


Review Article

Biological and Molecular Components for Genetically Engineering Biosensors in Plants

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Plants adapt to their changing environments by sensing and responding to physical, biological, and chemical stimuli. Due to their sessile lifestyles, plants experience a vast array of external stimuli and selectively perceive and respond to specific signals. By repurposing the logic circuitry and biological and molecular components used by plants in nature, genetically encoded plant-based biosensors (GEPBs) have been developed by directing signal recognition mechanisms into carefully assembled outcomes that are easily detected. GEPBs allow for *in vivo* monitoring of biological processes in plants to facilitate basic studies of plant growth and development. GEPBs are also useful for environmental monitoring, plant abiotic and biotic stress management, and accelerating design-build-test-learn cycles of plant bioengineering. With the advent of synthetic biology, biological and molecular components derived from alternate natural organisms (e.g., microbes) and/or *de novo* parts have been used to build GEPBs. In this review, we summarize the framework for engineering different types of GEPBs. We then highlight representative validated biological components for building plant-based biosensors, along with various applications of plant-based biosensors in basic and applied plant science research. Finally, we discuss challenges and strategies for the identification and design of biological components for plant-based biosensors.

1. Introduction

Environmental perturbations and threats jeopardize many ecosystems on Earth. Real-time monitoring of biological processes, environmental threats, and ecosystem responses, with informative spatial and temporal resolution, remains a challenge, as traditional monitoring strategies are typically based on laboratory analysis of samples collected at specific time points and locations [1–3]. Biosensors offer an alternative to traditional destructive sampling schemes. Molecules,

organisms, or devices in a biological context that sense specific stimuli or molecules and convert such signals into a quantitative or qualitative indicator can function as biosensors [4]. With the power of fluorescent proteins and other visible reporters, genetically encoded visible biosensors provide promising tools for large-scale environmental monitoring, high-resolution live-cell imaging, and so on.

Plants are natural biosensors, responding to various environmental stimuli and generating real-time signals for inter- and intracellular communication [5]. Native, signal-responsive

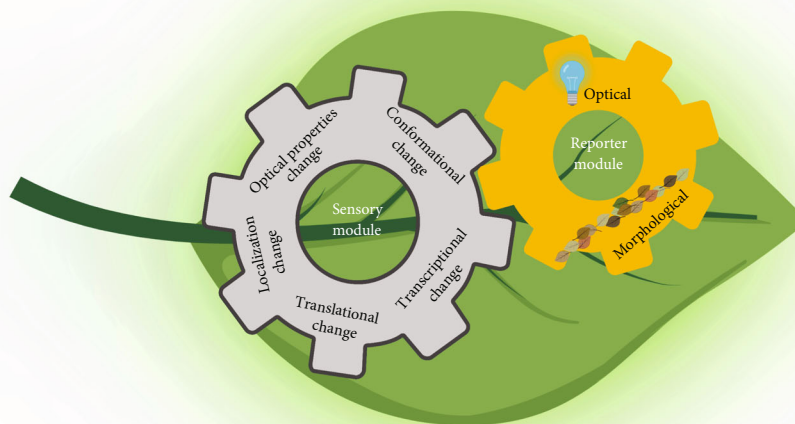


FIGURE 1: Conceptual framework of genetically encoded plant-based biosensors (GEPBs) design. GEPBs contain a Sensory Module and a Reporter Module. Five different mechanisms of Sensory Modules are presented in the gray gear, and two types of Reporters Module are presented in the yellow gear. The Sensory Module detects the environmental, chemical, or internal stimuli, and the Reporter Module provides the detectable signal.

promoters, signaling motifs (e.g. nuclear export signals (NESs)), and short amino acids sequences (i.e., degrons), have been used as sensory components for engineering genetically encoded plant-based biosensors (GEPBs) [6–8]. While GEPBs allow scientists to monitor molecular events, cell activities, and metabolic pathways in real-time, they also offer multiple desirable features for environmental monitoring. First, the integrated aboveground leaves and belowground root system allow plants to not only accept signals in the air, but to also sense the dynamic signals from a broad region of the soil [9]. Second, engineering biosensor in perennial plants species allows for cost-effective continuous monitoring of environmental conditions [9]. Third, with visible plant-based biosensors responsive to environmental factors, cumbersome sampling and laboratory analysis can be avoided [10].

An ideal plant-based biosensor should respond to specific stimuli and produce a quantifiable signal without disturbing the endogenous plant system. It has been difficult to develop such plant biosensor systems based solely on endogenous components due to the complicated crosstalk among different biological pathways. For instance, promoter-reporter systems derived from hormone signaling pathways (e.g., *DR5* and *TCS::GFP*) can be affected by native pathways [11]. Furthermore, many protein-degradation-based sensors (e.g., *DII-VENUS* and *GFP-DELLA*) are irreversible, and thus once triggered miss transient or dynamic signal changes [11, 12]. Hence, there is a need for new strategies to accelerate plant biosensor engineering.

Plant biosystem design or plant synthetic biology is an emerging and quickly advancing field, which aims to design elite plants with desirable traits [4, 13]. Synthetic biology potentially offers interchangeable components, standardized genetic circuit design, and Design-Build-Test-Learn (DBTL) cycles for rapidly developing plant-based biosensors [14]. The application of fluorescence proteins (FPs) in biosensor design is a good example demonstrating how synthetic biology utilizes universal components for building biosensors in various organisms. Standardization is important for plant biosystem design. Currently, there are no standard pipelines for choosing components to design and build genetic circuits as plant-based biosensors. In this review, we categorize plant-based biosensors based on the mode of action and list representative validated biological and molecular components for engineering each type of biosensor with the goal of proposing a standard roadmap for building genetically encoded plant-based biosensors. In addition, we discuss how to identify and design new biological components for bioengineering to expand the applications of plant-based biosensors.

2. Framework for Engineering Genetically Encoded Plant-Based Biosensors

Standardized components and frameworks are the first step towards a universal roadmap for building GEPBs. In general, GEPBs consist of a sensory element coupled to visible reporter proteins [11] (Figure 1). Based on whether biosensors rely on

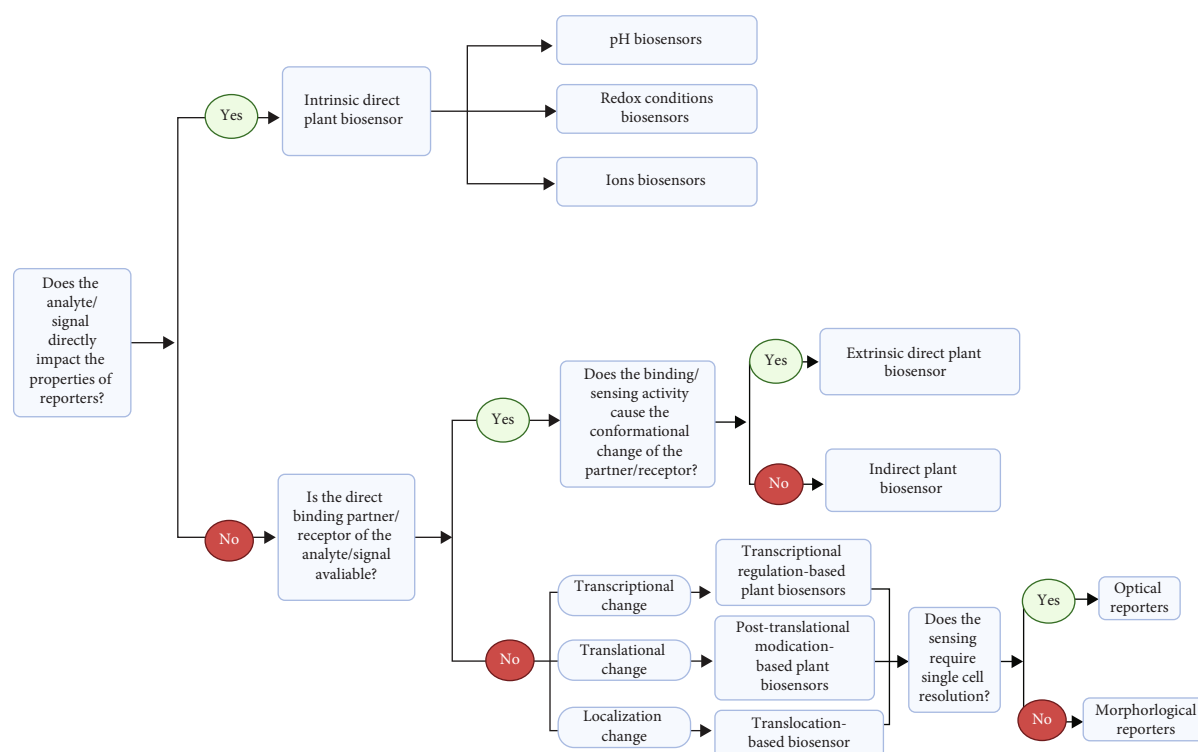


FIGURE 2: A dichotomous decision tree for the selection of appropriate genetically encoded plant-based biosensors.

the endogenous cellular processes, they can be categorized into two types: direct and indirect biosensors. Direct biosensors typically rely on fluorescence proteins (FPs) whose properties are altered by the sensing activities or interaction with analytes, while indirect biosensors consist of cellular components involved in transcription, posttranslational modification, or translocation.

Each biosensor type has advantages and limitations. Direct biosensors are a basic bioimaging tool with straightforward design principles, high sensitivity, and a wide range of resolution. Such direct biosensors produce reversible readouts that can reflect the real-time change of cellular processes. Alternatively, indirect biosensors rely on cellular process, e.g., transcription or translation, adding regulatable layers of output that can be fine-tuned. The genetic circuit design for indirect biosensors can also be used to produce metabolites or proteins as reporters. Hence, indirect biosensors offer more advanced tools with flexible designs that expand the biosensor toolbox to benefit plant biosystem design. However, because the output of indirect biosensors is usually irreversible, it is difficult to use indirect biosensors to monitor real-time dynamic cellular processes. In this section, strategies for designing different types of biosensors will be discussed and a decision map for applying different types of plant-based biosensors is illustrated in Figure 2.

2.1. Direct Plant Biosensors. Direct biosensors require no additional sensory module or only one sensory module directly interacting with the analytes. There are two types of direct biosensors, intrinsic and extrinsic direct biosensors. The intrinsic direct biosensors harbor reporters sensitive to the cellular environment, whereas the extrinsic direct biosensors contain

a sensory module whose structural change, causing a change in distance/orientation of two reporters, leading to signal changes [15]. Because the structural change is always reversible, direct biosensors allow detection of dynamic processes [16].

2.1.1. Intrinsic Direct Plant Biosensors. FPs can be readily detected by fluorescence microscopy without adding fluorescent dyes, making them useful visible reporters for noninvasive imaging (Figures 3(a) and 3(b)). For example, a phenol group on the chromophore allows pH to affect the optical properties of most green fluorescent protein (GFP) variants [17]. The structural basis of wild-type GFP (wtGFP) and the chromophore of GFP, including three consecutive amino acids S65, Y66, and G67 and residues responsible for fluorescence, have been identified [17]. Here, the excitation property of FPs is related to the ionization state of the chromophore, whose equilibrium is controlled by a hydrogen bond network that permits proton transfer to the neighboring amino acids when the chromophore is excited [18, 19]. This understanding has ushered in the opportunity for expanded FP engineering.

Most intrinsic direct biosensors were developed through targeted mutagenesis or random mutagenesis of the chromophore of FPs [20]. The abundance of available FPs facilitates potential applications for a wide variety of biosensors for pH, ion concentration, and redox conditions within plant cells [18, 21–24]. Some FPs emit different fluorescence intensity in various cellular environments, while other modified FPs have bimodal excitation/emission spectra, where the excitation/emission ratio reflects the change of cellular environmental conditions [25, 26]. This type of biosensor solely relies on the

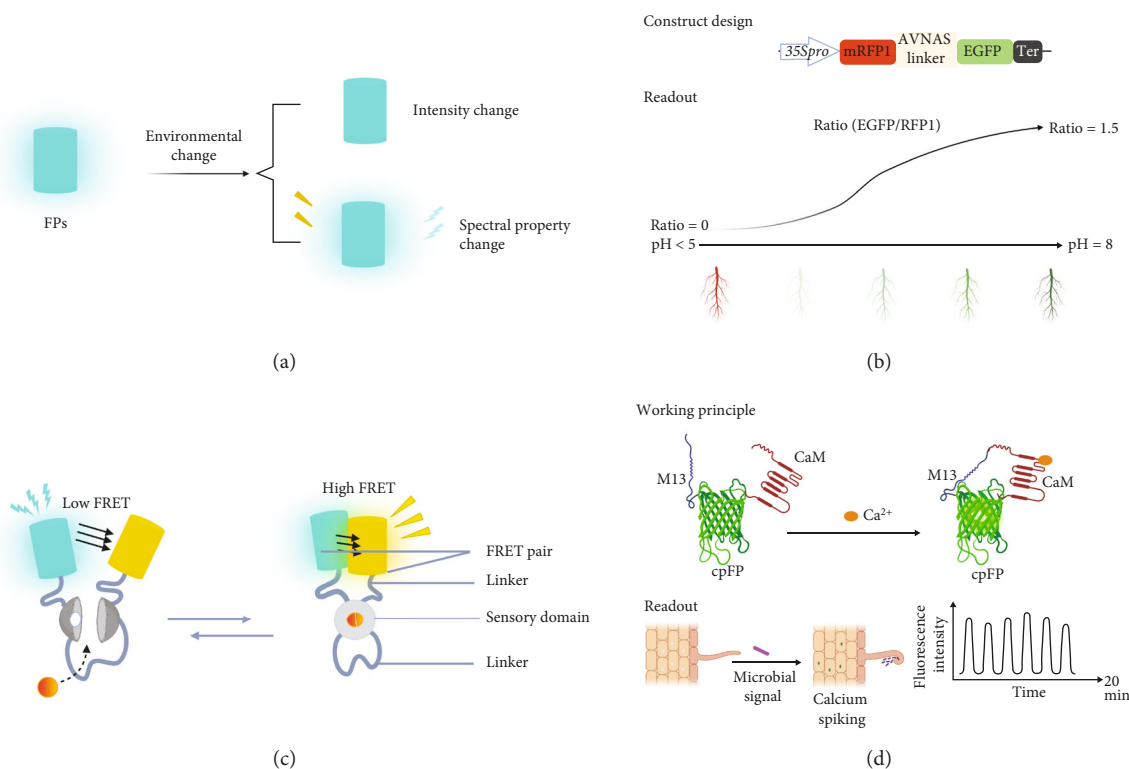


FIGURE 3: Design of direct plant biosensors. (a) Working principle for intrinsic direct plant biosensors where fluorescent proteins (FP) respond to an environmental change and induce a spectral change in the FP. (b) Illustration of the construct design and readout of pHusion in plants. Figures are redrawn from the publication of pHusion [51]. Pro indicates promoter and ter represents terminator. (c) Working principle for extrinsic direct plant biosensors, where the conformational change of the sensory module caused by binding activity leads to the FRET change. Figure is designed based on the strategy of FRET-based biosensors. (d) Illustration of working principle and application of G-GECO in plants. Figures are redesigned from the results in *Populus* [68].

spectral properties of FPs, so the intrinsic direct biosensors require the least number of components compared with other types of biosensors. The validated intensity-based and ratiometric intrinsic direct biosensors will be discussed in Section 3.

2.1.2. Extrinsic Direct Plant Biosensors. Different FPs can also be fused to a sensory module to enable the use of a fluorescence resonance energy transfer (FRET) signal as a readout and is known as a FRET-based biosensor (Figure 3(c)). In this circumstance, any conformational change in the sensory module will alter the distance/orientation of the two FPs and thereby modify the FRET efficiency [27]. Based on a similar principle, using different luciferase variants, bioluminescence resonance energy transfer (BRET)-based biosensors have been developed for imaging protein interactions in plant and mammalian cells and tissues [28, 29]. Because readout of FRET-based biosensors is excitation/emission ratio, this type of biosensor is ratiometric (i.e., the output is directly proportional to the input).

The tolerance of GFPs for circular permutations and insertion of entire proteins offers another strategy for building extrinsic direct plant biosensors [30]. The conformational changes in the insert can influence the spectral properties of these circularly permuted FPs. Hence, single circularly per-

tated FPs (cpFPs) can fuse with the sensory module to build extrinsic direct biosensors (Figure 3(d)). The readout of this type of extrinsic direct biosensors can be either ratiometric or intensimetric (i.e., intensity change depending on the design).

Based on a specific design principle, the direct binding partner/receptor for the analyte is necessary for designing extrinsic direct biosensors. Moreover, the structural change induced by the binding/sensing activity is another important factor to be considered for designing extrinsic direct biosensors. Modification of the sensory module can be applied for adjusting the analyte affinity [11]. Extrinsic direct plant biosensors that have been widely used for sensing various analytes will be presented in detail in Section 3.

2.2. Indirect Plant Biosensors. Direct binding partner/receptors are not always feasible in biosensor design. Under these circumstances, the downstream cellular processes induced by the binding/sensing activity can be applied as indicators for the signals, known as an indirect biosensor. Indirect biosensors need additional cellular processes to render a signal for a particular analyte or stimulus, and are typically grouped as transcription-based biosensors, posttranslational-based biosensors, and translocation-based biosensors. To build indirect plant-based biosensors, biological parts are usually

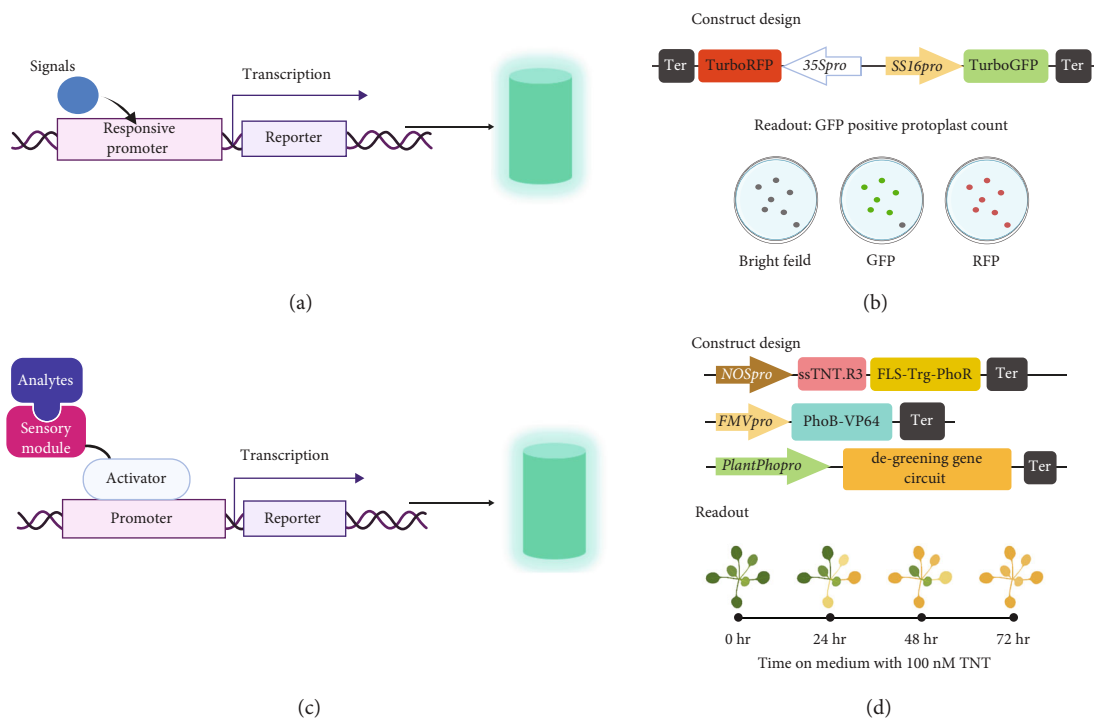


FIGURE 4: Design of transcriptional regulation-based plant biosensors. (a) Working principle for transcriptional regulation-based biosensors with responsive promoters as the sensory module, where the turquoise cylinder presents an optical signal from a fluorescent protein. (b) Illustration of the construct design and readout of SS16::GFP biosensor. Figures were redrawn from the results in *Populus* protoplasts [33]. Pro indicates promoter, and ter represents terminator. (c) Working principle for transcriptional regulation-based biosensors with synthetic TFs as the sensory module. (d) Illustration of constructs design and readout of TNT plant-based biosensor. Figures were adopted from phenotypic data of *Arabidopsis* [38].

found within the system under study. Because biological processes are complicated, indirect biosensors typically require a greater number of biological and molecular parts and are more complicated in comparison to direct biosensors.

2.2.1. Transcriptional Regulation-Based Plant Biosensors. If the binding/sensing activity causes a transcriptional change in the plant system, transcriptional regulation-based biosensors can be considered. Transcription factors (TFs) and promoters are two main components of plant transcriptional machinery that serve as sensory modules for transcriptional regulation-based biosensor design. There are two types of transcription-based biosensors depending on the sensory module (Figure 4). The first, known as a promoter-reporter system, utilizes promoters as the sensory module that regulates the transcription level of reporters (Figures 4(a) and 4(b)). A native plant gene promoter is the DNA sequence upstream of the transcription start sites (TSS) of a gene. A good example of transcription-based biosensors is β -glucuronidase or FPs driven by a synthetic or native hormone-responsive promoter for measuring phytohormone accumulation [31, 32]. However, because of the complex signaling networks within a plant system, applying endogenous plant promoters for sensory modules often results in low and complex patterns of readouts [33]. To enhance the specificity and sensitivity of the promoters, multiple core response elements can be used to create a synthetic promoter. For example, the synthetic DR5 promoter, consisting of 7-9 TGTCTC Aux

response element repeats, have been used to drive the expression of different reporters such as β -glucuronidase, fluorescent proteins, or luciferase to create a biosensor for auxin [31].

The second type of transcription-based biosensor uses synthetic TFs as the sensory module (Figure 4(c)). Here a TF is fused to a degron or conditionally stable ligand binding domain to construct a responsive synthetic activator/repressor regulated by posttranslational modifications [34, 35]. Although the responsive degrons or conditionally stable ligand binding domains can be directly fused with reporters to design post-translational regulation-based plant biosensors, the synthetic TFs can amplify the biosensor response and serve as a ligand-dependent controller for gene expression [35].

Endogenous signaling transduction systems (i.e., native plant promoters and TFs) can interfere with transcription-based biosensors. To overcome this concern, several orthogonal regulatory systems from *Saccharomyces* spp., bacteria, and other organisms have been developed for modulating transcription in plants [36, 37]. Likewise, a functional signal transduction system from bacteria has been engineered for plant transcriptional regulation-based biosensor design [38] (Figure 4(d)). The detail design strategies of those orthogonal regulators will be discussed in Section 3.

2.2.2. Posttranslational Modification-Based Plant Biosensors. A change in protein level, i.e., an accumulated reporter, has been utilized for biosensor design (Figure 5). Conditionally stable

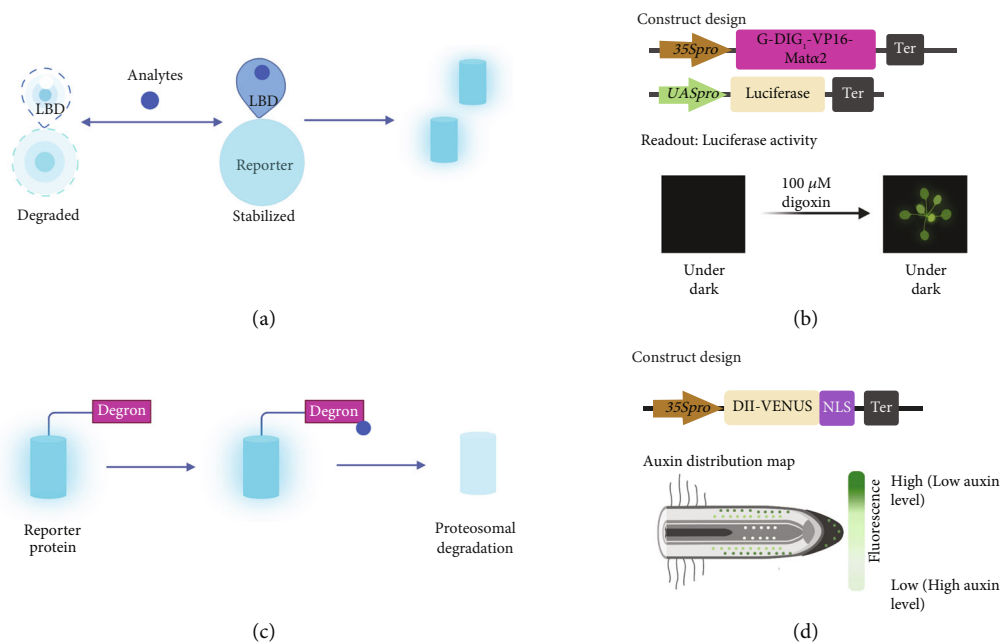


FIGURE 5: Design of posttranslational modification-based plant biosensors. (a) Working principle for posttranslational modification-based biosensors consisting of a conditionally stable ligand binding domain (LBD) fused with a reporter, where the turquoise cylinder presents an optical signal from a fluorescent protein. (b) Illustration of constructs design and application of digoxin plant-based biosensor. Figures were redrawn from results in *Arabidopsis* [35]. Pro indicates promoter and ter represents terminator. (c) Working principle for posttranslational modification-based biosensors consisting of a degron motif fused with a reporter. (d) Illustration of constructs design and application of DII-VENUS for mapping Auxin distribution. Figures were redrawn from results in *Arabidopsis* [6]. Pro indicates promoter, and ter represents terminator.

ligand-binding domains (LBDs) linked to reporters have been used as a general strategy to build small molecule biosensors [35]. Such engineered LBDs are degraded by the ubiquitin proteasome system until it binds to the signal molecules and thereby creates sensing/binding activity (Figure 5(a)). Currently, some conditionally stable LBDs have been engineered for sensing small molecules based on computational design [35, 39]. For example, an engineered LBD biosensor for digoxigenin has been applied in plants [35] (Figure 5(b)). A robust computational design is the first step for LBD engineering. Next, high-throughput experimental characterization is required for evaluating the ligand-dependent responses. Fluorescence-activated cell sorting (FACS) is a commonly used strategy. To obtain the ideal LBD-based biosensor, one round of optimization is usually needed. Error-prone PCR and site-saturation mutagenesis are two methods for creating a variable library of LBDs for characterization.

Another strategy is to apply a signal responsive degron as the sensory module coupled with a reporter gene (Figure 5(c)). The binding of the target analyte promotes degradation of the degron that thus yields a signal. A well-known degron-based biosensor DII-VENUS reporter system was developed by fusing the VENUS yellow fluorescent protein in frame to the degron motif of AtIAA28 [6] (Figure 5(d)). Jas9-VENUS has also been developed for mapping local changes in JA levels in *Arabidopsis* roots [40]. Fluorescence levels for these two biosensors are inversely correlated to endogenous phytohormone levels.

2.2.3. Translocation-Based Plant Biosensors. While transcriptional regulation-based and posttranslational modification-based biosensors monitor the input signal by changes in the abundance of reporters, and translocation-based biosensors utilize spatial location of reporters to measure signal levels. The localization of proteins can be tracked by fusing a FP to a protein of interest (Figure 6). The change in localization of the sensory module with a reporter can be used as a readout to monitor the input signal. This kind of biosensor is an ideal tool for studying protein localization, hormone signaling pathways, and protein phosphorylation levels [11, 27, 41]. For instance, because the brassinosteroid (BR) signaling promotes BRASSINAZOLE RESISTANT 1 (BZR1) nuclear localization, BZR1 fused with YFP can serve as a biosensor for BR signaling in *Arabidopsis* roots and hypocotyls [42] (Figures 6(a) and 6(b)).

Another example of translocation-based biosensors are kinase translocation reporters (KTRs) (Figures 6(c) and 6(d)). KTRs are comprised of an FP fused to a substrate recognition motif for a target kinase, where phosphorylation sites are attached to a negatively phospho-regulated nuclear localization signal (NLS) and a positively phospho-regulated nuclear export signal (NES) [43]. A nonphosphorylated KTR locates within the nucleus via its NLS. Once there, phosphorylation of the NES allows KTR to exit the nucleus, which leads to the conversion of a phosphorylation event into a nucleocytoplasmic shuttling event [41, 44].

Similarly, the intein-mediated conditional protein splicing (CPS) reaction has become an important strategy for protein

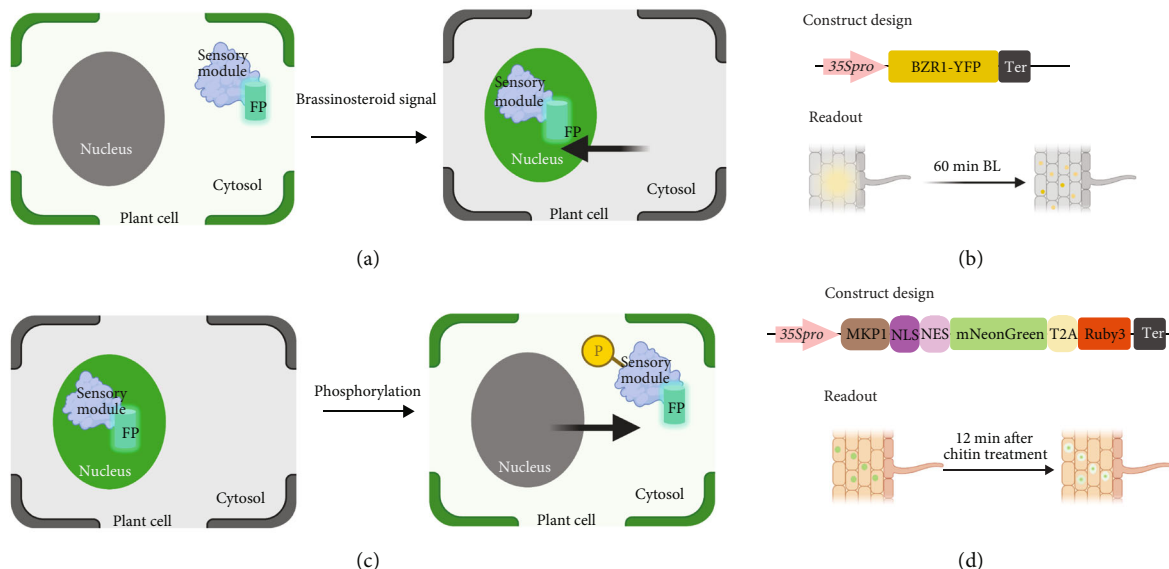


FIGURE 6: Design of translocation-based biosensors. (a) Illustration of translocation-based biosensors for brassinosteroid signaling pathway. (b) Illustration of the construct design and readout of BZR1-YFP biosensor. Yellow dots represent the accumulation of BZR1-YFP in nucleus, whereas the gradient yellow area represents the cytoplasmic BZR1-YFP signals. Figures were adopted from a study in *Arabidopsis* [42]. Pro indicates promoter, and ter represents terminator. (c) Illustration of translocation-based biosensors for phosphorylation activity. (d) Illustration of the construct design and readout of the KLR-MKP1 biosensor. Solid green spots represent the accumulation of KLR-MKP1 signals in the nucleus, whereas the green circle with gradient color change indicates the decrease fluorescence intensity in the nucleus. Figures were adopted from the results in *Arabidopsis* [96]. Pro indicates promoter, and ter represents terminator.

engineering [45, 46]. The intein-mediated split NLS and NES has also been applied for building translocation-based biosensors [47, 48]. Essentially, the split signal peptide (NLS or NES) is fused to a FP serves as a reporter. Upon the sensing activity, the signal peptide will be reconstituted via intein-mediated protein splicing, resulting in the translocation of signals. Thus far, this strategy has not been applied for building translocation-based biosensors in plants.

Translocation-based biosensors can also be used for detecting gene expression in real time. PP7 and MS2 RNA labeling technologies have been applied to building plant biosensors for gene expression [49]. Nascent RNA labeling with an RNA aptamer such as the MS2 or PP7 recruits FPs fused with an MS2 coat protein or PP7 bacteriophage coat protein to transcriptional loci [49]. The fluorescence intensity of these signals reflects the instantaneous rate of transcription [49].

3. Validated Biological Components for Different Types of Plant-Based Biosensors

Based on the framework discussed in Section 2, here biological components including sensory modules (promoter sequences, protein-coding sequences, and noncoding RNAs) and reporters (optical and morphological) are reviewed in the context of validated biological components for different types of plant biosensors. In this section, the application of frameworks mentioned above for designing various plant biosensors will be discussed in the context of further guidance for plant biosensor design.

3.1. Validated Biological Components for Direct Plant Biosensors. As mentioned in Section 2.1, FPs have been modified as intrinsic direct biosensors for sensing different analytes and changes of cellular environment. Representative biological components and design illustrations of intrinsic direct plant-based biosensors are listed in Table 1. With an additional sensory module, many extrinsic direct biosensors have been designed to sense direct signal binding activities. Validated sensory modules and design strategies for extrinsic direct plant-based biosensors are listed in Table 2.

3.1.1. Validated Components for Intrinsic Direct Plant Biosensors. Taking advantage of pH-dependent excitation and emission properties of FPs, a single FP can be used as an intrinsic direct plant biosensor for measuring pH within plant cells. An example is the ratiometric pHGFP that has been expressed in *Arabidopsis* for monitoring intracellular pH changes. This direct biosensor exhibited a dynamic range of 410 nm/470 nm excitation ratio for pH from 5.5 to 7.5 [50]. Tandem fusion of different FPs has also been applied for intrinsic direct plant biosensor design. The pH sensor named ‘pHusion’ consists of a monomeric red fluorescent protein (mRFP1) and an enhanced GFP [51]. Currently, three new ratiometric biosensors composed of two FPs in tandem have been generated for measuring a pH range of 3-8 within the plant cell apoplast [52].

Beyond the intrinsic pH sensitivity, ions near chromophores impact the spectral properties of FPs, which allows FPs to be engineered to measure the concentrations of various chemical ions within plant cells. YFP and its variants have

TABLE 1: Selected examples of validated biological parts for intrinsic direct plant biosensors. Coding sequences for listed biosensors are provided in supplemental data 1.

Name	Readout	Description	Biosensor target	Tested plant species	References
pHusion	Ratiometric	The tandem concatenation of enhanced green fluorescent protein (EGFP) and monomeric red fluorescent protein (mRFP1)	pH	<i>Arabidopsis thaliana</i>	[51]
PE-pHluorin	Intensity	Plant-solubility-modified ecliptic pHluorin	pH	<i>A. thaliana</i>	[131]
PR-pHluorin	Ratiometric	Plant-solubility-modified ratiometric pHluorin	pH	<i>A. thaliana</i>	[131]
Pt-GFP	Ratiometric	A ratiometric GFP variant from <i>Ptilosarcus gurneyi</i>	pH	<i>A. thaliana</i> , <i>Solanum tuberosum</i>	[132, 133]
Acidin2	Ratiometric	The tandem concatenation of mRFP and tagBFP2	pH	<i>A. thaliana</i>	[52]
Acidin3	Ratiometric	The tandem concatenation of mRFP and gamillus	pH	<i>A. thaliana</i>	[52]
Acidin4	Ratiometric	The tandem concatenation of mRFP and SYFP2	pH	<i>A. thaliana</i>	[52]
Clomeleon	Ratiometric	Cl ⁻ indicator (CFP-rTEV-YFP)	Chloride concentration	<i>A. thaliana</i>	[55, 56]
roGFP2	Ratiometric	A redox-dependent GFP variant that displays a bimodal excitation spectrum	Redox condition	<i>A. thaliana</i>	[61]
BS1	Intensity	A mutated dark GFP with a gRNA targeting the mutated region	CRISPR/Cas9	<i>A. thaliana</i> , <i>Nicotiana benthamiana</i> , <i>Populus tremula</i> × <i>alba</i> 717-1B4, <i>P. deltoides</i> WV94	[62]
BS2	Intensity	A mutated dark GFP with a gRNA targeting the mutated region	CRISPR/Cas9-based base editors	<i>A. thaliana</i> , <i>N. benthamiana</i> , <i>P. tremula</i> × <i>alba</i> 717-1B4, <i>P. deltoides</i> WV94	[62]

TABLE 2: Selected examples of validated biological parts for extrinsic direct plant biosensors. Coding sequences for listed biosensors are provided in supplemental data 2.

Name	Readout	Description	Biosensor target	Tested plant species	References
G-GECO	Intensity	Genetically encoded calcium indicators with improved single cpGFP for optical imaging (M13-cpGFP-CaM)	Ca ²⁺	<i>Arabidopsis thaliana</i> , <i>Populus tremula</i> × <i>alba</i> 717-1B4	[67, 68]
Cameleons	Ratiometric	Genetically encoded calcium indicators with two FPs (CFP/BFP-CaM-M13-GFP/YFP)	Ca ²⁺	<i>A. thaliana</i>	[134–137]
CALWY	Ratiometric	Genetically encoded zinc indicators with two FPs (cerulean-Atox1-WD4-citrine)	Zn ²⁺	<i>A. thaliana</i>	[71]
FLIPPi	Ratiometric	Genetically encoded phosphate indicators with two FPs (eCFP-PiBP-eYFP)	Pi	<i>A. thaliana</i>	[73]
cpFLIPPi	Ratiometric	Genetically encoded phosphate indicators with two FPs (eCFP-PiBP-cpVenus)	Pi	<i>A. thaliana</i>	[73]
ABSCUS1	Ratiometric	Genetically encoded ABA indicator with two FPs (edCerulean-PYL1-ABI1aid-edCitrine)	ABA	<i>A. thaliana</i>	[74]
AuxSen	Ratiometric	Genetically encoded IAA indicator with two FPs (aquamarine-TrpR-mNeonGreen)	IAA	<i>A. thaliana</i>	[12]
SED1	Ratiometric	Genetically encoded osmotic stress biosensor with two FPs (mCerulean3-AtLEA4-5-citrine)	Osmotic stress	<i>A. thaliana</i>	[75]

been constructed as a halide biosensor, where fluorescence decreased with increasing concentrations of chloride or nitrate [53, 54]. A ratiometric optical indicator for chloride concentration has been constructed by fusing the chloride-sensitive YFP and chloride insensitive cyan fluorescent protein [55]. This biosensor can be applied for the monitoring salt stress [56]. Engineering the metal binding sites of the Av-GFP resulted in a highly specific direct biosensor, eGFP20C, for monitoring mercury uptake [57]. Additional intrinsic direct biosensors can be developed by engineering the potential metal binding sites of FPs.

Another important application of intrinsic plant biosensors is real-time monitoring of plant cell redox conditions and energy physiology. In plants, redox reactions are involved in photosynthesis, respiration, and many other plant energy metabolism pathways [18]. Reactive oxygen species (ROS) are key signals in plant development and stress responses [18]. Genetically encoded intrinsic direct plant biosensors allow monitoring the dynamics of redox conditions and energy metabolites at high spatial resolution, which provides detailed insights into plant physiology [18, 58]. Structural changes in the FP β -barrel, redox-sensitive YFP (rxYFP), and redox-sensitive GFP (roGFP) have been engineered and used as intrinsic plant biosensors [59]. Among these, roGFP2 is the most commonly used because of its photostability, pH-insensitivity, and good signal-to-noise ratio [60, 61].

FPs can also be modified to detect the CRISPR machinery in plants. Intentionally inactivated GFPs that cannot emit fluorescence signals can be constructed in a system with an active CRISPR/Cas9 with a guide RNA targeting and repairing the mutated residue in GFP, restores the coding sequence and thus fluorescence. CRISPR/Cas-based genome engineering tools have been widely applied in various plant studies. However, off-target effects of CRISPR/Cas systems or CRISPR-based contaminating gene raise potential biosecurity risks [62]. Hence, a biosensor system to detect CRISPR/Cas systems at an early stage is needed.

In this regard, a plant-based biosensor has been developed using mutated GFP genes for detecting CRISPR/Cas-based genome engineering tools, such as based editors and prime editors [62]. Currently, studies focused on monitoring genome engineering tools are still at an early stage, and the developed biosensors can only monitor specific genome engineering tools. More effort is needed for building universal biosensors monitoring various CRISPR/Cas-based genome engineering invasions.

3.1.2. Validated Components for Extrinsic Direct Plant Biosensors. Extrinsic direct plant biosensors require an additional sensory module to directly interact with analytes. The sensory module can be fused with either a single cpGFP to make a biosensor or two different FPs to build a FRET-based biosensor. One of the most developed and widely applied extrinsic direct plant biosensor is the genetically encoded calcium indicator (GECI). The sensing module for Ca^{2+} is calmodulin (CaM), which recognizes a short polypeptide M13 in target protein [63]. Here, a single GFP GECIs is fused with the calmodulin-M13 to create a single circularly permuted FPs (cpFPs), where the presence of Ca^{2+} , calmodulin binds to the M13, inducing conformational changes of FP and inducing

its fluorescent properties [30, 64]. In addition, the GCaMP [65] and pericam [66] are two representative GECIs developed based on this strategy. With mutation of several amino acids adjacent to the chromophore, ratiometric-pericam and intensity based-pericam have been developed for monitoring the dynamic change of Ca^{2+} concentration. The cpGFP-based calcium indicator G-GECO has been applied for monitoring the calcium spiking triggered by an arbuscular mycorrhizal fungus in plants [67, 68]. The other widely adopted method for designing GECIs is the FRET-based biosensor. The principle is to flank the Ca^{2+} sensory module, CaM-M13 with two different FPs. Binding of the Ca^{2+} causes calmodulin to bind to M13, thus FRET between the flanking FPs [69]. For example, in yellow Cameleon-2, the CaM-M13 was fused with N-terminal CFP as the FRET donor and C-terminal YFP as the FRET acceptor [69]. FIP-CA indicators are another available design in which only the M13 is linked to two FPs with the engineered CaM fused to the C-terminus of this protein [70].

A similar design strategy has been applied in building plant biosensors for other ions. For instance, high-affinity FRET-based Zn^{2+} biosensors have been developed using two Zinc-binding domain as sensory modules [71]. Two Zn^{2+} binding domains, Atox1 and the fourth domain of ATP7B (WD4), were linked via a flexible linker and flanked by two FPs. This FRET-based biosensor has been applied for measuring the Zn^{2+} concentrations in Arabidopsis root cells [72]. In addition, the cyanobacterial inorganic phosphate, Pi binding protein, has been applied as sensory module flanked by eCFP as FRET donor and different FPs as FRET acceptors for building FRET-based biosensors detecting Pi in plants [73].

Phytohormone receptors can serve as sensory modules for building extrinsic direct phytohormone biosensors. For instance, potential ABA sensory domains (PAS) were selected from members of ABA coreceptor complexes for ABA FRET-based biosensors design [74]. Here, there were two types of designs: a single domain design, in which either a member of PYR/PYL/RCAR family of ABA receptors or a member of the PP2CA subfamily of ABA coreceptor phosphatases alone is inserted between two FPs, and a double domain design, in which the sensory module consists of a PYL/PYL/PCAR fused with a PP2CA via a linker [74]. After screening different ABA biosensor designs, ABACUS1, a FRET-based biosensor built with ABA receptor PYL and coreceptor PP2CAs, is characterized by an affinity of $\sim 80 \mu\text{M}$, was selected for ABA [74]. Auxin is another important phytohormone regulating plant development. Auxin biosensors provide effective tools for revealing the dynamics of auxin signaling during many developmental contexts. A novel FRET-based biosensor for auxin has been built using an engineered bacterial tryptophan repressor (TrpR) [12]. To build this biosensor, the selected TrpR variants with high affinity to IAA were flanked by Aquamarine as the FRET donor and mNeonGreen as the FRET acceptor [12].

Any protein conformational change caused by the surrounding environment without direct binding activity can also be monitored by extrinsic direct plant biosensors. Intrinsically disordered regions (IDRs) of a protein are domains that can be sensitive to the physical-chemical properties of its surrounding environment. Utilizing the *Arabidopsis* intrinsically

disordered AtLEA4-5 protein, whose conformational change is induced by water deficit, a FRET biosensor named SED1 was developed for monitoring water-associated stress in living bacteria, yeast, plant, and human cells [75].

3.2. Validated Components for Indirect Plant Biosensors. In contrast with direct biosensors, the sensory modules of indirect plant biosensors are involved in various biological processes. Because the readout of indirect plant biosensors is the quantity of reporter present, indirect biosensors are usually intensiometric. A ratiometric readout, though less common, can be obtained with a nonresponsive reporter for normalization. Without relying on the structural change of the FPs, morphological reporters can also be applied for indirect plant biosensors design. In this section, validated representative biological parts of indirect plant-based biosensors will be discussed and are listed in Tables 3–5.

3.2.1. Validated Components for Transcriptional Regulation-Based Plant Biosensors. The promoter-reporter systems are the simplest design for transcriptional regulation-based biosensors. In plants, promoters control genes expression patterns, and as noted above, promoter-reporter systems have been used for sensing phytohormones. For example, the expression of firefly luciferase driven by the abscisic acid (ABA)-inducible promoter has been developed to sense ABA levels in plants [76, 77]. A similar biosensor for investigating the dynamics of cytokinin using the synthetic promoter, TCS, has also been created [78]. Additionally, salicylic acid (SA) biosensors built with an SA responsive promoter, flagellin sensing 2 promoter, and a synthetic promoter have been utilized for monitoring biotic stress in plants [79].

Currently, novel cis sequences that respond to specific stimuli can be rapidly discovered and identified via bioinformatic tools and high-throughput gene expression profiles [80, 81]. To increase the accuracy of motif prediction, multiple bioinformatic tools should be applied for motif evaluation [81]. Once cis sequences have been identified synthetic responsive promoters can be designed by fusing multiple copies of a motif with a minimal 35S promoter. Both abiotic and biotic responsive synthetic promoters have been developed following this approach [33, 80, 81]. For instance, five synthetic promoters have been developed for building biosensors sensing drought or salt stress [33]. The *de novo* soybean cyst nematode-inducible synthetic promoters have been designed as biosensors monitoring soybean cyst nematode infection [81]. Using this method, pathogen elicitor-responsive synthetic promoters have been made for studying plant-pathogen interactions [80].

The output of promoter-reporter systems may be affected by cross talk from other pathways; the synthetic signal transduction system promises independent regulatory systems for building transcriptional regulation-based plant biosensors. For example, a bacterial periplasmic binding protein (PBP) was redesigned as a trinitrotoluene (TNT) receptor [38]. When TNT binds to this receptor, the conformational change of the PBP-TNT complex promotes its interaction with a bacterial chemotactic receptor (e.g., Trg). Here, the Trg was fused

with a histidine kinase (HK) to produce a chimeric kinase that transfers the TNT binding activity to Phosphorus-dependent gene expression [38]. A synthetic TF PhoB-VP64 and synthetic promoter PlantPho, together with the Trg-HK, makes a complete synthetic signal transduction system. The TNT receptor, together with synthetic signal transduction components and a synthetic reporter degreening gene circuit, were introduced to *Arabidopsis* to build a plant-based biosensor for monitoring TNT [38].

Finally, combining cis elements from yeast with plant minimal promoters has been used to create a set of synthetic promoters with various expression strengths. Together with different TFs, such as Gal4, MADS (MCM1), and GATA (Gat1), an orthogonal regulatory tool box for transcription-based biosensors has been created for plants [36]. Using a phosphate responsive promoter, *AtPht1.1* to drive the synthetic activator, an external phosphate biosensor was made in *Arabidopsis* [36]. In addition, dCas9-based synthetic TFs can be used to provide additional design options for transcription-based biosensors. For example, a synthetic hormone-responsive biosensor has been developed fusing the dCas9-based repressor with phytohormone inducible degrons [34].

3.2.2. Validated Components for Posttranslational Modification-Based Plant Biosensors. Posttranslational modification-based plant biosensors, such as degron-based biosensors, have been successfully design and tested based on ubiquitin-mediated protein degradation [82, 83]. Because proteins under hormone-dependent degradation are often regulators of phytohormone signaling pathways, degron-based biosensors are ideal tools to monitor the change of phytohormones in different plant tissues during various development stages. For example, gibberellin (GA) indicators have been developed by fusing GFP with DELLA proteins to monitor GA levels in hypocotyls during photomorphogenesis [11, 84]. By fusing the FP VENUS with auxin-inducible degron motif DII, a novel auxin biosensor was designed to map auxin distribution with single cell resolution [85]. Similarly, with the jasmonic acid (JA)-responsive degron motif of the JAZ repressors coupled with VENUS, the Jas9-VENUS biosensor was made for analyzing responses to JA in plants with cellular resolution [40]. The readouts of all these three biosensors are intensiometric, whereas the ratiometric version of these biosensors has been made by including another stable reporter. For example, the R2D2, a ratiometric auxin biosensor, has been made by including a mDII-tdTomato reporter for normalization [31]. Another ratiometric degron-based biosensor, Strigo-Quant, was engineered by linking AtSMXL6 with a firefly luciferase to quantify strigolactone (SL) activity and specificity [11, 86].

Computational design of ligand binding proteins promises novel components for biosensors sensing small molecules. As mentioned in Section 2, engineered conditionally stable LBDs have also been applied as sensory elements for plant-based biosensors. The computationally designed binding domains, such as DIG0 binding the plant steroid glycoside digoxin, progesterone binder (PRO0), and the potent analgesic fentanyl binder, have been applied in building

TABLE 3: Selected examples of validated biological parts for transcriptional regulation-based plant biosensors. Promoter sequences for listed “promoter-reporter” systems are provided in supplemental data 3.

Name	Readout	Description	Biosensor target	Tested plant species	References
RD29A::Luc	Intensity	Reporters driven by a native ABA and dehydration-responsive promoter	ABA	<i>Arabidopsis thaliana</i>	[76]
DR5::GFP/Luc	Intensity	Reporters driven by a synthetic auxin responsive promoter	Auxin	<i>A. thaliana</i> , <i>Populus tremula</i> × <i>alba</i> 717-1B4	[31, 138]
TCS::GFP	Intensity	Reporters driven by synthetic cytokinin responsive promoters	Cytokinin	<i>A. thaliana</i> , <i>Zea mays</i>	[139]
FLS2::GUS	Intensity	Reporters driven by salicylic acid responsive promoter	Salicylic acid	<i>Solanum tuberosum</i>	[79]
SD::TurboGFP	Intensity	Reporters driven by synthetic water-deficit stress responsive promoters	Water-deficit stress	<i>A. thaliana</i> , <i>P. tremula</i> × <i>alba</i> 717-1B4	[33]
SS16::TurboGFP	Intensity	Reporters driven by synthetic salt stress responsive promoters	Water-deficit stress	<i>A. thaliana</i> , <i>P. tremula</i> × <i>alba</i> 717-1B4	[33]
SCN::RFP	Intensity	Reporters driven by synthetic soybean cyst nematode responsive promoters	Soybean cyst nematode	<i>Glycine max</i>	[81]
ER::GUS	Intensity	Reporters driven by synthetic plant pathogen responsive promoters	Plant pathogen	<i>Nicotiana benthamiana</i>	[80]
TNT indicator	Intensity	Reporters controlled under a whole synthetic signaling transduction pathway (ssTNT.R3 → Fls-Trg-PhoR → PhoB-VP64 → PlantPho promoter::GUS/De-greening circuits)	TNT	<i>A. thaliana</i>	[38]
HACRs	Intensity	Reporters regulated by dCas9 based synthetic TFs (dCas9-degron-TPL repressor gRNAs +pUBQ1::Venus/luciferase)	Phytohormones	<i>A. thaliana</i>	[34]

TABLE 4: Selected examples of validated biological parts for posttranslational regulation-based plant biosensors. Coding sequences for listed biosensors are provided in supplemental data 4.

Name	Readout	Description	Biosensor target	Tested plant species	References
DELLA-reporter	Intensity	Proteins containing DELLA domain fused with GFP	Gibberellin	<i>Arabidopsis thaliana</i>	[84]
DII-reporter	Intensity	Degron motif of AtIAA28 fused with VENUS	Auxin	<i>A. thaliana</i>	[6]
Jas9-reporter	Intensity	Degron motif of JAZ proteins fused with VENUS	Jasmonic acid	<i>A. thaliana</i>	[40]
AtSMXL6-reporter	Intensity	SL-responsive degradation protein fused with luciferase	Strigolactone	<i>A. thaliana</i>	[86]
DIG1-reporter	Intensity	Conditionally stable plant steroid binding domain	Digoxin and progesterone	<i>A. thaliana</i>	[35]
PRG0-reporter	Intensity	Conditionally stable plant steroid ligand binding domain	Digoxin and progesterone	<i>A. thaliana</i>	[35]
Fen-reporter	Intensity	Conditionally stable fentanyl binding domain with GFP/Luc	Fentanyl	<i>A. thaliana</i>	[87]

plant-based biosensors [35, 39, 87]. Fusing these ligand binding domains with degrons and adding a transcriptional activation domain creates responsive synthetic transcriptional factors that can amplify the reporter signal of the biosensors [35].

3.2.3. *Validated Components for Translocation-Based Plant Biosensors.* Translocation-based biosensors reflect the change

of localization of reporters induced by the signals. This type of biosensor provides high resolution at the single cell level. Translocation-based biosensors have been used as tools for monitoring protein localization, phosphorylation activity, and gene expression. As mentioned in Section 2.2.3, the biosensor BZR1-CFP has been used in investigating the spatio-temporal brassinosteroid signaling in *Arabidopsis* [42]. Because the localization of transcription factors NLP7 is

TABLE 5: Selected examples of validated biological parts for translocation-based plant biosensors. Coding sequences for listed biosensors are provided in supplemental data 5.

Name	Readout	Description	Biosensor target	Tested plant species	References
BZR1-YFP	Subcellular localization of reporters	BZR1 protein fused with YFP	Brassinosteroid	<i>Arabidopsis thaliana</i>	[42]
NLP7-GFP	Subcellular localization of reporters	NLP7 protein fused with GFP	Nitrate	<i>A. thaliana</i>	[8]
PIPs indicator	Subcellular localization of reporters	Phospholipids-binding domains fused with FPs	Phosphatidylinositolphosphates (PIPs)	<i>A. thaliana</i>	[90]
KLR-MKP1	Subcellular localization of reporters	MKP1 docking domain fused with KLR (MKP1-bNLS-mNeonGreen-T2A-NES-mRuby3-SV40NLS)	Phosphorylation	<i>A. thaliana</i>	[96]
KLR-AP2C1	Subcellular localization of reporters	AP2C1 docking domain fused with KLR (AP2C1-bNLS-mNeonGreen-T2A-NES-mRuby3-SV40NLS)	Phosphorylation	<i>A. thaliana</i>	[96]
PP7- RNA reporter	Subcellular localization of reporters	An RNA aptamer recruiting PP7 BACTERIOPHAGE COAT PROTEIN fused FPs	Gene expression	<i>Nicotiana benthamiana</i> , <i>A. thaliana</i>	[49]
MS2- RNA reporter	Subcellular localization of reporters	An RNA aptamer recruiting MS2 COAT PROTEIN fused FPs	Gene expression	<i>N. benthamiana</i> , <i>A. thaliana</i>	[49]

regulated by nitrate via nuclear retention mechanism, the localization of NLP7-GFP can be used to monitor the nitrate level in *Arabidopsis* [8]. Similarly, phosphoinositide signaling is mediated by different lipid-binding domains via the direct recruitment of effector proteins to the plasma membrane [88, 89]. A multicolor/multi-affinity marker set has been built by fusing lipid-binding domains with FPs to visualize phosphoinositide dynamics in *Arabidopsis* [90].

Protein phosphorylation plays key roles in signaling networks of cell differentiation, plant development, and stress responses [44]. Kinase translocation reporters (KTRs) have been used to enable spatiotemporal visualization of protein kinase activity in plant cells [91]. Although many KTRs have been developed for mammalian cells, *Caenorhabditis elegans*, and zebrafish [92–95], only two translocation reporters have been designed in plant systems [96]. These two translocation reporters were made by fusing two mitogen-activated protein kinase (MAPKs) docking domains, MKP1 and AP2C1, with the kinase localization reporter (KLR). Both exhibit changes in subcellular localization in response to chitin [96].

It is always a challenge to build a biosensor for detecting the dynamic expression of target genes because most of the output data reflect the change at the protein level using protein-dependent reporters. Currently, PP7 and MS2 RNA labelling technologies have been used for monitoring regions of active transcription in plants [49]. Simpler RNA labeling technologies have been developed with the discovery of fluorescent RNA aptamers. Bai et al. [97] have used a fluorescent RNA aptamer 3WJ-4×Bro, which is a fluorescent tag used for visualizing the transcriptome in real time, to identify transcriptional activity.

4. Next-Generation Identification and Design of Biological Components for Engineering Plant-Based Biosensors

Advanced genome engineering technologies (e.g., CRISPR/Cas tools) offer exciting prospects with respect to next-generation plant-based biosensors; however, there are several unique challenges that must be addressed. A challenge of plant-based biosensor design is validation due to tedious tissue- or cell-level assays. Advancements in protein-engineering technologies are largely hampered by the lack of high-throughput screening systems in plants. To solve this problem, single cell transient assay systems using FACS could be applied for high-throughput screening in plants. Apart from these technical challenges, plant biosystems have inherently complex circuitry logic, spanning and intersecting multiple layers of biochemical, molecular, and cellular processes. Engineering across these multiple layers remains a grand challenge [98]. Additional biological components, involved in alternate levels of gene regulation, are still needed for addressing this challenge. In this section, principles and strategies of designing biological parts for engineering plant-based biosensors will be discussed.

4.1. Principles for the Design of Sensory Elements for Plant Biosensors. To design extrinsic direct biosensors and indirect biosensors, domains, motifs, promoters, etc. can be used as sensory modules for targeted or specific analytes. In the first approach, conformational changes of the sensory module is caused by binding with the signal molecules. In the second approach, the sensory module is used to regulate the transcription level of reporters by binding with the analyte.

Native and synthetic responsive promoters are sensory modules with this feature. In the third approach, the sensory module is used to change the translational level of reporters and thus give a readout when sensing the signal molecules. In the fourth approach, binding with the analyte is used to change localization of the biosensor and thus the movement of the biosensor is used as a readout.

In addition to the four features, analyte binding specificity and affinity are two additional key factors that should be considered when designing the sensory module in biosensors. These two factors will influence the sensitivity of biosensors. Computational design of ligand-binding domains has also been applied to engineer LBDs with higher specificity and affinity [35, 39, 87].

4.2. Principles for Choosing Reporters for Plant Biosensors.

There are two types of reporter modules, optical reporters (FPs and Luc) and morphological reporters (e.g., color markers and herbicide/antibiotic resistant marker). Optical reporters can be applied for monitoring signal changes at the cellular level, whereas the morphological reporters are usually used to reflect signal changes at the whole-plant level. The choice of reporters for direct biosensors is limited to optical reporters. For indirect biosensors, other than optical reporters, morphological reporters can be applied. Emerging examples for application of morphological reporters are the synthetic RUBY markers that have been widely utilized for transgenic plant selection [99].

Identifying the ideal reporter is important for plant biosensor design. Key to this identification is an easily detectable signal. Fluorescent proteins are being implemented for biosensor design because their fluorescence signals can be reliably detected and imaged. A new reporter RUBY that converts tyrosine to vividly red betalain can be detected without the need of special equipment or chemical treatment [99]. Another potential reporter for biosensor is eYGFPUV, which has been successfully used as a reporter for plant transformation [100, 101]. Both RUBY and eYGFPUV could be used as suitable reporters for building transcriptional- or translational-based biosensors. Additionally, reporters fused to a sensory module need themselves to be insensitive to the analyte. Likewise, the reporters should be expressed efficiently resulting in no toxicity to the chosen system [100]. Another important factor for choosing the reporter is the maturation time and half-life. This factor is especially important for building degraon-based biosensors. For example, the VENUS fast maturing yellow fluorescent protein (YFP) has been fused with DII domain to overcome the technical limitation of GFP maturation time, where GFP maturation time is often longer than Aux/IAA half-lives [6]. Alternatively, many biosensors need to monitor signals in real time. The accumulation of proteins may not allow the biosensor to reflect the real-time change of the signal. In this case, a reporter with a short half-life should be considered. Luciferase reaction can emit bioluminescence within a short time frame, and therefore a luciferase reporter is also a good choice for real-time signal monitoring.

4.3. Identification of Natural Biological Components for Biosensor Engineering in Plants.

Plant system biology has pro-

vided a large amount of biological parts for biosensor design from its detailed characterization of molecular components in plant systems [102]. Many sensory modules are being discovered through basic plant biology studies. The knowledge of protein-protein interactions and upstream regulators of signaling pathways is essential for choosing the right parts for designing biosensors. Currently, the rapid accumulation of omics data is accelerating progress towards gene, promoter, and motif discovery [103].

Transgenic overexpression lines and knock-out mutants are used to validate predicted parts. However, traditional plant tissue culture is time consuming and labor intensive, creating a bottleneck for parts mining. Recently, progress has been made in plant transformation using developmental regulators. For example, overexpression of developmental regulators, such as *Baby Boom*, *Wuschel*, GROWTH-REGULATING FACTOR 4 (GRF4), and its cofactor GRF-INTERACTING FACTOR 1 (GIF1), have dramatically increased the efficiency and speed of regeneration in different plant species [104, 105]. In addition, developmental regulators have been used together with gene editing reagents to generate gene-edited plants through *de novo* meristem induction, thereby, bypassing the tissue culture process [106].

4.4. Modification of Natural Biological Components for Biosensor Engineering in Plants.

Naturally occurring biological components are involved in complex networks and usually involve crosstalk with different signaling pathways. The lack of understanding of the mechanisms involved in signaling pathway crosstalk is limiting for biosensor development. An alternate route to the modification of natural biological components may be achieved via protein engineering. Directed evolution has been a successful method for protein engineering. This approach has been used to generate a library of variants followed by screening to identify desirable designs [107]. Computational modeling offers another approach for protein engineering. For instance, using computational modeling, metal binding sites have been engineered into green fluorescence protein for sensing Cu^{2+} , Ni^{2+} , or Co^{2+} [108]. The features of naturally occurring binding sites should be considered when developing a computational method for engineering ligand-binding proteins [39]. Such that, the binding of the ligands should be energetically favorable. Secondly, the overall shape of the binding site should be complementary to the ligand. Thirdly, the structure of the unbound protein should be stable. Based on these principles, a robust computational method for the design of high affinity and specificity ligand-binding-proteins has been developed [39]. Finally, machine-learning-guided directed evolution has been applied in protein engineering to enable the optimization of protein functions in a data driven manner [107]. Longstanding campaigns around protein structure design have successfully been used to design new biosensors [109].

4.5. Design of New-to-Nature Components for Engineering Biosensors in Plants.

The engineering of synthetic plant-based biosensors requires components that allow for sensing, signal processing, and output [98]. The synthetic plant-based biosensors consist of orthogonal components that function

independent from the plant endogenous signaling pathway or network. A synthetic promoter can be designed by combining a core promoter region with signal-responsive motifs serving as the sensing module for a transcriptional-based biosensor [98, 110]. The most widely used core promoter is the minimal CaMV 35S promoter. Currently, three databases, PLACE, PlantCARE, and TRANSFAC, are available for the selection of cis-regulatory elements with known functions [110].

AI-based frameworks are being applied for promoter analysis and prediction in plants [111, 112]. The TSSP-TCM was the first tool to predict and identify plant promoters using the support vector machine (SVM) algorithm [113]. Currently, many computational tools of plant promoter prediction have been developed [114–116]. The PromPredict program using DNA degree of stability features of promoter regions showed accurate promoter prediction in *Arabidopsis* and rice genomes [117]. AI-based frameworks for *de novo* promoter design and prediction have also been developed in *E. coli* [118, 119]. These AI-based frameworks lay the foundation for the future promoter design work in plants. The conserved phytohormone-responsive and stress-inducible cis elements have been identified via overlapping results of various bioinformatical tools [33, 120–122].

Another useful class of biological components is based on synthetic transcription factors (TFs). Utilizing DNA-binding domains and activation domains from different organisms, synthetic TFs have been constructed. For instance, the transcription activator-like effectors (TALEs), dead Cas9 fused with VP64, and others, have been used to build synthetic TFs in plants [110, 123].

In addition to synthetic sensory modules, synthetic reporters are also important for engineering plant-based biosensors. Although the FPs and luciferase can generate facile readout signals, the requirement of fluorescence microscopes and expensive substrate limited the use of these reporters. Currently, several synthetic reporters that can overcome these limitations have been developed for plant system. For instance, the synthetic RUBY reporter, including all the enzymes for betalain biosynthesis, has been generated to visualize transgenic events [99]. A fungal bioluminescence pathway (FBP) can create luminescence *in planta* without additional substrate addition [124].

4.6. The Challenges Specific to Constructing a Multicellular Biosensor to Monitor the Environment. One of the advantages of using plants to build sensors for environmental monitoring is their ability to change morphology. Plant tissues and cells deeply penetrate the soil and extend up into the air, enabling them to sample the environment broadly and continuously. While this morpho-physiology is beneficial for sampling, it creates unique challenges for the implementation of GEPBs. For example, if a signal is sensed in one or a few cells in the plant, only those cells would report it. Thus, unless every cell was monitored continuously, which is impractical and infeasible, the detected signal would be invisible. Additionally, if the signal was perceived in cells that were hidden from view, such as roots in soil, the signal would not be visible unless the plant was excavated. These challenges indicate that biosensors need to be created with systems capable of amplifying reporter signals and transmitting them throughout the plant.

Signal amplification is essential to convert signal perception in a subset of cells in the plant to a response that is easily measured. There are several synthetic signaling systems that have been developed, such as transcriptional feedback loops [125] and engineered kinase cascades [126, 127], that can be used to engineer systemic reporter signal amplification. However, such systems would need to be calibrated to prevent auto-activation or a loss of correlation between the strength of a signal and the reporter output. Once locally amplified, this signal would also need to be transmitted to regions of the plant that were accessible to measurement for the plant-based biosensor to be useful. Engineering the mobility of reporter signal through the plant could be implemented at either the RNA or protein level. At the RNA level, fusion of tRNA-like sequences to messenger RNAs has been demonstrated to confer systemic mobility to them, enabling transport through the phloem [128, 129]. This strategy has been utilized by groups to both confer mobility to reporters across graft junctions and to enhance the mobility of viral vectors [128, 129]. At the protein level, reporter mobility could be engineered by cloning domains from the movement proteins of plant viruses, which have evolved to enable such transport [130]. Both these strategies are generic and could be broadly applied to many different reporters.

5. Conclusion

The goal of engineering for plant-based biosensors is to design and build biosensors with high specificity and sensitivity. It would be ideal to engineer plant-based biosensors to reflect real-time dynamics of analytes without the need for complicated equipment to detect the signal.

In this review, we outline a general framework for engineering different type of biosensors. We highlight representative biological components (e.g., FPs, natural sensory modules, synthetic reporters, and synthetic sensory modules) that have been successfully applied in plant-based biosensors design, and we conclude with a look to the future discussing synthetic sensory modules.

The items listed in Tables 1–5 serve as a guide for generating a more comprehensive catalog of biological components for GEPBs. We propose the following strategies for identification and curation of more biological components for plant-based biosensor engineering:

- (1) Selecting the promoters of responsive genes to specific analytes, TFs responsive to specific signals, or proteins that interact with analytes from the literature to develop plant-based biosensors for specific analytes
- (2) Designing new synthetic biological components for plant-based biosensor engineering with *de novo* protein design
- (3) Applying new natural or synthetic reporters with facile readout properties for plant-based biosensor engineering

Currently, it is still a challenge to identify biological components in order to build reliable plant-based biosensors for various analytes. This is, in part, due to the fact that

molecular events in plants are complicated and the function of many biological components still need further characterization. Second, large genomic databases or resources are lacking for many plant species, which makes it difficult to apply AI-based modeling for designing biological components for plant-based biosensor engineering. Third, high-throughput screening systems are also lacking in plants for validating new biological components for plant-based biosensor engineering. All these challenges represent substantial opportunities for future plant synthetic biology research. Additional efforts are also needed in plant biotechnology, including improved CRISPR-based genome engineering, rapid transformation systems, and high-throughput phenotyping systems, which would accelerate Design-Build-Test-Learn cycles for plant synthetic biology.

Disclosure

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Conflicts of Interest

The authors declare that they have no conflicts of interest regarding the publication of this article.

Authors' Contributions

YL and XY conceived the idea and drafted the manuscript. YL and MH designed the figures. All authors have read and contributed to the content, edited, and reviewed it.

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Supplementary Materials

Coding sequences for listed biosensors are provided in supplemental data 1-supplemental data 5. (*Supplementary Materials*)

References

- [1] H. E. Joe, H. Yun, S. H. Jo, M. B. G. Jun, and B. K. Min, "A review on optical fiber sensors for environmental monitoring," *International Journal of Precision Engineering and Manufacturing-Green Technology*, vol. 5, no. 1, pp. 173–191, 2018.
- [2] G. Hanrahan, D. G. Patil, and J. Wang, "Electrochemical sensors for environmental monitoring: design, development and applications," *Journal of Environmental Monitoring*, vol. 6, no. 8, pp. 657–664, 2004.
- [3] M. Campas, R. Carpentier, and R. Rouillon, "Plant tissue- and photosynthesis-based biosensors," *Biotechnology Advances*, vol. 26, no. 4, pp. 370–378, 2008.
- [4] X. Yang, J. I. Medford, K. Markel et al., "Plant Biosystems design research roadmap 1.0," *BioDesign Research*, vol. 2020, p. 8051764, 2020.
- [5] A. G. Volkov and D. R. A. Ranatunga, "Plants as environmental biosensors," *Plant Signaling & Behavior*, vol. 1, no. 3, pp. 105–115, 2006.
- [6] G. Brunoud, D. M. Wells, M. Oliva et al., "A novel sensor to map auxin response and distribution at high spatio-temporal resolution," *Nature*, vol. 482, no. 7383, pp. 103–106, 2012.
- [7] M. Fukuda, S. Asano, T. Nakamura et al., "CRM1 is responsible for intracellular transport mediated by the nuclear export signal," *Nature*, vol. 390, no. 6657, pp. 308–311, 1997.
- [8] C. Marchive, F. Roudier, L. Castaings et al., "Nuclear retention of the transcription factor NLP7 orchestrates the early response to nitrate in plants," *Nature Communications*, vol. 4, no. 1, p. 1713, 2013.
- [9] J. P. Adams, A. Adeli, C. Y. Hsu et al., "Plant-based FRET biosensor discriminates environmental zinc levels," *Plant Biotechnology Journal*, vol. 10, no. 2, pp. 207–216, 2012.
- [10] E. S. Alves, B. B. Moura, A. N. V. Pedroso, F. Tresmondi, and S. R. Machado, "Cellular markers indicative of ozone stress on bioindicator plants growing in a tropical environment," *Ecological Indicators*, vol. 67, pp. 417–424, 2016.
- [11] A. Walia, R. Waadt, and A. M. Jones, "Genetically encoded biosensors in plants: pathways to discovery," *Annual Review of Plant Biology*, vol. 69, no. 1, pp. 497–524, 2018.
- [12] O. Herud-Sikimić, A. C. Stiel, M. Kolb et al., "A biosensor for the direct visualization of auxin," *Nature*, vol. 592, no. 7856, pp. 768–772, 2021.
- [13] J. I. Medford and D. M. McCarthy, "Growing beyond: designing plants to serve human and environmental interests," *Current Opinion in Systems Biology*, vol. 5, pp. 82–85, 2017.
- [14] C. Garagounis, N. Delkis, and K. K. Papadopoulou, "Unraveling the roles of plant specialized metabolites: using synthetic biology to design molecular biosensors," *New Phytologist*, vol. 231, no. 4, pp. 1338–1352, 2021.
- [15] S. Okumoto, A. Jones, and W. B. Frommer, "Quantitative imaging with fluorescent biosensors," *Annual Review of Plant Biology*, vol. 63, no. 1, pp. 663–706, 2012.

- [16] E. A. Lemke and C. Schultz, "Principles for designing fluorescent sensors and reporters," *Nature Chemical Biology*, vol. 7, no. 8, pp. 480–483, 2011.
- [17] R. Bizzarri, M. Serresi, S. Luin, and F. Beltram, "Green fluorescent protein based pH indicators for in vivo use: a review," *Analytical and Bioanalytical Chemistry*, vol. 393, no. 4, pp. 1107–1122, 2009.
- [18] S. J. Mueller-Schuessele, M. Schwarzlaender, and A. J. Meyer, "Live monitoring of plant redox and energy physiology with genetically encoded biosensors," *Plant Physiology*, vol. 186, no. 1, pp. 93–109, 2021.
- [19] K. Brejc, T. K. Sixma, P. A. Kitts et al., "Structural basis for dual excitation and photoisomerization of the *Aequorea victoria* green fluorescent protein," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 94, no. 6, pp. 2306–2311, 1997.
- [20] R. N. Day and M. W. Davidson, "The fluorescent protein palette: tools for cellular imaging (vol 38, pg 2887, 2009)," *Chemical Society Reviews*, vol. 40, no. 12, pp. 5923–5923, 2011.
- [21] N. C. Shaner, P. A. Steinbach, and R. Y. Tsien, "A guide to choosing fluorescent proteins," *Nature Methods*, vol. 2, no. 12, pp. 905–909, 2005.
- [22] T. Nagai, K. Ibata, E. S. Park, M. Kubota, K. Mikoshiba, and A. Miyawaki, "A variant of yellow fluorescent protein with fast and efficient maturation for cell-biological applications," *Nature Biotechnology*, vol. 20, no. 1, pp. 87–90, 2002.
- [23] A. W. Nguyen and P. S. Daugherty, "Evolutionary optimization of fluorescent proteins for intracellular FRET," *Nature Biotechnology*, vol. 23, no. 3, pp. 355–360, 2005.
- [24] M. Sadoine, Y. Ishikawa, T. J. Kleist et al., "Designs, applications, and limitations of genetically encoded fluorescent sensors to explore plant biology," *Plant Physiology*, vol. 187, no. 2, pp. 485–503, 2021.
- [25] G. Miesenbock, D. A. De Angelis, and J. E. Rothman, "Visualizing secretion and synaptic transmission with pH-sensitive green fluorescent proteins," *Nature*, vol. 394, no. 6689, pp. 192–195, 1998.
- [26] M. Bencina, "Illumination of the spatial order of intracellular pH by genetically encoded pH-sensitive sensors," *Sensors*, vol. 13, no. 12, pp. 16736–16758, 2013.
- [27] V. V. Uslu and G. Grossmann, "The biosensor toolbox for plant developmental biology," *Current Opinion in Plant Biology*, vol. 29, pp. 138–147, 2016.
- [28] T. Yoshida, A. Kakizuka, and H. Imamura, "BTeam, a novel BRET-based biosensor for the accurate quantification of ATP concentration within living cells," *Scientific Reports*, vol. 6, no. 1, 2016.
- [29] X. D. Xu, M. Soutto, Q. Xie et al., "Imaging protein interactions with bioluminescence resonance energy transfer (BRET) in plant and mammalian cells and tissues," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 104, no. 24, pp. 10264–10269, 2007.
- [30] G. S. Baird, D. A. Zacharias, and R. Y. Tsien, "Circular permutation and receptor insertion within green fluorescent proteins," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 96, no. 20, pp. 11241–11246, 1999.
- [31] C. Y. Liao, W. Smet, G. Brunoud, S. Yoshida, T. Vernoux, and D. Weijers, "Correction: Corrigendum: Reporters for sensitive and quantitative measurement of auxin response," *Nature Methods*, vol. 12, no. 11, pp. 1098–1098, 2015.
- [32] T. Ulmasov, J. Murfett, G. Hagen, and T. J. Guilfoyle, "Aux/IAA proteins repress expression of reporter genes containing natural and highly active synthetic auxin response elements," *Plant Cell*, vol. 9, no. 11, pp. 1963–1971, 1997.
- [33] Y. Yang, J. H. Lee, M. R. Poindexter et al., "Rational design and testing of abiotic stress-inducible synthetic promoters from poplar cis-regulatory elements," *Plant Biotechnology Journal*, vol. 19, no. 7, pp. 1354–1369, 2021.
- [34] A. Khakhar, A. R. Leydon, A. C. Lemmex, E. Klavins, and J. L. Nemhauser, "Synthetic hormone-responsive transcription factors can monitor and re-program plant development," *eLife*, vol. 7, article e34702, 2018.
- [35] J. Feng, B. W. Jester, C. E. Tinberg et al., "A general strategy to construct small molecule biosensors in eukaryotes," *eLife*, vol. 4, 2015.
- [36] M. S. Belcher, K. M. Vuu, A. Zhou et al., "Design of orthogonal regulatory systems for modulating gene expression in plants," *Nature Chemical Biology*, vol. 16, no. 8, pp. 857–865, 2020.
- [37] J. A. Brophy, K. J. Magallon, L. Duan et al., "Synthetic genetic circuits as a means of reprogramming plant roots," *Science*, vol. 377, no. 6607, pp. 747–751, 2022.
- [38] M. S. Antunes, K. J. Morey, J. J. Smith et al., "Programmable ligand detection system in plants through a synthetic signal transduction pathway," *PLoS One*, vol. 6, no. 1, article e16292, 2011.
- [39] C. E. Tinberg, S. D. Khare, J. Dou et al., "Computational design of ligand-binding proteins with high affinity and selectivity," *Nature*, vol. 501, no. 7466, pp. 212–216, 2013.
- [40] A. Larrieu, A. Champion, J. Legrand et al., "A fluorescent hormone biosensor reveals the dynamics of jasmonate signalling in plants," *Nature Communications*, vol. 6, no. 1, p. 6043, 2015.
- [41] M. Ahmed, K. M. Koo, P. N. Mainwaring, L. G. Carrasco, and M. Trau, "Phosphoprotein biosensors for monitoring pathological protein structural changes," *Trends in Biotechnology*, vol. 38, no. 5, pp. 519–531, 2020.
- [42] J. Chaiwanon and Z. Y. Wang, "Spatiotemporal brassinosteroid signaling and antagonism with auxin pattern stem cell dynamics in *Arabidopsis* roots," *Current Biology*, vol. 25, no. 8, pp. 1031–1042, 2015.
- [43] S. Regot, J. J. Hughey, B. T. Bajar, S. Carrasco, and M. W. Covert, "High-sensitivity measurements of multiple kinase activities in live single cells," *Cell*, vol. 157, no. 7, pp. 1724–1734, 2014.
- [44] L. Zhang, Y. Takahashi, and J. I. Schroeder, "Protein kinase sensors: an overview of new designs for visualizing kinase dynamics in single plant cells," *Plant Physiology*, vol. 187, no. 2, pp. 527–536, 2021.
- [45] G. Yuan, H. Lu, K. De et al., "An intein-mediated split-nCas9 system for base editing in plants," *ACS Synthetic Biology*, vol. 11, pp. 2513–2517, 2021.
- [46] H. Wang, L. Wang, B. Zhong, and Z. Dai, "Protein splicing of inteins: a powerful tool in synthetic biology," *Frontiers in Bioengineering and Biotechnology*, vol. 10, 2022.
- [47] C. Kang, S. Kim, E. Lee, J. Ryu, M. Lee, and Y. Kwon, "Genetically encoded sensor cells for the screening of glucocorticoid receptor (GR) effectors in herbal extracts," *Biosensors-Basel*, vol. 11, no. 9, 2021.
- [48] H. Jeon, E. Lee, D. Kim et al., "Cell-based biosensors based on InteIn-mediated protein engineering for detection of

- biologically active signaling molecules,” *Analytical Chemistry*, vol. 90, no. 16, pp. 9779–9786, 2018.
- [49] S. Alamos, A. Reimer, K. K. Niyogi, and H. G. Garcia, “Quantitative imaging of RNA polymerase II activity in plants reveals the single-cell basis of tissue-wide transcriptional dynamics,” *Nature Plants*, vol. 7, no. 8, pp. 1037–1049, 2021.
- [50] N. Moseyko and L. J. Feldman, “Expression of pH-sensitive green fluorescent protein in *Arabidopsis thaliana*,” *Plant, Cell & Environment*, vol. 24, no. 5, pp. 557–563, 2001.
- [51] K. S. K. Gjetting, C. K. Ytting, A. Schulz, and A. T. Fuglsang, “Live imaging of intra- and extracellular pH in plants using pHusion, a novel genetically encoded biosensor,” *Journal of Experimental Botany*, vol. 63, no. 8, pp. 3207–3218, 2012.
- [52] H. Moreau, I. Gaillard, and N. Paris, “Genetically encoded fluorescent sensors adapted to acidic pH highlight subdomains within the plant cell apoplast,” *Journal of Experimental Botany*, 2022.
- [53] L. J. V. Galiotta, P. M. Haggie, and A. S. Verkman, “Green fluorescent protein-based halide indicators with improved chloride and iodide affinities,” *FEBS Letters*, vol. 499, no. 3, pp. 220–224, 2001.
- [54] R. M. Wachter and S. J. Remington, “Sensitivity of the yellow variant of green fluorescent protein to halides and nitrate,” *Current Biology*, vol. 9, no. 17, pp. R628–R629, 1999.
- [55] T. Kuner and G. J. Augustine, “A genetically encoded ratio-metric indicator for chloride: capturing chloride transients in cultured hippocampal neurons,” *Neuron*, vol. 27, no. 3, pp. 447–459, 2000.
- [56] I. Lorenzen, T. Aberle, and C. Plieth, “Salt stress-induced chloride flux: a study using transgenic *Arabidopsis* expressing a fluorescent anion probe,” *Plant Journal*, vol. 38, no. 3, pp. 539–544, 2004.
- [57] R. R. Chapleau, R. Blomberg, P. C. Ford, and M. Sagermann, “Design of a highly specific and noninvasive biosensor suitable for real-time *In Vivo* imaging of mercury(II) uptake,” *Protein Science*, vol. 17, no. 4, pp. 614–622, 2008.
- [58] A. J. Meyer, A. Dreyer, J. M. Ugalde, E. Feitosa-Araujo, K. J. Dietz, and M. Schwarzländer, “Shifting paradigms and novel players in Cys-based redox regulation and ROS signaling in plants - and where to go next,” *Biological Chemistry*, vol. 402, no. 3, pp. 399–423, 2021.
- [59] G. T. Hanson, R. Aggeler, D. Oglesbee et al., “Investigating mitochondrial redox potential with redox-sensitive green fluorescent protein indicators,” *Journal of Biological Chemistry*, vol. 279, no. 13, pp. 13044–13053, 2004.
- [60] M. Schwarzländer, M. D. Fricker, C. Müller et al., “Confocal imaging of glutathione redox potential in living plant cells,” *Journal of Microscopy*, vol. 231, no. 2, pp. 299–316, 2008.
- [61] A. J. Meyer, T. Brach, L. Marty et al., “Redox-sensitive GFP in *Arabidopsis thaliana* is a quantitative biosensor for the redox potential of the cellular glutathione redox buffer,” *Plant Journal*, vol. 52, no. 5, pp. 973–986, 2007.
- [62] G. Yuan, M. M. Hassan, T. Yao et al., “Plant-Based Biosensors for Detecting CRISPR-Mediated Genome Engineering,” *ACS Synthetic Biology*, vol. 10, no. 12, pp. 3600–3603, 2021.
- [63] A. Crivici and M. Ikura, “Molecular and structural basis of target recognition by calmodulin,” *Annual Review of Biophysics and Biomolecular Structure*, vol. 24, no. 1, pp. 85–116, 1995.
- [64] E. A. Souslova, V. V. Belousov, J. G. Lock et al., “Single fluorescent protein-based Ca²⁺ sensors with increased dynamic range,” *BMC Biotechnology*, vol. 7, no. 1, 2007.
- [65] J. Nakai, M. Ohkura, and K. Imoto, “A high signal-to-noise Ca²⁺ probe composed of a single green fluorescent protein,” *Nature Biotechnology*, vol. 19, no. 2, pp. 137–141, 2001.
- [66] T. Nagai, A. Sawano, E. S. Park, and A. Miyawaki, “Circularly permuted green fluorescent proteins engineered to sense Ca²⁺,” *Proceedings of the National Academy of Sciences of the United States of America*, vol. 98, no. 6, pp. 3197–3202, 2001.
- [67] Y. X. Zhao, S. Araki, J. Wu et al., “An expanded palette of genetically encoded Ca²⁺ indicators,” *Science*, vol. 333, no. 6051, pp. 1888–1891, 2011.
- [68] K. R. Cope, A. Bascaules, T. B. Irving et al., “The ectomycorrhizal fungus *Laccaria bicolor* produces Lipochitooligosaccharides and uses the common symbiosis pathway to colonize populus roots,” *Plant Cell*, vol. 31, no. 10, pp. 2386–2410, 2019.
- [69] A. Miyawaki, J. Llopis, R. Heim et al., “Fluorescent indicators for Ca²⁺ based on green fluorescent proteins and calmodulin,” *Nature*, vol. 388, no. 6645, pp. 882–887, 1997.
- [70] A. Persechini, J. A. Lynch, and V. A. Romoser, “Novel fluorescent indicator proteins for monitoring free intracellular Ca²⁺,” *Cell Calcium*, vol. 22, no. 3, pp. 209–216, 1997.
- [71] J. L. Vinkenborg, T. J. Nicolson, E. A. Bellomo, M. S. Koay, G. A. Rutter, and M. Merckx, “Genetically encoded FRET sensors to monitor intracellular Zn²⁺ homeostasis,” *Nature Methods*, vol. 6, no. 10, pp. 737–740, 2009.
- [72] V. Lanquar, G. Grossmann, J. L. Vinkenborg, M. Merckx, S. Thomine, and W. B. Frommer, “Dynamic imaging of cytosolic zinc in *Arabidopsis* roots combining FRET sensors and RootChip technology,” *New Phytologist*, vol. 202, no. 1, pp. 198–208, 2014.
- [73] P. Mukherjee, S. Banerjee, A. Wheeler et al., “Live imaging of inorganic phosphate in plants with cellular and subcellular resolution,” *Plant Physiology*, vol. 167, no. 3, p. 628, 2015.
- [74] A. M. Jones, J. Å. H. Danielson, S. N. ManojKumar, V. Lanquar, G. Grossmann, and W. B. Frommer, “Abscisic acid dynamics in roots detected with genetically encoded FRET sensors,” *eLife*, vol. 3, article e01741, 2014.
- [75] C. L. Cuevas-Velazquez, T. Velloso, K. Guadalupe et al., “Intrinsically disordered protein biosensor tracks the physical-chemical effects of osmotic stress on cells,” *Nature Communications*, vol. 12, no. 1, p. 5438, 2021.
- [76] V. Chinnusamy, B. Stevenson, B. H. Lee, and J. K. Zhu, “Screening for gene regulation mutants by bioluminescence imaging,” *Science’s STKE*, vol. 2002, no. 140, p. pl10, 2002.
- [77] M. C. Alvarado, L. M. Zsigmond, I. Kovács, A. Cséplő, C. Koncz, and L. M. Szabados, “Gene trapping with firefly luciferase in *Arabidopsis*. Tagging of stress-responsive genes,” *Plant Physiology*, vol. 134, no. 1, pp. 18–27, 2004.
- [78] S. Bencivenga, S. Simonini, E. Benková, and L. Colombo, “The transcription factors BEL1 and SPL are required for Cytokinin and auxin signaling during ovule development in *Arabidopsis*,” *Plant Cell*, vol. 24, no. 7, pp. 2886–2897, 2012.
- [79] H. M. Abd El-Halim et al., “Evaluation of two promoters for generating transgenic potato plants as salicylic acid biosensors,” *Biologia Plantarum*, vol. 64, pp. 535–540, 2020.

- [80] J. Koschmann, F. Machens, M. Becker et al., "Integration of bioinformatics and synthetic promoters leads to the discovery of novel elicitor-responsive cis-regulatory sequences in Arabidopsis," *Plant Physiology*, vol. 160, no. 1, pp. 178–191, 2012.
- [81] W. S. Liu, M. Mazarei, Y. Peng et al., "Computational discovery of soybean promoter cis-regulatory elements for the construction of soybean cyst nematode-inducible synthetic promoters," *Plant Biotechnology Journal*, vol. 12, no. 8, pp. 1015–1026, 2014.
- [82] B. L. Moss, H. Mao, J. M. Guseman et al., "Rate motifs tune auxin/Indole-3-acetic acid degradation dynamics," *Plant Physiology*, vol. 169, no. 1, pp. 803–813, 2015.
- [83] K. Murase, Y. Hirano, T. P. Sun, and T. Hakoshima, "Gibberellin-induced DELLA recognition by the gibberellin receptor *GID1*," *Nature*, vol. 456, no. 7221, pp. 459–463, 2008.
- [84] A. Dill, H. S. Jung, and T. P. Sun, "The DELLA motif is essential for gibberellin-induced degradation of RGA," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 98, no. 24, pp. 14162–14167, 2001.
- [85] L. R. Band, D. M. Wells, A. Larrieu et al., "Root gravitropism is regulated by a transient lateral auxin gradient controlled by a tipping-point mechanism," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 109, no. 12, pp. 4668–4673, 2012.
- [86] S. L. Samodelov, H. M. Beyer, X. Guo et al., "StrigoQuant: a genetically encoded biosensor for quantifying strigolactone activity and specificity," *Science Advances*, vol. 2, no. 11, 2016.
- [87] M. J. Bick, P. J. Greisen, K. J. Morey et al., "Computational design of environmental sensors for the potent opioid fentanyl," *eLife*, vol. 6, 2017.
- [88] J. H. Hurley and T. Meyer, "Subcellular targeting by membrane lipids," *Current Opinion in Cell Biology*, vol. 13, no. 2, pp. 146–152, 2001.
- [89] P. Varnai and T. Balla, "Live cell imaging of phosphoinositide dynamics with fluorescent protein domains," *Biochimica et Biophysica Acta-Molecular and Cell Biology of Lipids*, vol. 1761, no. 8, pp. 957–967, 2006.
- [90] M. L. A. Simon, M. P. Platre, S. Assil et al., "A multi-colour/multi-affinity marker set to visualize phosphoinositide dynamics in Arabidopsis," *Plant Journal*, vol. 77, no. 2, pp. 322–337, 2014.
- [91] T. Kudo, S. Jeknić, D. N. Macklin et al., "Live-cell measurements of kinase activity in single cells using translocation reporters," *Nature Protocols*, vol. 13, no. 1, pp. 155–169, 2018.
- [92] J. Kim, S. Lee, K. Jung et al., "Intensometric biosensors visualize the activity of multiple small GTPases in vivo," *Nature Communications*, vol. 10, no. 1, 2019.
- [93] B. Sparta, M. Pargett, M. Minguet, K. Distor, G. Bell, and J. G. Albeck, "Receptor level mechanisms are required for epidermal growth factor (EGF)-stimulated extracellular signal-regulated kinase (ERK) activity pulses," *Journal of Biological Chemistry*, vol. 290, no. 41, pp. 24784–24792, 2015.
- [94] C. de la Cova, R. Townley, S. Regot, and I. Greenwald, "A Real-Time Biosensor for ERK Activity Reveals Signaling Dynamics during *C. elegans* Cell Fate Specification," *Developmental Cell*, vol. 42, no. 5, pp. 542–553.e4, 2017.
- [95] V. Mayr, C. Sturtzel, M. Stadler, S. Grissenberger, and M. Distel, "Fast dynamic In Vivo monitoring of Erk activity at single cell resolution in DREKA zebrafish," *Frontiers in Cell and Development Biology*, vol. 6, 2018.
- [96] K. Seitz and P. J. Krysan, "Expanding the toolkit of fluorescent biosensors for studying mitogen activated protein kinases in plants," *International Journal of Molecular Sciences*, vol. 21, no. 15, p. 5350, 2020.
- [97] J. Y. Bai, Y. Luo, X. Wang et al., "A protein-independent fluorescent RNA aptamer reporter system for plant genetic engineering," *Communications*, vol. 11, no. 1, 2020.
- [98] A. R. Leydon, H. P. Gala, S. Guiziou, and J. L. Nemhauser, "Engineering synthetic signaling in plants," *Annual Review of Plant Biology*, vol. 71, no. 1, pp. 767–788, 2020.
- [99] Y. B. He, T. Zhang, H. Sun, H. Zhan, and Y. Zhao, "A reporter for noninvasively monitoring gene expression and plant transformation," *Horticulture Research*, vol. 7, no. 1, p. 152, 2020.
- [100] G. L. Yuan, H. Lu, D. Tang et al., "Expanding the application of a UV-visible reporter for transient gene expression and stable transformation in plants," *Horticulture Research*, vol. 8, no. 1, p. 234, 2021.
- [101] G. Yuan, H. Lu, D. J. Weston et al., "Reporter genes confer new-to-nature ornamental traits in plants," *Horticulture Research*, vol. 9, 2022.
- [102] T. A. Bowen, J. K. Zdunek, and J. I. Medford, "Cultivating plant synthetic biology from systems biology," *New Phytologist*, vol. 179, no. 3, pp. 583–587, 2008.
- [103] X. J. Ran, F. Zhao, Y. Wang et al., "Plant regulomics: a data-driven interface for retrieving upstream regulators from plant multi-omics data," *Plant Journal*, vol. 101, no. 1, pp. 237–248, 2020.
- [104] J. M. Debernardi, D. M. Tricoli, M. F. Ercoli et al., "A GRF-GIF chimeric protein improves the regeneration efficiency of transgenic plants," *Nature Biotechnology*, vol. 38, no. 11, pp. 1274–1279, 2020.
- [105] K. Lowe, E. Wu, N. Wang et al., "Morphogenic Regulators-Baby boom and Wuschel Improve monocot transformation," *Plant Cell*, vol. 28, no. 9, pp. 1998–2015, 2016.
- [106] M. F. Maher, R. A. Nasti, M. Vollbrecht, C. G. Starker, M. D. Clark, and D. F. Voytas, "Plant gene editing through de novo induction of meristems," *Nature Biotechnology*, vol. 38, no. 1, pp. 84–89, 2020.
- [107] K. K. Yang, Z. Wu, and F. H. Arnold, "Machine-learning-guided directed evolution for protein engineering," *Nature Methods*, vol. 16, no. 8, pp. 687–694, 2019.
- [108] T. A. Richmond, T. T. Takahashi, R. Shimkhada, and J. Bernsdorf, "Engineered metal binding sites on green fluorescence protein," *Biochemical and Biophysical Research Communications*, vol. 268, no. 2, pp. 462–465, 2000.
- [109] A. Quijano-Rubio, H. W. Yeh, J. Park et al., "De novo design of modular and tunable protein biosensors," *Nature*, vol. 591, no. 7850, pp. 482–487, 2021.
- [110] W. S. Liu and C. N. Stewart, "Corrigendum to "Plant synthetic promoters and transcription factors" [Curr. Opin. Biotechnol. 37 (2016) 36–44]," *Current Opinion in Biotechnology*, vol. 38, pp. 203–203, 2016.
- [111] A. K. M. Azad, S. Shahid, N. Noman, and H. Lee, "Prediction of plant promoters based on hexamers and random triplet pair analysis," *Algorithms for Molecular Biology*, vol. 6, no. 1, 2011.
- [112] F. Anwar, S. M. Baker, T. Jabid et al., "Pol II promoter prediction using characteristic 4-mer motifs: a machine learning approach," *BMC Bioinformatics*, vol. 9, no. 1, 2008.

- [113] I. A. Shahmuradov, V. V. Solovyev, and A. J. Gammerman, "Plant promoter prediction with confidence estimation," *Nucleic Acids Research*, vol. 33, no. 3, pp. 1069–1076, 2005.
- [114] P. Civan and M. Svec, "Genome-wide analysis of rice (*Oryza sativa* L. subsp. japonica) TATA box and Y patch promoter elements," *Genome*, vol. 52, no. 3, pp. 294–297, 2009.
- [115] J. C. F. Silva, R. M. Teixeira, F. F. Silva, S. H. Brommonschenkel, and E. P. B. Fontes, "Machine learning approaches and their current application in plant molecular biology: a systematic review," *Plant Science*, vol. 284, pp. 37–47, 2019.
- [116] I. A. Shahmuradov, R. K. Umarov, and V. V. Solovyev, "TSSPlant: a new tool for prediction of plant pol II promoters," *Nucleic Acids Research*, vol. 45, no. 8, article gkw1353, 2017.
- [117] C. Morey, S. Mookherjee, G. Rajasekaran, and M. Bansal, "DNA free energy-based promoter prediction and comparative analysis of Arabidopsis and rice genomes," *Plant Physiology*, vol. 156, no. 3, pp. 1300–1315, 2011.
- [118] M. Zhao, Z. Yuan, L. Wu, S. Zhou, and Y. Deng, "Precise prediction of promoter strength based on a de novo synthetic promoter library coupled with machine learning," *ACS Synthetic Biology*, vol. 11, 2022.
- [119] Y. Wang, H. Wang, L. Wei, S. Li, L. Liu, and X. Wang, "Synthetic promoter design in *Escherichia coli* based on a deep generative network," *Nucleic Acids Research*, vol. 48, no. 12, pp. 6403–6412, 2020.
- [120] G. Thijs, K. Marchal, M. Lescot et al., "A Gibbs sampling method to detect overrepresented motifs in the upstream regions of coexpressed genes," *Journal of Computational Biology*, vol. 9, no. 2, pp. 447–464, 2002.
- [121] T. L. Bailey, J. Johnson, C. E. Grant, and W. S. Noble, "The MEME suite," *Nucleic Acids Research*, vol. 43, no. W1, pp. W39–W49, 2015.
- [122] S. L. Nystrom and D. J. McKay, "Memes: a motif analysis environment in R using tools from the MEME suite," *PLoS Computational Biology*, vol. 17, no. 9, p. e1008991, 2021.
- [123] A. Papikian, W. Liu, J. Gallego-Bartolomé, and S. E. Jacobsen, "Site-specific manipulation of *Arabidopsis* loci using CRISPR-Cas9 SunTag systems," *Nature Communications*, vol. 10, no. 1, p. 729, 2019.
- [124] A. Khakhar, C. G. Starker, J. C. Chamness et al., "Building customizable auto-luminescent luciferase-based reporters in plants," *eLife*, vol. 9, article e52786, 2020.
- [125] T. L. To and N. Maheshri, "Noise can induce bimodality in positive transcriptional feedback loops without bistability," *Science*, vol. 327, no. 5969, pp. 1142–1145, 2010.
- [126] C. J. Bashor, N. C. Helman, S. Yan, and W. A. Lim, "Using engineered scaffold interactions to reshape MAP kinase pathway signaling dynamics," *Science*, vol. 319, no. 5869, pp. 1539–1543, 2008.
- [127] B. Groves, A. Khakhar, C. M. Nadel, R. G. Gardner, and G. Seelig, "Rewiring MAP kinases in *Saccharomyces cerevisiae* to regulate novel targets through ubiquitination," *eLife*, vol. 5, article e15200, 2016.
- [128] W. N. Zhang, C. J. Thieme, G. Kollwig et al., "tRNA-related sequences trigger systemic mRNA transport in plants," *Plant Cell*, vol. 28, no. 6, pp. 1237–1249, 2016.
- [129] A. Khakhar, C. Wang, R. Swanson et al., "VipariNama: RNA viral vectors to rapidly elucidate the relationship between gene expression and phenotype," *Plant Physiology*, vol. 186, no. 4, pp. 2222–2238, 2021.
- [130] A. Sambade, K. Brandner, C. Hofmann, M. Seemanpillai, J. Mutterer, and M. Heinlein, "Transport of TMV movement protein particles associated with the targeting of RNA to Plasmodesmata," *Traffic*, vol. 9, no. 12, pp. 2073–2088, 2008.
- [131] J. B. Shen, Y. Zeng, X. Zhuang et al., "Organelle pH in the *Arabidopsis* endomembrane system," *Molecular Plant*, vol. 6, no. 5, pp. 1419–1437, 2013.
- [132] A. Schulte, I. Lorenzen, M. Böttcher, and C. Plieth, "A novel fluorescent pH probe for expression in plants," *Plant Methods*, vol. 2, no. 1, 2006.
- [133] A. Pecherina, M. Grinberg, M. Ageyeva et al., "Whole-Plant Measure of Temperature-Induced Changes in the Cytosolic pH of Potato Plants Using Genetically Encoded Fluorescent Sensor Pt-GFP," *Agriculture-Basel*, vol. 11, no. 11, p. 1131, 2021.
- [134] R. M. Parton, S. Fischer-Parton, A. J. Trewavas, and M. K. Watahiki, "Pollen tubes exhibit regular periodic membrane trafficking events in the absence of apical extension," *Journal of Cell Science*, vol. 116, no. 13, pp. 2707–2719, 2003.
- [135] G. J. Allen, J. M. Kwak, S. P. Chu et al., "Cameleon calcium indicator reports cytoplasmic calcium dynamics in Arabidopsis guard cells," *Plant Journal*, vol. 19, no. 6, pp. 735–747, 1999.
- [136] M. C. Bonza, G. Loro, S. Behera, A. Wong, J. Kudla, and A. Costa, "Analyses of Ca²⁺ accumulation and dynamics in the endoplasmic reticulum of Arabidopsis root cells using a genetically encoded Cameleon sensor," *Plant Physiology*, vol. 163, no. 3, pp. 1230–1241, 2013.
- [137] S. Kosuta, S. Hazledine, J. Sun et al., "Differential and chaotic calcium signatures in the symbiosis signaling pathway of legumes," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 105, no. 28, pp. 9823–9828, 2008.
- [138] Y. R. Chen, Y. S. Yordanov, C. Ma, S. Strauss, and V. B. Busov, "DR5 as a reporter system to study auxin response in *Populus*," *Plant Cell Reports*, vol. 32, no. 3, pp. 453–463, 2013.
- [139] E. Zurcher, D. Tavor-Deslex, D. Lituiev, K. Enkerli, P. T. Tarr, and B. Müller, "A robust and sensitive synthetic sensor to monitor the transcriptional output of the cytokinin signaling network in plants," *Plant Physiology*, vol. 161, no. 3, pp. 1066–1075, 2013.