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Overview of New Paradigms in the Field of Plant Sciences

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Short Commentary

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Paradigm shifts are the core of scientific revolutions. They change how we view the world, the questions that scientists consider worth asking and the manner of doing science. There is often talk of paradigm shifts in reference to a global change of theory, such as the eclipsing of the geocentric by the heliocentric world vision (Copernican theory), the discovery of plate tectonics, the particular theory of heredity (Mendelian theory), or the discovery that DNA is the physical carrier of inheritance. Furthermore, paradigm shifts are used to refer to drastic changes occurring at a narrower scale, and triggering a number of backbone modifications in conceptual systems within the concerned disciplines.

Recent biology is passing through a critical cross-road from reductionist concepts and methodologies towards the post-genomic, holistic, systems-based analyses of integrated and communicative networks of life processes. As a fundamental part of biology, plant sciences have been witnessing a number of paradigm shifts that have become evident since the dawn of this 21st century, which I treat here after.

THE EMERGENCE OF COMPUTATIONAL BIOLOGY

An increasing number of biological studies are focusing on the computational analysis of genomic and transcriptomic sequences from model and non-model plant species. Computational approaches have been developed to examine gene finding, gene expression, transcriptome assembly, and conserved elements identification, through computer programs.

AFTER PLANT GENOMES, PLANT PHENOMES

The terms genotype and phenotype were introduced by the Danish plant physiologist and geneticist Wilhelm Johannsen in 1909. An individual's genotype denotes the constitution of parts or all of its genetic material, while its phenotype may comprise any characteristic or trait.

Just as the genome and proteome signify all of an organism's genes and proteins, the phenome is the set of all phenotypes expressed by a cell, tissue, organ, organism, or species.

Entire genomes are now rapidly sequenced at steadily declining costs and ever increasing speed. Next Generation Sequencing methods provide opportunities to get the complete genotype and epigenotype not only of a single individual of a genus or species, but even of a population or a phylogenetic group, to reveal punctual, sometimes rare, differences along the genome. High-density Single Nucleotide Polymorphism (SNP) genotyping, first pioneered in the human HapMap project, have become tractable for any organism and are now routinely applied to plants, for the design of molecular markers associated with quantitative trait loci (QTLs) or genes, and for studying the diversity and evolutionary dynamics of several plant species ^[1]. SNP databases are available for a great number of plants.

Phenomics, the study of the phenome, is a rapidly emerging area of science, which seeks to characterize phenotypes in a rigorous and formal way, and link these traits to the associated gene variants (alleles). The phenotypic parameters that could be studied include morphological measures (e. g. tree height or wheat yield), metabolic measures (e. g. nutrient uptake), and molecular measures (e. g. transcript profiles). Because phenomics is the science of large-scale phenotypic data collection and analysis, it has been greatly enhanced by the increasing development of high throughput technologies, which made phenomics results increasingly powerful. Therefore, plant genome science is moving beyond the era of reference and model plants to study in depth any plant that has characteristics of interest to science and society.

GENOMIC SELECTION: THE FUTURE OF MARKER - ASSISTED SELECTION

The mission of plant breeding is to develop high-yield varieties to increase crop productivity to meet the need of human populations. Genomic selection is an upgrading form of marker-assisted selection for quantitative traits, and it differs from the traditional marker-assisted selection in that markers in the entire genome are used to predict genetic values. Genomic selection holds the promise to be more efficient than the traditional marker-assisted selection for traits controlled by polygenes. Genomic selection is also cost-saving due to early selection before phenotypes are measured. When applied to hybrid breeding, genomic selection is even more efficient because genotypes of hybrids (hybrid performance) are predetermined by their inbred parents [2].

FROM AN OBSOLETE “JUNK DNA” DOGMA TO A NEW PARADIGM OF “MULTI -TASK DNA”

Genomes are much more complex and dynamic as we ever anticipated. Plant genomes often have high proportions of non-coding DNA sequences. Rather than to constitute ‘junk DNA’, non-coding sequences are, nowadays, more thought to be part of multitask networks integrating coding DNA [3]. Often plant genomes are exposed to a selective pressure due to multiple biotic and abiotic stresses, and mutations in genes can occur. The definition of ‘what is a gene’ remains far from being surrounded by biologists and thus, we are learning to be careful in dealing with the concepts of under-expression, knocking-out, or overexpression of any particular gene [4,5]. It is increasingly clear that when mutations occur in single genes, the dynamic genome can actively regain the lost balance, via extensive re-shufflings of non-coding DNA, and even through subtle re-arrangements of chromatin structure and genome architecture.

INSIGHTS INTO THE AMAZING WORLD OF TRANSPOSABLE ELEMENTS

Plant genomes are packed with transposable elements (TEs) and a proportion of them that contain protein-coding sequences are often (wrongly) annotated as genes. In rice for instance, it was estimated that only 40,000 of the more than 55,000 annotated genes are really genes and that the other 10,000 to 15,000 are TEs [6,7]. TEs include various families that move via copy-and-paste (class I) and cut-and-paste (class II) mechanisms. Copy-and-paste TEs can dramatically increase the size of a plant genome.

Transposon biology is an intriguing area of research and relies on relatively complete genomes so that TEs are captured in sequence contigs and can be accurately annotated. There are conventional schemes for classification of TEs, but annotation of non-LTR TEs is complicated by the lack of structural clues, which complicates both their prediction and classification. Another complication is that in genomes produced by short read DNA sequencing technology, TEs are often missed in the assembly due to their repetitive nature. The proportion of repetitive DNA across 55 completely sequenced plant genomes ranges from 3 to 85% with a median of 43% and TEs, specifically cut-and-paste TEs (LTRs), represent the majority of that repetitive DNA [8]. Capturing and annotating these genomic components is important as it is becoming increasingly clear that TEs can be domesticated to function in gene regulation and as structural components of the genome.

SMALL RNAs: ANOTHER AMAZING WORLD

Although RNA was initially considered to be a passive intermediate in the flow of information from DNA to protein, the regulatory capacity of RNA is now well established. Over the past few years, it has been revealed that there is a world of small non-coding RNAs that not only regulate gene expression on post-transcriptional and transcriptional levels, but also affect the organization and modification of chromatin.

Further complicating annotation is that there are many expressed non-coding RNAs that are functionally important, but not considered genes in a traditional sense [9]. Small RNA precursors are often not included in a genome annotation, but are important for plant development and silencing of TEs [10]. Small RNAs and other non-coding RNAs are often annotated and curated separately from genome annotations in dedicated databases. Among small RNAs, the category of microRNAs (miRNAs) have very small sizes of ~22 nucleotides; and they constitute the most sophisticatedly characterized small RNA category that was shown to play essential regulatory roles in gene expression in plants [11].

FROM THE “CELL THEORY” TO A NEW PARADIGM OF “SYSTEMS CELL BIOLOGY”

Eukaryotic cells organisation shows numerous supracellular situations; the most dramatic one is represented by plants where all cells are interconnected via plasmodesmata into a supracellular organism [5]. This connectively indicates that the

currently valid dogma of the 'Cell Theory' is approaching its replacement with a new updated concept of a more extended basic unit of eukaryotic and plant life ^[12].

Systems biology is defined as a framework for conducting a rigorous analysis of the complexity of biological systems at all levels of cellular organization, with the goal to achieve a thorough understanding of how information is transmitted and interpreted by cells ^[13]. Systems biology is commonly associated with large-scale "omics" technologies such as genomics, proteomics, and functional genetics that are used to explore the state of a system under investigation ^[14].

PLANT NEUROBIOLOGY: A VERY PROVOCATIVE NEW IDEA IN PLANT SCIENCES

The past ten years have witnessed the birth and propagation of a provocative idea in the plant sciences. Its proponents have suggested that higher plants have nerves, synapses, the equivalent of a brain localized somewhere in the roots, and an intelligence. The idea has attracted a number of adherents, and meetings have been held in different host countries to address the topic, and an international society devoted to 'plant neurobiology' has been founded (<http://www.plantbehavior.org/neuro.html>) ^[15].

Plant scientists recognize that plant cells do share features in common with animal cells. To name just a few: plant cells show action potentials, their membranes harbor voltage-gated ion channels, and there is evidence of neurotransmitter-like substances. Equally, in a broader sense, signal transduction over distance is a property of plants and animals. Yet the idea of "plant neurobiology" is presently strongly controverted between both its proponents and opponents ^[16,17]. Whereas the first claim that a plant neuronal informational system is behind plants behaving as "knowledge accumulating systems", the latter think that this new concept is built on just superficial analogies and have concerns about its scientific validity ^[16].

CONCLUSION

After complete sequencing of numerous plant genomes, from the first *Arabidopsis thaliana*, until the most recently released oak, *Quercus robur*, genome, it is clear that our understanding of the plant complex life has been modified ^[18,19]. New concepts and fields of research are developing as a result of creative thinking and technological development. Their true success will be measured by the long-term scientific benefits that the plant science research community will gain. We think that the majority of these changes in paradigms and conceptional methods will be of major and wide-reaching importance for the issues of genetic resources conservation, genetic breeding and food security, and contribute to a deeper understanding of the true complexity of plant systems. I, finally, trust that Journal of Botanical Sciences will be an important platform for exchange of these ideas.

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