theory generally does not make dynamics explicit, since the welfare optimum can only be reached by some unspecified dynamical process in such a situation.

The second condition for dynamics to apply is that each step in the process helps generate additional information for approaching the welfare optimum. From this, we deduce that the iterative process only applies where feedback from action to information occurs rapidly. Therefore, among such cases the relevant question is: is information only local? If the entire welfare function is known, then the correct metaphor is that of optimization, dynamics is not relevant, and the welfare optimum is not equilibrium. When faced with a non-convex economics problem, it is important to recognize the correct metaphor, which affects both the language employed to describe that problem as well as conclusions reached from analysis.

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12. As the authors furthermore discuss, failure to mitigate emissions rapidly could render what was previously the global optimum solution unreachable, due to physical and economic constraints. In reconsidering the policy goal the starting position would then be irreversibly different, presenting a new problem, and the original problem would then be improperly posed. This merely reflects the difficulty of simplifying a time-dependent dynamic optimization problem to the very different static one of choosing a single quantity, the maximum global warming.

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OPINION

Weedomics a need of time

Niraj Tripathi

Weeds are the plants, found simultaneously with crops and out-compete them in more or less every aspect. Competitive characters and tolerance to various abiotic and biotic stresses are the significant qualities which can be identified amongst a variety of weed species and can be transferred into crop plants for their advancement. Plant molecular biology includes the study of cellular processes, their genetic management and links with alterations in their adjoining. Advancement and accessibility of the sophisticated molecular tools offers us liberty to play with different metabolic pathways at molecular level and to transfer the desirable genetic materials into crop plants, thus breaking the reproductive barriers for interspecific and intergeneric transfer of the genetic material. Advanced plant molecular biology tools offer fabulous promises for elucidating these imperative traits from weed species in detail and further exploration for the diverse aspects of crop improvement in future. The large scale studies connecting entire genetic, structural, or functional machinery are called 'omics'. Major segments of omics consist of genomics, transcriptomics, proteomics, metallomics, metabolomics, ionomics and phenomics. At present these advances are frequently used in crop improvement. However, success of such approaches requires joint efforts from scientists to work mutually with expertise in weed science, molecular breeding and plant physiology. So the combined omic approaches in weed species (weedomics) for crop improvement may play a significant role in changing climatic conditions for food security (Figure 1).

Genomic helps in clarification of taxonomy and evolutionary relationships, uncover evidence of closely related species that cannot be morphologically distinguished (cryptic species) and hybridization events, elucidate methods of reproduction, determine population structure and origins of target weeds. These may help in biological control of invasive weeds. Advances in weed genomics can contribute to crop improvement by better understanding of the biological mechanisms and improved screening methods for selecting superior genotypes more efficiently which possess novel genes to provide resistance against adverse climatic conditions and biotic stresses. A wide range of defense mechanisms are activated that increases plant tolerance against adverse conditions to avoid damage imposed by stresses. The first step toward stress response is stress signal recognition and subsequent molecular, biochemical and physiological responses activated through signal transduction[1]. Understanding such responses is important for effective management of stress. Weeds possess higher level of stress tolerance and their transcriptome profiling may

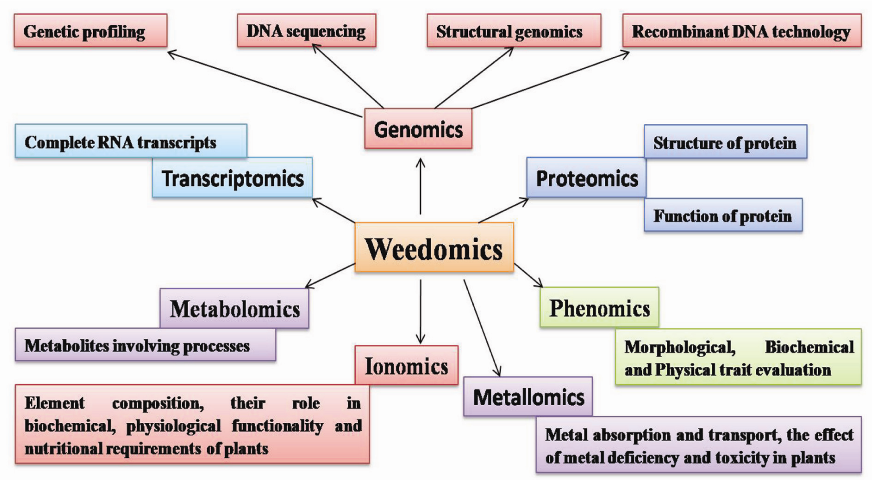

Figure 1. Weedomics and its relation with different omic approaches.

provide an opportunity to study plant response regulation and to identify genes involved in stress tolerance mechanisms. Several high-throughput techniques have been developed for transcriptome analysis due to the advancement in sequencing technology[2]. Stress tolerance mechanisms involve stress perception, followed by signal transduction, which changes expression of stress-induced genes and proteins. Proteomics deals with structural and functional features of all the proteins in an organism. This approach in weeds is important to understand complex biological mechanisms including the plant responses to stress tolerance and post-translational changes during stresses. A single gene can translate in several different proteins and a few genes can lead to a diverse proteome. Some common proteins involved in redox systems, carbon metabolism, photosynthesis, signalling and amino acid metabolism have been found in plants to be associated with various stress responses. These candidate proteins can directly link to genetic regulation of stress response in weeds. Metabolomic studies in plants aim to identify and quantify the complete range of primary and secondary metabolites involved in biological processes. Therefore metabolomics provides a better understanding of biochemical pathways and molecular mechanisms. Some weeds have been found as source of nutritionally important components. The knowledge of genes, transcripts and proteins involved cannot alone help to understand the biological process completely until knowledge of metabolites that are involved becomes available. Metabolomics in weeds may be an important way to understand various synthetic pathways producing nutritionally and pharmaceutically important compounds. Ionomics is the study of elemental composition of an organism that mostly deals with high-throughput identification and quantification. It is important to understand element composition and their role in biochemical, physiological functionality and nutritional requirements of plants. However plants require many other elements and those are not uniformly distributed among different soil types. Plants have evolved with diverse element uptake ability at different locations because of diverse soil types[3]. The elemental composition of a plant is controlled by multiple factors including element availability, uptake capability of roots, transport and external environment which control physiological processes such as evapotranspiration. Because of such parameters, the plant ionome has become responsive and precise so that the element profile reflects different physiological states. Accurate phenotyping is important to understand any biological system.

Phenome is not limited to the visible morphology of an organism. The phenotype is a physical and biochemical trait of an organism. Phenomics is a study involving high-throughput analysis of phenotype. Phenotype is the ultimate resultant from the complex interactions of genetic potential between an organism and environment. In plant breeding, genetic improvement through omics approaches is being conducted to achieve ideal phenotype that will ensure higher and stable yield under diverse environmental conditions. Therefore phenomics integrated with other omics approaches has the most potential in the plant breeding. New techniques that have greatly improved the identification, localization and quantification of metals within plant tissues have led to the science of metallomics. Plants need many different metal elements for growth, development and reproduction, which must be mobilized from the soil matrix and absorbed by the roots as metal ions. Plants are challenged by environmental metal ion concentrations that fluctuate from low to high toxic levels, and have therefore evolved mechanisms to cope with such phenomena. Many weed such as *Arundo donax* possess the capabilities to perform better in higher metal toxicity and they grow in polluted soil areas. Metallomics may provide insight into the molecular mechanisms of metal absorption and transport by weeds, also considering the effect of metal deficiency and toxicity.

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