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Short title: Nt-acetylation-independent turnover of SQE1

Nt-acetylation-independent turnover of SQUALENE EPOXIDASE 1 by Arabidopsis DOA10-like E3 ligases

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Abstract

The Acetylation-dependent (Ac/) N-degron pathway degrades proteins through recognition of their acetylated N-termini (Nt) by E3-ligases called Ac/N-recognins. To date, specific Ac/N-recognins have not been defined in plants. Here we used molecular, genetic, and multi-omics approaches to characterise potential roles for Arabidopsis (*Arabidopsis thaliana*) DEGRADATION OF ALPHA2 10 (DOA10)-like E3-ligases in the Nt-acetylation-(NTA-) dependent turnover of proteins at global and protein-specific scales. Arabidopsis has two ER-localised DOA10-like proteins. *At*DOA10A, but not the *Brassicaceae*-specific *At*DOA10B, can compensate for loss of yeast (*Saccharomyces cerevisiae*) *Sc*DOA10 function. Transcriptome and Nt-acetylome profiling of an *Atdoa10a/b* RNAi mutant revealed no obvious differences in the global NTA profile compared to wildtype, suggesting that *At*DOA10s do not regulate the bulk turnover of NTA substrates. Using protein steady-state and cycloheximide-chase degradation assays in yeast and Arabidopsis, we showed that turnover of ER-localised SQUALENE EPOXIDASE 1 (*At*SQE1), a critical sterol biosynthesis enzyme, is mediated by *At*DOA10s. Degradation of *At*SQE1 *in planta* did not depend on NTA, but Nt-acetyltransferases indirectly impacted its turnover in yeast, indicating kingdom-specific differences in NTA and cellular proteostasis. Our work suggests that, in contrast to yeast and mammals, targeting of Nt-acetylated proteins is not a major function of DOA10-like E3 ligases in Arabidopsis and provides further insight into plant ERAD and the conservation of regulatory mechanisms controlling sterol biosynthesis in eukaryotes.

Introduction

N-terminal (Nt) acetylation (NTA) is a highly prevalent chemical modification that is applied to around 60 % of cytosolic proteins in yeast and more than 80% in humans and plants (Arnesen et al. 2009; Bienvenut et al. 2012; Aksnes et al. 2015). NTA is performed by N-acetyltransferase (NAT) enzymes, which catalyse the transfer of an acetyl moiety from acetyl-CoA to the α-amino group of specific Nt-residues in substrate proteins (Starheim et al. 2012). In eukaryotes, most NTA is carried out co-translationally by five ribosome-anchored NATs (NATA-NATE), with experimentally determined substrate specificities in yeast, animals, and plants (Linster *et al.*, 2015, Aksnes *et al.*, 2019, Huber *et al.*, 2020). Furthermore, post-translational NTA also occurs in plants and animals via monomeric NATs that function away from the ribosome exit tunnel (Aksnes et al. 2019; Giglione and Meinnel 2021). These include membrane-bound NATF (Aksnes et al. 2015; Aksnes et al. 2017; Linster et al. 2020), a family of at least 6 plant-specific plastidic GNATs, that also catalyse lysine-acetylation (Dinh et al. 2015; Koskela et al. 2018; Bienvenut et al. 2020), and cytosolic NATH, which specifically Nt-acetylates actin in animals (Drazic et al. 2018; Wiame et al. 2018).

The addition of an acetyl group has the effect of neutralising N-terminal charge and increasing hydrophobicity, which can influence protein fate in several ways, for example by promoting protein-protein interactions and directing protein localisation by increasing membrane affinity (Linster and Wirtz 2018; Ree et al. 2018). NTA also impacts protein folding, with deletions of NATA and particularly NATB causing the accumulation of misfolded protein aggregates in yeast (Friedrich et al. 2021). Furthermore, NTA has been shown to promote or prevent protein degradation depending on the protein target and cellular context.

In yeast and humans, acetylation of N-termini can destabilise certain proteins through the creation of Ac/N-degrons that target them for proteolysis via the acetylation-dependent (Ac/)N-degron pathway (Hwang et al. 2010; Park et al. 2015; Shemorry et al. 2013). This degradation pathway was identified in yeast (*Saccharomyces cerevisiae*), where DEGRADATION OF ALPHA2 10 (DOA10) and NEGATIVE ON TATA-LESS 4 (NOT4) E3 ligases were shown to function as Ac/N-recognins that target substrates via recognition of their Nt-acetylated N-termini (Hwang et al. 2010; Shemorry et al. 2013). Ac/N-degron pathway substrates have also been identified in humans (*Homo sapiens*), and are recognised by the human *Sc*DOA10 homolog, MEMBRANE-ASSOCIATED RING-CH-TYPE FINGER 6 (MARCH6)/TEB4 (Nguyen et al. 2019; Park et al. 2015). In Arabidopsis (*Arabidopsis thaliana*), NTA of an MMD-initiating isoform of SUPPRESSOR OF NPR1,

CONSTITUTIVE 1 (SNC1) by NATA was shown to induce degradation, suggesting the Ac/N-degron pathway may also function in plants, though to date no plant Ac/N-recognins have been identified (Xu et al. 2015). Interestingly however, NTA of an alternative MD-initiating isoform of SNC1 by NATB was shown to have a stabilising effect, indicating that Nt-variants of the same protein can be differentially targeted for degradation (Xu et al. 2015; Gibbs 2015). Recently, the NATA-interacting HUNTINGTIN INTERACTING PROTEIN K (HYPK) protein in rice (*Oryza sativa*) was also shown to be degraded following N-terminal acetylation (Gong et al. 2022). Since most cellular proteins are Nt-acetylated, degradation via the Ac/N-degron pathway is proposed to be conditional, with substrates only degraded when their acetylated N-termini are not internalised within a protein's structure or shielded by a binding partner (Shemorry et al. 2013).

The discovery of the Ac/N-degron pathway partially conflicted with the historical view that NTA increases protein half-life by blocking ubiquitination of the N-terminus (Hershko et al. 1984). Recent studies have also suggested that NTA does not act as a broad or universal degradation signal. High throughput screening studies have independently shown that unstructured NTA reporter substrates of NATA and NATB were generally stable, and that mutations of NATA or NATB did not increase the abundance of their endogenous targets (Kats et al. 2018; Friedrich et al. 2021). Indeed, NTA has also been reported to block other Nt-processing events such as Met-excision, arginylation and the binding of N-recognins, thereby potentially protecting proteins from other degradative mechanisms such as the Arg/N-degron pathway (Kats et al. 2018; Park et al. 2015; Kim et al. 2014). One such protein is Arabidopsis SIGMA FACTOR-BINDING PROTEIN1 (SIB1), which is stabilised following NTA by NATB (Li et al. 2020). Kats *et al*. (2018) also observed that whilst mutation of *Sc*DOA10 did stabilise many normally unstable reporter proteins, turnover of these peptides was largely defined by Nt-hydrophobicity rather than NTA itself. Additionally, in human cells, NTA by NATA was shown to protect nascent proteins from degradation by preventing their unwanted interaction with IAP E3 ligases that might otherwise trigger ectopic apoptosis (Mueller et al. 2021). Moreover, an analogous proteome-wide role for NTA in protein stabilisation was also recently uncovered in Arabidopsis, where stress-responsive NATA activity (Linster et al. 2015) was shown to mask non-Ac/N-degrons that would otherwise target NATA substrates for proteasomal degradation by as-yet-unknown E3 ligases (Linster et al. 2022; Gibbs et al. 2022).

The best characterised Ac/N-recognin, *Sc*DOA10, is a RING-type E3 ligase that localises to the endoplasmic reticulum (ER) and nuclear envelope, and which was identified as a major component of the endoplasmic-reticulum-associated protein degradation (ERAD)

system that degrades misfolded ER proteins (Swanson et al. 2001). *Sc*DOA10 is one of two ERAD E3 ligases and is primarily responsible for the ubiquitination of proteins with cytosolic degrons (ERAD-C) (Hirsch et al. 2009; Strasser 2018) although targeting of degrons within the ER membrane and retrotranslocase activity have also been reported for *Sc*DOA10 (Habeck et al. 2015; Schmidt et al. 2020). Two putative homologs of *Sc*DOA10 have been identified in Arabidopsis: *At*DOA10A, also known as ECERIFERUM9 (CER9)/ SUPPRESSOR OF DRY2 DEFECTS1 (SUD1), and *At*DOA10B (Liu et al. 2011). *Atdoa10a* mutants display a range of phenotypes, including altered cuticular wax composition, improved drought tolerance and ABA hypersensitivity during germination (Lu et al. 2012; Zhao et al. 2014). Mutations in *AtDOA10A* were also shown to repress the pleiotropic phenotypes caused by a point mutation in the sterol biosynthesis gene *SQUALENE EPOXIDASE 1* (*SQE1)/ DROUGHT HYPERSENSITIVE2* (*DRY2*) by downregulating 3-HYDROY-3-METHYLGLUTARYL-COA REDUCTASE (HMGR), an upstream enzyme of the pathway (Doblas et al. 2013). It is still unclear if either *At*DOA10 homolog plays a major role in the plant ERAD system (Li et al. 2017; Huber et al. 2021). Furthermore, potential Ac/N-recognin functions for *At*DOA10s have not yet been investigated and no physiological substrates of *At*DOA10s have been identified.

Here, we sought to functionally characterise both putative *At*DOA10 orthologs with a view to establishing whether they function as Ac/N-recognin E3 ligases of the as-yet-uncharacterised Ac/N-degron pathway in plants. Our global and protein-specific results uncover a previously unknown function for *At*DOA10s in the homeostatic regulation of sterol biosynthesis through controlling *At*SQE1 turnover, and suggests that their primary function in Arabidopsis is unrelated to the Ac/N-degron pathway and the bulk degradation of Nt-acetylated proteins.

Results

Structure, functional conservation, and phylogeny of Arabidopsis DOA10-like proteins

To identify putative DOA10 homologs in Arabidopsis, we searched for protein sequences with homology to full-length *Sc*DOA10 from *Saccharomyces cerevisiae*, which, in accordance with previous studies, identified two DOA10-like proteins encoded by the genes At4g34100 (*At*DOA10A/CER9/SUD1) and At4g32670 (*At*DOA10B) (Doblas et al. 2013; Lu et

al. 2012; Liu et al. 2011). These share 22.87% and 19.23% amino acid identity with *Sc*DOA10, respectively, and 35.66% with each other (Fig.1a-b and Fig. S1). Identity is particularly high in the N-terminal RING-CH domain, an atypical variant of the classic RING domain that provides ubiquitin-ligase activity, and the TEB4/DOA10 (TD) domain, which influences interactions with the cognate ubiquitin conjugase 6 (UBC6) E2 enzyme in yeast (Fig.1b) (Doblas et al. 2013; Kreft and Hochstrasser 2011). Both *At*DOA10s also have an extended C-terminal region containing 13-16 predicted transmembrane (TM) domains (Fig. S2a,b), similar to the experimentally confirmed 14 TM domains in *Sc*DOA10 (Fig. 1a) (Kreft et al. 2006).

To determine whether *At*DOA10A and *At*DOA10B represent functional homologs of *Sc*DOA10, we assessed their capacity to complement the yeast *Scdoa10Δ* mutant. We cloned both proteins as C-terminal GFP fusions driven by the *GPD* promoter, transformed them into *Scdoa10Δ*, and confirmed expression using RT-PCR (Fig. 1c). In growth assays, *Scdoa10Δ* displayed relative insensitivity to hygromycin, which was reverted in mutants expressing *At*DOA10A-GFP (to a greater extent than WT yeast, possibly due to over expression of the transgene), but unaffected in lines expressing *At*DOA10B-GFP (Fig. 1d). Thus, *At*DOA10A, but not the C-terminally truncated *At*DOA10B (Fig. 1a), is able to compensate for the loss of endogenous *Sc*DOA10 activity in yeast, indicating at least partial conservation of function for this putative ortholog.

To understand the nature of the Arabidopsis DOA10 gene duplication, we constructed a phylogenetic tree of DOA10-like protein sequences identified via BLASTP from a range of diploid flowering plant genomes, including diverse monocots, dicots and several members of the *Brassicaceae* family (Fig. 1e). We found that many, though not all, plant species had two DOA10-like proteins. Whilst most DOA10-like sequences clustered into defined branches that split the monocots and dicots, *At*DOA10B was part of a separate *Brassicaceae*-specific clade, grouping with similar DOA10B-like sequences from lyre-leaved rock cress (*Arabidopsis lyrata*), field mustard (*Brassica rapa*) and pink shepherd's-purse (*Capsella rubella*). In contrast, where two putative orthologs were identified in other species, both sequences occurred together in species-specific pairs within the main *At*DOA10A-like clade - e.g., pineapple (*Ananas comosus*), poplar (*Populus trichocarpa*), and soybean (*Glycine max*). This suggests that the truncated DOA10B-like variant emerged in the *Brassicaceae* lineage.

_At_DOA10A and _At_DOA10B are broadly expressed and localise to the endoplasmic reticulum

We developed transgenic lines expressing C-terminal GUS fusions of *At*DOA10s driven by 2kb of the endogenous promoter (*pAtDOA10A/B::AtDOA10A/B-GUS*). Histochemical staining revealed that both proteins are broadly detectable in 7-day and 14-day old seedlings, particularly in roots, which showed enrichment in the primary root meristem, lateral root primordia and vasculature (Fig. 2a). A complementary RT-qPCR analysis of relative *AtDOA10A/B* mRNA abundance also identified transcripts for both proteins across a range of seedling and adult tissues, suggesting broad roles for *At*DOA10s in diverse cell types (Fig. 2b). Corroborating the reduced levels of *At*DOA10B-GUS staining relative to AtDOA10A-GUS, *AtDOA10B* mRNA abundance was much lower than *AtDOA10A* (approx. 20-fold) across all tissue types.

To determine *At*DOA10 subcellular localisation, we isolated total protein from the *pAtDOA10A/B::AtDOA10A/B-GUS* transgenics and prepared soluble and microsomal fractions. Anti-GUS immunoblotting revealed exclusive enrichment of *At*DOA10A/B-GUS in the microsomal fractions, alongside the known ER marker Calnexin (CNX) 1/2 (Fig. 2c). We also examined the subcellular localisation of an eYFP-*At*DOA10A transgene in transiently transformed *Nicotiana benthamiana* leaf epidermal cells. Here, eYFP-*At*DOA10A co-localised with the ER marker *At*VMA12-RFP (Fig. 2d). Thus, *At*DOA10s are ER-localised, like yeast *Sc*DOA10 and human MARCH6/TEB4.

Generation and phenotypic assessment of *AtDOA10A* and *B* mutants

We obtained homozygous *Atdoa10a* and *Atdoa10b* T-DNA insertional mutants and confirmed the knockouts by RT-PCR (Fig. 3a and Fig. S3a). Although only *At*DOA10A was able to complement *Scdoa10Δ*, we postulated that both AtDOA10s could have overlapping or redundant functions in Arabidopsis. As such, we attempted to make a double mutant, but the proximity of the two genes (separated by 0.57 Mb) meant that a crossover event was likely to be very rare; in accordance with this, we were unable to identify any double mutants and instead took an RNAi approach. We designed two different RNAi constructs that targeted the first and second exons of *AtDOA10B* (Fig. 3a) and transformed these into *Atdoa10a*. RT-qPCR analysis of the derived progeny led to the identification of two independent lines with reduced *AtDOA10B* mRNA (~50% Col-0 levels): *Atdoa10a/b RNAi 3-7* and *RNAi 4-2* (Fig. 3b). Despite screening several lines, we did not identify any with stronger depletion.

No major phenotypic differences between lines were observed when grown under standard conditions, though mutant rosettes were slightly smaller than WT rosettes, in accordance with previous observations for *Atdoa10a* (Fig. 3c) (Huber et al. 2021). *At*DOA10A was previously linked to ABA signalling and the control of cuticle development,

with *Atdoa10a* mutants displaying seed ABA hypersensitivity and drought tolerance phenotypes (Zhao et al. 2014; Lu et al. 2012). We also observed ABA hypersensitivity of *Atdoa10a* seeds (Fig. 3d), and showed that WT sensitivity was restored in *Atdoa10a* lines complemented with *pDOA10A::AtDOA10A-YFP* (Fig. S3b). In contrast, the *Atdoa10b* single mutant had no obvious phenotype, and ABA sensitivity of *Atdoa10a/b RNAi 4-2* resembled that of the *Atdoa10a* single mutant, suggesting that *At*DOA10A and *At*DOA10B do not have additive or redundant roles in ABA-related responses.

RNA-seq and Nt-acetylome profiling indicate that *At*DOA10s do not regulate global turnover of Nt-acetylated proteins

We carried out an RNA-seq analysis of 10-day old *Atdoa10a/b RNAi 4-2* seedlings grown under long day conditions, which identified 447 differentially expressed genes (DEGs; 217 up, 230 down) relative to Col-0 (False Discovery Rate (FDR) adjusted p-value (q)<0.05) (Fig. 4a and Supplemental dataset 1). Amongst these, 89 had a fold-change of two or more. This modest number of DEGs likely reflects the fact that plants were grown under ambient, non-stressed conditions. Nonetheless, Gene Ontology (GO) analysis uncovered several enriched GO-terms that are consistent with potential roles for *At*DOA10s in protein quality control or ERAD, including: cellular component term *perinuclear region of the cytoplasm* (18.1 fold enrichment, 2.05E-07 FDR); biological process terms *protein folding* (4.63 enrichment, 6.31E-03 FDR) and *protein refolding* (fold enrichment 10.18, 1.50E-02 FDR), and; molecular function term *unfolded protein binding* (5.14 fold enrichment, 1.61E-02 FDR). We also carried out RNA-seq analysis on 10-day old NAT-depleted plants: *amiNAA10* (i.e., *NATA*) knockdown and *Atnaa20* (i.e., *NATB*) mutant seedlings. We hypothesised that there might be some overlap in the transcriptome of *Atdoa10a/b* and *nat* mutants, due to shared ectopic stabilisation of Ac/N-degron protein targets. As expected, given NATA's role in acetylating 40% of cytosolic proteins, *amiNAA10* seedlings had the greatest number of DEGs (7,139), with *Atnaa20* having fewer (2,486). Interestingly, nearly 70% of the *Atdoa10a/b* RNAi annotated DEGs (307/444) were also differentially expressed in either NAT-mutant transcriptome (Fig. 4b), with 75% of *Atdoa10a/b-amiNAA10* and 78% of *Atdoa10a/b-naa20* shared DEGs occurring in the same direction (i.e., up in both or down in both; supplementary dataset S1).

If *At*DOA10s function as general Ac/N-recognins of the Ac/N-degron pathway, an accumulation of Nt-acetylated proteins would be expected in plants lacking *At*DOA10 function compared to Col-0. This could manifest as either an increase in the total levels of Nt-acetylated proteins, or increased ratio of acetylated to non-acetylated variants of a

particular protein(s). We performed quantitative Nt-acetylome profiling on total protein extracts from both Col-0 and *doa10a/b RNAi 4-2* seedlings using the "stable isotope labelling protein N-terminal acetylation quantification (SILProNAQ)" method (Bienvenut et al. 2017a), with data processed using the EnCOUNTer tool (Bienvenut *et al*., 2017b) (Supplemental dataset 2). A total of 651 and 594 N-termini were identified in Col-0 and *Atdoa10a/b RNAi 4-2*, respectively, with 426 common to both lines (Fig. 4c and d). In both genotypes, approximately half of these N-termini were Nt-acetylated (48% in Col-0 and 49% in *Atdoa10a/b*). We were able to quantify a total of 342 unique N-termini (277 in Col-0 and 256 in *Atdoa10a/b RNAi 4-2*). In Col-0 58% (161/277) were either fully or partially acetylated, which was similar to 59% observed for *Atdoa10a/b RNAi 4-2* (151/256). Global NTA variation comparisons based on either N-terminal position (Fig. 4e) or cellular sub-compartment (Fig. S4) showed no differences in overall NTA level in *Atdoa10a/b RNAi* 4-2 vs Col-0, and a similar distribution in NTA-frequency was observed for all natural amino acids at the N-terminal position (Fig. 4f). Moreover, relative quantification of Nt-acetylated peptides shared between *Atdoa10a/b RNAi 4-2* and WT identified no proteins with significantly (i.e., FDR<5%) increased or decreased NTA (Fig. 4g). Collectively, these Nt-profiling findings suggest that strong depletion of *At*DOA10 levels does not affect the overall turnover of Nt-acetylated proteins.

Proteolytic turnover of *At*SQE1 requires *At*DOA10A and *At*NAA20 in heterologous yeast degradation assays

Whilst the *Atdoa10a/b RNAi 4-2* double mutant had no clear differences in global NTA, *At*DOA10s could still play a role in targeting specific Nt-acetylated protein substrates for degradation. We took a targeted approach to identify a potential physiological substrate to use for investigating protein turnover in finer molecular detail. Mutations in *At*DOA10A were previously shown to suppress phenotypic defects in the *dry2* mutant, which lacks SQE1 activity. Here, defects arise due to a build-up of toxic intermediates, and a secondary mutation in *At*DOA10A alleviates this by downregulating HMGR enzyme activity, which functions several steps ahead of squalene synthesis (Doblas et al. 2013). Moreover, in yeast and mammals, SQE homologs (Ergosterol Biosynthesis 1 (ERG1) in yeast and squalene monooxygenase (SM) in mammals) localise to the ER membrane and are direct proteolytic targets of *Sc*DOA10 and *Hs*MARCH6/TEB4, respectively (Foresti et al. 2013; Sharpe et al. 2020; Zelcer et al. 2014). Similarly, Arabidopsis SQE1 is predicted to have transmembrane regions and localise to the ER, although it does not contain a predicted N-

terminal secretory signal peptide (Fig. S2 c,d). Given the evolutionary conservation of DOA10-like E3 ligases and their roles in modulating sterol biosynthetic pathways, we postulated that Arabidopsis SQE1 turnover might also be regulated by *At*DOA10s.

We used WT and mutant yeast strains as a heterologous system for expressing *At*SQE1 and monitoring its stability by immunoblotting. Steady-state levels of *At*SQE1-HA were higher in *Scdoa10Δ* than WT yeast, and this could be reverted when *At*SQE1-HA was co-expressed with *At*DOA10A-YFP, but not *At*DOA10B-YFP (Figs. 5a and b). Next, we monitored *At*SQE1-HA turnover rates using cycloheximide (CHX) chase assays, which revealed rapid degradation of *At*SQE1-HA in WT yeast cells, but relative stabilisation in *Scdoa10Δ* (Fig. 5c). Moreover, the enhanced stability was partially reverted when *At*DOA10A-YFP was co-transformed into *Scdoa10Δ* (Fig. 5d).

*At*SQE1 initiates with the residues Met-Glu- (ME-) and should retain its initiator Met during translation and be targeted by ribosome-associated NATB (comprising NAA20 catalytic and NAA25 auxiliary subunits) (Aksnes et al. 2019). It was previously shown that 99% of ME-initiating proteins undergo NTA in humans (Aksnes et al. 2016), with similarly high numbers in yeast and Arabidopsis (Fig. S5 and Supplemental Dataset 3). It was also shown that human *HsNAA20* can complement Arabidopsis *Atnaa20* mutants, but that yeast *ScNAA20* cannot (Huber et al. 2020). Whether *At*NAA20 can compensate for loss of *Sc*NAA20 function is unknown. To investigate whether *At*SQE1-HA turnover is mediated by Nt-acetylation and the Ac/N-degron pathway, we also monitored *At*SQE1-HA stability in the yeast *Scnaa20Δ* mutant (Fig. 5c and e). Similar to *Scdoa10Δ*, and potentially consistent with the Ac/N-degron pathway, we saw strong enhancement of *At*SQE1-HA stability relative to WT, which was almost completely reverted when *At*NAA20 was co-expressed. This indicates that NATB activity is required for *At*SQE1 turnover and reveals that Arabidopsis *At*NAA20 can functionally replace *Sc*NAA20.

Impact of N-terminal mutagenesis on *At*SQE1 stability suggests indirect effects of Nt-acetyltransferases on protein turnover in yeast

To further investigate the connection between NTA and *At*SQE1 degradation, we developed a series of Nt-mutagenized variants of *At*SQE1 that are predicted to be blocked for NTA, or which are targeted by different cognate NATs (Fig. 6a, Fig. S5 and Supplemental dataset 3): (1) MP-SQE1, which should undergo Met-excision by methionine aminopeptidases (MetAPs) but no further Nt-acetylation, as Nt-Proline residues are not acetylated (Goetze et al. 2009); (2) MK-SQE1, which should be rarely acetylated (Arnesen et al. 2009), and (3) MA-SQE1, which would instead be Nt-acetylated by NATA/NAA10 following initiator Met removal by MetAP. We hypothesised that MP- and MK-SQE1-HA

would be stable in WT yeast if turnover is dependent on NTA, but instead found that their steady-state levels were in fact reduced relative to WT ME-*At*SQE1-HA (Fig. 6b), perhaps due to codon differences impacting translation (Kozak 1997). Moreover, when expressed in *Scdoa10Δ*, relative abundance increased for all proteins, but the ratios between them were maintained, suggesting that *Sc*DOA10 targets all three Nt-variants and that their direct NTA is not critical for degradation.

In accordance with these steady-state analyses (Fig. 6b), we found that mutant MP-*At*SQE1-HA rapidly degraded following CHX treatment, similarly to WT ME-*At*SQE1-HA (Fig. 6c). We also observed stabilisation of WT ME-*At*SQE1-HA in *Scnaa10Δ* mutant cells (Fig. 6d), which lack a functional NATA enzymatic complex; this was unexpected, since ME- is not a target sequence for NATA activity. Finally, we examined the stability of mutant MA-*At*SQE1-HA, where the N-terminus is remodelled from a NATB to a NATA target. Like all other variants, MA-*At*SQE1-HA was unstable in WT yeast, but was surprisingly still stable in the non-cognate Sc*naa20Δ* mutant in addition to *Scdoa10Δ* (Fig. 6e,f). Collectively, these assays indicate that degradation of *At*SQE1 via DOA10 in yeast is indirectly influenced by NATA and NATB activity.

Nt-acetylation-independent turnover of *At*SQE1 by *At*DOA10 in Arabidopsis

To test *At*SQE1 stability *in planta*, we generated a range of stable transgenic Arabidopsis lines expressing Nt-variants of *At*SQE1-Myc driven by the constitutive 35S CaMV promoter. WT ME-*At*SQE1-Myc was expressed in Col-0, *Atdoa10a*, *Atdoa10b*, *Atdoa10a/b RNAi 4-2* and *Atnaa20*, whilst mutant non-acetylatable MP-AtSQE1-Myc was expressed in Col-0 only. For each construct we identified two independent transgenics and confirmed their expression by RT-qPCR (Fig. S6a). Both the ME- and MP- Nt-variants of *At*SQE1-Myc localised to the ER in Col-0 (Fig. 7a). Thus, *At*SQE1 resides in the same cellular compartment as *At*DOA10s (like in yeast and mammals), and the introduced E2P N-terminal mutation does not disrupt this subcellular targeting. CHX chase assays revealed that WT ME-*At*SQE1-Myc was unstable after 24 h of translational shutdown with CHX in all genetic backgrounds tested, except for the *Atdoa10a/b RNAi 4-2* double mutant (Fig 7b). This was consistent across two independent transgenic lines (Fig. 7b and Fig. S6b). A shorter CHX experiment corroborated this finding, showing that WT ME-*At*SQE1-Myc is turned over in WT within 6 h, but remains stable in the *Atdoa10a/b RNAi 4-2*, or if co-incubated with proteasome inhibitor bortezomib (Fig 7c and Fig. S6c). Mutant MP-*At*SQE1-Myc was also unstable in Col-0 (Fig 7b). These data reveal that proteasomal degradation of *At*SQE1 requires both *At*DOA10 proteins *in planta* and that this turnover is neither

dependent on indirect NAT activity (in contrast to yeast; Figs 5 and 6) nor direct NTA of *At*SQE1 by NATB.

Potentially consistent with the fact that *At*SQE1 accumulates in *Atdoa10a/b RNAi 4-2*, we observed extreme epinasty in seedlings of this mutant relative to Col-0, a phenotype that has previously been shown to coincide with altered sterol biosynthesis (Fig. 7d) (Carland et al. 2010). Precise control of sterol synthesis pathway enzymes is required to regulate and maintain appropriate levels of phytosterols and their intermediates in Arabidopsis (De Vriese et al. 2021). In human and yeast systems, SQE expression and stability are influenced by the accumulation or consumption of different sterols and pathway intermediates, but how such feedback works in Arabidopsis is currently unknown (Foresti et al. 2013; Gill et al. 2011; Scott et al. 2020; Leber et al. 2001). We investigated whether chemical inhibition of Arabidopsis sterol synthesis impacts *At*SQE1 stability via *At*DOA10s through treating seedlings with the chemical lauryldimethylamine oxide (LDAO), a dual inhibitor of both the cycloartenol synthase (CAS) enzymes, which cyclise 2,3-oxidosqualene (the direct product of *At*SQE1) to produce cycloartenol, and cycloeucalenol cycloisomerase (CPI) enzymes, which act further downstream (Darnet et al. 2020). We observed extremely rapid turnover of ME-*At*SQE1-Myc protein in response to LDAO treatment, occurring within just 30 minutes (Fig. 7e). This was specific to ME-*At*SQE1-Myc and not a consequence of general protein turnover nor ER disruption due to LDAO's detergent properties, since ER-localised CNX1/2 proteins were unaffected. Interestingly however, LDAO was still able to induce rapid turnover of ME-*At*SQE1-Myc in *Atdoa10a/b RNAi 4-2* (Fig. 7e). We also directly inhibited AtSQE1 using terbinafine, a non-competitive inhibitor of squalene epoxidase enzymes (Nowosielski et al. 2011); this led to strong accumulation of *At*SQE1-Myc (Fig. 7f), likely caused by positive feedback through reduced degradation given that expression was driven by the constitutive 35S CaMV promoter.

Discussion

In yeast and humans, DOA10 E3 ligases function as Ac/N-recognins that target functionally diverse proteins for degradation via recognition of their acetylated N-termini (Park et al. 2015; Hwang et al. 2010; Shemorry et al. 2013). In plants, the Ac/N-degron pathway and its associated Ac/N-recognins are yet to be characterised, although it was previously shown that NTA of rice HYPK and a specific Nt-isoform of Arabidopsis SNC1 triggers their degradation (Xu et al. 2015; Gong et al. 2022). Whilst HYPK and SNC1 are potential plant Ac/N-degron pathway targets, the Arabidopsis SIB1 protein was recently

shown to be stabilised by NATB-mediated NTA (Li et al. 2020). Moreover, large-scale studies in yeast, humans and plants have established broader roles for NTA in proteome stabilisation (Kats et al. 2018; Friedrich et al. 2021; Mueller et al. 2021; Linster et al. 2022; Gibbs et al. 2022). Therefore, the relationship between protein NTA and degradation is complex, and is likely to vary depending on protein identity and cellular context. Here, we investigated Arabidopsis *At*DOA10-like E3 ligases, focussing specifically on their potential function as Ac/N-recognins. Nt-acetylome profiling revealed no apparent differences in the accumulation of Nt-acetylated proteins in *Atdoa10a/b RNAi* vs Col-0, suggesting that depletion of *At*DOA10 proteins does not influence the bulk turnover of Nt-acetylated proteins. However, the proteins identified and quantified in our comparative Nt-acetylome analysis represent only a small proportion of total potential Ac/N-degron substates, which means we cannot rule out that *At*DOA10s may have specific roles in targeting a more constrained set of Nt-acetylated proteins. Alternatively, other E3 ligases, for example, putative orthologs of the NOT4 Ac/N-recognins (Shemorry et al. 2013; Gibbs et al. 2016), may function as primary Ac/N-recognins in plants.

We identified the ER-resident *At*SQE1 protein, a rate-limiting enzyme in the sterol biosynthesis pathway (Rasbery et al. 2007), as a target of *At*DOA10s. Turnover of *At*SQE1 requires functional *At*DOA10s and was not linked to acetylation of its N-terminus *in planta*, since its stability was unaltered when its putative cognate NAT, NATB, was deleted (Fig. 7b). Surprisingly however, we found that *At*SQE1 stability was indirectly influenced by NAT activity when heterologously expressed in yeast. Partial or complete NATA or NATB inactivation led to enhanced stabilisation regardless of the Nt-variant being assayed (Figs 5 and 6), which may be due to indirect effects on other proteins linked to translational or proteolytic machineries; the ERAD protein *Sc*Der1, for example, requires NTA by NATB for stability (Zattas et al. 2013). Our cross-kingdom analysis of *At*SQE1 stability has therefore uncovered differences in the ways in which NTA can influence proteostasis in yeast and plants, suggesting that caution should be applied when investigating the connection between NTA and protein turnover, and particularly when extrapolating between organisms.

In contrast to yeast and humans, the Arabidopsis genome encodes for two DOA10-like E3 ligases. *At*DOA10A, but not *At*DOA10B, was able to complement *Scdoa10Δ* yeast, with respect to both hygromycin sensitivity and turnover of heterologously expressed *At*SQE1 (Figs. 1 and 5). Whilst both *At*DOA10s are smaller than *Sc*DOA10, *At*DOA10B is particularly truncated (Fig. 1a), and appears to be restricted to the Brassicaceae clade (Fig. 1e), which could explain its inability to complement *Scdoa10Δ*. This may be the result of incompatibility between *At*DOA10B and components of the endogenous yeast ubiquitination machinery, since in Arabidopsis *At*SQE1 degradation was only inhibited in the *Atdoa10a/b*

RNAi double mutant. Despite this example of functional redundancy, other evidence points to additional paralog-specific activities. For instance, *Atdoa10a* single mutants display a range of phenotypes that do not manifest in *Atdoa10b,* and which are not amplified in *Atdoa10a/b RNAi* lines, including altered cuticular wax composition and strong ABA hypersensitivity (Fig. 3d) (Lu et al. 2012; Zhao et al. 2014).

DOA10s in yeast and humans are major E3 ligases of the ERAD system (Ravid et al. 2006), whilst roles for AtDOA10s in the Arabidopsis ERAD system are still unclear (Liu et al. 2011; Huber et al. 2021; Li et al. 2017). This may be due to functional redundancy, a concept supported by our observations that turnover of ER-resident AtSQE1 is dependent on both AtDOA10s. Interestingly though, AtDOA10B was shown to physically associate with the ERAD-associated ubiquitin-conjugase 32 (UBC32) (Cui et al. 2012), and be transcriptionally induced by L-azetidine-2-carboxylic acid (AZC), a proline analogue that causes protein misfolding (Kim et al. 2017). We also observed significant upregulation of AtDOA10B, but not AtDOA10A, in response to the ERAD elicitor tunicamycin (Fig. S7). This suggests that AtDOA10s have both redundant and distinct roles linked to different cellular processes, and that the AtDOA10B paralog may have evolved to take on a more prominent role in stress-associated, rather than constitutive, ERAD in Arabidopsis. Further analysis of the transcriptomic, proteomic, and physiological response of *Atdoa10a* and *b* mutants to ER- and protein misfolding stresses will shed further light on the roles these proteins play in ERAD and protein homeostasis.

Sterol biosynthesis is sensitive to fluctuations in enzyme activity and substrate availability at each stage. For example, a build-up of cholesterol in animals feeds back to downregulate the pathway and redirect precursor flux, whilst increases in lanosterol abundance has a similar effect in yeast (Gill et al. 2011; Scott et al. 2020; Foresti et al. 2013). In plants, a build-up of squalene and/or its precursors is toxic but can be counteracted by a reduction of HMGR enzyme activity, which is enhanced when *At*DOA10A is knocked out (Doblas et al. 2013). Our LDAO assays reveal that ectopic build-up of downstream sterol intermediates also triggers feedback mechanisms to downregulate sterol production in plants, in this case promoting *At*SQE1 destabilisation, possibly through an alternative E3 ligase or an autophagic mechanism (Fig. 7e). In contrast, direct inhibition of AtSQE1 with terbinafine led to increased accumulation of *At*SQE1 (Fig. 7f). Interestingly, *Sc*DOA10 was previously shown to target multiple enzymes of the sterol biosynthesis pathway in yeast, indicating that it is a master regulator of this biochemical pathway (Scott et al. 2020). The fact that *At*DOA10s influence both HMGR activity and SQE1 stability also points to central functions for DOA10s in coordinating sterol production at several steps in plants (Fig. 8). Whether *At*DOA10s control turnover of other Arabidopsis SQEs (Rasbery et al. 2007), remains to be determined, though the Brassicaceae-specific *AtSQE5* (Laranjeira

et al. 2015) was significantly downregulated in the *Atdoa10a/b RNAi 4-2* transcriptome, potentially suggesting negative feedback. Furthermore, direct interaction and ubiquitination of AtSQE1 by AtDOA10s needs to be confirmed biochemically. A more detailed analysis of the connection between *At*DOA10s, *At*SQEs and other components of the sterol synthesis pathway in Arabidopsis will provide further insight into the complexities of sterol homeostasis in plants.

To conclude, our work suggests that DOA10-like E3 ligases, in contrast to their putative yeast and mammalian homologs, do not play a major role in the degradation of Nt-acetylated proteins in Arabidopsis, suggesting that the plant Ac/N-degron pathway is less highly conserved across kingdoms than other N-degron pathways, and that its E3 ligase component(s) await discovery. Furthermore, we uncover conservation of a DOA10-SQE regulatory module across 1.5 billion years of evolution, which suggests that homeostatic mechanisms controlling sterol biosynthesis have ancient origins.

Materials and Methods

Arabidopsis growth conditions and transgenic lines

Arabidopsis (*Arabidopsis thaliana*) lines were obtained from the Nottingham Arabidopsis Stock Centre (NASC), apart from *amiNAA10* and *naa20* (Huber et al. 2020; Linster et al. 2015). *AtDOA10A/B-GUS/YFP* transgenics were produced by cloning the genomic sequences of *AtDOA10A/B* (At4g34100 and At4g32670), including ~2 kb of upstream sequence, into the Gateway® entry vectors pDONR™221/pENTR™/D-TOPO™ (Invitrogen) before ligation into pGWB533/pGWB540 (Nakagawa et al. 2007). *AtDOA10B* RNAi target sequences were cloned into pK7GWIWG2(I) (Karimi et al. 2002). The *AtSQE1* (At1G58440) CDS was cloned into pENTR™/D-TOPO™ (Invitrogen) and subsequently pGWB17 (Nakagawa et al. 2007) to produce *35S::AtSQE1-Myc*; the E2P mutation was introduced via a mismatched forward primer. Expression clones were transformed into *Agrobacterium tumefaciens* (GV3101 pMP90) for Arabidopsis transformation via floral dip (Zhang et al. 2006). All cloning and genotyping primers are listed in Supplementary Table 1.

Arabidopsis plants were grown on soil (Levington M3 compost, vermiculite and perlite; 4:2:1 ratio), in long day (16 h light at 22°C) or short day (8 h light at 22°C) conditions. For sterile growth, seeds were surface sterilised (10% v/v bleach), plated onto half-strength Murashige & Skoog (½ MS) medium (1% w/v agar, pH 5.7), stratified at 4°C for 48 hours and grown in long days. ABA (Sigma Aldrich) was added directly into the ½ MS growth medium to the appropriate concentration. LDAO (Cayman Chemical Company) treatments were carried out on 7-day old seedlings in water supplemented with 100 µg ml^{-1} LDAO.

Terbinafine hydrochloride (20μM) (Sigma-Aldrich) was applied to seedlings in the same manner as cycloheximide (see below). All experiments involving chemical treatment of Arabidopsis were conducted at least three times.

Yeast assays

Yeast (*Saccharomyces cerevisiae*) cells used were homozygous diploid BY4743 cells derived from the S288C strain (Dharmacon yeast KO collection, Horizon Discovery). Yeast were transformed with *AtDOA10A*, *AtDOA10B* and *AtNAA20* (At1g03150) in the pAG416GPD-ccdB-EGFP vector (Addgene plasmid #14196, Susan Lindquist) and *AtSQE1* in the pAG413GPD-ccdB-HA vector (Addgene plasmid #14238, Susan Lindquist), or the corresponding empty vectors. Transformation was performed by the lithium acetate method: A 1μl loop of cells was added to 2μg of expression clone and 100μl of transformation buffer (33% v/v polyethylene glycol 3350, 0.33M lithium acetate, 0.66% v/v β-mercaptoethanol). Cells were briefly vortexed, incubated at 37°C for 45 minutes (200rpm), then spread on synthetic drop-out (DO) media (Formedium) and incubated at 30°C. Non-transformed cells were grown on yeast-extract peptone dextrose (YPD). G418 (Sigma-Aldrich) was added to media used for the growth of mutant strains. For hygromycin treatments, cells were grown overnight in liquid DO media and diluted to an OD_{600} of 1.0. A serial dilution of each culture was then spotted onto plates containing DO media with added hygromycin B (TOKU-E) (50-75μg ml^{-1}).

Reverse transcription PCR (RT-PCR) and reverse transcription quantitative PCR (RT-qPCR)

RNA was extracted from snap-frozen samples using an RNeasy minikit (QIAGEN) and analysed by NanoDrop™ 1000 spectrophotometer (ThermoFisher Scientific). 1.5μg of RNA was treated with RQ1 DNase (Promega) and cDNA was synthesised using oligo(dT) primers and SuperScript™ II Reverse Transcriptase (ThermoFisher Scientific). For semi-quantitative RT-PCR, synthesised cDNA was used in PCR reactions specific to the gene of interest and *ACTIN7*. RT-qPCR was performed on 45ng template cDNA using Brilliant III Ultra-Fast SYBR® Green QPCR Master Mix with Low ROX (Agilent), using an AriaMx Real-time PCR System (Agilent). Relative expression was calculated using the $2^{-\Delta\Delta CT}$ method (Livak and Schmittgen 2001) normalised to *ACTIN7.* All primers used are listed in Supplementary Table S1.

Phylogenetic tree construction

Putative DOA10-like protein sequences were identified by BLASTP at NCBI using *Sc*DOA10 as the template sequence. Sequences were aligned in SEAVIEW5 using the

Clustal O method and the phylogenetic tree was constructed using SEAVIEW5 and BIONJ (BIO Neighbour-Joining) method (Gouy et al. 2021), where Poisson Correction and bootstrap testing is performed with 1000 iterations.

Histochemical staining

Arabidopsis seedlings were incubated in GUS stain solution (100mM phosphate buffer (pH 7.0), 2mM X-gluc (X-GLUC Direct) 0.1% v/v Triton-X-100, 1mM potassium ferricyanide, 1 mM potassium ferrocyanide) at 37°C for 24 hours. Seedlings were cleared and fixed in 3:1 ethanol:acetic acid, mounted onto microscope slides in 50% v/v glycerol and imaged on a dissecting microscope. At least three biological repeats were conducted for each transgenic line.

Cell Fractionation

Cell fractionation was performed based on Abas & Luschnig (2010). Tissue was lysed by grinding in extraction buffer (100 mM Tris-HCl (pH 8.0), 5% v/v glycerol, 10 mM EDTA, 10mM EGTA, 5mM KCl, 1mM DTT) supplemented with cOmplete™, Mini, EDTA-free Protease Inhibitor Cocktail (Roche), and precleared by centrifugation at 630xg (10 minutes). High-speed centrifugation (21000xg) was then carried out for 2 hours (4°C) to pellet the microsomal fraction. The supernatant (soluble fraction) was removed for analysis, the pellet washed with 150µl of wash buffer (100mM Tris-HCl (pH 8.0), 5mM EDTA, 150mM NaCl) and resuspended in buffer (10mM Tris-HCl (pH 8.0), 0.5mM EDTA, 150mM NaCl). A $1/5^{th}$ volume of 5x sample buffer (300mM Tris-HCl (pH 6.8), 50% v/v glycerol, 25% β-mercaptoethanol, 10% SDS, 0.05% bromophenol blue) was added for analysis by SDS-PAGE and immunoblotting. Fractionation experiments were conducted at least twice for each transgenic line.

Confocal Microscopy

The *AtDOA10A* CDS (pDONR221) was cloned into pB7WGY2.0 to produce *35S::eYFP-AtDOA10A*, and transiently co-expressed in *Nicotiana benthamiana* epidermal cells with the ER marker VMA12-RFP (Viotti et al. 2013) via *A. tumefaciens*-mediated transformation (Kong et al. 2015). After 72 h, leaves were additionally infiltrated with 2 µg μL^{-1} 4′,6-diamidin-2-phenylindol (DAPI, Sigma-Aldrich) in ddH_2O supplemented with 1:20,000 v/v Triton-X (100%). Fluorescence was analyzed by confocal laser scanning microscopy using a Nikon automated Ti inverted microscope equipped with a Yokagawa CSU-X1 confocal scanning unit, a Hamamatsu C9100-02 EMCCD camera, and a Nikon S Fluor 40× numerical aperture 1.3 oil-immersion objective (Nikon). Images were taken in five

channels (RFP, 561/615; DAPI, 405/445nm; EYFP, 488/527nm; autofluorescence, 485/705nm; and brightfield) and processed with Fiji image analysis software.

RNA-sequencing

RNA was extracted from biological triplicates of pooled 10-day old seedlings grown vertically on ½ MS plates, and samples were sequenced and analysed by Novogene UK. Briefly, mRNA was purified from total RNA using poly-T oligo-attached magnetic beads. After fragmentation, the first strand cDNA was synthesized using random hexamer primers followed by the second strand cDNA synthesis. The library was ready after end repair, A-tailing, adapter ligation, size selection, amplification, and purification. The library was checked with Qubit and real-time RT-qPCR for quantification and bioanalyzer for size distribution detection, before pooling and sequencing on Illumina platforms to generate >20M pair-end clean reads. Sequencing quality control, mapping, quantification, and differential gene expression analysis were carried out using HISAT2 software, RPKM calculations for each gene, and DESeq2 and EdgeR packages in R were used to generate lists with differentially expressed genes as described. GO enrichment analysis was carried out at geneontology.org (Ashburner et al. 2000; Mi et al. 2019).

Nt-acetylome profiling

Three biological replicates of 10-day old Arabidopsis Col-0 wild-type (WT) and *AtDOA10a/b* RNAi 4-2 seedlings (~400 mg for each sample) were processed following exactly the previously described SILProNAQ protocol (Bienvenut et al. 2017a). Following protein extraction and Bradford assay, 1mg of proteins were denatured then labelled on their N-termini and lysine ε-amino groups using N-acetoxy-[$^2H_3$] succinimide (25 µmol/mg). The labelled proteins were subjected to trypsin digestion (100 U/mg protein) and the resulting peptide mixtures were fractionated on a Strong Cation eXchange (SCX) chromatography column (Polysulfoethyl A, 200x2.1 mm, 5 µm, Hichrom, UK) to separate the acetylated N-termini and the non-acetylated internal peptides. N-termini-enriched fractions (fractions 2-11) were individually analysed by LC-MS/MS on an LTQ-Orbitrap Velos mass spectrometer. Raw data files were processed by Mascot Distiller, using the latest Araport-11 database for identification, and with mass tolerance settings of 10 ppm and 0.5 Da for the parent and fragments ions respectively. Quantification results were exported then parsed by the EnCOUNTER script (Bienvenut et al. 2017b) to obtain the datasets. Manual consolidation was then performed on all samples. This included combining the biological replicates of

each condition, averaging their NTA levels and the corresponding standard deviations, as well as calculating, ratios and p-values (two-tailed t-test).

Cycloheximide chases and protein extractions

Yeast cycloheximide (CHX) chases were performed according to the protocol described by (Buchanan et al. 2016). Transformed colonies were grown overnight in liquid DO media at 30°C before subculturing into 30ml fresh media to an OD_{600} of 0.2. The secondary cultures were then grown at 30°C to an OD_{600} of 1.0, then 8 ml of culture was pelleted by centrifugation before resuspending in 3.2 ml fresh 30°C DO media with 250µg ml^{-1} CHX (in DMSO) and briefly vortexing. 950µl samples were removed at specified time points, added to 50µl of ice-cold Stop Mix (1M NaN_3, 100µg ml^{-1} BSA), centrifuged (30 seconds) at 6500xg and snap-frozen. Total protein was extracted from pellets in 50µl of extraction buffer (0.1M NaOH, 50mM EDTA, 2% v/v β-mercaptoethanol, 2% v/v SDS), heated to 90°C for 20 minutes, with 0.67µl 3M acetic acid added halfway through. 12.5µl of sample buffer (250mM Tris-HCl (pH 6.8), 50% v/v glycerol, 0.05% bromophenol blue) was subsequently added. Cells were then pelleted by centrifugation and the supernatant was used for analysis.

Arabidopsis CHX chases were performed on seedlings grown vertically for 7 days, then transferred to liquid ½ MS for a further 3 days, at which point 300 µg ml^{-1} CHX +/- 50 µM bortezomib was added. At specified time points, 30 seedlings were blotted dry and snap-frozen. Total protein was extracted by grinding in lysis buffer (10mM Tris-HCl (pH 8.0), 150mM NaCl, 0.5mM EDTA, 0.1% v/v SDS, 1% v/v Trition-X-100) with added cOmplete™, Mini, EDTA-free Protease Inhibitor Cocktail (Roche). Following pelleting of cell debris, $1/5^{th}$ volume 5x sample buffer (above) was added to the supernatant prior to SDS-PAGE. All CHX chases were conducted three to four times.

SDS-PAGE and Immunoblotting

SDS-PAGE and immunoblotting were performed using the BIO-RAD Mini-PROTEAN system. Protein concentrations were quantified via Bradford assay, separated on 10% v/v polyacrylamide gels, transferred to a PVDF membrane, and blocked in 5% non-fat milk in TBST. Membranes were probed with primary antibodies: 1:4000 anti-β-Actin (Abcam ab184220), 1:5000 anti-β-Tubulin (Sigma-Aldrich T8328), 1:2500 anti-AtCNX1/2 (Agrisera AS12 2365), 1:4000 anti-AtUGPase (Agrisera AS05 086), 1:1000-1:3000 anti-GUS (Sigma-Aldrich G5420), 1:1000 anti-GFP/YFP (ROCHE 11814460001), 1:4000 anti-HA (Sigma-Aldrich H3663), 1:1000 anti-Myc (Antibodies.com A85281). Horseradish peroxidase-conjugated anti-mouse (Sigma-Aldrich A5278) or anti-rabbit (Cell Signalling Technology 7074) secondary antibodies were subsequently added to allow development with Pierce™

ECL Western Blotting Substrate (ThermoFisher Scientific) and ECL Hyperfilm film (Amersham). Band densities were quantified relative to the most intense band following normalisation to actin/tubulin using Fiji image analysis software. All stability assays were conducted at least three times.

Accession Numbers

RNA-seq data are available at the NCBI GEO database with accession codes GSE236282 (for *doa10a/b RNAi 4-2* and its related Col-0 WT, *amiNAA10*, and *Atnaa20* data sets) and GSE161571 (for Col-0 WT datasets related to *amiNAA10* and *Atnaa20* analyses). Nt-acetylome data are available at the Proteomics Identification Database (PRIDE) with accession code PXD043217.

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Author contributions

D.J.G, R.D.E and M.B conceived and designed the study. R.D.E, M.B, JB.B, L.A, X.C, J.C.C, T.M, M.W, C.G and D.J.G performed research and analysed data. D.J.G and R.D.E wrote the manuscript. All authors revised and approved the article.

Figure Legends

Figure 1. Structure, functional conservation and phylogeny of Arabidopsis DOA10-like proteins. (A) Schematic diagram of Arabidopsis (At) DOA10 proteins compared to the single yeast (Sc) homolog. Key domains and features are shown. (B) Percentage identity between Arabidopsis and yeast DOA10 proteins. Values are shown for total protein length, and the RING-CH and TD regions. See also Figure S1. (C) Transgene-specific RT-PCR (using 5' and 3' primer pairs) confirming *AtDOA10A/B-GFP* expression in *Scdoa10Δ* mutant yeast cells. (D) The *Scdoa10Δ* yeast mutant is insensitive to hygromycin relative to WT cells. *At*DOA10A-GFP can complement this phenotype, whereas *At*DOA10B-GFP cannot. Spots represent 10-fold dilutions from left to right. (E) Inferred phylogenetic tree of full-length DOA10-like protein homologs identified in various diploid angiosperm species, yeast and human (*Hs*MARCH6). Two main groups are identified: (i) a DOA10A-like clade, which is split between monocot and dicot lineages, and (ii) a DOA10B-like clade that is comprised of Brassicaceae-derived sequences only. Bootstrap values are shown and the separate Brassicaceae groupings are highlighted with a blue box. At, *Arabidopsis thaliana*; Al, *Arabidopsis lyrata*; Br, *Brassica rapa*; Cr, *Capsella rubella*; Os, *Oryza sativa*; Bd, *Brachypodium distachyon*; Ac, *Ananas comosus*; Sl, *Solanum lycopersicum*; Ca, *Capsicum*

anuum; Gm, *Glycine max*; Mt, *Medicago truncatula*; Pt, *Populus trichocarpa*; Rc, *Ricinus communis*. Tree not drawn to scale.

Figure 2. *At*DOA10A and *At*DOA10B are broadly expressed in seedlings and localise to the endoplasmic reticulum. (A) Histochemical staining of 7- and 14-day old Arabidopsis seedlings expressing *pDOA10A/B::AtDOA10A/B-GUS*. Scale bar for all images: 1mm. (B) RT-qPCR of endogenous *AtDOA10A* and *B* mRNA in different seedlings and adult tissues (note the Y-axis Log_{10} scale). Relative expression levels were calculated through normalisation to *AtACT7* and are the average of three biological repeats. Horizontal line shows mean. (C) anti-GUS immunblot of microsomal and soluble protein extracts from seedlings expressing *pDOA10A/B::AtDOA10A/B-GUS* (expected sizes: *At*DOA10A-GUS, ~195 kDa; *At*DOA10B-GUS, ~170kDa – although both are detected at around 250 kDa). Anti-CNX1/2 (microsomal) and anti-UGPase (soluble) control blots confirming efficacy of the fractionation are shown. (D) Confocal images of *N. benthamiana* leaf pavement cells transiently co-expressing eYFP-*At*DOA10A and the ER-marker protein *At*VMA12-RFP showing co-localisation of YFP and RFP signals. Nuclei are stained with DAPI, and chloroplast auto-fluorescence is also shown. Scale bar: 10µm.

Figure 3. Generation and phenotypic assessment of *At*DOA10A and B mutants. (A) Schematic of *AtDOA10A* and *B* genes, showing 5'/3' UTR (black) and exons (grey), T-DNA IDs and insertion sites, position of RNAi construct sequences and RT-qPCR primers used in (B). (B) RT-qPCR of endogenous *AtDOA10B* in the *Atdoa10A* control line and homozygous RNAi lines *3-7* and *4-2*, using primer pairs (P1 and P2) upstream and downstream of the RNAi target sequence. Expression levels were normalised to *AtACT7* and expression in the RNAi lines is shown relative to the endogenous levels of *DOA10B* in the untransformed *Atdoa10A* mutant. Data are the average of three biological repeats. Horizontal line shows the mean. (C) Rosettes of 6-week-old WT, *Atdoa10a*, *Atdoa10b* and *Atdoa10a/b RNAi 4-2* lines grown under short days. Images were digitally extracted for comparison. Scale bar: 2cm (D) 7- and 14-day old seedlings grown on control or 0.5µM ABA-supplemented ½ MS plates. Scale bar: 5mm.

Figure 4. RNA-seq and Nt-acetylome profiling indicate that AtDOA10s do not regulate global turnover of Nt-acetylated proteins. (A) Volcano plot of Up and Down DEGs in 10-day old seedlings of *Atdoa10a/b RNAi 4-2* vs Col-0. Orange data points represent mRNAs that are >2-fold up or down ($log_{10}(q)>5$). (B) Venn diagram showing overlap in total DEGs (excluding non-annotated mRNAs) relative to Col-0 between 10-day old seedlings of *Atdoa10a/b RNAi 4-2, amiNAA10 and naa20.* (C) Summary table of N-terminal profiling. (D)

Venn diagrams showing numbers and overlap of (i) identified N-termini and (ii) quantified N-termini in *Atdoa10a/b RNAi 4-2* vs Col-0. (E) Global NTA variations comparison in *Adoa10a/b RNAi 4-2* and Col-0. For each sample, the peptides were sorted in decreasing order of %NTA (quantitated only). Each Nt-peptide was assigned a number corresponding to its relative position. These protein numbers are plotted with matching NTA yield (%), either for all Nt-acetylation positions, protein Nt-positions (pos. 1 or 2), or downstream Nt-acetylation (pos. >2) (F) Relative abundance of acetylated Nt-residues (shown as %) in *Atdoa10a/b RNAi 4-2* and Col-0. (G) Relative comparison of NTA levels between *Atdoa10a/b RNAi 4-2* and Col-0, for peptides quantified in both datasets, showed no significant ($p < 0.05$) differences.

Figure 5. Proteolytic turnover of *At*SQE by *At*DOA10A and *At*NAA20 in heterologous yeast degradation assays. (A) Anti-HA immunoblot showing steady state levels of AtSQE1-HA in WT vs *Scdoa10*Δ yeast cells. Anti-ACTIN bands are shown on the same blot. CBB: coomassie brilliant blue loading control. (B) Steady-state protein (immunoblot) and mRNA (RT-PCR) levels of AtSQE1-HA expressed in WT vs *Scdoa10*Δ +/- co-expression with *At*DOA10A or *At*DOA10B. (C) Cycloheximide (CHX) chase of *At*SQE1-HA in WT, *Scdoa10*Δ *and Scnaa20*Δ yeast cells (immunoblot and quantified relative density). (D) Cycloheximide chase showing that co-expression of *At*DOA10A destabilises *At*SQE1-HA in *Scdoa10*Δ yeast cells (immunoblot and quantified relative density). (E) Cycloheximide chase showing that co-expression of *At*NAA20 destabilises *At*SQE1-HA in *Scnaa20*Δ yeast cells (immunoblot and quantified relative density).

Figure 6. Impact of N-terminal mutagenesis on AtSQE1 stability suggests indirect effects of Nt-acetyltransferases on protein turnover in yeast. (A) Summary of N-terminal (Nt) mutants and predicted respective NAT activities. (B) Steady-state protein levels of *At*SQE1-HA Nt-variants in WT and *Scdoa10*Δ yeast cells (C) Cycloheximide (CHX) chase of WT ME- and mutant MP-*At*SQE1-HA in WT yeast cells (immunoblot and quantified relative density). (D) Cycloheximide (CHX) chase of WT ME-*At*SQE1-HA in WT and *Scnaa10*Δ yeast cells (immunoblot and quantified relative density). (E) Cycloheximide (CHX) chase of mutant MA-*At*SQE1-HA in WT and *Scnaa20*Δ yeast cells (immunoblot and quantified relative density). (**F**) Cycloheximide (CHX) chase of mutant MA-*At*SQE1-HA in WT and *Scnaa10*Δ yeast cells (immunoblot and quantified relative density).

Figure 7. Nt-acetylation-independent turnover of *At*SQE1 by *At*DOA10 in Arabidopsis. (A) Microsomal and soluble protein extracts from seedlings expressing WT ME- and mutant MP-*At*SQE1-Myc. Anti-CNX1/2 (microsomal) and anti-UGPase (soluble) control blots

confirming efficacy of the fractionation are shown. (B) Cycloheximide (CHX) chase of WT ME- and mutant MP-*At*SQE1-Myc variants in WT Col-0 and different mutant backgrounds. Independent transgenics have different starting expression levels (see Fig. S6A) and so comparisons of protein levels can only be directly made between time points within lines. (C) Cycloheximide (CHX) chase of WT ME-*At*SQE1-HA in Col-0 and *Atdoa10a/b RNAi 4-2* seedlings (immunoblot and quantified relative density). (D) 7-day old seedlings on ½ MS showing epinasty in *Atdoa10a/b RNAi 4-2*. scale bar: 5mm. (E) LDAO chase of WT ME-*At*SQE1-Myc in Col-0 and *Atdoa10a/b RNAi 4-2* seedlings (immunoblot and quantified relative density). (F) Terbinafine chase of WT ME-*At*SQE1-Myc in Col-0.

Figure 8. Summary of the mevalonate (MVA) and sterol synthesis pathways in Arabidopsis: (1) DOA10 negatively regulates SQE1 stability (this study) and positively regulates HMGR activity (Doblas *et al*. 2013) in plants, yeast and humans. Yeast and animal SQEs were previously shown to be targets of DOA10 (Foresti *et al.* 2013; Zelcer et al. 2014), indicating conservation of this regulatory module across three eukaryotic kingdoms. (2) NATA and B were shown to indirectly contribute to AtSQE1 turnover in yeast (this study), but not in Arabidopsis. (3) LDAO, an inhibitor of several downstream enzymatic steps, also negatively regulates AtSQE1 levels via DOA10-independent mechanism(s). (4) Terbinafine, a chemical inhibitor of SQE enzymatic activity (Nowosielski et al., 2011), indirectly promotes accumulation of AtSQE1 (this study), likely through positive feedback. Dashed lines denote indirect effects.

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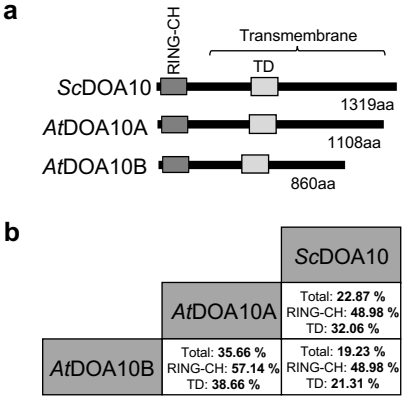
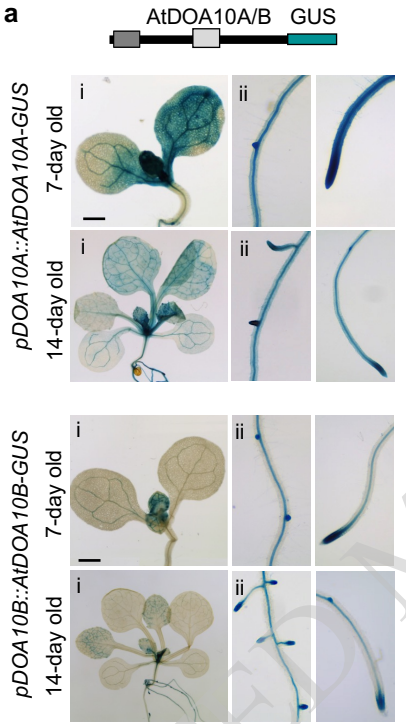
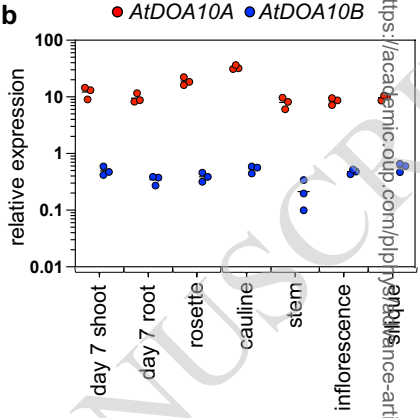
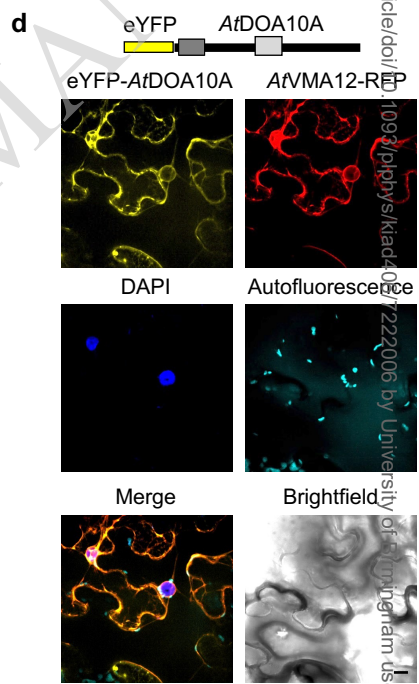
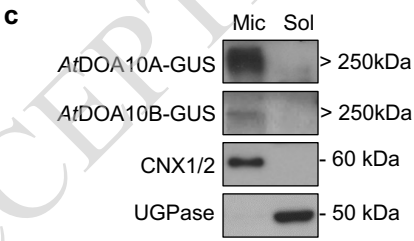
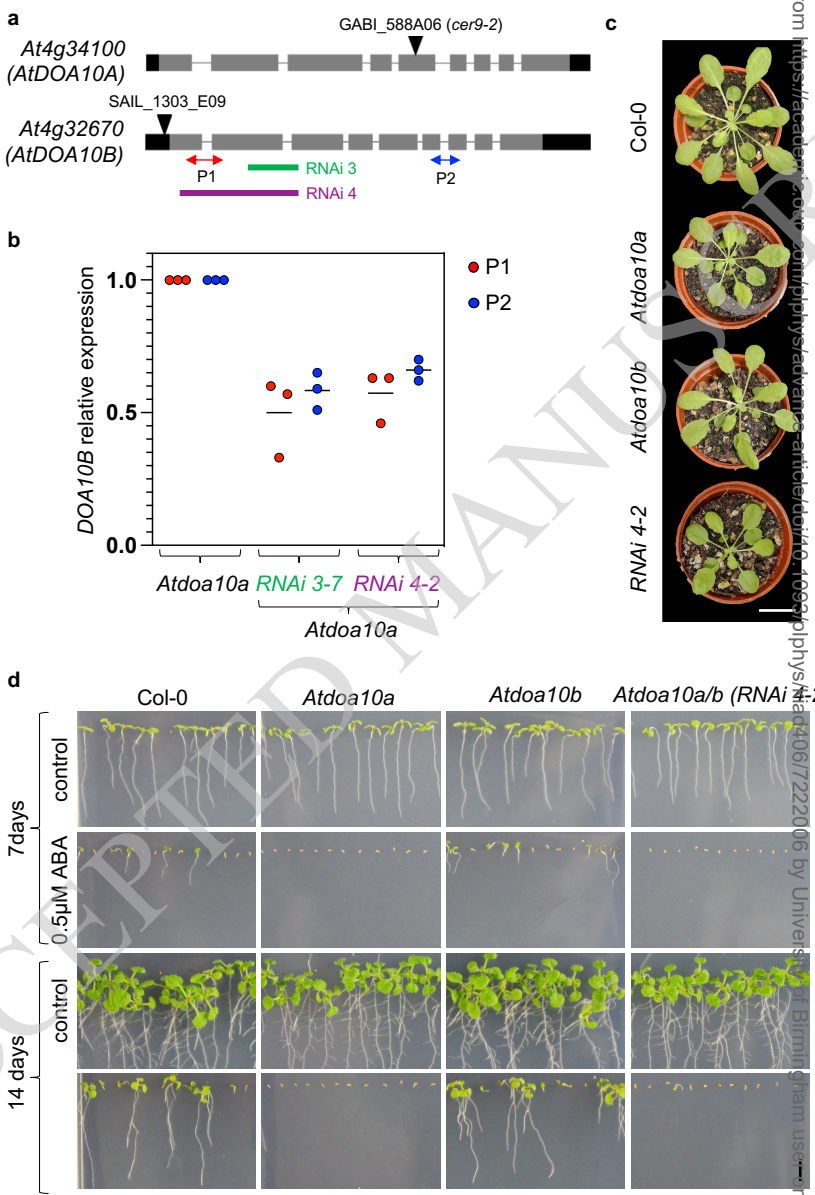


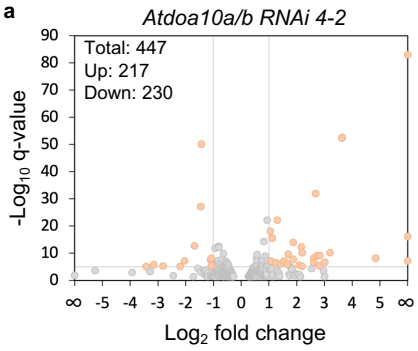


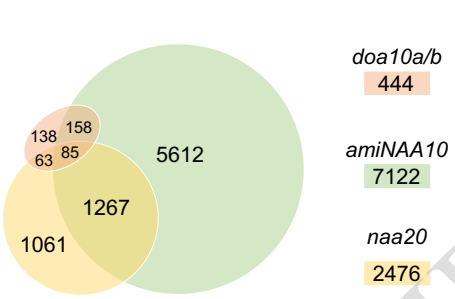






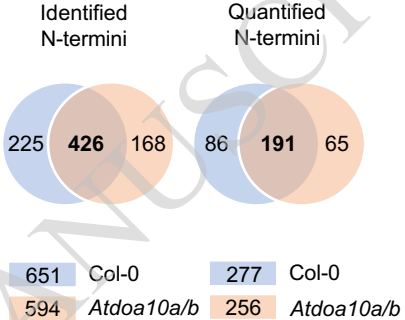


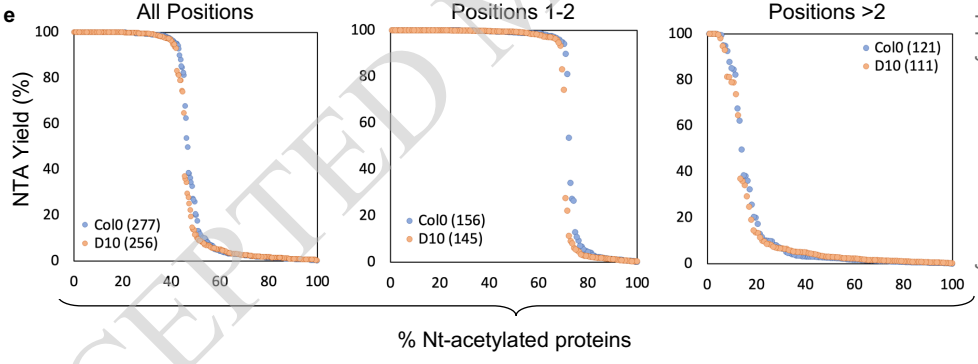


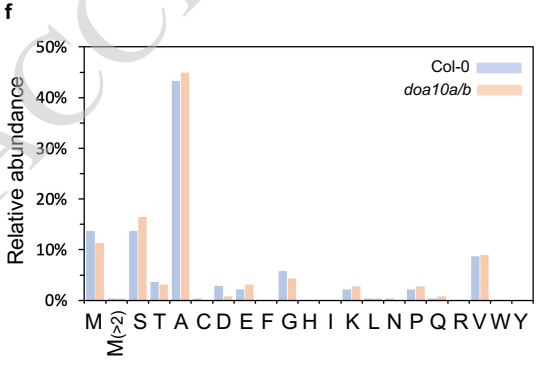


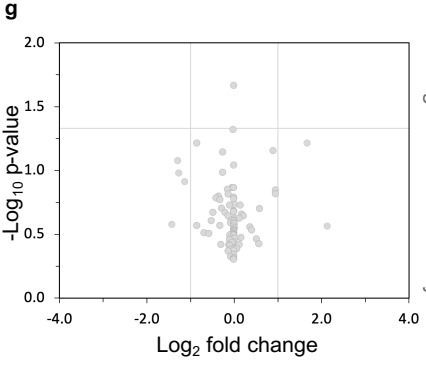
c

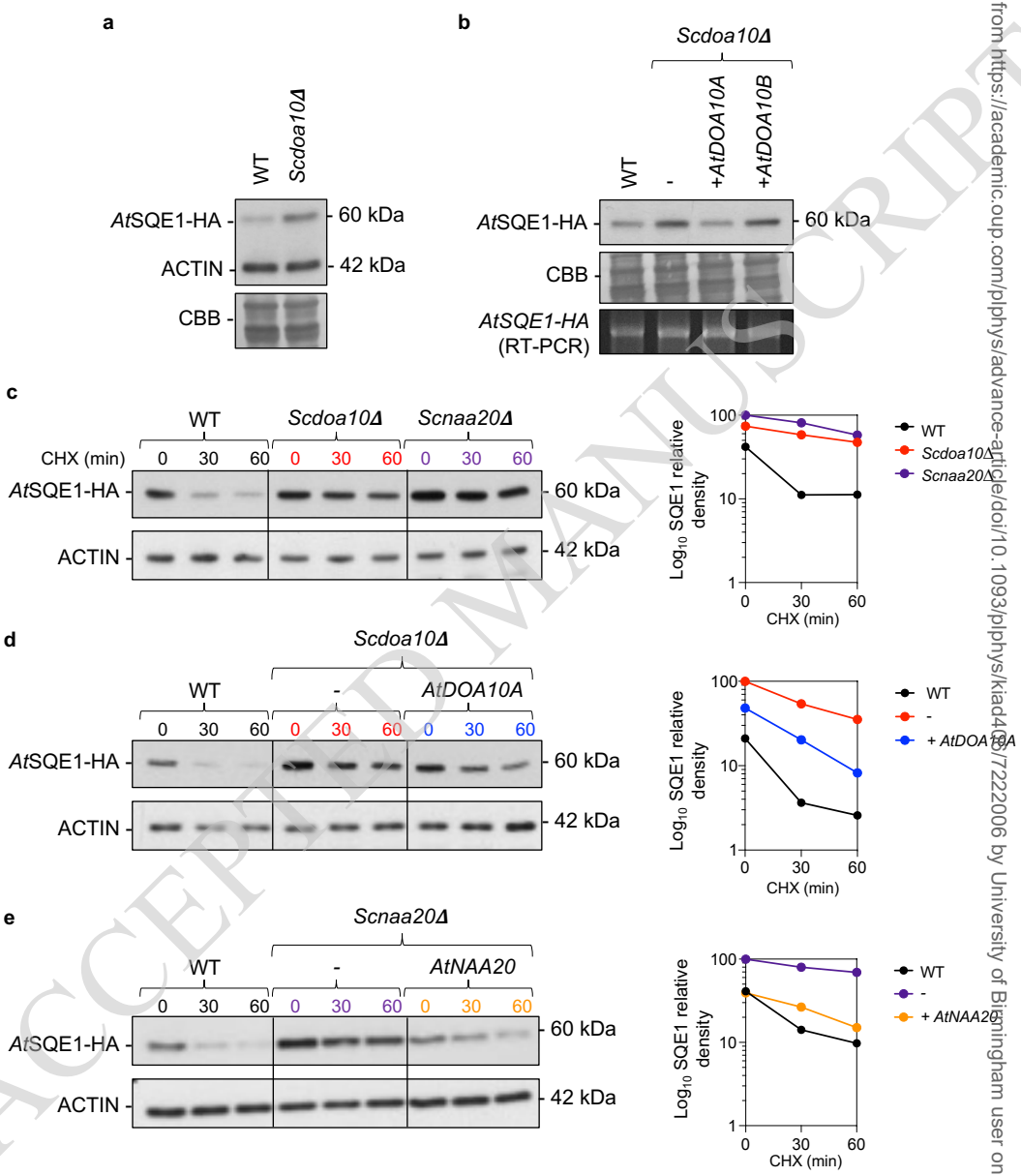
	N-ter peptides	Total	Pos. 1-2	Pos. > 2
Col-0	**Identified N-termini**	**651**	**337**	**314**
	NTA	311	252	59
	Free	337	85	252
	NTA/Free	3	0	3
	Quantitated NTA	**277**	**156**	**121**
	NTA > 95%	116	108	8
	5% ≤ NTA ≤ 95%	45	14	31
	NTA < 5%	116	34	82
Atdoa10a/b	**Identified N-termini**	**594**	**334**	**260**
	NTA	292	252	40
	Free	301	81	220
	NTA/Free	1	1	0
	Quantitated NTA	**256**	**145**	**111**
	NTA > 95%	104	98	6
	5% ≤ NTA ≤ 95%	47	11	36
	NTA < 5%	105	36	69





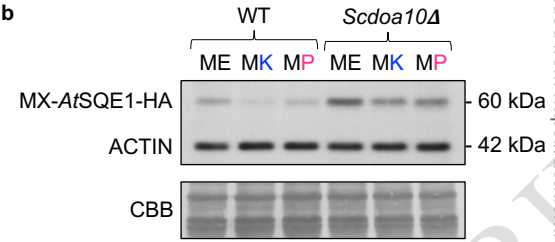


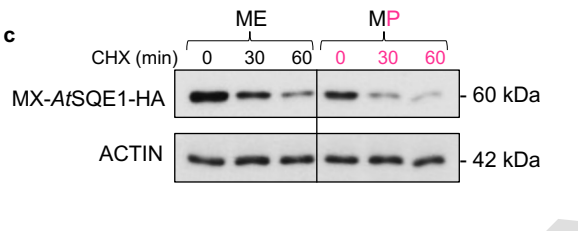


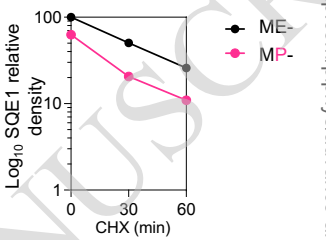


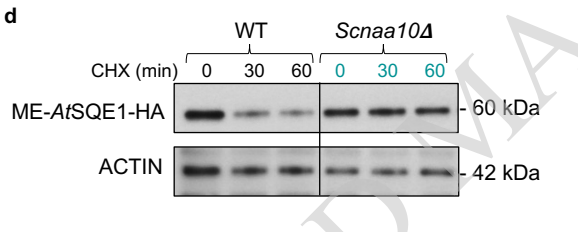
a

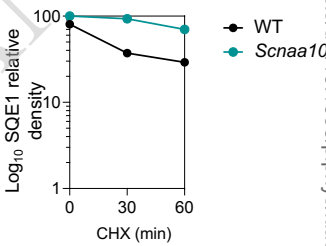
SQE1-Nt	NAT
ME-	NATB/Naa20
MP-	Not acetylated
MK-	Rarely acetylated
MA-	NATA/Naa10

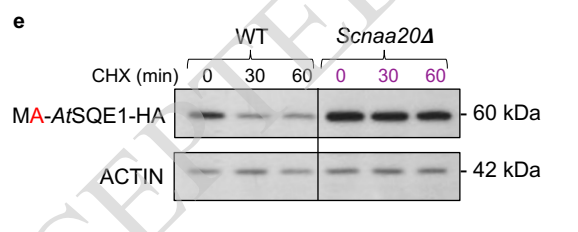


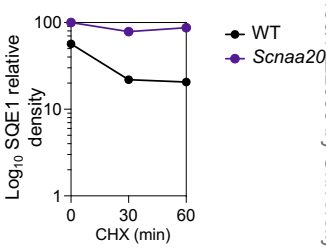


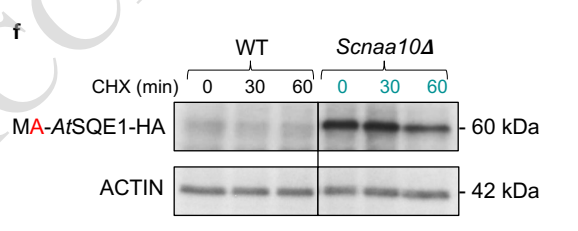


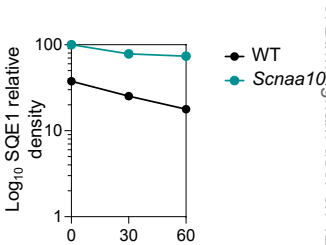


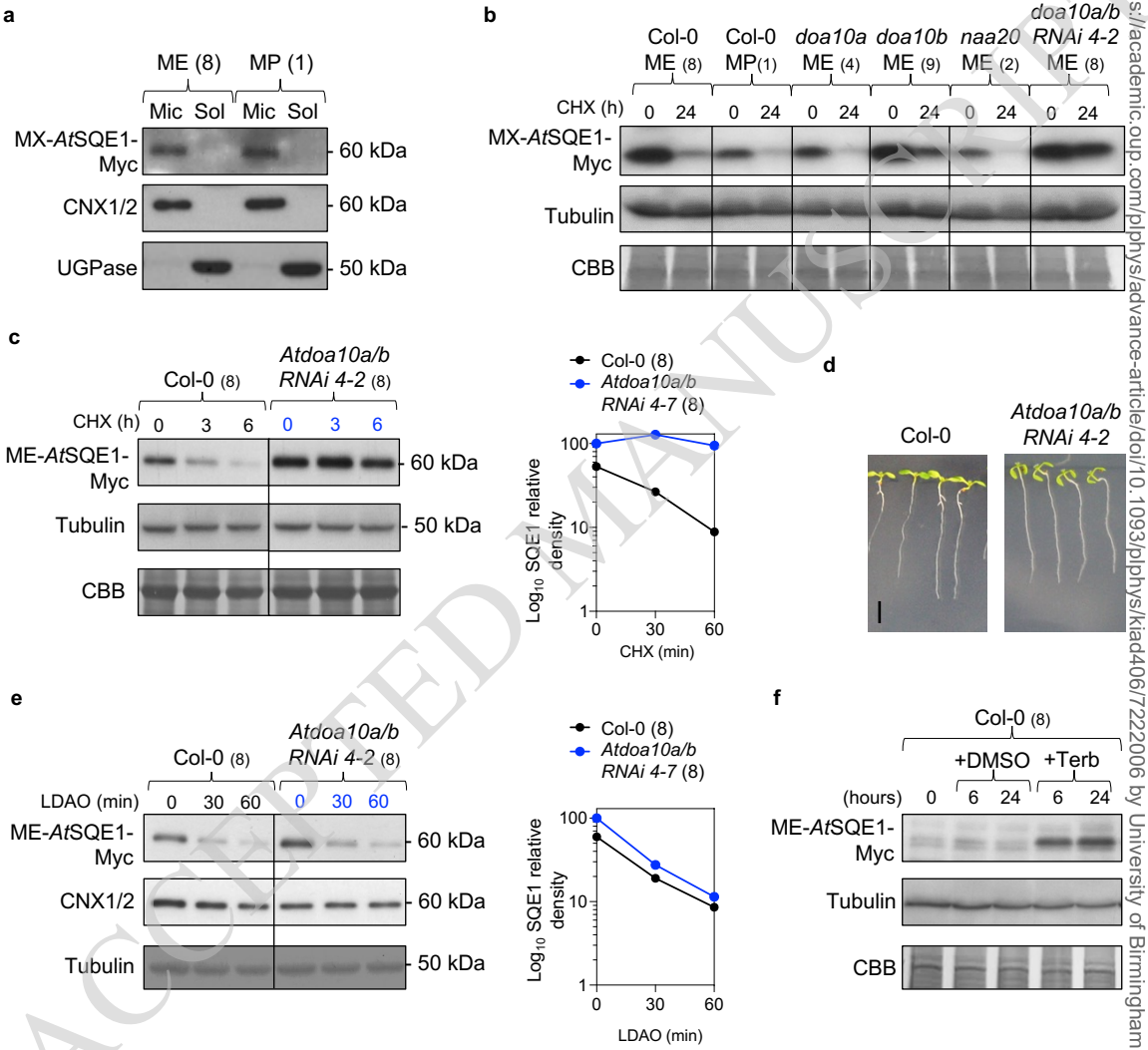


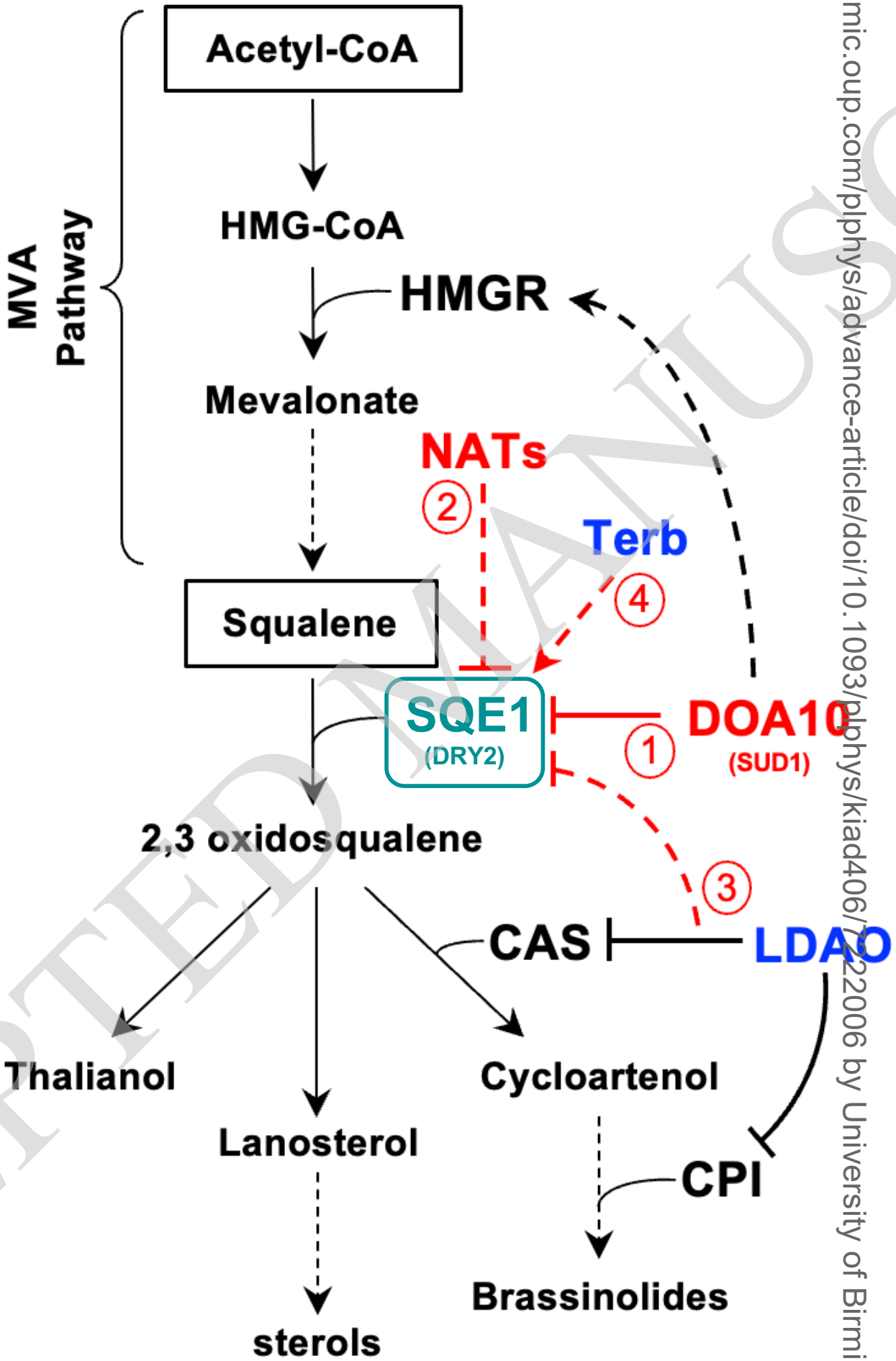












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