Dynamic regulation of AtDAO1 and GH3 modulates auxin homeostasis

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The hormone auxin is a key regulator of plant growth and development, and great progress has been made understanding auxin transport and signaling. Here we show that auxin metabolism and homeostasis are also regulated in a complex manner. The principal auxin degradation pathways in Arabidopsis include oxidation by AtDAO1/2 and conjugation by GH3s. Metabolic profiling of dao1-1 root tissues revealed a 50% decrease in the oxidation product oxIAA, an increase in the conjugated forms IAA-Asp and IAA-Glu of 438-fold and 240-fold respectively, while auxin remains close to wild type. By fitting parameter values to a mathematical model of these metabolic pathways we show that, in addition to reduced oxidation, both auxin biosynthesis and conjugation are increased in dao1-1. We then quantified gene expression in planta, and found that transcripts of AtDAO1 and GH3 genes are increased in response to auxin, over different time scales and concentration ranges. Including this regulation of AtDAO1 and GH3 in an extended model reveals that auxin oxidation is more important for auxin homeostasis at lower hormone concentrations, while auxin conjugation is most significant at high auxin levels. Finally, embedding our homeostasis model in a multicellular simulation to assess the spatial effect of the dao1-1 mutant shows that auxin increases in outer root tissues, in agreement with the dao1-1 mutant root hair phenotype. We conclude that auxin homeostasis is dependent on AtDAO1, acting in concert with GH3, to maintain auxin at optimal levels for plant growth and development.

Significance Statement

Auxin is a key hormone regulating plant growth and development. We combine experiments and mathematical modeling to reveal how auxin levels are maintained within normal physiological limits via feedback regulation of genes encoding key metabolic enzymes. In particular, we describe how regulation of auxin oxidation, via transcriptional control of AtDAO1 expression, is important at low to normal auxin concentrations. In contrast, higher auxin levels lead to increased GH3 expression and auxin conjugation, thereby reducing hormone concentration. Integrating this understanding into a multicellular model of root auxin dynamics successfully predicts that the dao1-1 mutant has an auxin-dependent longer root hair phenotype. Our findings reveal the importance of auxin homeostasis to maintain this hormone at optimal levels for plant growth and development.
The principal degradation pathways in Arabidopsis include irreversible conjugation by GH3s and oxidation by AtDAO1/2 (Fig. 1A). In the roots of dao1-1 knockout seedlings, oxidised IAA (oxIAA) levels are halved and the conjugated forms IAA-Asp and IAA-Glu are increased by 438 and 240-fold respectively, whereas the level of IAA is only increased by 20% (statistically insignificant) (Fig. 1B). These root data are consistent with metabolite profiling from whole seedlings and different tissues [11].

To investigate whether the conceptual model of the main IAA degradation pathways summarised in Fig. 1A is consistent with the metabolite data given in Fig. 1B a linear ordinary differential equation (ODE) model was formulated (see Materials and Methods, SI Appendix). The model simulates the biosynthesis of IAA and its subsequent conversion to IAA-glc via UGT, to IAA-Asp and IAA-Glu via GH3, and to oxIAA via AtDAO1/2. IAA-glc and oxIAA can both be conjugated further to form oxIAA-glc, and this, along with the conjugates IAA-Asp and IAA-Glu, are then degraded at fixed rates. We calculated steady state levels of the model variables in the wild type, modeled the mutant by setting the rate of AtDAO1-mediated IAA-oxidation in dao1-1 to zero (\(d_i = 0\), where the * notation indicates a parameter value in the dao1-1 mutant), and estimated model parameters to best fit the data in Fig. 1B. The model is able to reproduce the observed reductions in [oxIAA] and [oxIAA-glc], whilst maintaining levels of [IAA] and [IAA-glc], but yields only an 8% increase in the levels of conjugated auxin ([IAA-Asp]/[IAA-Glu]), far less than the experimentally observed changes of greater than 200-fold (Fig. 1C). Thus our mathematical modeling predicts that a decrease in oxidation rate alone is not sufficient to account for the massive increase in conjugation products and IAA homeostasis in dao1-1.

To explore whether increased GH3 conjugation rates in dao1-1 can explain the data, we increased those rates 10-fold in our model so that \(g_a = 10g_a\) and \(g_g = 10g_g\). Along with the knock out of AtDAO1, this surprisingly results in only a 13% increase in the level of [IAA-Asp] and [IAA-Glu] conjugates and decreases in all other metabolites (Fig. 1D). We conclude that altering GH3 conjugation rates is insufficient in isolation to explain the metabolic data. We therefore tested in our model whether increasing the auxin biosynthesis rate

Fig. 1. A metabolic model suggests the dao1-1 mutant may have altered rates of metabolism other than IAA oxidation. (A) The principal degradation pathways in Arabidopsis include irreversible conjugation by GH3s and oxidation by DAO1/2. (B) In the dao1-1 knockout, oxidised IAA (oxIAA) levels are halved and conjugated forms, IAA-Asp and IAA-Glu are increased by more than 438 and 240-fold respectively, while the level of IAA is increased by only 20%. Asterisks indicate statistically significant differences from Col-0 (P<0.05, Student’s t-test). (C,D) Mathematical modeling predicts that a decrease in oxidation rate alone is not sufficient to account for the increase in conjugation products and IAA homeostasis in dao1-1, and increasing GH3 conjugation rates does not lead to a better qualitative match. (E) Increasing both IAA biosynthesis and GH3 conjugation rates in the dao1-1 simulation can qualitatively match metabolomic data.

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in dao1-1 ($\lambda^* = 10\lambda$) as well as GH3-mediated conjugation rates could capture the experimentally observed behaviour of the dao1-1 mutant compared to wild type. Fig. 1E shows that increasing both IAA biosynthesis and GH3 conjugation rates in the dao1-1 simulation can qualitatively match metabolomic data. Hence, auxin homeostasis appears to be maintained in the IAA oxidase mutant dao1-1 by adjusting conjugation and synthesis rates.

Systems analysis reveals that in addition to reduced oxidation, both IAA biosynthesis and conjugation are increased in dao1-1. Next we sought experimental evidence for changes in conjugation and synthesis rates, before attempting more precise fitting of our model to the data. Quantitative RT-PCR shows that the mRNA expression level of GH3.3 is 2.7 times higher in dao1-1 than in wild type (Fig. 2A), and additional metabolite profiling in whole seedlings shows the levels of the three IAA precursors IAM, IPyA and IAN all drop significantly in the dao1-1 mutant relative to wild type (Fig. 2B), indicating a higher IAA biosynthetic rate in dao1-1.

To further establish the plausibility of increased IAA biosynthesis and GH3 conjugation in the dao1-1 mutant, model parameters were fitted to the steady state metabolite data for [IAA], [oxIAA], [IAA-Asp], [IAA-Glu], [IAA-glc] and [oxIAA-glc] in both wild type and dao1-1. To fix the IAA synthesis rate in dao1-1 ($\lambda^*$), we assume that IAM, IPyA and IAN have constant production rates (which do not vary between w.t. and dao1-1), and that each is converted to IAA at a rate that is different in dao1-1 compared to w.t... It follows that $\lambda^*$ is inversely proportional to the corresponding drop in auxin precursor concentrations (0.74 averaged across IAM, IPyA and IAN), giving $\lambda^* = 1.36$. We then allowed the remaining parameters, including $g_9, g'_9$ and $g_9, g'_9$ (the respective rates, in w.t. and dao1-1, of GH3 mediated conjugation to [IAA-Asp] and [IAA-Glu]), to take any values within a wide range of fixed bounds. The parameter fitting used a hybrid genetic algorithm plus local minimum search which sought to minimise the squared difference between model steady state and metabolite data, for both w.t. and dao1-1. We found that, with conjugation rates free to vary in dao1-1, a wide range of parameter sets can fit the quantitative data. (Fig. 2C).

Running the parameter fitting algorithm a number of times, we generated 100 different parameter sets which all result in good agreement of the model with data (well within the bounds of statistical experimental error). Plotting the distribution of each of the fitted parameter values shows that there is a limited degree of variability in some parameters between parameter sets (Fig. 2C). Fig. 2D shows that the predicted relative changes between w.t. and dao1-1 match those observed for the six key metabolites. Fig. 2E and F show that the rates of conjugation via GH3 increase more than 400-fold (to IAA-Asp) and more than 200-fold (to IAA-Glu) in dao1-1 compared to w.t., consistently across parameter sets.

Dynamic regulation of AtDAO1 and GH3 by auxin allows a context-dependent homeostatic response to changes in auxin. As expected for important components of the auxin homeostasis machinery, AtDAO1 and GH3 genes are auxin inducible [11, 16]. Affymetrix-based transcriptomic analysis of auxin treated root tips revealed that GH3.3 mRNA is induced very rapidly (peaking at two hours) while AtDAO1 mRNA is induced more slowly (peaking at the final, four hour time-point). RT-qPCR-based transcriptomic analysis also showed that GH3.3 is up regulated 2.7-fold in dao1-1 (Fig. 2A), and around 200-fold in wild type seedlings exposed to IAA (Fig. 3A, S1). In contrast, IAA-treated w.t. seedlings show at most a 75% increase in AtDAO1 expression (Fig. 3A, S1). We conclude that AtDAO1 and GH3.3 are upregulated by auxin, over different timescales and concentration ranges and with...
different fold-changes in response.

To investigate the effect of these nonlinear feedbacks on auxin homeostasis we incorporate them into an extended model (Fig. 3B) in which the expression of both AtDAO1 and GH3 increase as the concentration of IAA increases. To model these nonlinearities we use Hill functions (Equations [2b]-[2c]), where the threshold parameters \(k_d\) and \(k_g\) determine the level of IAA at which gene expression reaches half-maximum, and the Hill coefficients \(n_d\) and \(n_g\) determine the sharpness of the transition from low to high expression. In the case of AtDAO1 we see at most a doubling of the mRNA level from basal expression under IAA treatment, with no sharp switch in expression observed (Fig. 3A, S1), which suggests a half-maximum threshold similar to the basal IAA concentration. Hence, we fix \(k_d = 1\) and the Hill coefficient \(n_d = 1\), and fit the remaining model parameters to the steady state metabolic wild type and dao1-1 data. The fitted nonlinear model shows good agreement with the data (Fig. S4) and demonstrates that a small increase in IAA biosynthesis rate (36%) can result in a much larger (> 100-fold) increase in the level of IAA-Asp and IAA-Glu conjugates.

Fig. 3C uses the estimated and fitted parameters to compare the contribution of the GH3 and AtDAO1 pathways to IAA degradation. While the contribution of AtDAO1 increases slightly over the range shown and is still active even at low levels of IAA, conjugation rates are much lower at and below basal levels (\(\text{IAA} \leq 1\)) but rapidly increase as IAA increases, so that for high levels of IAA (\(\text{IAA} \geq 2\)) the conjugation pathway is dominant.

Fig. 3D-F shows the temporal response of the model after changing the [IAA] input rate, \(\lambda\), from the basal steady-state value (\(\lambda = 1\)). To compare the relative importance of the AtDAO1 and GH3 degradation pathways, as well as the ‘full’ model with both up-regulated by IAA, we also show three alternate versions, one where only AtDAO1 is induced by auxin, one where only GH3 is induced by auxin, and one where neither response is induced. With the full model there is a clearly a homeostatic response, with a transient peak, after which the steady-state level of IAA is much lower than the steady-state level without any AtDAO1/GH3 induction. For a large change in IAA input (Figure 3D) this homeostasis is much more rapid and pronounced than for a relatively small change in IAA input (Figure 3E). This difference in homeostatic responses is due to variations in the magnitude and speed of AtDAO1 and GH3 responses to increased IAA as can be inferred from the simulations where the inducibility of one or the other is switched off. In the absence of GH3 induction, homeostasis is greatly reduced for a 10-fold increase in IAA input (Fig. 3D), while for a 2-fold reduction the homeostatic response is largely unchanged from the full model (Fig. 3F).

Conversely, in the absence of AtDAO1 regulation the homeostatic effect is only slightly reduced for a 10-fold IAA increase, while it is undetectable for a 2-fold-reduction in IAA input. For a 2-fold increase in IAA input both the AtDAO1 and GH3 pathways contribute to IAA homeostasis (Fig. 3E).

Mathematical modeling of these feedbacks on auxin degradation suggests AtDAO1 is more effective for auxin homeostasis at lower auxin concentrations, while GH3s are much more important at high auxin levels. This is illustrated further in Figure 3G, which shows the IAA steady state for a range of values of the auxin input rate \(\lambda\), for each of the model variants described above. Here, \(\text{IAA} = 1\) corresponds to typical physiological levels. Around this level and below the AtDAO1 degradation pathway is the more active, but above this level the GH3 pathway becomes more active, and eventually is much more important than AtDAO1 in removing large quantities of excess IAA.

Multicellular root modeling predicts auxin accumulation in epidermal tissues. We developed a spatial model for auxin transport and metabolism, combining our compartmental model for IAA metabolism and IAA-dependent induction of AtDAO1 and GH3 (described above), with the multicellular model for IAA transport described in [17]. The multicellular model is based on actual root cell geometries and auxin influx and efflux carrier subcellular localizations. The IAA concentration is defined in each cell, together with terms for the rates of carrier-dependent transport between cells.

Following [17], we prescribed PIN, AUX and LAX carrier distributions in our virtual root tissues, with the PIN carriers polarised according to reports in the literature and our own observations using anti-PIN antibodies. The model also incorporates a weak background efflux to account for low levels of nonpolar PIN and for the presence of other transporters such as ABCB. We specified small auxin production rates within every cell and higher auxin production in the QC and columella initials. The model also captured auxin diffusion through the apoplast, as measured by [18]. We treated auxin concentrations as uniform within each cell, due to the small size of cells in this region and relatively rapid auxin diffusion within the cytoplasm compared to within the apoplast [18–20]. This is in contrast with the larger cells further from the root tip, where subcellular variations in auxin have previously been considered [21, 22].

The resulting model can be described by a system of ODEs for the auxin concentrations within each cell and each segment of apoplast. For details and model parameter values see SI Appendix, [17]. As done previously, we included a flux of auxin from the shoot by prescribing a non-zero auxin concentration within the stele cells at the boundary of the modeled tissue. In the epidermal, cortical, and endodermal cells we assume that the auxin concentrations have reached their far-field asymptotic values, hence setting them equal to those in neighbouring (rootward) cells of the same type. This implies an appropriate shootward flux of auxin through the outer tissue layers [19]. Starting from an initial condition in which all remaining concentrations equal zero, we simulated the ODEs until the concentrations and fluxes reached a steady state.

Embedding our homeostasis model into a multicellular context allows us to predict the effect of the dao1-1 mutant on IAA levels and distribution in root tissues when compared to the wild type. Simulations using our combined transport and homeostasis model predict that the wild type IAA distribution (Fig. 4A) is in good agreement with spatial patterns inferred from the DII-VENUS fluorescent auxin signalling sensor [17]. Though the spatial pattern in the dao1-1 mutant is similar to w.t., the total concentration of IAA was predicted to increase by 26%, consistent with the metabolite data (Fig. 1B). Very interestingly, the simulated increase in auxin is predicted to be spatially inhomogeneous, with auxin concentrations in outer root tissues increased > 40% (Fig. 4B). The predicted increase in IAA in the dao1-1 mutant outer root tissues is consistent with the observed extra elongated root hair phenotype, which
is known to be auxin dependent [23].

Fig. 3. AIDAOI transcriptional regulation by IAA provides sensitivity at low auxin concentrations, whilst GH3 regulation contributes to homeostasis at high auxin concentrations. (A) Affymetrix data showing AIDAOI and GH3.3 transcript abundance in micro-dissected root tips at time points after IAA treatment. (B-G) Mathematical modeling of these feedbacks on auxin degradation suggests AIDAOI is more effective in auxin homeostasis at lower auxin concentrations, while GH3 is responsible for much more at high levels of auxin. (B) Submodel for IAA metabolism indicating the IAA-dependent transcription of AIDAOI and GH3. (C) Effective AIDAOI and GH3 dependent IAA degradation rates at steady state for fixed levels of IAA input. (D,E) Temporal response to a 10- and 2-fold increase in IAA input with different combinations of modeled regulation. GH3 regulation is dominant. In each case the model is shown with both AIDAOI and GH3 inducible by auxin, only AIDAOI inducible, and only GH3 inducible. (F) Temporal response to a 2-fold decrease in IAA input with different combinations of modeled regulation. AIDAOI regulation is dominant. (G) The steady-state patterns seen in (D)-(F) are found across a wide range of IAA input rates.

Fig. 4. Multicellular simulation, showing auxin accumulation in outer tissues of the root apex in dao1-1 relative to wild type. (A) Predicted IAA in the wild type simulation, relative to the fixed reference value of IAA=1 in the stele at the shootward end of the tissue, as defined in the boundary conditions. (B) In dao1-1, auxin is up to 40% higher in the epidermis, which is consistent with increased RSL4 expression causing the increased root hair phenotype seen in the dao1-1 mutant [11].

Discussion

Our systems-based study has revealed that auxin homeostasis is controlled by highly redundant regulatory mechanisms involving auxin oxidation, conjugation and synthesis pathways. These auxin homeostasis regulatory mechanisms are also highly non-linear, involving multiple feedback loops that control the expression of AtDAO1 IAA oxidase and GH3 IAA conjugation enzymes. These regulatory mechanisms also operate across a range of spatial and temporal scales and auxin concentrations. For example, AIDAOI and GH3 exhibit contrasting slow and rapid temporal expression dynamics, respectively. These differences are critical in the timing of AtDAO1 and GH3 induction by auxin and likely to be functionally important. The slow auxin induction of AtDAO1 ensures that perturbations in this signal can still cause a desired developmental response, while helping the cell maintain an optimal level of auxin. GH3 on the other hand is only induced when auxin is high and so may be expressed rapidly in order to remove excess auxin as quickly as possible. The triggering of the GH3 degradation pathway at high levels of auxin is possibly a stress response to excess auxin levels, and is likely in effect during many lab experiments when large amounts of exogenous auxin is applied. However, Kramer and Ackelsberg [24] recently suggested that the GH3 conjugation pathway may be important at sites of high auxin accumulation during normal growth such as lateral root primordia or within the shoot apical meristem.

Despite these myriad auxin homeostasis mechanisms operating in plants, our multicellular model predicted that disrupting just the IAA oxidase AtDAO1 is still able to perturb auxin levels in selected root tissues. This included elevating auxin levels...
in the dao1-1 mutant epidermis (Fig. 4B), the tissue from which root hairs originate and enlarge in an auxin-dependent manner.

Datta et al. [25] have recently demonstrated that root hair length is directly proportional to the abundance of a bHLH transcription factor RSL4 whose expression is auxin inducible. Hence, we would predict (based on our multicellular model simulations) that RSL4 and root hair length would increase in proportion to the >40% increase in auxin levels in the dao1-1 mutant epidermis. Consistent with our model predictions, Porco et al [11] report similar increases in RSL4 mRNA abundance and root hair length in the dao1-1 mutant epidermis experimentally. Hence, we reason that auxin levels may also be perturbed in other dao1-1 mutant tissues and/or stages of development. This helps explain why, despite the highly redundant organisation of the auxin homeostasis, dao1-1 exhibits a number of subtle auxin-related mutant phenotypes in root, shoot and floral tissues [11, 12].

Materials and Methods

\[ G \] representing GH3s. \[ D \] and \[ G \] are assumed to be produced

Plant material and growth conditions. Arabidopsis thaliana Columbia-0 (Col-0) was used as wild type in all experiments. All T-DNA insertion mutants were obtained from the NASC (Nottingham Arabidopsis Stock Centre). Wild type and mutant plants were grown as described in [11].

RNA isolation and analysis. Sterilized seeds were plated on half MS media and stratified at 4°C for 24h to synchronize germination then transferred to a controlled growth chamber. 7 day old seedlings on plates were then transferred to MS media containing 1uM IAA for 7 or 10 days. RNA was extracted from root tips and used for microarray analysis with the Affymetrix ATH1 array.

IAA metabolite profiling. Arabidopsis thaliana wild type Col-0 and the dao1-1 mutant were grown under LD conditions for 7 or 10 days. Whole seedlings or dissected tissues were collected in 5 replicates (20 mg tissue per sample). Sample purification and quantification of IAA metabolites was performed as described in [26].

Mathematical models and parameter estimation. Here we summarize our mathematical models of the auxin homeostasis network. For full details of all models, definitions of model variables and parameters, and parameter estimation, see SI appendix.

IAA metabolism model: The simplest model of the pathway shown in Figure 1A has a constant rate of IAA biosynthesis (\( \lambda \)), and linear rates of degradation and conversion from one form of auxin to another:

\[
\frac{d[IAA]}{dt} = \lambda - (u_f + g_0 + g_1 + d_1) [IAA] + u_r [IAA-gluc] \]  
\[
\frac{d[oxIAA]}{dt} = (d_1 + d_2) [IAA] - \mu_s [oxIAA] \]  
\[
\frac{d[IAA-Asp]}{dt} = g_0 [IAA] - \mu_p [IAA-Asp] \]  
\[
\frac{d[IAA-Glu]}{dt} = g_0 [IAA] - \mu_p [IAA-Glu] \]  
\[
\frac{d[IAA-gluc]}{dt} = u_f [IAA] - (u_r + \mu_s) [IAA-gluc] \]  
\[
\frac{d[oxIAA-gluc]}{dt} = \mu_s [oxIAA] + \mu_p [IAA-gluc] - \mu_p [oxIAA-gluc]. \]

Inducible AtDDAO1-GH3 model: We extend Equations (1a)-(10) by assuming that the rate of conversion of IAA to oxIAA (\( d_1 \)) is proportional to the level of a new variable \( [D] \) representing AtDDAO1, and the rates of conjugation of IAA to IAA-Asp (\( g_0 \)) and IAA-Glu (\( g_0 \)) are proportional to the level of another new variable in response to \( [IAA] \), represented by Hill functions, and to decay linearly, so that:

\[
g_0 = g_0 [G], \quad g_0 = g_0 [G], \quad d_1 = d_1 [D]. \]  
\[
\frac{d[D]}{dt} = \frac{d_1}{[IAA]^n_p + [IAA]^n_d} - [D]. \]  
\[
\frac{d[G]}{dt} = g_0 \left( \frac{[IAA]^n_p}{[IAA]^n_d + [IAA]^n_g} - [G]. \right. \]

Multicellular model: see the SI Appendix.

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9. Tanaka K et al. (2014) Ugt74d1 catalyzes the glucosylation of 2-oxindole-3-acetic acid in the
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1 Linear ODE model of IAA degradation

To investigate whether the conceptual model of the main IAA degradation pathways summarised in Fig. 1A (main text) is consistent with the metabolite data given in Fig. 1B (main text) a simple linear ordinary differential equation model was formulated, as described below in Sections 1.1 and 1.2. The model simulates the biosynthesis of IAA and its subsequent conversion to IAA-glc via UGT, to IAA-Asp and IAA-Glu via *GH3*, and to oxIAA via *AtDAO1/2*. IAA-glc and oxIAA can both be conjugated further to form oxIAA-glc, and this, along with the conjugates IAA-Asp and IAA-Glu, are then degraded at fixed rates (to prevent accumulation of these products in the model system).

1.1 Model reactions

In the following the empty set notation is used to denote a fixed pool of molecules from and into which model variables can be respectively synthesised and degraded. We assume all substrates such the amino acids Asp and Glu are available in excess so that this pool is neither depleted or increased. For a review of the IAA metabolic pathways modelled here see [27].

We initially consider the input of IAA to the system to be at some fixed rate $\lambda$:

$$ \emptyset \xrightarrow{\lambda} \text{IAA}. $$

This IAA synthesis step is considered in more detail, taking into account quantitative IAA precursor data, in Section 2.

The oxidative pathway is modelled by the conversion of IAA to oxIAA by the combined action of *AtDAO1* and *AtDAO2* with respective rate constants $d_1$ and $d_2$, the subsequent conversion of oxIAA to oxIAA-glc with rate $\mu_x$, and finally the degradation of oxIAA-glc with rate $\mu_p$:

$$ \text{IAA} \xrightarrow{d_1 + d_2} \text{oxIAA} \xrightarrow{\mu_x} \text{oxIAA-glc} \xrightarrow{\mu_p} \emptyset. $$

*GH3* mediated conjugation is modelled by two pathways, one which models the conjugation of IAA with Aspartic acid with rate $g_a$ to produce IAA-Asp, and another which models the conjugation of IAA with Glutamate with rate $g_g$ to produce IAA-Glu:

$$ \text{IAA} \xrightarrow{g_a} \text{IAA-Asp} \xrightarrow{\mu_a} \emptyset, \quad \text{IAA} \xrightarrow{g_g} \text{IAA-Glu} \xrightarrow{\mu_g} \emptyset, $$
where \( \mu_a \) and \( \mu_g \) are the respective degradation rates of IAA-Asp and IAA-Glu.

Finally the conversion of IAA to IAA-glc via UGT is modelled with rate constant \( u_f \), with the reverse reaction also included with rate \( u_r \). IAA-glc can also be converted to oxIAA-glc with rate \( \mu_u \), which as previously stated degrades with rate \( \mu_p \):

\[
\text{IAA} \xrightarrow{u_f} \text{IAA-glc} \xrightarrow{\mu_u} \text{oxIAA-glc} \xrightarrow{\mu_p} \emptyset.
\]

### 1.2 Model equations

Using the law of mass action, we cast the set of the reactions described in Section 1.1 as a set of ordinary differential equations for six variables:

\[
\begin{align*}
\frac{d[IAA]}{dt} &= \lambda - (u_f + g_a + g_g + d_1 + d_2)[IAA] + u_r[IAA-glc] \quad (1a) \\
\frac{d[oxIAA]}{dt} &= (d_1 + d_2)[IAA] - \mu_x[oxIAA] \quad (1b) \\
\frac{d[IAA-Asp]}{dt} &= g_a[IAA] - \mu_a[IAA-Asp] \quad (1c) \\
\frac{d[IAA-Glu]}{dt} &= g_g[IAA] - \mu_g[IAA-Glu] \quad (1d) \\
\frac{d[IAA-glc]}{dt} &= u_f[IAA] - \mu_u[IAA-glc] - u_r[IAA-glc] \quad (1e) \\
\frac{d[oxIAA-glc]}{dt} &= \mu_x[oxIAA] + \mu_u[IAA-glc] - \mu_p[oxIAA-glc] \quad (1f)
\end{align*}
\]

Time is dimensionless, scaled by the dimensional biosynthesis rate (\( \lambda_w \)), divided by the IAA concentration in wild type ([IAA]_w), so that for wild type \( \lambda = 1 \). All other model species are nondimensionalised by scaling with [IAA]_w.

### 1.3 dao1-1 mutant simulations

We use the * superscript notation to indicate the mutant value when parameter values may differ from their wild type values in the dao1-1 simulations. For example the wild type rate of \( AtDAO1 \) mediated oxidation is denoted \( d_1 \), while the value in the dao1-1 mutant is denoted \( d_1^* \).

The simplest way to model the dao1-1 knock-out mutant is to set \( d_1^* = 0 \) in Equation (1). However, if this is the only difference between the wild type and mutant simulations, it is not possible to get good agreement between the model steady states and the metabolic data (Figs. 1C, S2) when running the parameter fitting algorithm (see Section 3). The best-fit parameter set is given in Table S1 and used as the base parameter set for further modifications of parameter values in the dao1-1 simulations (Figure 1D-E, main text).

Based on this fitting of the initial model, and with support from further experimental data (Figure 2A,B, main text) in subsequent parameter fitting exercises we may also allow the IAA synthesis rate (\( \lambda^* \)) and the conjugation rates (\( g_a^* \) and \( g_g^* \)) to vary from their wild type values in the dao1-1 mutant simulations. Figure 1D, main text uses the parameters in Table S1, except \( g_a^* = 10g_a \) and \( g_g^* = 10g_g \), while in Figure 1E \( g_a^* = 10g_a \), \( g_g^* = 10g_g \) and \( \lambda^* = 10\lambda \).
IAA precursors

To fix the IAA synthesis rate in dao1-1 ($\lambda^*$), we assume that IAA precursors have constant production rates (which do not vary between w.t. and dao1-1), and that each precursor is converted to IAA at a rate that is different in dao1-1 compared to wild type.

If we denote the pool of IAA precursors $[IAA_p]_w$ in w.t. and $[IAA_p]_m$ in dao1-1 and assume they are governed by the following:

$$\frac{d[IAA_p]_w}{dt} = \delta - \lambda[IAA_p]_w,$$

$$\frac{d[IAA_p]_m}{dt} = \delta - \lambda^*[IAA_p]_m,$$

where $\delta$ is the constant synthesis rate and $\lambda$ and $\lambda^*$ are the respective conversion rates to [IAA], then at steady state we can rearrange to obtain:

$$\lambda^* = \frac{[IAA_p]_m}{[IAA_p]_w}.$$

It follows that $\lambda^*$ is inversely proportional to the corresponding drop in auxin precursor concentrations (0.74 averaged across IAM, IPyA and IAN from the whole-seedling metabolite data shown in Fig. 1 of the main text), giving $\lambda^* = 1.36$ (since $\lambda = 1$).

Parameter fitting

During the parameter fitting and all other single compartment simulations the systems of ODEs were solved from zero initial conditions in Matlab using the function ode15s. To simulate wild type plants the model(s) were run with one parameter set to steady state, and the same model was run with another parameter set to represent the dao1-1 mutant. The steady state values were then compared with the data.

For the parameter estimation problems described below, we used the genetic algorithm (function ga) followed by local minimum search (function fmincon) from the Matlab Optimisation toolbox to minimize the error between the data and model simulations. The objective function to be minimised was:

$$f = \sum_{i \in X} \left( \frac{M^w_i - D^w_i}{\sigma^w_i} \right)^2 + \sum_{i \in X} \left( \frac{M^d_1 - D^d_1}{\sigma^d_1} \right)^2$$

where $M$ represents model steady state values, and $D$ data points with associated error $\sigma$. The superscript $wt$ denotes the wild type (Col-0), while $dao1$ denotes the dao1-1 knock out model variant and mutant plants. $X$ is the set of metabolites IAA, oxIAA, IAA-Asp, IAA-Glu, IAA-glc and oxIAA-glc, the data for which is normalised relative to the wild type IAA measurement, consistent with the non-dimensional models. Unless stated all parameters were identical in the wild type and dao1-1 simulations, save the mutant value for the AtdAO1 oxidation rate $d^*_1 = 0$, and constrained between $10^{-4}$ and $10^4$. In all cases the wild type IAA production rate ($\lambda$) was fixed = 1.

The results of the parameter fitting in the simplest case, where only $d^*_1 = 0$ differs from wild type in the dao1-1 simulation, are shown in Fig. 1 (main text) and Fig. S2, and the parameters given in Table S1 (Set 1).
In Fig. 2 (main text) the linear model (Equations (1a)-(1f)) was fitted against the data, with $g_a^*$ and $g_g^*$ free to vary within the default constraints while $\lambda^*$ was fixed = 1.36 (Section 2). The representative parameter set used to produce Fig. 2D and Fig. S3 is given in Table S1 (Set 2).

4 Inducible AtDAO/GH3 model

4.1 Model formulation

The model is as the initial model (Equations (1a)-(1f)) except that the rate of conversion of IAA to oxIAA is proportional to the level of a new variable $[D]$ representing the level of AtDAO1, and the rates of conjugation of IAA to IAA-Asp and IAA-Glu are proportional to the level of another new variable $[G]$ representing the level of GH3, so that:

\[
g_a = \hat{g}_a[G] \tag{3a}\\
\]

\[
g_g = \hat{g}_g[G] \tag{3b}\\
\]

\[
d_1 = \hat{d}_1[D] \tag{3c}\\
\]

where $\hat{g}_a$, $\hat{g}_g$ and $\hat{d}_1$ are new parameters.

$[D]$ and $[G]$ are themselves produced at rates nonlinearly dependent on the level of [IAA], represented by Hill functions, so that:

\[
\frac{d[D]}{dt} = \eta_d \left( \frac{[IAA]^{n_d}}{k_d^{n_d} + [IAA]^{n_d}} - [D] \right), \tag{3d}\\
\]

\[
\frac{d[G]}{dt} = \eta_g \left( \frac{[IAA]^{n_g}}{k_g^{n_g} + [IAA]^{n_g}} - [G] \right). \tag{3e}\\
\]

4.2 Parameter fitting

The inducible model was also fitted to the same metabolic data, using the same algorithm as the linear model (Section 3). The only parameter which differed from w.t. in dao1-1 was $\lambda^*$, which was again fixed = 1.36. $n_g$ and $k_g$ were found using the parameter fitting but constrained $1 \leq n_g \leq 9$ and $10^{-4} \leq k_g \leq 10$. This upper bound on $k_g$ was selected to ensure the response of GH3 occurs within approximate physiological bounds of the level of IAA. The parameters $n_d$, $k_d$, $\eta_d$ and $\eta_g$ do not directly affect the fit with the metabolic data and were instead separately estimated based on the available GH3 and AtDAO1 mRNA expression data and fixed during the parameter fitting algorithm. We fit the remaining model parameters to the steady state metabolic wild type and dao1-1 data. Since we see at most a doubling of the mRNA level from basal expression under IAA treatment, with no sharp switch in expression observed (Fig. S1A), we fix both the Hill coefficient ($n_d$) and the binding threshold ($k_d$) = 1. $\eta_d$ and $\eta_g$ affect the respective timescales over which AtDAO1 and GH3 can change. We estimate that gene expression will evolve over a slower timescale than biosynthesis, with AtDAO1 changing more slowly than GH3 so we set $\eta_d = 0.005$ and $\eta_g = 0.01$.

The representative fitted parameter set used to produce Fig. 3D-H main text and Figs. S4, S5 is given in Table S1 (Set 3), and is used as the basis for parameterisation of the multi-cellular model.
4.3 Model variants

For each of the model variants described below the model was run to steady state (using the parameters in Table S1) with $\lambda = 1$, then using these results as the initial conditions for a new set of simulations for $\lambda \in \{0.5, 2.0, 10.0\}$, the time-courses shown in Fig. 3E-G (main text) were plotted. The steady state of each model variant is also plotted for $0.05 \leq \lambda \leq 20$ in Fig. 3H (main text).

4.3.1 Only \textit{AtDAO1} induced

The induction of \textit{GH3} is switched off by setting:

$$\frac{d[G]}{dt} = 0,$$

with the initial condition that $[G]$ is equal to its steady state value in Equation (3e) when $[IAA] = 1$, i.e.:

$$[G] = \frac{1^{ng}}{k^{ng} + 1^{ng}}.$$

4.3.2 Only \textit{GH3} induced

Similarly, we switch off the induction of \textit{AtDAO1} by setting:

$$\frac{d[D]}{dt} = 0, \quad [D] = \frac{1^{nd}}{k^{nd} + 1^{nd}}.$$

4.3.3 No induction

Both inducible pathways are switched off by setting:

$$\frac{d[D]}{dt} = 0, \quad [D] = \frac{1^{nd}}{k^{nd} + 1^{nd}}, \quad \frac{d[G]}{dt} = 0, \quad [G] = \frac{1^{ng}}{k^{ng} + 1^{ng}}.$$

5 Multicellular model

The multicellular model is based on that of [17], in which auxin transport is embedded in a realistic root cell geometry, using a vertex-based data structure from the OpenAlea modeling framework [28], with experimentally observed locations for the PIN, AUX and LAX auxin efflux and influx carriers. To incorporate the \textit{AtDAO1/GH3} homeostasis model we replace the linear production and degradation of IAA in [17] with the production and non-linear degradation defined in Equations (1a) & (3a)-(3c), so that in general terms for every cell $i$:

$$\frac{d[IAA]_i}{dt} = \alpha \text{ metabolism}_i + \text{ transport}_i,$$

where $\alpha = 0.001$ (as in [17]) is a constant of proportionality to ensure that the relative contribution of metabolism and transport remains similar in the two models. All remaining model variables are simulated in every cell as in the inducible model.

The metabolism terms are identical to the right hand side of Equation (1a), with the IAA inducible versions of $g_u$, $g_g$ and $d_1$ as defined in Equations (3a)-(3e). Parameter values are as estimated by the fitting algorithm as defined in Table S1, with two exceptions. To
maximise the number of cells in which the IAA homeostasis model works at basal levels of IAA in the same way as described in the single compartment models (i.e. relatively low GH3 conjugation, and intermediate levels of AtDAO1 oxidation), we set the thresholds in the Hill functions for \([G]\) and \([D]\) 5× higher so that \(k_d = 5.0\) and \(k_g = 11.6135\). \(\lambda = 1\) (wild-type) and \(\lambda^* = 1.36\) (\(dao1-1\) mutant) in all cells except in the quiescent centre and columella initials, where \(\lambda = 10\) and \(\lambda^* = 13.6\), again reflecting the cell-type specific differences modelled in [17].

The transport terms, parameter values, initial conditions and efflux/influx carrier positions are identical to those defined in [17]. In summary, movement of IAA (denoted \([Auxin]\) in [17]) is simulated between every cell and its neighbouring apoplastic compartments, and between every apoplastic compartment and neighbouring apoplastic compartments (via quasi-steady state concentrations of IAA at the vertices between apoplastic compartments) using the following model:

\[
\frac{d[IAA]_i}{dt} = \alpha \text{ metabolism}_i + \frac{1}{A_i} \sum_{j \in C_i} \sum_{k=1}^{N_{ij}} S_{ijk} J_{ijk}, \\
\frac{d[IAA_a]_{ijk}}{dt} = \frac{1}{\delta} (J_{ij} + J_{jk}) + \frac{1}{S_{ijk}} \sum_{m \in V_{ijk}} J_{ijkl},
\]

(5a)

(5b)

where \([IAA]_i\) and \(A_i\) respectively denote the IAA concentration and area of cell \(i\), and \([IAA_a]_{ijk}\) and \(S_{ijk}\) are, respectively, the IAA concentration and segment length of the \(k^{th}\) apoplastic compartment between cells \(i\) and \(j\).

\(C_i\) is the set of neighbouring cells to cell \(i\), \(N_{ij}\) is the number of apoplastic compartments between cells \(i\) and \(j\), and \(V_{ijk}\) is the pair of vertices adjacent to apoplastic compartment \(ijk\). \(\delta\) is a parameter defining the apoplast width.

Finally, \(J_{ij} \) is the flux from apoplast compartment \(ijk\) into cell \(i\) and \(J_{ijkl}\) is the flux into apoplastic compartment \(ijk\) from one of two neighbouring vertices \(l \in V_{ijk}\). Both \(J_{ij} \) and \(J_{ijkl}\) are defined as in [17].

For the boundary conditions, as done previously we included a flux of auxin from the shoot by prescribing a non-zero auxin concentration within the stele cells at the shootward boundary of the modeled tissue [17]. In the epidermal, cortical, and endodermal cells we assume that the auxin concentrations have reached their far-field asymptotic values, hence setting them equal to those in neighbouring (rootward) cells of the same type. This boundary condition is slightly different to that in [17], which sets the boundary cells to have zero auxin concentration, and implies an appropriate shootward flux of auxin through the outer tissue layers [19] — moreover, we have checked that this modification makes no significant difference to the model predictions.
Supplementary Figure Legends

**Figure S1:** qRT-PCR IAA dose response data showing *AtDAO1* and *GH3.3* mRNA expression levels increasing with IAA. 7 day old seedlings were treated with the stated IAA concentrations for 4 hours.

**Figure S2:** Best fit between simple *dao1-1* knock-out model and metabolic data, using Equations (1a)–(1f) and parameter values from Table S1 (Set 1).

**Figure S3:** Representative fit between *dao1-1* simulation (with $d_1^* = 0$, $\lambda^* = 1.36$, and $g_a^*$ and $g_g^*$ free to vary) and metabolic data, using Equations (1a)–(1f) and parameter values from Table S1 (Set 2).

**Figure S4:** Representative fit between model with inducible *AtDAO1* and *GH3* and metabolic data, showing absolute concentrations of auxin and its metabolites, using Equations (3a)–(3e) and parameter values from Table S1 (Set 3).

**Figure S5:** Representative fit between model with inducible *AtDAO1* and *GH3* and metabolic data, showing auxin and metabolite concentrations in *dao1-1* relative to wild type, using Equations (3a)–(3e) and parameter values from Table S1 (Set 3).
wild type

- model
- data

dao1

concn. / w.t. IAA
Supplementary Table Legend

Table S1: Representative fitted parameter sets for the various models for auxin homeostasis. **Set 1**: simple *AtDAO1* knockout model (*d*\textsubscript{i} = 0 in *dao1-1* simulation), using Equations (1a)–(1f). Parameters with superscript * are for the *dao1-1* case. Here we assume *g*\textsubscript{a} = *g*\textsuperscript{*} \textsubscript{a}, *g*\textsubscript{g} = *g*\textsuperscript{*} \textsubscript{g}, \(\lambda = \lambda^*\). **Set 2**: fitted parameter set, using Equations (1a)–(1f), for *dao1-1* simulation with \(d^*_i = 0\), \(\lambda^* = 1.36\), and *g*\textsuperscript{*} \textsubscript{a} and *g*\textsuperscript{*} \textsubscript{g} free to vary within the default constraints. **Set 3**: Representative fitted parameter set for model with inducible *AtDAO1* and *GH3*, used to produce Fig 3. (main text) and as the basis for the parameterisation of the multi-cellular model. See SI text for parameter constraints.
**SUPPLEMENTARY TABLE 1:** Dynamic Regulation of *AtDAO1* and *GH3* modulates auxin homeostasis

<table>
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<th>Parameter</th>
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<th>Set 2: <em>dao1-1</em> differs in rates of IAA oxidation, biosynthesis and conjugation</th>
<th>Set 3: <em>dao1-1</em> only differs in rate of IAA oxidation, but <em>AtDAO1</em> and <em>GH3</em> are auxin inducible</th>
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