

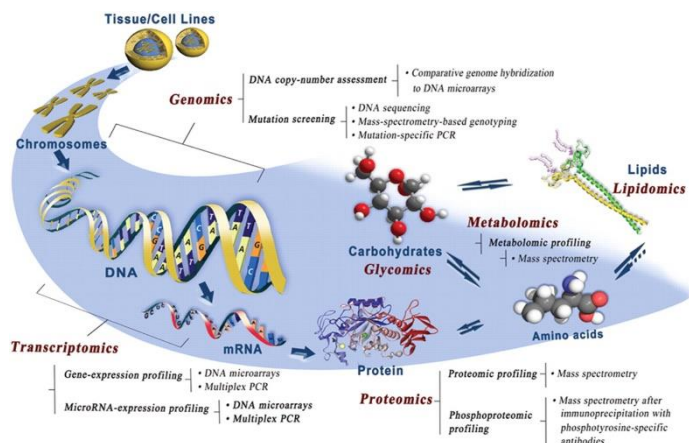
# Omics Technologies in Seed Science and Technology

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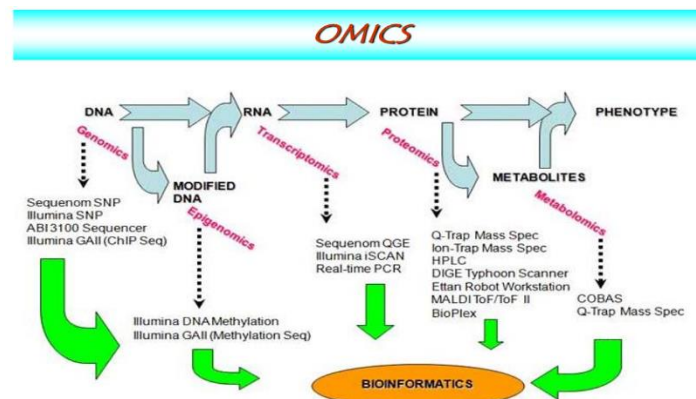
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OMICS denotes a suite of integrated methodologies wielded in the interrogation of the intricate roles, interdependencies, and physiological manifestations of the diverse molecular constituents constituting the cellular framework of an organism. These methodologies are principally geared towards the holistic and indiscriminate detection of genes (genomics), messenger RNA (transcriptomics), proteins (proteomics), and metabolites (metabolomics) within a designated biological specimen. This pursuit, characterized by its comprehensive and unbiased nature, is often dubbed high-dimensional biology, epitomizing the amalgamation of these investigative modalities, a phenomenon known as systems biology.



As the global population burgeons, the demand for sustenance derived from agricultural crops escalates proportionately. Conventional methodologies employed to discern favorable crop traits for incorporation into breeding programs often prove insufficient in delineating specific gene-trait associations. Consequently, there has been a paradigmatic shift towards the fusion of traditional plant breeding practices with emergent omics technologies. Leveraging the wealth of recently elucidated crop genome sequences, twenty-first century omics methodologies embark on an exploration of gene functionality across four cardinal disciplines: genomics, elucidating the comprehensive expression patterns of DNA across the genome; proteomics, interrogating the global functions and expression profiles of proteins; transcriptomics, delving into the regulatory mechanisms governing RNA dynamics; and interactomics, scrutinizing the

intricate interplay among proteins within cellular networks. This integrated approach holds promise in uncovering pivotal constituents ripe for exploitation in enhancing seed quality and augmenting yield potential. (Ryan *et al.*, 2015).



Metabolomics technology is a cutting-edge scientific discipline aimed at the comprehensive detection and analysis of small molecules, which frequently serve as pivotal determinants in various aspects of seed quality, disease resilience, antioxidant efficacy, and beyond. Among the essential small metabolites scrutinized are organic acids, amino acids, sugars, volatile compounds, as well as secondary metabolites including alkaloids and phenolic compounds, alongside pigments such as carotenoids and anthocyanins. These intricate molecular constituents collectively contribute to the intricate biochemical milieu governing plant physiology and response to environmental stimuli. (Saito and Matsuda, 2010).

Proteomics stands as an indispensable facet of organismal biology, constituting a vast array of biological constituents, encompassing structural elements vital for cellular architecture, enzymatic catalysts essential for metabolic orchestration, and signal transduction mediators crucial for cellular communication. Leveraging proteomics technologies offers a profound understanding of protein attributes and functionalities, thus presenting a potent avenue for advancing seed development and augmenting seed yield. Meanwhile, transcriptomics, the comprehensive assessment of all mRNA molecules or transcripts generated within a given cellular context, epitomizes genome-wide expression profiling. This approach illuminates the intricate transcriptional

landscape, shedding light on the dynamic interplay of genetic regulatory networks governing cellular processes. (Zhang *et al.*, 2010).

Blanca E Barrera-Figueroa *et al.* (2011) employing deep sequencing techniques, extracted small RNA sequences from two distinct cowpea genotypes, namely CB46, characterized by drought sensitivity, and IT93K503-1, renowned for drought tolerance, cultivated under both adequately watered and drought-induced stress conditions. Subsequently, we aligned these small RNA reads to the cowpea genome, facilitating the identification of a total of 157 miRNA genes, distributed across 89 families. Notably, within this cohort, 44 miRNAs exhibited associations with drought stress, with 30 displaying upregulation and 14 manifesting downregulation under the arid conditions. This comprehensive analysis provides valuable insights into the regulatory dynamics orchestrated by miRNAs in response to drought, thus enhancing our understanding of the molecular mechanisms underlying cowpea resilience to water scarcity.

Lipid peroxidation stands as a pivotal process governing seed longevity and viability, exerting a profound influence on the storage potential of rice grains. Within this biochemical cascade, the enzyme lipoxygenase 3 (LOX3) emerges as a key catalyst, orchestrating the oxidative degradation of lipids. Remarkably, the downregulation of LOX3 expression within the rice endosperm has been demonstrated to confer heightened grain storability. Notably, comparative analysis between the wild-type (WT) and the TS-91 transgenic line, engineered to exhibit antisense suppression of LOX3, revealed a marked disparity in germination rates. Specifically, the germination rate of TS-91 surpassed that of the WT counterpart by a substantial margin, exhibiting a 29% increase following artificial aging for 21 days and a remarkable 40% augmentation subsequent to natural aging over a span of 12 months. These findings underscore the pivotal role of LOX3 in modulating seed longevity and underscore the potential utility of targeted genetic interventions for enhancing grain storability in rice cultivars (Huibin Xu *et al.*, 2014).

Tsutomu Furukawa *et al.* (2006) A recent study elucidated that the incorporation of the DFR gene into a previously characterized Rcrd mutant led to a phenotypic alteration, transitioning the resultant rice grains from their initial brown hue to a striking red coloration. This transformation served as compelling evidence implicating the Rd locus as the genetic locus governing the synthesis of the DFR protein. Moreover,

comprehensive analyses revealed a discernible accumulation of proanthocyanidins within the transgenic lines subsequent to the introduction of the Rd gene into the Rcrd genetic background. These findings underscore the pivotal role played by the Rd gene in mediating the biosynthesis of proanthocyanidins, shedding light on the intricate regulatory mechanisms governing rice pigmentation and offering insights into potential strategies for enhancing desirable traits in rice cultivars.

Revilla *et al.* (2009) concluded that a comparative study was conducted on the sweet corn inbred lines P39 and EP44, wherein seeds preserved for a duration of 22 years were subjected to analysis utilizing simple sequence repeats (SSRs). Notably, polymorphic SSRs were identified between the viable and non-viable seed populations across six distinct genetic loci, encompassing genes associated with pivotal biological processes such as pathogenesis-related protein 2, superoxide dismutase 4, catalase 3, opaque endosperm 2, and metallothionein1, all known to exert significant influences on germination dynamics. These findings collectively underscore the existence of genetic variability within aged seed stocks of these inbred lines, illuminating the intricate interplay between genetic determinants and seed longevity, thereby offering valuable insights into strategies for preserving and enhancing seed viability over prolonged storage periods.

## Conclusion

In the contemporary era, the integration of twenty-first-century omics technologies stands as an indispensable facet in the quest for enhanced seed development and augmented crop yields. The convergence of genomics, transcriptomics, proteomics, and interactomics has furnished biologists with a wealth of intricate data pertaining to diverse facets of biological processes. This multifaceted approach offers unparalleled insights into global gene functionalities, dynamic alterations in gene expression profiles, discernment of protein identities and functionalities, and elucidation of intricate protein-protein interaction networks. Such comprehensive elucidation of seed developmental physiology and morphology serves as a cornerstone for bridging the chasm between fundamental biological knowledge and its pragmatic application towards the enhancement of seed quality and crop productivity. Consequently, these advancements are pivotal in laying the groundwork for the establishment of a modern seed industry and the formulation of robust plant breeding programs, thereby facilitating the

imperative goal of bolstering global food production to meet the demands of an ever-expanding populace.

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