



Integrated omics for increasing plant production and health-related nutrition under extreme conditions: The Indonesia perspective

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ABSTRACT Despite Indonesia being a megadiverse country that provides germplasm for breeding to produce improved future varieties, significant threats are faced related to biodiversity extinction. Such threats, for example habitat degradation and climate change, which lead to extreme conditions, must be addressed as they have contributed to stresses at the molecular level and affect plant production and health-related nutrition. Integrated omics approaches have been applied to address the problems, as well as to produce varieties with superior traits, which are critical factors in achieving improved plant production and better naturally derived human nutrition. The paper discusses the omics research agenda in Indonesia; Indonesian biodiversity of nutraceutical plants and how omics can increase its production. Besides, current progress of omics application in Indonesia, policies and regulations to enhance integrated omics research are elucidated. By applying these approaches in Indonesia, breeding for better traits to support human needs and improve health quality will be greatly accelerated in the future.

KEYWORDS Extreme conditions; Health-related nutrition; Indonesia; Nutraceutical plants; Omics; Production

1. Introduction

Indonesia, lying on the equator area, is rich in biodiversity. At least two-third non fish vertebrate species as well as high plant species in the world find their home. The tropical rain forests in Indonesia provide critical habitats for endemic species, high economical reservoir, such as timber and non-timber products that can support the livelihood as well as germplasm source for breeding to produce improved varieties in the future (Dawson et al. 2014).

Indonesia biodiversity is enriched with the diversity of native nutritious edible fruits (Hermanto et al. 2013) as well as pharmaceutical plants (Elfahmi et al. 2014; Pratami et al. 2024). Plant health-related nutrition refers to the nutrients and bioactive compounds in plants that contribute to the health and well-being of humans when consumed. These nutrients play crucial roles in preventing chronic diseases, boosting the immune system, and maintaining overall health.

The knowledge of the native nutritional and medicinal plants usage is transferred between generation. Various studies have documented a long historical relationship between the use of natural resources and various ethnic groups in the Indonesia (Katili et al. 2015; Silalahi et al. 2018; Situmorang et al. 2015; Yusro

et al. 2014; Sianipar et al. 2023). However, during the transfer, this knowledge is prone to be eroded. It is inevitable that the younger generation does not know and understand the benefits of species (Gurib-Fakim 2006; Okui et al. 2021). Good documentation of the plant's usage and characteristics until genome level is crucial for its sustainability.

The plant genetic resources are not only preserved in forest, but also in agricultural land. However, limited information on the beneficial species and land mismanagement threatens the existence of genetic resources. The loss of genetic resources results not only in deterioration of plant characteristics but also increase of the crop loss due to new pest and diseases as well as unfavourable environmental conditions (Temesgen 2021; Salgotra and Chauhan 2023). The changes of global meteorological pattern characterized by rising temperatures, unpredicted rainfall, frequent drought and unexpected flood threat the plant growth and yield (Raza et al. 2019; Chele et al. 2024).

As the population increases, there will be more demand on food. To increase food supply for a growing population and enhance the health quality at the same time, breeders have developed new cultivars with higher yield, as well as enhanced resistance/tolerance to biotic

and abiotic pressures as well as the production of high nutrition plants. Abiotic and biotic stresses are perceived and responded through signaling components (Hastilestari 2021; Hastilestari et al. 2018; Sgherri et al. 2017). This signal should be captured as early as possible to trigger defence mechanism and damage mitigation for maintaining their survival and yield. Then, they adapt the changes through physiological responses (Pantouw et al. 2022; Hastilestari and Pantouw 2015; Hastilestari 2015).

Herein lies the promise of omics technologies in supporting plant vigor in dynamic environments. Omics technologies cover cutting edge scientific techniques such as genomics, metabolomics, proteomics, transcriptomics and more (Yang et al. 2021). These technologies not only create a comprehensive data at molecular level but also provide tools to understand the pathway as well as engineer crops suited to the climate change (Roychowdhury et al. 2023; Sarfraz et al. 2025). These technologies have been widely used in many countries, however, the application in Indonesia that is rich in biodiversity is awaiting for broader application.

In this article, our focus will be on unlocking potential germplasm for nutraceutical purposes in Indonesia that is rich in biodiversity. Then challenges and threats in the dynamic environment are discussed. Furthermore, how omics technologies can provide breakthrough in Indonesia for harnessing food security and public health will be elucidated. Besides, legal and regulations framework will be presented to protect overutilization of natural germplasm. This holistic approach is essential to reach the increasing global demand for food and enhancing public health through better nutrition.

2. Omics research agenda in Indonesia

The key thematic areas dealing with omics in Indonesia were illustrated in Figure 1. This map consists of 3 clusters (1) Indonesia, diversity and Jamu; (2) Omics, research and technology; (3) food, multiomic, omics approach and rice. This map indicated that omics research in Indonesia was generated dealing with Jamu (Herbal drink) and diversity. It was also dealing with omics, research and technology. This omics research was applied to study food.

3. Potential Diversity for nutraceutical in Indonesia

3.1. Pharmaceutical plants biodiversity

Indonesia is rich in biopharmaceutical plants, that are utilized as traditional medicine, cooking spices, and natural cosmetic ingredients. The herbal medicines have many benefits for the body such as increasing energy and immunity. There are two types of biopharmaceutical plants produced in Indonesia namely: rhizome biopharmaceutical plants which include ginger, galangal, kencur, turmeric, lempuyang, temulawak, temu ireng, temu kunci, dringo, and non-rhizome biopharmaceutical plants

include cardamom, kejobeling, mengkudu, sambiloto, and aloe vera (Gandhi 2024). The production of the main herbal commodities is depicted in Figure 2.

From Figure 2, it can be noticed that ginger (*Zingiber officinale*) and turmeric (*Curcuma longa*) are commodities frequently used by the communities. The production of ginger decreased in 2023 compared to 2022, but the production of turmeric increased slightly. In Indonesia, there are 3 types of ginger ("sunti" ginger/red ginger, elephant ginger, and "emprit" ginger) that are widely cultivated in mainly in Java and Sumatera islands (Aryanta 2019). Those type of ginger are usually used for cooking spice, herbal medicine and drinks (Yulianti et al. 2023). Essential oil contents in Sunti ginger (red ginger), elephant ginger and emprit ginger are 2.58–2.72%, 0.82–1.68% and 1.5–3.3% respectively (Yulianti et al. 2023; Aryanta 2019). The active substances in essential oils, including: shogaol, gingerol, zingerone, and other natural antioxidants have properties to prevent and treat various diseases (Masya et al. 2023; Handayani et al. 2022; Siregar et al. 2022).

The use of *C. longa* as a cooking spice has long been carried out by various community in Indonesia. In addition to its culinary application, the rhizome of this species demonstrates therapeutic potential as an alternative treatment, a finding corroborated by existing

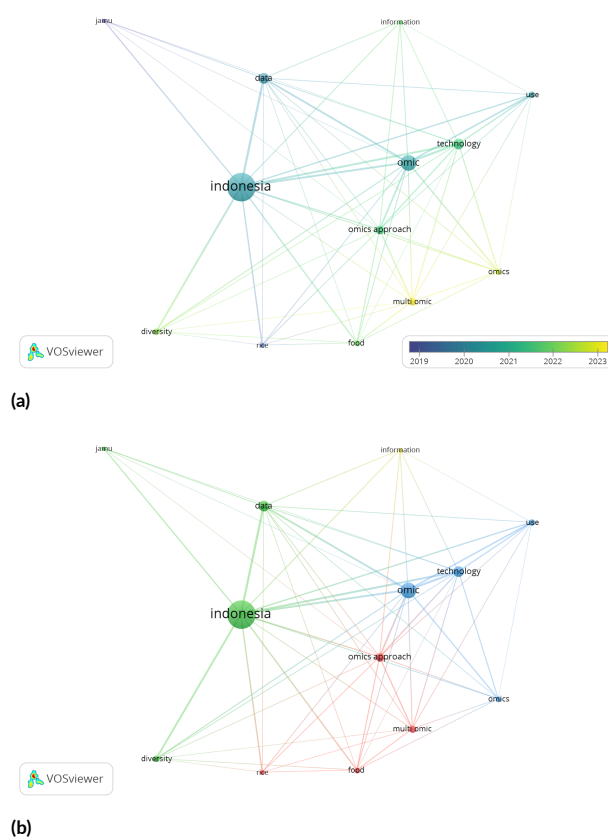


FIGURE 1 (a) Network visualization of Omics Research in Indonesia. (b) Network visualization of Omics Research in Indonesia based on Google Scholar data in 2019–2022.

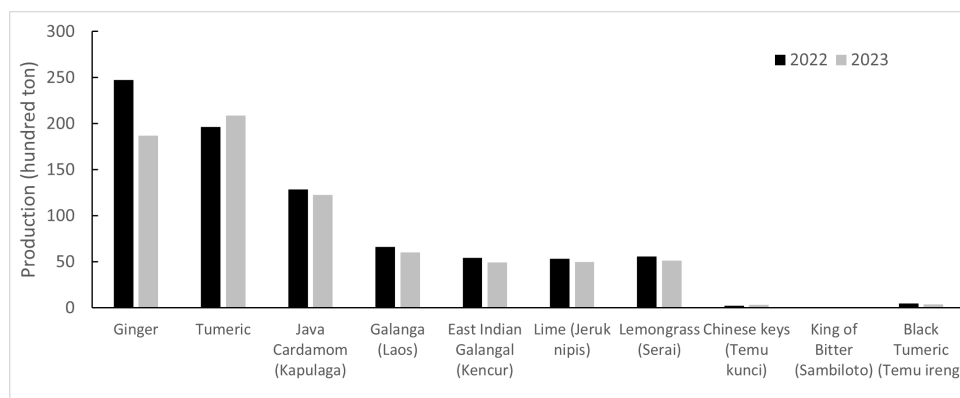


FIGURE 2 Production of the main Indonesian biopharmaceutical plants in 2022 and 2023 (hundred ton) (Badan Pusat Statistik (BPS) 2024)

studies (Fuloria et al. 2022; Pujimulyani et al. 2025). The active substances in essential oils in turmeric encompasses (+)-camphor, (-)-transcaryophyllene, 1,8-cineole, citral, citronellal, citronellol, eugenol, geraniol, α -humulene, D-limonene, ($\pm$)-linalool, methyl chavicol, (-)- α -terpineol, terpinen-4-ol, methyl cinnamate, and methyl eugenol (Phanthong et al. 2013). Pujimulyani et al. (2025) have reported that Indonesian turmeric varieties contain more antioxidant and phenolic compound compared to the ones in Philippines.

The demand for biopharmaceutical commodity continues to increase as part of healthy lifestyle, especially in the health beverage industry such as herbal medicine, herbal tea, and spice-based supplements (Mao et al. 2019). In addition, the global trend towards natural and plant-based products encourages the use of these commodities in various functional beverage formulations, either in the form of extracts, powders, or concentrates (Gupta et al. 2023). With proven health benefits and broad market opportunities, ginger and turmeric are strategic raw material that needs to be developed sustainably to meet the needs of the health beverage industry.

Production of biopharmaceutical commodities in Indonesia, as shown in Figure 1, tend to slightly decrease whereas the domestic demand increases especially for herbal industries (Badan Pusat Statistik (BPS) 2024). One of the factors contributing to low production is genetic factors. There have been wide variabilities in the yield depend on the genotypes and environment factors but not so many superior varieties have been developed with high productivity and resistance to environmental stress (Yunita et al. 2023). Environmental factors such as land suitability, soil conditions, water availability, and pathogen pressure determine the yield (Liliane and Shelton Charles 2020). Therefore, it is essential to increase productivity by producing superior varieties through breeding and strategic cultivation technologies.

Prior to breeding approach, comprehensive analysis of metabolic components is crucial (Maulida et al. 2024). Control of raw material sources is essential to ensure the availability of uniform plant materials on an industrial scale, especially through the selection of super-

ior seeds and efficient cultivation techniques (Marcelino et al. 2023). On the industry side, there is a gap to maintain large-scale production due to limited standardized herbal medicinal raw material (Tambare et al. 2021). This encourages development of a more controlled raw material at genomic, proteomic and metabolic level, as well as technology-based herbal medicinal raw material production system to ensure the quality and availability of raw materials in a sustainable manner. If this sustainable system has been developed, expansion to utilization of other nutraceutical plants is possible (Table 1).

3.2. Staple food biodiversity

There are numerous species that support human diet globally. These varieties are precious resource to underpin food security and nutrition security. In agriculture, the term agricultural biodiversity is identified as the variety of domesticated plants, livestock and microbes used for food and farming (Jago et al. 2024).

In Indonesia, the main food crops that are widely planted are rice followed by corn and other vegetables (Figure 3). In this agricultural country, rice types are divided into 4 groups based on its morphological characteristics, namely indica (cere), japonica (gundil), javanica (bulu), and hybrid types (Silitonga et al. 2003). Isozyme analysis shows that the diversity of indica type rice characters is greater than japonica; from the kinship relationships, it is reported that indica and japonica rice derive from the same wild rice species, but environmental selection and genetic changes induce differences in their appearance (Ganjari 2020). New varieties released after 2004 have been equipped with Glycemic Index (GI) data and cultivation recommendation so the farmers will actively identify varieties that are suitable for the environmental conditions of their area (Suprihatno et al. 2009).

Beside commodities presented in Figure 3, Indonesia is also wealthy in plant genetic resources for food and agriculture (PGRFAs) (Borelli et al.). The PGRFAs are source of invaluable germplasm for the development of local food resources and for the development of science. Potential germplasm for supporting food security are tuberous plants. Tubers such as konjac (*Amorphophalus*

TABLE 1 Potential nutraceutical plants in Indonesia.

Varieties	Plant parts	Function	Pharmaceutical form	Potential Metabolite	Area	Reference
<i>Musa paradisiaca</i> var. Kepok	Corm	reducing sugar blood rate	oral administration, with potential dose 200 mg/g (w/w)	Flavonoid, Saponin, Tanin, Triterpenoid	Jakarta	Wenas et al. (2020)
<i>Musa paradisiaca</i> var. Kepok	Fruit peel	antifungal: <i>Candida albicans</i>	Ethanol extract of fruit peels		South Kalimantan	Ariani and Riski (2018)
Pegagan (<i>Centella asiatica</i> (L.) Urban.)	Leaf	Antianxiety, skin cells regeneration, skin care	Secondary metabolites	Alkaloid, Saponin, Flavonoid, Steroid, Triterpenoid	DI Yogyakarta	Sutardi (2017)
Belimbing wuluh (<i>Averrhoa bilimbi</i>)	Leaf	Antioxidative and anti-inflammatory	Ethanol extract of leaf	Tanin, Saponin, Steroid	West Java	Hasim et al. (2019)
Mengkudu (<i>Morinda citrifolia</i>)	Fruit	Reducing blood pressure	Oral administration, simplicial powder	Terpenoid, Ascorbic acid, Scolopetin, Xerone	Southeast Asia	Febriansa et al. (2024)
Sirih hijau (<i>Piper betle</i> Linn.)	Leaf	Anti-bacterial	Pure extract	Phenolic compound	Indonesia	Pratiwi and Muderawan (2016)
Papaya	leaves	Antibacterial	Oral administration	Phenolic, flavonoid	Indonesia	Sianipar et al. (2023)

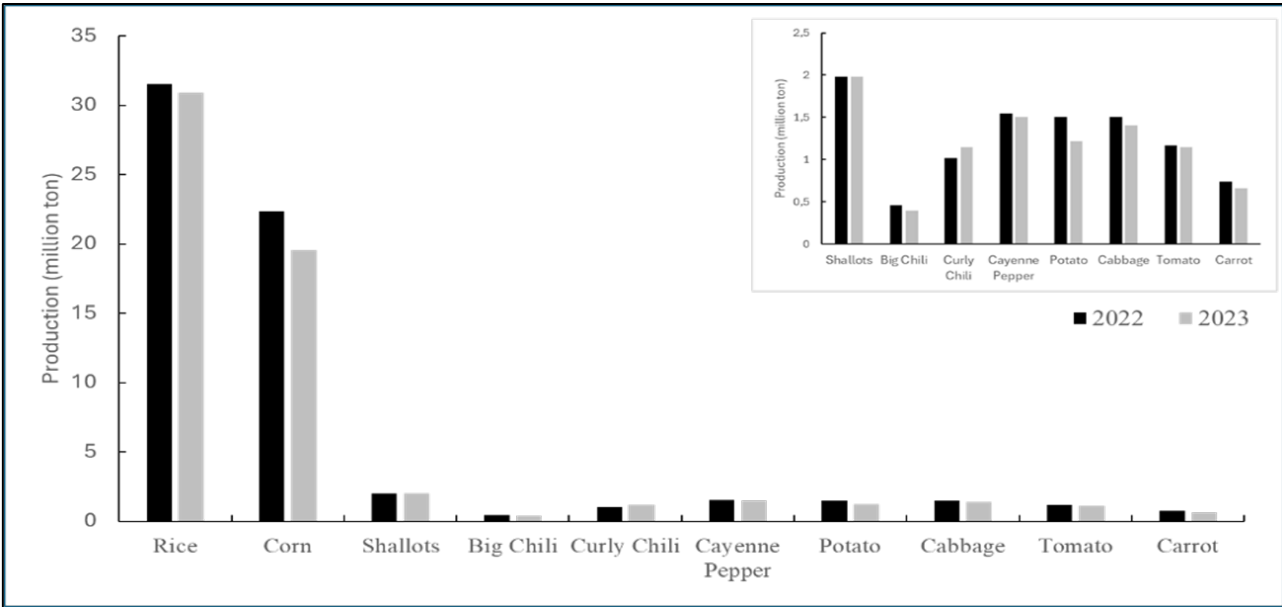


FIGURE 3 Production of the main Indonesian staple plants in 2022 and 2023 (million ton) (Badan Pusat Statistik (BPS) 2024)

konjac), taro (*Colocasia* spp.), and yam (*Dioscorea* spp.) have been consumed in emergency situation as safeguard of food security which are culturally inherited (Indriyatno et al. 2024; Sari and Prasetyo 2022). These plants have advantage of being able to grow in various different environmental conditions and can be developed in agroforestry systems. *Dioscorea* genus that can be found in Indonesia are for example *D. bulbifera*, *D. alata*, *D. esculenta* var. *spinosa*, *D. esculenta* var. *apiculata*, and *D. pentaphyla* with carbohydrate contents range from 66–77%, protein content (3–11%), fat content around 5% and low percentage of fiber (Indriyatno et al. 2024).

4. Challenge and threat to preserve nutraceutical species

Climate change and irresponsible human activities may destroy the environment and cause degradation. Forest degradation is a condition in which forests experience a decline in the level of diversity of fauna and flora due to human activities such as continuous cutting of illegal trees and from natural weather disasters (Sembiring et al. 2023; Vázquez-Grandón et al. 2018).

Moreover, staple food production such as rice and soybean has been reported to decline drastically due to the rise

of temperature (Ray et al. 2019) which only 1 °C rise reduced up to around 3% rice and soybean yield, more than 5% of wheat and maize yield (Zhao et al. 2017). Water-logging has also impacted yield of barley and maize (Ren et al. 2018) although the applying auxins and cytokinin could encourage stomatal conductance and photosynthetic capability.

Extreme climate changes have occurred everywhere which will affect plant growth, morphology and physiology (Gray and Brady 2016). Drought reduces grain yield via reduction in antioxidant potential, photosynthetic rate, and carbohydrate-metabolic enzymes (Ulfat et al. 2021). This ratio change is an effect of transpiration rate, decrease of the Rubisco enzyme activity in carbon assimilation and the shift of shoots to root accumulation. However, in maize, high CO₂ and temperature do not increase seed yield. The effect of climate change on plants is worse if multiple stress factors exist.

The predicted increase in global temperature ranges from 1.0 to 3.7 °C which affects the rise in CO₂ and other greenhouse effects (Gray et al. 2016), which will be worse with the enhanced frequency, intensity, and duration of heat waves. Climate change has increased the frequency and intensity of extreme weather events, changing rain patterns, and also temperatures and sea levels (Bolan et al. 2024). Rainfall volume and pattern changes occurred in many parts of Indonesia for decades (Sudarman et al. 2024). On one hand, there has been an increase of extreme rainfall in coastal area; on the other hand, there has been decrease of annual rainfall in 26 rain stations in East Java (Boer and Buono 2008). Rainfall patterns also reduce water availability in reservoirs functioning as irrigation sources. The Citarum watershed fluctuated depended on the annual average values of rainfall that occur in the western and eastern side areas, with a value of 4,000 mm/year, and the minimum value of 1,200 mm occurred in 2018–2019. Analysis using machine learning methods indicates a decreasing trend in water level estimates for all stations, as well as estimates of groundwater recharging (Susandi et al. 2024). It also happened in Kedung Ombo, Gajah Mungkur, as well as Jatiluhur reservoirs, which function as a rice field irrigation source in the northern part of Java. Three main issues related to global climate change, which influence agriculture sector agriculture, are: 1) rain patterns changes, 2) extreme climate events (floods and droughts), and 3) enhanced air temperatures and sea levels (Suranny et al. 2022).

Therefore, with such conditions, if farmers continue to apply planting patterns under normal conditions, then crop failure will occur more frequently. There has been a shift in planting season due to the changes in rainfall amount in certain areas in Indonesia which affected main crops especially rice, is sensitive to stresses such as drought or submersion. Besides that, agriculture systems such as soil type, plant varieties, planting system, and land and water management play a role in the plant's yield (Kopittke et al. 2019).

Plant responses to various environmental pressures are highly variable. Advances in genetics such as genomics, transcriptomics, proteomics are not easy to dissect the defence system or increase plant resistance (Liu et al. 2014). This development makes it easier to study stress signalling pathways, such as signalling pathways (signal perception, signal transduction, gene expression against stress, physiological processes and metabolic reactions). Recent studies show that plants can respond to multiple stressors rather than to a single stressor by expressing specific genes under certain stress conditions. However, plants, with their ability, can adapt to face the environment and manage environmental stresses with the following mechanisms.

First, plants receive extracellular stimulation through sensors/receptors in their cell walls or membranes. Next, the signal turns into an intracellular signal through inositol phosphate, sugar, reactive oxygen species (ROS), calcium ions (Ca²⁺), cyclic nucleotides (cAMP and cGMP), and nitric oxide (NO). Furthermore, these components will give rise to signal transduction (Newton et al. 2016). The following processes are protein phosphorylation and dephosphorylation, which is carried out with the help of protein kinases and phosphatases, in most signalling pathways, and this is quite effective in conveying the signalling mechanism. Protein kinase or phosphatase will activate the transcription factor at the end of the phosphorylation chain and then bind the transcription factor precisely to the *cis*-element in the promoter region associated with gene repression and modulate the transcription process (Baoxiang et al. 2023). At the same time, upstream components regulate transcription factors at the transcript level and change at the posttranscriptional level, such as ubiquitination and silencing. After post-transcription, it will influence gene responses in regulating physiological activities and metabolic reactions (Simeunovic et al. 2016; Zhu 2016).

5. Integrated omics: Progress in Indonesia

Recently, an integrated approach that leverages omics has opened a new frontier in breeding plant traits precisely, using functional markers which often have a genetic link with phenotypic traits. The term of integrated omics refers to the comprehensive and combined analysis of the various “omes” such as genome, transcriptome, proteome, metabolome within a biological system. In the context of plant production and health-related nutrition, integrated omics can play a pivotal role in enhancing crop yield, improving resistance to diseases, and increasing the nutritional quality of plants. Using cutting-edge bioinformatics tools and machine learning techniques to integrate and analyze multi-omics data enable significant regulatory networks and pathways underpinning plant traits.

Indonesia, as one of the world's most biodiverse countries, holds immense potential for -omics applications (genomics, transcriptomics, proteomics, metabolomics, and microbiomics) in agriculture, health, and conservation. Recent bibliometric and empirical

TABLE 2 Genomics based research evident in Indonesia from 2020-2025.

Approach	Focus of works	Reference
Genome mining analysis and mass spectrometry (MS)	Indonesian Microbial Biodiversity	Handayani et al. (2021)
Pangenome assembly pipeline	Pangenome study across genus boundaries and identifies genes that differentiate between Musaceae species,	Rijzaani et al. (2021)
Illumina NextSeq 500	Chloroplast genome of <i>Myristica teysmannii</i> (Myristicaceae), an endemic and endangered species from Indonesia	Ariati et al. (2023)
Illumina/PacBio sequencing and de novo assembly	Whole-genome sequencing of <i>Ganoderma boninense</i> , the causal agent of basal stem rot disease in oil palm.	Utomo et al. (2024)
Illumina/ MinION sequencing and de novo assembly	Genetic diversity, contributes to conservation and breeding of red meranti (<i>Rubroshorea johorensis</i>)	Nugroho et al. (2025a)
MinION Oxford Nanopore Technologies	<i>Cinnamomum burmanni</i> (Nees & T.Nees) Blume (Lauraceae) genome	Salindeho et al. (2024)
Comparative genomics analysis of chloroplast genome annotation	Genomes across seven <i>Salacca</i> species	Arshad et al. (2024)
Whole genome sequencing	Identify genome-wide DNA polymorphisms in Lim 1 and 2 of <i>Coffea liberica</i> in order to gain insights into its capacity for adaptation in peatlands	Melia et al. (2025)

studies, as mentioned above, reveal a growing trend in the use of these tools, although significant gaps and opportunities remain. Continued efforts in research, infrastructure development, and international collaboration will be essential to fully harness the potential of -omics in understanding and preserving Indonesia’s unique genetic heritage. Herewith, a breakdown of each omics implementation, significant gaps, and opportunities in Indonesia.

5.1. Genomic

Genomic approaches are typically used to pinpoint precise genetic markers associated with the targeted traits. However, due to their complicated variations in structure and transposable elements, predicted genes hardly reflect the corresponding proteins that express the desired traits/characteristics (Ling et al. 2021). In plants, genomic technology enables to identify genes associated with desirable traits such as high yield, disease resistance, and improved nutritional content.

Marker-assisted selection combines with genomic selection can then be used to breed plants with these traits. Key applications in increasing plant production include genome-wide association studies (GWAS): This crucial tool is used to identify genetic variants linked to high-yield traits, and its application in understanding germplasm diversity is a significant step forward in utilizing genetic resources for crop improvement (Alemu et al. 2024). Marker-assisted selection (MAS): Using genetic markers to select plants with desired traits more efficiently; CRISPR/Cas9 and Other: Genome editing tools: Precisely editing genes to improve yield and resilience. GWAS technology may be conducted in hundreds of the accession of germplasm without segregation’s population. The synergetic relationship between GWAS and genome editing is a testament to the power of these technologies in advancing plant breeding. While GWAS is a major tool to iden-

tify genes underlying complex traits, providing targets for genome editing to generate engineered alleles, improved genome editing enables the validation of gene function under different genetic backgrounds, which can inform the method research of GWAS (Tibbs Cortes et al. 2021).

Between 2000 and 2024, there has been a notable increase in DNA barcoding research aimed at identifying Indonesia’s vast biodiversity. Genomic research has extended to native species, plant-associated microbiomes, and plant pathogens, which focused on genetic diversity, molecular marker development, and genome sequencing. These studies are crucial for conservation efforts and breeding programs, emphasizing the importance of understanding local genetic variations (Table 2). While progress is evident, comprehensive genomic data across species remain limited.

5.2. Transcriptomic

Transcriptomics studies on different types of plants can assist researchers in elucidating gene function and regulatory processes for breeding selection, such as for yield improvement or increasing nutrition value, which benefits human health. Compared to genomic research, transcriptomic study provides more in-depth understanding of gene regulation transcripts and expression at the core of the problem. Transcriptome can be used to assess overall transcriptional activity. In addition, the transcriptome changes over time and space because it includes information on secondary metabolic pathways and variations in gene expression at different times and spatial regions. Even in the same species or cultivar, plants grow variously depending on the conditions and periods. These transcript differences are important for plant functional genome mining studies, gene regulatory domain development, genetic diversity (dominant and recessive genes), and bioactive compounds. Transcriptome is the total number of RNA molecules transcribed from a particular tissue or cell at a

given functional or developmental stage, including mRNA (messenger RNA) and nc-RNA (non-coding RNA). This approach enhances research for understanding the functions of cells, tissues, and organisms. (Wang 2021; Tyagi et al. 2021).

Transcriptomic analysis has been used for elucidating genes in biosynthesis and metabolism pathways and regulation for various plants, such as food, horticulture, industrial and medicinal crops in multiple purposes such as nutrient uptake, organs development, stress responses to different environments (Ren et al. 2024; Wang et al. 2023b; Dai et al. 2023; Nguyen et al. 2021). Transcriptomic analyses and physiological experiments on rice (*Oryza sativa*) revealed that deficient in N and P inhibit rice growth and utilization of other nutrients. *Garp-type Transcriptional Repressor 1 (NIGT1)* gene, as a transcription factor for nitrate-inducible, was reported encoded protein is a positive regulator of P homeostasis and a negative regulator of N acquisition in rice. A transcriptomic study in *Brassicaceae* species revealed a conserved shade avoidance syndrome (SAS) mechanism exhibits distinct responses to shade, which provides comprehensive information to develop new shade-tolerant cultivars that are suitable for high-density indoor farms (Nguyen et al. 2021; Tyagi et al. 2021). Initiation of seed development, maturation, and accumulation of storage products in vegetable and grain pea (*Pisum sativum*) triggered by complex regulatory network (Zorin et al. 2023; Verma et al. 2016). Besides important traits for increasing productivity for food crops, transcriptomic has also been used for plant-producing bioactive compounds beneficial for health, such as *Astragalus membranaceus*. Understanding the biosynthesis pathway of bioactive compound, phenylpropanoid, the main bioactive substance of *A. membranaceus*, has also been revealed from *A. membranaceus* (Wang et al. 2023b; Kang et al. 2024).

Bibliometric analyses reveal that Indonesia is making

notable strides in transcriptome research, especially in the areas of plant variety, agriculture, and microbiomes under extreme environment (Table 3). In Indonesia metatranscriptomics is beginning to be used for understanding microbial functions, gene expression with environmental adaptation and plant-microbe interactions, to discover bioactive compounds with potential health benefits, though mostly studies focus on a few major crops, at a pilot scale, while Indonesia's vast plant biodiversity is under-explored. Though there is need for improvement in a number of areas, the incorporation of transcriptomic. The know-how of pathways, cycles, and regulation of gene/s interest will significantly impact plant improvement and management. The genome-wide comparison of gene expression patterns can uncover novel biological relationships. When gene expression profiles of two independent experiments are highly correlated, it can be concluded that the treatments, genotypes, organs, or other experimental variables were correlated.

5.3. Proteomic

Proteomic approaches are conducted to gain a comprehensive understanding of functional insights into how this genetic product (composition, structure, functional, and expression) influences the molecular mechanism at the post-transcriptional stage associated with the phenotypic trait (Chawade et al. 2016). In plants, stress-associated proteins play a crucial role in enhancing tolerance against abiotic stresses and defence against pathogens (Shukla et al. 2021; Liu et al. 2019), as well as plant development, have been identified with the help of the proteomic technique (Figure 3). Wheat, maize, soybean, tomato and rice have been the most extensively exploited crop plants for proteomic analysis to identify protein associated with yield and environmental resilience traits (Zenda et al. 2021; Khan et al. 2021; Pratap et al. 2024). As it has been many years Indonesia's scientists have been working on banana in-

TABLE 3 Transcriptomics recent research evident in Indonesia from 2020-2025.

Approach	Focus of works	Reference
RNA-seq and BGISEQ- 500 platform	Transcriptomic of banana response against pathogen, reveal pathogenesis-related genes and gene functions in the plant system, and research development to design blood disease-resistance <i>Ralstonia syzigii</i> subsp. <i>celebesensis</i> and <i>Ralstonia solanacearum</i>	Prakoso et al. (2020)
RNA-seq and de novo transcriptome analysis	De novo transcriptome assembly data for sengon (<i>Falcataria moluccana</i>) trees to study differences in gene expressions between resistant and susceptible accessions, and to identify candidate genes involved in boktor stem borers (<i>Xystrocera festiva</i> Pascoe)	Siregar et al. (2021)
RNA-seq Illumina HiSeq 2000	Transcriptomic dataset for early inflorescence stages of oil palm in response to defoliation stress	Apriyanto and Ajambang (2022)
RNA-seq and gene regulatory network (GRN) analysis for DEGs	Transcriptomic changes over time in adult oil palms under waterlogging condition	Lim et al. (2023)
RNA-seq Illumina HiSeq™ 2000, DEGs analysis	Delay the ripening process in banana	Dwivany et al. (2024)
RNA Sequencing (RNA-seq) and de novo transcriptome analysis	De novo assembly, gene annotation, and molecular marker development of in nutmeg (<i>Myristica fragrans</i> Houtt.)	Rostiana et al. (2025)

TABLE 4 Identified protein using proteomics in banana.

Technique	Number of proteins identified	Protentional for translational research	Reference
nanoLC-MS/MS (quantitation:iTRAQ)	3477 proteins from plantains seedlings	809 proteins promising for antioxidation to develop cold-tolerant banana variety	Yang et al. (2012)
LC-MS/MS	26 proteins from mature green banana fruit	Some proteins related with chitinases, involved in metabolism of carbohydrates and ethylene	Toledo et al. (2012)
CPPL+ nanoLC-MS/MS	1131 protein from banana fruit	Some proteins are involved in fruit ripening and to identify allergen	Vanderschuren et al. (2013)
LC-MS/MS	1363 proteins from plantain fruit 1344 proteins from cavendish fruit	59 peptides specific to B alleles, and 47 peptides as A alleles specific	Campos et al. (2018)
LC-MS/MS	1201 proteins from cavendish and plantain fruits	proteins involved in several roles include the oxidation-reduction of polyphenols, the synthesis and degradation of starch, and the metabolism of sugar, the breakdown of cell walls,	Bhuiyan et al. (2020)
PMF and MS/MS	25 proteins from somatic embryo of banana cv. Grand nine	Identified proteins were expressed during the somatic embryo development	Kumaravel et al. (2020)

TABLE 5 Proteomics research in Indonesia (2020-2025).

Technique	Focus of works	Reference
Nano LC-MS/MS (quantitation:iTRAQ)	The anthocyanin composition in Java black rice	Sari et al. (2021)
Chromatography-Mass Spectrometry (LC-MS/MS)	Identification of Nephrotettix virescens vector protein transmitting the tungro virus in rice	Senoaji et al. (2021)
LC/MS-MS	in silico proteomics and in vivo analysis of Tacorin, a bioactive protein fraction from <i>Ananas comosus</i> (L.) Merr. Stem	Rahayu et al. (2024)
LC-HRMS	Differentiate authentic <i>Pangasius hypophthalmus</i> meat from pork adulteration meat	Windarsih et al. (2022)
LC-MS/MS	Identifying spermatozoa proteins in Indonesian native Madura bulls	Rosyada et al. (2023)
Peptide fractionation and LC-MS/MS	Examine the seminal plasma and sperm proteins of Toraya buffalo to uncover those critical for reproductive functions.	Maulana et al. (2025)

cluding the wild species and strengthening the research through a research scheme entitled “Collection, Characterization and Pre-breeding of Indonesian Wild Bananas” which combining conventional breeding and genome editing as well as applying other omics technology. Although research on plant proteomics in Indonesia is not as extensive as on animals, it will be intensified to keep the pace faster to join the international scientists whose results are listed in Tables 4 and 5.

With the use of next-generation sequencing (NGS), mass spectrometry (MS), and an array of protein libraries in the UniProt database, the proteomic approach is one of the prominent methods to investigate the protein landscape in biological and biochemical systems, offering insight into cellular functions and expressions in plant growth and development, metabolic processes, plant genetic variations, and plant defence mechanism, which are plausible tools to develop innovative strategies to improve crop productivity, quality and resilience (Table 4) (Molendijk and Parker 2021; Li and Keller 2023).

Proteomics research in Indonesia, particularly concerning more in animal rather than in plant diversity, plant production and plant health-related nutrition (Table 5).

While there is a growing interest in omics technologies, proteomics has not yet been widely adopted or extensively studied within the Indonesian scientific community.

5.4. Metabolomic

Metabolomics, a branch of omics, plays a crucial role in characterizing and quantifying metabolites in cellular biological systems. Like other omics studies, metabolomics utilizes data analysis techniques developed for transcriptomics and proteomics. The data sets produced by metabolomics are highly diverse and can even exceed the number of samples. Metabolomics analysis data is instrumental in characterizing synthetic strains (Tanaka et al. 2023), bioactive compounds (Ruviano et al. 2019; Santos et al. 2019) and understanding plant–microbe interactions (Olanrewaju et al. 2024).

Metabolomic profiling to elucidate plant metabolites is challenging because more connections between proteomes and metabolomes are needed. In metabolomics, no technique or single equipment can be used to analyze all metabolites in a metabolome. Instead, different technology is required to provide the most significant metabolite coverage. Common approaches involve coupling a

chromatographic separation to mass spectrometry, including gas chromatography-mass spectrometry (GC-MS), liquid chromatography-mass spectrometry/LC-MS (Ruviano et al. 2019; Santos et al. 2019; Borges et al. 2019), and capillary electrophoresis-mass spectrometry/CE-MS (Komatsu et al. 2014). And another approach is nuclear magnetic resonance/NMR (Cuperlovic-Culf et al. 2019) and an assortment of direct injection-mass spectrometry (DIMS) methods.

Metabolomics is a research field integrating analytical chemistry, statistics, and biochemistry to analyse quantitative changes in metabolite levels. It allows researchers to link genotype to phenotype by studying these metabolites (Shen et al. 2023). Metabolomics research in Indonesia is an emerging and growing field, with increasing activity in various sectors, particularly in natural products, food science, and health (Armas et al. 2024). Indonesia, with its rich biodiversity, is leveraging metabolomics to explore and identify bioactive compounds from its vast plant resources.

Collaboration research was conducted by the National University of Indonesia with the National Research and Innovation Agency (BRIN) and Rutgers – the State University of New Jersey of the United States for Pioneering Metabolomic Libraries from Indonesian plants. The creation of the first metabolomic library of Indonesian plant species, the Indonesia Metabolome and Genome Innovation and Conservation (MAGIC) Library, is a significant step, aiming to foster collaborative research into plant metabolomics and natural products. This initiative utilizes technologies like Rapid Metabolome Extraction and Storage (RAMES) for ethical and efficient sample collection (Armas et al. 2024).

Metabolomics is still developing and being explored for its potential to understand the nutritional content, bioactive compounds, safety, and quality of traditional and local food sources, and various spices. This is crucial for food diversification efforts. There were some publications about applying metabolomics analysis on Indonesian Plants (Table 6).

Some challenges in facilitating research about metabolomics are infrastructure and instrumentation, data analysis and bioinformatics, standardization, skilled personnel, and funding (Hao et al. 2025; Peters et al. 2018; Johnson and Gonzalez 2012). Collecting metabolomics data requires access to advanced metabolomics instrumentation, such as high-resolution mass spectrometry, nuclear magnetic resonance, etc. The complexity of metabolomics data requires specialized bioinformatics expertise and robust data processing platforms (Chen et al. 2022). So, there is a need for more trained researchers and technical staff in metabolomics, requiring continued educational and training initiatives. While some national and international funding exists, securing consistent and substantial funding for large-scale metabolomics projects can be a limitation.

On the contrary, there are many opportunities to develop metabolomics analysis in Indonesia because In-

donesia has unique and extensive biodiversity presents an unparalleled opportunity for novel discoveries in natural products, drug development, and functional foods (Armas et al. 2024). Research on metabolomic of Indonesian chilli pepper have commenced in 2010 which was combined with molecular markers measuring the composition of both semi-polar and volatile metabolites in fruit pericarp, using untargeted LC-MS and headspace GC-MS platforms while the ongoing research has been using different varieties and different approaches of metabolomic integrated with transcriptomic to investigate the expression of gene regulating the polyphenol compounds in unripe and ripe fruits. Integrating metabolomics with traditional Indonesian knowledge of plants and health offers a powerful approach for scientific validation and innovation. Metabolomics can significantly contribute to addressing food security challenges and improving public health through personalized nutrition and disease prevention strategies (Johnson and Gonzalez 2012). The increasing availability of more affordable and efficient metabolomics technologies can facilitate wider adoption and research. Building stronger national and international collaborative networks can accelerate research progress and knowledge exchange.

5.5. Paving desired increased plant production through genome editing

Plant whole-genome sequencing studies have enabled the discovery of several genes and regulatory elements that govern various characteristics (Vekemans et al. 2021). By combining inexpensive sequencing technologies with computational bioinformatics tools and high throughput phenotyping methods, we can improve the detection of genes that control significant agronomic variables related to food production and quality (Steinwand and Ronald 2020). Multi-omics investigations yield a comprehensive understanding of organisms' diverse genetic, protein, metabolite, and ion profiles. Hence, the integration of multi-omics technologies presents a significant chance to expedite the process of identifying genes that regulate agriculturally significant characteristics in plants, including conventional food crops. This integration can also hasten improvement programs by employing traditional breeding methods and cutting-edge gene editing technologies. Genome editing, as a cutting-edge technology, is a breakthrough that will help meet the growing need for food while facing limited resources. Due to inter-specific hybridization hurdles, conventional breeding faces a significant problem in developing desired cultivars. The primary challenges in traditional crossing in the banana genus include polyploidy, a lengthy production cycle, the sterility of most cultivars, and the limited genetic variety in this genus germplasm (Ortiz and Swennen 2014). This approach is enabling the introduction or modification of specific and relevant features in a single step. In addition, these molecular tools, such as CRISPR-Cas9, TAL-ENs, and ZFNs, function as molecular scissors, enabling precise modification of specific DNA sequences with un-

TABLE 6 The research on metabolomics approaches in Indonesia.

Function	Approach	Reference
Metabolite profiling of Indonesian coffees based on their regional origin.	nuclear magnetic resonance (NMR)	Happyana et al. (2020)
identifying and quantifying metabolic changes associated with <i>Ganoderma resistance</i> in oil palm roots	nuclear magnetic resonance (NMR)	Nugroho et al. (2025b)
Understanding metabolite changes during soybean fermentation to improve the quality and nutritional value of tempe	gas chromatography-mass spectrometry (GC-MS)	Prativi et al. (2023)
Characterize the metabolic profiles of leaves from cloves (<i>Syzygium</i> spp.) varieties	gas chromatography-mass spectrometry (GC-MS)	Kusuma et al. (2024)
Metabolomic profile of Indonesia Betel Quids.	gas chromatography-mass spectrometry (GC-MS)	Zhang et al. (2022)
Identify antihyperglycemic and antioxidant compounds from <i>Melastoma malabathricum</i> L. leaf	liquid chromatography-mass spectrometry (LC-MS)	Lestari et al. (2024)

precedented accuracy. This method allows for scientists to create or enhance advantageous characteristics in crops, such as disease resistance, improved nutrition, and drought tolerance.

In horticulture crop research, TALENs, ZFNs, and CRISPR-Cas9 have been utilised as genome editing techniques. They offer researchers the ability to precisely modify genes associated with desired traits in horticultural crops, facilitating the development of improved varieties. TALENs and ZFNs employ modified DNA-binding proteins that can be tailored to target particular genomic sequences selectively (Gaj et al. 2013). Like CRISPR-Cas9, these technologies cause specific DNA cutting and subsequent alterations at the intended locations in the genome. TALENs utilise DNA-binding domains that originate from transcription activator-like effectors (TALEs), proteins usually found in bacteria that cause plant diseases (Sun and Zhao 2013). Engineered TALE domains selectively attach to particular DNA sequences and are combined with a nuclease domain to induce DNA cleavage (Joung and Sander 2013). On the other hand, ZFNs are a type of hybrid protein that merge designed zinc finger DNA-binding domains with the FokI nuclease domain obtained from the FokI restriction enzyme (Li et al. 2011). Zinc finger domains are specifically engineered to identify specific DNA sequences, while the FokI domain precisely cuts the DNA at the intended location (Pattanayak et al. 2014).

The Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and the accompanying CRISPR-associated (Cas) proteins have become well-known for their user-friendly characteristics, high effectiveness, and versatility in modifying genetic material in various organisms, including horticulture crops. This potent tool allows for accurate modification of plant genomes by leveraging the defence mechanism of bacteria against viral infections (Rao et al. 2022), enables researchers to focus on particular genes linked to desirable features and introduce alterations to improve agricultural characteristics (Rasheed et al. 2022). This high level of accuracy enables the implementation of beneficial mutations, gene interruption, and the replacement of precise DNA sequences, resulting in targeted modifications in

characteristics such as resistance to diseases, ability to withstand environmental stress, nutritional content, and crop productivity.

The CRISPR-Cas9 system consists of two essential components: the Cas9 nuclease and the guide RNA (gRNA). Type II CRISPR systems utilize the RNA-guided endonuclease Cas9 to recognize/identify and cut double-stranded DNA (dsDNA) targets using conserved RuvC and HNH nuclease domains. The cleavage induced by Cas9 is strictly dependent on a protospacer adjacent motif (PAM) in the target DNA (Karvelis et al. 2017).

The SpyCas9 effector protein, derived from *Streptococcus pyogenes*, is a single polypeptide chain consisting of 1,368 amino acids. When bound to dual-component guide RNAs composed of CRISPR RNA (crRNA) and trans-acting CRISPR RNA (tracrRNA), the Cas effector protein transforms into a fully operational nuclease. The two RNA components can be physically combined to create a unified guide RNA (sgRNA) (Park and Choe 2019). Cas9 is a nuclease that can cause blunt double-strand breaks (DSBs) at almost any target DNA locus with a 5'-NGG-3' protospacer-adjacent motif (PAM) at the 3' end. Then, DSBs facilitate the generation of specific point mutations, insertions, deletions, or substitutions within the target DNA locus, via homologous recombination (HR) or nonhomologous end joining (NHEJ). These mutations may result in loss of function for the gene of interest. Since the HR pathway uses a homologous sequence as a template to repair the DSBs, this pathway can be utilized to precisely integrate of the desired genes into the genome (Park and Choe 2019). The CRISPR/Cas9 technique application on various crops, along with the specific genes targeted and the resulting modified genetic traits, is presented in Table 7. Some of those were conducted in Indonesia to improve crops such as rice (Santoso et al. 2020), chilli pepper (Kurniawati et al. 2020), oil palm (Budiani et al. 2019), and on medicinal plants such as *Artemisia annua* (Koerniati and Simanjuntak 2020). On going gene editing research on cassava conducted at BRIN which commenced in 2022 is to address drought tolerance as well as increase nutrition content especially iron. The results will be published in 2025–2026.

TABLE 7 Crops subjected to genome editing techniques, modified genetic traits in various plant species in Indonesia.

Crops	Modified Gene(s)	Trait/Function	Reference
<i>Artemisia annua</i>	SQS	Sterol biosynthesis	Koerniati and Simanjuntak (2020)
Chilli pepper	PCNA	Resistant to geminivirus	Kurniawati et al. (2020)
Rice	<i>OsGA20ox-2</i>	Semi-dwarf	Santoso et al. (2020)
Oil Palm	<i>EgEMLP</i>	Resistant to <i>Ganoderma</i>	Budiani et al. (2019)
Tomato	<i>E8</i> , phytoene desaturase (<i>PDS</i>), <i>SIDE</i> LLA	Enhanced fruit ripening, delayed fruit senescence, reduced plant height	Wai et al. (2020)
Potato	<i>StCDF1</i>	Increased tuberization and yield	Gonzales et al. (2021)
Wheat	<i>TaGW2</i> , Puroindoline genes	Enhanced thousand grain weight, improved grain quality	Henry et al. (2018)
Citrus	<i>CsPDS</i>	Improved disease resistance, reduced ethylene production	Yang et al. (2023)
Strawberry	<i>FaTM6</i>	Petal and stamen development	Martín-Pizarro et al. (2019)
Grape	<i>VvWRKY52</i> , <i>VvWRKY2</i>	Enhanced disease resistance, improved abiotic stress tolerance	Capriotti et al. (2020)
<i>Brassica oleracea</i>	<i>XccR5-89.2</i>	Improved resistance to blackleg disease	Afrin et al. (2019)
Mushroom (<i>Agaricus bisporus</i>)	Polyphenol oxidase (<i>PPO</i>) genes	Reduced browning and improved shelf life	Waltz (2016)
Banana	<i>MaACO1</i>	Promotes the shelf life of banana	Hu et al. (2021)
Carrot	<i>DcCCD4</i>	Different colored taproots in carrots	Li et al. (2021)
Strawberry	<i>FaGAST1</i>	Increased fruit size	Abdullah et al. (2021)
<i>Cucumis melo</i>	<i>CmACO1</i>	Extends the shelf-life	Nonaka et al. (2023)
<i>Capsicum annuum</i>	<i>CaERF28</i>	Anthraxnose resistance	Mishra et al. (2021)
Rose	<i>RhEIN2</i>	Ethylene insensitivity in rose	Wang et al. (2023a)
Melon	<i>elF4E</i>	Virus resistance and male sterility	Pechar et al. (2022)
Tomato	<i>SIMAPK3</i>	Reduced drought tolerance	Wang et al. (2017)
<i>Brassica napus</i>	<i>FAD2</i>	Catalyzes the desaturation of oleic acid	Okuzaki et al. (2018)
Kiwi fruit	<i>AcBFT</i>	Reduce plant dormancy	Herath et al. (2022)
Tomato	<i>SIMYC2</i>	Fruit resistance to <i>Botrytis cinerea</i>	Shu et al. (2021)
Soybean	<i>GmFATB1</i>	Reduce saturated fatty acids	Ma et al. (2021)
Kiwi fruit	<i>AcCBF3</i>	Dwarf plants and enhanced freezing tolerance	Wang (2021)
Sweet Potato	<i>IbGBSSI</i> and <i>IbSBEII</i>	Improvement of starch quality	Wang et al. (2019)
Papaya	Phytoene desaturase (<i>CpPDS</i>)	Inducing a visually scorable albino phenotype	Brewer and Chambers (2022)
Eggplant	<i>SmelPPO4</i> , <i>SmelPPO5</i> , and <i>SmelPPO6</i>	Reduces fruit flesh browning	Maioli et al. (2020)
Cassava	<i>elF4E</i>	Reduces cassava brown streak disease symptom	Gomez et al. (2019)

On going gene editing research to improve banana resistance to banana bunchy top virus (BBTV) and *Fusarium* TR (Tropical Race)-4, nutrition content and tolerance to drought are conducted by BRIN researchers with their partners both national and international institutions. The approach being used in banana is direct gene transfer using electroporator into the protoplast or embryogenic callus although the procedure and the ratio of successful regeneration is still further improved.

Although genetically modified organism (GMO) Banana has been produced by the Queensland University of Technology and approved by the Government of Australia for the production (Hathy et al. 2024), scientists are seeking on non-transgene improved banana due to global community preference. Therefore, efforts to produce those

gene edited banana are enhanced to anticipate future devastation attacking commercial banana as had been faced in the past causing enormous damage to the production of Gros Michel due to *Fusarium* disease (Altendorf 2019). As a consequence, in mid-1950s, the first strain (Race 1) of *Fusarium* wilt outbreak which was facilitated by the monoculture and intensive plantation cultivation techniques and concentrated transport routes of the commercial banana industry, the production of Gros Michel that the export industry was forced to switch its entire production to the *Fusarium* wilt-resistant Cavendish variety. This was unavoidable as the total losses to trade in Gros Michel bananas at the time amounted to a current equivalent of USD 2.3 billion.

The DNA-free CRISPR system does not involve in-

TABLE 8 CRISPR/Cas9-based genome editing in various plants, target genes and delivery methods.

Plant species	Target genes	Delivery method	References
<i>Arabidopsis thaliana</i>	<i>AtPDS3, AtFLS2, AtRACK1b</i>	Protoplast, co-transfection and <i>Agrobacterium</i> infiltration	Li et al. (2013)
<i>Nicotiana benthamiana</i>	<i>NbPDS</i>	<i>Agrobacterium</i> infiltration	Nekrasov et al. (2013)
	<i>NbpdS</i>	<i>Agrobacterium</i> infiltration	Upadhyay et al. (2013)
	<i>NbPDS</i>	<i>Agrobacterium</i> infiltration	Belhaj et al. (2013)
<i>Triticum aestivum</i>	<i>TaMLO</i>	<i>Agrobacterium</i> infiltration	Shan et al. (2013)
	<i>Tainox, TaPDS</i>	<i>Agrobacterium</i> infiltration	Upadhyay et al. (2013)
	<i>TaMLO-A1</i>	<i>Agrobacterium</i> infiltration	Wang et al. (2014)
<i>Sorghum bicolor</i>	<i>DsRED2</i>	<i>Agrobacterium</i> infiltration	Jiang et al. (2013a)
<i>Citrus sinensis</i>	<i>CsPDS</i>	<i>Agrobacterium</i> infiltration	Jiang et al. (2013b)

tegrating foreign DNA elements; therefore, it may alleviate the regulatory issues associated with transgenic crops and their easy acceptance. Moreover, the deliberate alteration of a gene through the utilization of CRISPR/Cas technology, resulting in mutations, sometimes resembles to the use of mutagenic substances that are legally acceptable. CRISPR/Cas9-based genome editing has been successfully established in various fruit crops, which has set an example for its applicability and usefulness (Table 8).

6. Challenges and Opportunities

The synergism of all legal framework, national and international policies and conventions and the implementation of the regulations are challenging. In order to protect the biodiversity from overexploitation, the Government of Indonesia has released Government Regulations No. 6 year 2007 about Forest Management and Preparation of Forest Management Plans, and Forest Utilization. In this regulation, the utilization forest resources for pharmaceutical purposes, viz cultivating medicinal plants could be awarded for non-timber forest utilization. Government Regulation No. 28 year 2011 about the Management of Natural Reserve Areas and Nature Conservation Area expresses the government commitment to provide opportunity for the community to utilize forest areas for pharmaceutical purposes sustainably.

Government Regulation Number 8 year 1999 about the Utilization of Plant and Animal Article 35 states that utilization of certain types of medicinal plants collected from natural habitat shave to sustainable considering the population in the wild, carrying capacity, and its diversity and must comply with conservation principles. Determination of the quota for export and import of wildlife (biodiversity) is managed by a Secretariat of Biodiversity Scientific Authority BRIN to maintain the balance of Indonesian biodiversity.

The Government of Indonesia has also committed to conservation efforts for biological resources through the utilization of genetic resources regulated in Law No. 11 year 2013 regarding the Nagoya Protocol as well as the

Cartagena Protocol of the Convention on Biological Diversity (CBD) about access to Genetic Resources and Fair Profit Sharing from its Use of the Convention Biodiversity, and biosafety of genetically engineered organisms.

Inadequate or poorly enforced omics-based agricultural products and nutrition-based plant products policies can hinder sustainable practices and innovation. Coordination and collaboration of research on omics especially in Indonesia will enhance better result achievements considering the existing human resources, infrastructures and research funds. Increasing capacity building on mastering this technology for agriculture and health-related plant products and its data analysis is prerequisite. Tariffs, quotas, and other trade restrictions can limit market access related to omics-based products for user utilization.

Other challenges are big data management, interpretation, cost, variability of environmental factors. Integrating and interpreting vast amounts of data from different omics platforms are complex and requires advanced bioinformatics tools. High-throughput omics technologies can be expensive and may not be accessible to all research institutions, particularly in developing countries. Plants' responses to environmental factors are highly variable, and omics data must be interpreted in the context of these variations.

To tackle these problems, integrated and sustainable approaches to obtain superior genotypes, efficient irrigation systems, soil conservation techniques, and nutrient management to maintain soil fertility and water availability, strengthening agricultural and health-related nutrition producing plants policies, and promoting research and development in sustainable agriculture are essential.

By addressing these challenges through a combination of scientific, technological, and policy-driven approaches, plant production can become more resilient, sustainable, and productive, ensuring food security, nutrition-based plant products, health and environmental health.

7. Conclusion and Way Forward

Integrated omics is a powerful approach that can revolutionize some attributes such as plant production and

health-related nutrition. To enable the development of crops that are not only high-yielding and resilient but also nutritionally superior, it is crucial to have a comprehensive key traits molecular background. This holistic approach is essential for meeting the growing global demand for food and improving public health through better nutrition. By integrating omics, researchers can identify key genetic and biochemical pathways to target for enhancing yield, stress tolerance, and nutrient use efficiency. The implementation of GWAS including the interaction of Genetic and Environment is a great opportunity for the development of more effective approaches for various aspects of plant breeding.

Increasing plant production using omics technologies which involves the integration of various high-throughput approaches is possible as plant growth and development are enhanced by understanding and manipulating genetic through new technologies such as genome editing, molecular, and biochemical aspects. Enhancing and strengthening collaborations among universities/research institutions within Indonesia and abroad, private sectors, other government agencies as well as society and communities are necessary. Legal framework and synergism of national and international policy and regulations covering trade and access and benefit sharing need to be ensured. Future directions involve the development of more cost-effective including simplifying procedures from extraction stage and accessible omics technologies, improved bioinformatics tools for data integration, and a more focus on translating research findings into practical applications in the field.

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Authors' contributions

ES and BRH designed the concept. ES, AAAA, AA, SK, EIR, EL, DJM, CFP, and BRH analyzed the data. ES, AAAA, AA, SK, EIR, EL, DJM, CFP, and BRH wrote the paper.

Competing interests

All authors have examined the manuscript and declare no competing interests.

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