant Ionomics: An Important Component of Functional Biology. InMetabolic Adaptations in Plants During Abiotic Stress 2018 Sep 3 (pp. 147-154). CRC Press.
17. Chen A, Hansen TH, Olsen LI, Palmgren M, Husted S, Schjoerring JK, Persson DP. Towards single-cell ionomics: a novel micro-scaled method for multi-element analysis of nanogram-sized biological samples. Plant Methods. 2020 Dec;16:1-3.
18. Fikas AA. A Combinatorial Approach of Ionomics, Quantitative Trait Locus Mapping, and Transcriptome Analysis to Characterize Element Homeostasis in Maize. Washington University in St. Louis; 2019.

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