Variable Effects of C-Terminal Fusions on FLS2 Function: Not All Epitope Tags Are Created Equal\[CC-BY\]

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Receptor-like kinases (RLKs) are the largest family of proteins in plants and are responsible for perceiving the vast majority of extracellular stimuli. Thus, RLKs function in diverse processes, including sensing pathogen attacks, regulating symbiotic interac-
tions, transducing hormone and peptide signals, and monitoring cell wall status. However, despite their fundamental role in plant biology, very few antibodies are available against RLKs, which necessitates the use of epitope tags and fluorescent protein fusions in biochemical analyses such as immunoblot analysis and intracellular visualization. Epitope tags are widely used and are typically assumed to be benign, with no influence on protein function. FLAGELLIN SENSITIVE2 (FLS2) is the receptor for bacterial flagellin and often is used as a model for RLK function. Previous work implies that carboxyl-terminal epitope fusions to FLS2 maintain protein function. Here, a detailed complementation analysis of Arabidopsis (Arabidopsis thaliana) fls2 mutant plants expressing various FLS2 C-terminal epitope fusions revealed highly variable and unpredictable FLS2-mediated signaling outputs. In addition, only one out of four FLS2 epitope fusions maintained the ability to inhibit plant growth in response to flg22 treatment comparable to that in the wild type or control untagged transgenic lines. These results raise concerns over the widespread use of RLK epitope tag fusions for functional studies. Many of the subtleties of FLS2 function, and by extension those of other RLKs, may have been overlooked or inappropriately interpreted through the use of RLK epitope tag fusions.
protein function vary depending on cell type, further complicating functional validation in one system being used to inform another (Jiang et al., 2012). Detailed work also indicates that multiples of an epitope tag, such as FLAG, MYC, or HA repeats, are more likely to disrupt function than a single tag (Georgieva et al., 2015).

FLAGELLIN SENSITIVE2 (FLS2) and BRASSINOSTEROID INSENSITIVE1 (BRI1), in conjunction with their coreceptor BRASSINOSTEROID-ASSOCIATED KINASE1 (BAK1), are the receptors for bacterial flagellin (Gómez-Gómez and Boller, 2000; Zipfel et al., 2004; Chinchilla et al., 2007; Heese et al., 2007) and brassinosteroids (Friedrichsen et al., 2000; Li et al., 2002; Nam and Li, 2002), respectively. They are the most well-characterized leucine-rich repeat (LRR)-RLK pairings, with a range of tools and known signaling outputs available for their investigation. In particular, FLS2 and BAK1 are used frequently as the model system for LRR-RLK-mediated signaling during immune responses. FLS2 and BAK1 rapidly heterodimerize upon the perception of flagellin by FLS2 and downstream signaling responses are initiated, which include reactive oxygen species bursts, MAPK activation, and changes in gene expression (Chinchilla et al., 2007; Heese et al., 2007). Previous work has shown that BAK1, fused to various C-terminal epitopes, is able to interact with FLS2 in a flagellin-dependent manner but shows greatly reduced potency in terms of activating downstream signaling outputs (Ntoukakis et al., 2011). Interestingly, brassinosteroid signaling is largely unaffected by C-terminal tags on either BAK1 or BRI1 (Geldner et al., 2007; Ntoukakis et al., 2011), indicating that the effect of epitope tags on function is not easily predictable. Therefore, studies using BAK1 C-terminal fusions during the examination of pathogen-associated molecular pattern (PAMP)-triggered immune responses should be planned and interpreted appropriately (Ntoukakis et al., 2011). Historically, FLS2-epitope fusions have been assumed to be functional, as they confer flagellin responsiveness to the natural fls2 mutant accession Wassilewskija-0 (Zipfel et al., 2004; Robatzek et al., 2006) and reportedly complement fls2 mutant lines (Chinchilla et al., 2006). However, comparative assays of functionality or quantitative complementation analyses have not been shown explicitly, and, to the best of our knowledge, there are no published data on fls2 loss-of-function mutant defects being restored to wild-type levels by physiologically relevant expression of FLS2 epitope fusions. We recently began working on FLS2 signaling, using our own and others’ Arabidopsis lines expressing epitope-tagged FLS2 in fls2 mutant backgrounds, and have discovered that C-termally tagged FLS2 constructs do not behave in a consistent or predictable manner with respect to signaling outputs. Here, we demonstrate that three out of four FLS2 C-terminal epitope fusions are greatly impaired in their ability to restore flg22-mediated growth inhibition, suggesting that many FLS2 C-terminal epitope fusions are, at best, only partially functional. We present complementation assays for FLS2 C-terminal fusions as a resource for the community and identify the best constructs to use in future work.

RESULTS
The Effect of C-Terminal Epitope Tags on FLS2-Mediated Signaling Is Unpredictable

FLS2 recognizes flg22, the elicitor-active epitope of bacterial flagellin (Felix et al., 1999), and subsequently forms a dimer with BAK1 (Chinchilla et al., 2007; Heese et al., 2007). This interaction leads to increased activation of MAPK cascades, which is one of the earliest observable signaling outputs of PAMP-triggered immunity (PTI; Nühse et al., 2000). During work to characterize the flg22-induced responses of various forms of FLS2, we consistently observed that all lines expressing FLS2-mGFP6 fusions exhibited greatly reduced MAPK activation compared with that in wild-type Columbia-0 (Col-0) plants. Therefore, we set out to test whether C-terminal epitope tags impair FLS2 signaling or if these observations were a peculiarity of the mGFP6 tag. To this end, we used the previously published fls2-101/FLS2-pro:FLS2-3xHA line (Dunning et al., 2007) and two fls2/FLS2-pro:FLS2-3xMYC-EGFP lines (Mbengue et al., 2016). We also generated fls2/FLS2-pro:FLS2-EGFP lines as well as fls2/FLS2-pro:FLS2 control lines without epitope tags. The constructs in these two lines, and the FLS2pro:FLS2-mGFP6 constructs described above, use the same promoter region and open reading frame described previously (Zipfel et al., 2004). For comparative purposes, linker, peptide epitope, and GFP sequences appended to the FLS2 C terminus used in this study are shown in Supplemental Figures S1 and S2. All generated epitope-tagged FLS2 transgenic lines were tested for FLS2 expression, and those lines showing a range of mRNA expression to control for expression level effects were selected for further study. fls2/FLS2-pro:FLS2 control lines were selected to cover the range of mRNA expression observed between the tagged lines under investigation and Col-0 to control for expression-level effects (Fig. 1; Supplemental Fig. S3). All plant lines displayed 3:1 antibiotic selection segregation in the T2, and quantitative PCR analysis indicated that each line carried the transgene integrated at a single locus. Comparison of transgene copy number in T3 lines with FLS2 expression level showed very little correlation, suggesting that expression levels are likely dictated by transgene insertion site rather than transgene copy number (Fig. 1; Supplemental Fig. S3).

It was not possible to directly compare protein levels between the different tagged and untagged forms of FLS2, as the only α-FLS2 antibody available, raised against the extreme C terminus of FLS2 (Chinchilla et al., 2006; Hurst et al., 2017), shows variable and apparently reduced sensitivity toward epitope-tagged FLS2 (e.g. compare relative signal intensity for α-FLS2...
and α-GFP in Fig. 1 and Supplemental Fig. S3 for fls2/FLS2:3xMYC-EGFP and fls2/FLS2:FLS2-EGFP). This is likely due to the tags, by virtue of being attached to the C terminus of FLS2, partially disrupting the epitope recognized by the α-FLS2 antibody, with different tags affecting antibody binding to varying degrees. Therefore, it is not appropriate to draw quantitative comparisons between FLS2 levels in different lines using this antibody, which is important to note for future studies comparing different tagged and untagged FLS2 lines. A similar situation was observed for BAK1 when an antibody raised against the C terminus was used to probe tagged and untagged BAK1-expressing lines (Ntoukakis et al., 2011). Despite this, immunoblot analysis using antibodies against mGFP6, EGFP, MYC, or HA epitopes revealed signal at the appropriate M_r from the epitope-tagged FLS2-expressing lines, indicating that FLS2 protein was present. Relative FLS2 mRNA and FLS2 protein levels within each set of lines correlated, with the exception of fls2/FLS2:FLS2-EGFP #10.7, where high mRNA levels did not translate into higher protein levels. Although we do not have an explanation for this, sufficient FLS2-EGFP protein was produced to be detected by both anti-EGFP and anti-FLS2 immunoblot analysis. Interestingly, in FLS2-3xMYC-EGFP-expressing lines, an untagged FLS2-sized band was frequently observed, albeit weaker than the α-FLS2 signal from Col-0-derived FLS2 or full-length FLS2-3xMYC-EGFP, which is reactive with the FLS2 antibody but not MYC or GFP antibodies. This suggests the presence of a cleavage product where both 3xMYC and EGFP have been removed, leaving a form of FLS2 that closely resembles wild-type FLS2.

After flg22 treatment, FLS2-3xHA- and FLS2-mGFP6-expressing lines showed little MAPK6/3 activation, whereas MAPK6/3 activation in FLS2-EGFP-
3xMYC-EGFP-, and untagged FLS2-expressing lines were essentially indistinguishable from that in Col-0 (Fig. 2A). These data indicate that the presence of a C-terminal tag can have an impact on flg22-mediated FLS2 signaling outputs. RLKs have been shown to act in large multicomponent complexes (Jordá et al., 2016; Yeh et al., 2016), raising the possibility that the presence of the epitope tag in mGFP6- or HA-tagged lines could act as a general suppressor of PTI signaling. The elongation factor-Tu receptor EFR activates MAPK cascades in an almost identical manner to FLS2 during the perception of bacterial pathogens (Zipfel et al., 2006). Therefore, FLS2-3xHA- and FLS2-mGFP6-expressing lines were treated with the elongation factor-Tu-derived peptide elf18 and showed normal MAPK induction when compared with that in Col-0 (Fig. 2B). This demonstrates that the effect of mGFP6 or HA epitope tags on FLS2 is restricted to the outputs of FLS2-mediated signaling rather than PTI responses in general.

PAMP perception leads to transcriptional reprogramming and defense gene expression (Asai et al., 2002). In light of our conflicting MAPK activation data, we decided to test whether epitope-tagged FLS2-expressing lines exhibit changes in PAMP-induced gene expression. After flg22 treatment, typical early (NHL10; Zipfel et al., 2004) and late (PRI; Robatzek and Somssich, 2002) PAMP-induced genes were up-regulated in Col-0 but not in fls2 mutants (Fig. 2, C and D; Supplemental Fig. S4). However, fls2 plants expressing epitope-tagged FLS2 variants showed variable PAMP-triggered gene induction when compared with that in Col-0 (Fig. 2, C and D; Supplemental Fig. S4). Lines expressing FLS2-3xHA or FLS2-mGFP6 showed little to no gene induction compared with that in Col-0, whereas lines expressing untagged FLS2 or 3xMYC-EGFP-tagged FLS2 appeared capable of activating all tested genes in response to flg22 (Fig. 2, C and D; Supplemental Fig. S4). FLS2-EGFP-expressing lines were capable of inducing gene expression but did not appear to be quite as effective as untagged or 3xMYC-EGFP-tagged lines at inducing early MAPK-mediated response genes such as NHL10 (Fig. 2C; 1-h induction), whereas late salicylic acid-mediated response genes such as PRI were induced similar to that in Col-0 (Fig. 2D; Supplemental Fig. S4, C and D; 24-h induction). These data further substantiate the hypothesis that epitope tags can impact upon FLS2 functionality in terms of activating PAMP-responsive outputs, regardless of the mediating pathway, but not in a manner that can be readily predicted. Basal expression levels of NHL10 and PRI are almost nil under non-flg22-challenged conditions; the presence of any FLS2 transgene tested here, regardless of expression level or copy number, failed to elevate either PRI or NHL10 expression compared with that in either unchallenged Col-0 or fls2 mutant plants (Supplemental Fig. S5). This is similar to the observations made using MAPK activation and suggests that the transgenes do not affect plant physiology or outputs in the absence of flg22.

C-Terminal Epitope Tags Can Impair FLS2-Mediated Growth Inhibition

One of the responses to prolonged PAMP treatments such as flg22 is the inhibition of both seedling shoot and root growth, which often is used as an assay for the overall combined outputs and long-term effects of receptor pathway activation (Gómez-Gómez et al., 1999; Gómez-Gómez and Boller, 2000). Therefore, in light of our unexpected data above on the varied functionality of FLS2 epitope fusions, we determined whether the lines tested also show variation in overall output resulting from long-term PAMP exposure. Interestingly, all FLS2 C-terminal fusions, with the exception of that in FLS2-3xMYC-EGFP-expressing lines, show impaired ability to inhibit seedling growth after flg22 treatment when compared with that in Col-0. Untagged FLS2-expressing lines essentially showed slightly greater or comparable growth inhibition to that in Col-0 (Fig. 3A), despite FLS2 being present at lower levels than in FLS2-3xMYC-EGFP-expressing lines. This implies that untagged FLS2 is still more active than the most potent tagged form of FLS2. These data indicate that the presence of a tag contributes more to the observed outcome of FLS2-mediated growth inhibition after flg22 treatment than FLS2 expression level (Fig. 3B).

Combined, these data indicate that C-terminal tagging of FLS2 can affect several PTI responses in a manner that cannot be easily predicted based solely on which epitope tag is used. Furthermore, the overall outcome of FLS2 signaling is consistently reduced in all FLS2 C-terminal fusion-expressing lines, with the potential exception of FLS2-3xMYC-EGFP-expressing plants. It is theoretically possible that the lines with mGFP6-, EGFP-, and HA-tagged FLS2, despite expressing FLS2 and producing detectable FLS2 protein, do not produce stable FLS2 protein and that this leads to diminished responses compared with that in Col-0. Arguing against this is the strong MAPK activation and gene induction in the EGFP-tagged FLS2 lines and the partial rescue of growth inhibition in mGFP6- and EGFP-tagged FLS2 lines. This again suggests that the FLS2 antibody recognizing the C-terminal epitope, as used here and described previously (Chinchilla et al., 2006), is not suitable for comparing levels of the various tagged and untagged forms of FLS2. These data combined make the effect of a given tag on FLS2 outputs very difficult to predict.

DISCUSSION

Epitope fusions are a common tool in molecular biology and are indispensable for many cell biology applications or where antibodies are not available for a protein of interest. As the use of epitope tagging has become standard practice, it is easy to forget that the epitope itself may impact upon function by altering protein conformation, obscuring ligand-binding surfaces, or hindering protein-protein interactions. Deleterious
Figure 2. Plants expressing epitope-tagged FLS2 show variable MAPK activation and gene induction in response to elicitation by flg22. A, MAPK activation in fsl2 mutant seedlings expressing FLS2 tagged with 3xHA, mGFP6, EGFP, or 3xMYC-EGFP or untagged FLS2 in response to 100 nM flg22 as determined over time by immunoblot analysis. MAPK assays of Col-0 FLS2pro:FLS2-3xMYC-EGFP lines were included for completeness but were not taken further, as no deleterious effects were observed and no conclusion about complementation could be drawn. B, MAPK activation in seedlings expressing 3xHA- or mGFP6-tagged FLS2 in response to 100 nM elf18, as determined over time by immunoblot analysis. Blots in A and B were probed with α-p42/44 (active MAPK; pMPK6/3) and α-MPK6 (total) as loading controls. C and D, Expression analysis of NHL10 (C) and PR1 (D) after elicitation with 100 nM flg22 for 0-15 minutes or 100 nM elf18 for 0-15 minutes.
or anomalous effects of fused epitopes on protein function are not limited to FLS2, as reported here, but also have been identified for 20% of tested mammalian proteins (Stadler et al., 2013). The effects of fused epitope tags on RLK function have been shown in a study on BAK1 (Ntoukakis et al., 2011) and seem likely to also affect ERECTA (ER). An ER<sub>pro</sub>:ER-LUC construct showed complementation in only 27% of recovered transformants compared with 100% complementation for an ER<sub>pro</sub>:ER construct, but expression levels of ER-LUC fusions compared with wild-type ER levels were not determined and the significance or possible implications were not discussed further (Kosentka et al., 2017). Alongside BAK1 and BRI1, FLS2 is probably the best-studied RLK in plants, and much of the published work utilizes epitope-tagged forms. FLS2 has been reported to be functional when transformed into Ws-silwskija-0 accession plants (a natural fls2 mutant) as 3xMYC-EGFP or 3xMYC fusions (Zipfel et al., 2004; Robatzek et al., 2006), but, as those articles state, these data are gain-of-function analyses, not complementation assays; there is no reference for wild-type activity. In our work, we found that FLS2-3xHA- and FLS2-mGFP6-expressing lines were broadly impaired in all FLS2 responses tested. FLS2-EGFP-expressing lines showed an intermediate phenotype, while only those lines expressing FLS2-3xMYC-EGFP were able to complement the gene induction, MAPK activation, and seedling growth inhibition phenotypes of fls2 mutants. Interestingly, FLS2-mGFP6- and FLS2-EGFP-expressing lines show similar growth inhibition despite FLS2-mGFP6 conferring minimal MAPK activation and reduced gene induction and FLS2-EGFP conferring wild-type levels of MAPK activation and only mildly affected gene induction. This suggests that, whereas MAPK and gene induction are differentially affected in these lines, other aspects of the flg22 response leading to growth inhibition not measured here are possibly less affected in FLS2-mGFP6-expressing lines.

Alternatively, absolute levels of MAPK activation and gene induction may not be closely correlated with the outcomes of growth inhibition experiments. This makes the effects of tags on each specific aspect or outcome of FLS2 function very difficult to predict. These unexpected and potentially variable effects of tags on FLS2 appear to have gone unreported, likely because the constructs are at least partially functional (Dunning et al., 2007; Hemsley et al., 2013; Figs. 1–3), unlike in the case of BAK1, where all tested C-terminal tags abolish function during PTI signaling (Ntoukakis et al., 2011). The effects of FLS2 expression levels on functional outcomes are reported to be nonlinear, with several orders of magnitude increase in expression required to increase measured outputs a few fold (Gómez-Gómez and Boller, 2000). In wild-type plants, FLS2 receptors have an EC<sub>50</sub> of ~0.2 nm but a K<sub>d</sub> of ~1.3 nm for flg22 (Bauer et al., 2001). This indicates that FLS2 signaling responses are saturated long before all receptor-binding sites are occupied; therefore, a 10-fold increase in FLS2 expression is not going to increase outputs 10-fold, particularly under treatment conditions commonly used, where flg22 concentrations range from 100 nm to 10 μM. In fact, our observations suggest that a 10-fold increase in FLS2 expression (e.g. FLS2<sub>pro</sub>:FLS2 line 1.3) has, at most, a 1.2-fold effect on growth inhibition and minimal effect on MAPK activation or gene expression compared with that in Col-0 or other FLS2<sub>pro</sub>:FLS2 lines with lesser untagged FLS2 expression. It is also a formal possibility that other factors, such as BAK1 or downstream components, are present in rate-limiting amounts. Therefore, elevated FLS2 expression would have limited additional effect, as extra activated FLS2 receptor would be reduced in its ability to transduce signal. As the FLS2 promoter and coding sequence used in all of the lines studied here are identical and multiple independent transformants for each construct show the same phenotype regardless of FLS2 expression level, the observed variation must be the result of either the epitope tag or the vector T-DNA sequence. The vector effect likely can be excluded, as our own fls2/FLS2<sub>pro</sub>:FLS2-EGFP and fls2/FLS2<sub>pro</sub>:FLS2 lines use the same vector series (Karimi et al., 2002).

Interestingly, a 3xHA tag (Dunning et al., 2007) of ~3 kD adopting a largely disordered conformation (Georgieva et al., 2015) is apparently more effective at reducing FLS2 responses compared with the ~27-kD, highly stable and structured mGFP6 or EGFP fusions. While this is outwardly counterintuitive, exposed, terminal regions of disorder, such as MYC or HAA repeat peptide tags, have been suggested to have deleterious effects on protein function (Georgieva et al., 2015). BAK1-3xHA constructs also were unexpectedly impaired in BR responses despite being strongly expressed (Ntoukakis et al., 2011), indicating that C-terminal 3xHA tags may impair RLK function more than would otherwise be expected given their size. The linker between FLS2 and mGFP6 contains two Pro residues (Supplemental Fig. S2), and Pro is an amino acid known to produce inflexible linkers with reduced mobility (Radford et al., 1987). This may explain the difference in functionality observed between FLS2-mGFP6 and FLS2-EGFP, as the EGFP linker is predicted to be highly flexible and,
therefore, less likely to sterically hinder downstream interactions (Supplemental Fig. S2). The most widely used and published FLS2 epitope fusion, demonstrated to be most active based on our data, is the FLS2-3xMYC-EGFP construct (Robatzek et al., 2006). In this construct, the highly disordered 3xMYC epitope (Georgieva et al., 2015) separates EGFP from FLS2 more than that in any other construct tested (Supplemental Fig. S2). This may reduce steric hindrance by GFP to a greater extent than that resulting from any

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Figure 3. flg22-mediated growth suppression can be impaired in plant lines expressing epitope-tagged FLS2. A, Average relative seedling mass (flg22 treated/untreated) of seedlings grown in 1 µM flg22 for 10 d (14 d post germination). Data are averages of at least two independent biological replicates. Error bars show ±. Asterisks denote statistically significant differences compared with that of the Col-0 control (*, *P* < 0.1; **, *P* < 0.05; and ***, *P* < 0.01) determined by one-way ANOVA and Tukey’s HSD test. B, Growth inhibition data shown in A plotted against FLS2 mRNA expression data from Figure 1A. Gray and white data points represent Col-0 and fls2/FLS2<sup>−/−</sup> mutants, respectively, used as controls for each indicated genotype/experiment. x axis (FLS2 expression) error bars represent RQMIN and RQMAX and constitute the acceptable error level for a 95% confidence interval according to Student’s t test; y axis (growth inhibition) error bars show ±. Statistically significant differences are as for A and Figure 1A but are omitted here for clarity. C, Summary table of FLS2 responses in all lines used in this study. Differences compared with that in Col-0 for each response are indicated: ++, strong increase; +, mild increase; o, no change; –, mild decrease; and – –, strong decrease.
of the other constructs used here and allow for a more native conformation of the FLS2 C terminus and better access for interacting proteins. However, it is worth noting that, in FLS2-3xMYC-EGFP-expressing lines, an α-FLS2 reactive band is observed frequently at the size expected for full-length FLS2. This band is not detected by either α-MYC or α-GFP antibody, suggesting that this cleavage product contains a C terminus very similar to, or only slightly longer than, that of native FLS2. Therefore, it cannot be ruled out that this cleavage product may be able to function like untagged FLS2 and provide a greater degree of flag22 responsiveness in FLS2-3xMYC-EGFP-expressing lines than would be expected given the behavior of other epitope-tagged FLS2 lines. It should be noted that we have not tested this construct for complementation of every FLS2-mediated output described in the literature.

A possible explanation for the deleterious effects of epitope tagging on RLK outputs identified here or reported previously (Ntoukakis et al., 2011; Kosentka et al., 2017) involves a weak kinase activity (e.g. FLS2 or ER; Schwessinger et al., 2011) in the receptor/coreceptor pairing. It may well be the case that epitope tags impact upon all RLKs, but the effects are minor or unnoticed if both RLK partners are strong kinases (e.g. BRI1 or BAK1; Schwessinger et al., 2011) and able to compensate for the negative effects of the tag. Therefore, the use of RLK C-terminal fusions may reduce researchers’ ability to properly observe and differentiate the effects of various mutant forms of RLKs on signaling or interactions. As a result, many intricacies and details of RLK signaling may have been obscured (Dunning et al., 2007; Sun et al., 2012; Hemsley et al., 2013; Kosentka et al., 2017), and potentially false-negative, uninterpretable, or inappropriate conclusions may have been reached in other studies that, therefore, have gone unpublished.

While this study indicates that untagged forms of FLS2 provide the best possible approach for testing the functionality of FLS2 variants, it is of course impossible to avoid epitope tags altogether. Much of the vital cell biology data on RLK localization and trafficking (Robatzek et al., 2006; Beck et al., 2012; Choi et al., 2013; Liang et al., 2013; Spallek et al., 2013; Smith et al., 2014; Mbengue et al., 2016) could not have been achieved without the presence of GFP or similar marker proteins, and the field would be much poorer for their absence. However, as FLS2 (this study), BAK1 (Ntoukakis et al., 2011), and ER (Kosentka et al., 2017) function have now all been shown to be affected by C-terminal epitope tags, we suggest that any functional study on RLKs using epitope tags should be designed and interpreted with care; the functionality of epitope tag fusions should not be assumed, and full quantitative complementation studies of each output of interest should precede further evaluation. Possible alternative solutions to C-terminal tagging not yet considered by the RLK field are the use of tags internal to the protein sequence or the use of innocuous tags (Georgieva et al., 2015). In the case of FLS2, the obvious and immediate solution is to base all future constructs on FLS2-3xMYC-EGFP (Robatzek et al., 2006), but it would be interesting to determine whether a 3xMYC or other long and flexible linker between the RLK of interest and GFP provides a generic solution to the issue of C-terminal RLK tags.

## MATERIALS AND METHODS

### Plant Lines and Growth Conditions

All Arabidopsis (Arabidopsis thaliana) lines used are of the Col-0 ecotype. The FLS2 mutant alleles, fls2 (SAIL_691C4; Ziepel et al., 2004) and fls2-101, as well as fls2-103/FLS2-1, A1 lines (Dunning et al., 2007) and fls2/FLS2-3xMYC-EGFP (Mbengue et al., 2016), have been described previously. fls2/FLS2-3xMYC-EGFP (pMDC107 based; Curtis and Grossniklaus, 2003) and fls2/FLS2-3xEGFP (pH7FWG0 based; Karimi et al., 2002) were created for this study using a construct with the same promoter region and open reading frame of FLS2 lacking a stop codon, as found in the FLS2-3xMYC-EGFP construct and described previously (Ziepel et al., 2004; Robatzek et al., 2006). fls2/FLS2-3x constructs were created using the same FLS2 fragment as for mGFP6- and EGFP-tagged lines but with a stop codon introduced and cloned into pK7WG0 (Karimi et al., 2002). Transgenic Arabidopsis plants were generated by Agrobacterium tumefaciens-mediated floral dip transfection (Clough and Bent, 1998) and selected for homozygosity at T3. Plant material for the experiments was grown on 0.5× Murashige and Skoog (MS) medium and 0.8% (w/v) phytagar under a 16/8-h light/dark cycle at 20°C in MLR-350 growth chambers (Panasonic).

### Transgene Copy Number Determination

Genomic DNA was extracted from Arabidopsis plate-grown seedlings (Edwards et al., 1991). Real-time PCR determination of copy number was performed using SYBR Green and the ΔΔCt method as described previously (Buhner and Baldwin, 2004). Validated primer pairs used were against NHL10 (endogenous control) and FLS2 (target for copy number determination).

### Gene Expression Analysis

Gene expression levels were analyzed using reverse transcription quantitative PCR. For this, 10 seedlings of each genotype 10 d post germination were treated with 1 µM flg22 for the indicated times. The 10 seedlings from each genotype at each time point for each treatment were pooled before further analysis. RNA was extracted using the RNeasy kit with on-column DNase digestion according to the manufacturer’s instructions (Qiagen). Two micrograms of RNA was reverse transcribed using a High Capacity cDNA Reverse Transcription kit (Applied Biosystems). All transcripts were amplified using validated gene-specific primers. Expression levels were normalized against PEX5 (Asg525760; Wilm et al., 2008; Dunning et al., 2012). Each sample was analyzed in triplicate (technical replicates) for each primer pair within each biological replicate. Relative quantification (RQ) was achieved using the ΔΔCt method (Yuan et al., 2006; Schmittgen and Livak, 2008). RQMIN and RQMAX define the range of possible RQ values calculated from the standard error of ΔΔCt using a 95% confidence interval derived from the t-distribution. Significant differences between samples in a biological replicate were defined by non-overlapping 95% confidence intervals. Fully independent biological replicates were performed over a period of 2 years, with each genotype only being present once in each replicate.

### MAPK Activation

MAPK activation was performed essentially as described previously (Schwessinger et al., 2011). Six seedlings of each genotype 10 d post germination were treated with 100 nM flg22 or eti18 as appropriate for the indicated times in 2 mL of 0.5× MS medium. The six seedlings from each genotype at each time point for each treatment were pooled before further analysis. Fully independent biological replicates were performed over a period of 2 years, with each genotype only being present once in each replicate.
**Supplemental Data**

The following supplemental materials are available.

**Supplemental Figure S1.** Alignment of GFP sequences found in vectors used in this study.

**Supplemental Figure S2.** Alignment of FLS2 and appended C-terminal sequences in the constructs used in this study.

**Supplemental Figure S3.** Supporting data for Figure 1: biological replicates.

**Supplemental Figure S4.** Supporting data for Figure 2: biological replicates.

**Supplemental Figure S5.** Supporting data for Figure 2 and Supplemental Figure S4.

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