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Spatiotemporal distribution of ROS production, delivery and utilization in Arabidopsis
root hairs

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Abstract

Fluorescent selective probes for reactive oxygen species (ROS) detection in living cells are
versatile tools for documentation of ROS production in developmental or stress reactions in
plants. We employed staining of *Arabidopsis thaliana* with CM-H_2DCFDA, CellRox Deep
Red and Amplex Red for functional characterization of spatiotemporal mode of ROS

production, delivery and utilization during root hair formation. Using high-resolution live-cell
imaging and semi-quantitative analysis we characterized an ability of employed selective
probes to reveal subcellular localization of ROS production and accumulation from bulge
formation to tip growth of root hairs. The data show a sensitivity of CM-H$_2$DCFDA to ROS
in cytoplasm, CellRox Deep Red to ROS in mitochondria and root hair-specific sensitivity of
Amplex Red to ROS in apoplast and mitochondria. This dynamic and high-resolution study of
ROS production and utilization opens new opportunities for precise speciation of particular
ROS involved in root hair formation process.

Introduction

Root hairs are tubular outgrowths of specialized root epidermal cells, trichoblasts. A specific
feature of the formation of root hairs is a spatiotemporal change in the polarity, driving the
cell expansion. From the trichoblast expanding by a diffuse cell growth, a fundamental change
in expansion mode occurs, and the root hair itself is further elongated only by polarized tip
growth (Dolan et al., 1994; Baluška et al., 2000). Root hairs increase the total surface of the
root, which significantly improves the absorption of water and nutrients. They also support
the anchoring of the plant in the soil and enable symbiotic interactions with the beneficial
microflora in the rhizosphere (Gilroy and Jones, 2000). The establishment, maintenance and
regulation of the tip growth is conditioned by the maintenance of the polar organization of the
tip-growing cell. Membrane transport processes, temporal and spatial regulation of exocytosis
and endocytosis, as well as selective recycling of vesicles play a central role in this
maintenance. Polar tip growth, including the maintenance of root hair polarity itself, requires
regulated directional transport, dynamic properties of the cytoskeleton, maintenance of
physiological gradients in the tip and, last but not least, signaling cascades (Baluška et al.,
2000; Šamaj et al., 2006). Pollen tubes and root hairs are model objects for the study of tip
growth in plants.

The formation of a bulge on the outer cell wall of the trichoblast represents a transitional
phase between the diffuse growth of the epidermal cell and the tip growth of the root hair.
From a mechanical, as well as a functional point of view, it is a rebuilding of the cell wall,
which occurs primarily by local loosening of bonds. There is a local decrease in the pH of the
cell wall (Bibikova et al., 1998), a localized increase in the concentration of proton ions in the
cytoplasm (Bibikova et al., 1997). This is associated with an increase in xyloglucan
endotransglycosylase activity (Vissenberg et al., 2001) and specific expression of expansin 7

and 10 in trichoblasts (Cho and Cosgrove, 2002). The creation of a proton gradient is also closely connected with the production of reactive oxygen species (Foreman et al., 2003). The mechanism regulating tip growth of root hairs requires a tip-focused gradient of Ca^{2+} in the cytosol, which regulates the activity of vesicular trafficking, generation of reactive oxygen species (ROS), and organization of the cytoskeleton in growing tip. Ca^{2+}- permeable ion channels are localized at the apical plasma membrane (Miedema et al., 2008) and ROS are generated by NADPH oxidase AtrbohC/RHD2. The ROS production is regulated by ROP GTPases (Foreman et al., 2003) and the whole process is interconnected by a positive feedback mechanism, which determines root hair polarity and tip growth (Carol et al., 2005; Takeda et al., 2008). Tip-focused accumulation of ROS is tightly associated also with tip growth of pollen tubes. AtABCG28, an ABC transporter, is responsible for ROS accumulation at the tip of the growing *Arabidopsis thaliana* pollen tubes (Do et al., 2019). In tip-growing cells, NADPH oxidases, highly regulated transmembrane proteins that use cytosolic NADPH, produce superoxide ($O_2^{\bullet-}$) at the apoplastic side of the plasma membrane, which is then converted to hydrogen peroxide (H_2O_2) by the activity of the superoxide dismutase in the apoplast (Demidchik, 2018). Hydrogen peroxide can diffuse to the cytoplasm of the tip-growing cells via aquaporins, forming there a tip-focused gradient of ROS (Bienert and Chaumont, 2014).

For quantitation of H_2O_2 in living cells quite extensively is used the oxidation of 2'-7' dichlorofluorescin (H_2DCF) to 2'-7'dichlorofluorescein (DCF). Important parameter is good permeability of the diacetate form, H_2DCFDA and its acetomethyl ester H_2DCFDA-AM through plasma membrane of living cells. Probes are taken up by cells and nonspecific cellular esterases cleave off the lipophilic groups, resulting in a trapping the charged compound inside the cell. Oxidation of H_2DCF by ROS in cells converts the molecule to 2',7' dichlorodihydrofluorescein (DCF), which is highly fluorescent. Although DCF was believed to be specific for H_2O_2, some evidences indicate that other ROS such as nitrate and hypochlorous acid can oxidize H_2DCF (Hoffman et al., 2008). However, albeit this probe can react with other ROS, due to its high sensitivity, it has been widely used to monitor H_2O_2 production in plants (Swanson et al., 2011). The CellRox Deep Red is a fluorescent reagent that detects superoxide and hydroxyl radicals (Alves et al., 2015). It is a cell-permeant dye weakly fluorescent while in a reduced state, however, it exhibits strong and photostable fluorescence upon oxidation by ROS. Amplex Red is a most commonly used fluorogenic substrate, which serves as hydrogen donors in conjugation with horseradish peroxidase (HRP)

enzyme to produce intensely fluorescent product. Amplex Red serves in this case a potent and

sensitive probe, as increasing amounts of H_2O_2 in cells leads to increasing amounts of specific

fluorescent product. Amplex Red is oxidized by H_2O_2 in the presence of HRP and converts to

resorufin (Reszka et al., 2005).

In tip-growing cells, fluorescence localization of ROS using CMH$_2$DCFDA or DCFH$_2$-DA

was quite commonly employed. In pollen tubes, it was utilized for H_2O_2 detection (Potocký et

al., 2007; Do et al., 2019). The same approach was used for localization of ROS production in

Arabidopsis roots upon salt stress-induced signal transduction (Leshem et al., 2007) and in

root hairs of Arabidopsis upon treatment with LY294002, a phosphatidylinositol 3-kinase

(PI3K) - specific inhibitor (Lee et al., 2008). Alternatively, to test the possibility that the ROS

produced by mitochondria might influence the tip growth of pollen tubes, a CellRox Deep

Red probe, detecting superoxide and hydroxyl radicals was used (Do et al., 2019). In the

absence of ROS it remains in its reduced state with no fluorescence, which is rapidly induced

upon oxidation during cellular oxidative stress. CellRox Deep Red can be used to measure

cellular ROS in the cytoplasm because it detects hydroxyl better than superoxide (Alves et al.,

2015). In our knowledge, Amplex Red was not used for study of ROS production, distribution

and utilization during root hair formation process.

Sensitive fluorescent probes were so far not utilized for subcellular discrimination between

ROS sources in growing root hairs. Mapping of the origin, subcellular location of the

production and dynamics of ROS utilization during bulge formation and tip growth of root

hairs has not been documented and remains unknown. In this study, live-cell imaging using

high-resolution spinning disk fluorescence microscopy supplemented with semi-quantitative

analysis was used for functional characterization of spatiotemporal mode of ROS production,

delivery and utilization in Arabidopsis root hairs from bulge formation to tip growth.

Results

ROS detection by fluorescent probes in Arabidopsis root apex

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Staining of *Arabidopsis thaliana* root apex with CM-H$_2$DCFDA, CellRox Deep Red and

Amplex Red, probes for selective ROS detection in living cells, provided slightly different

staining pattern. In the elongation and differentiation zones, all epidermal cells were stained

with CM-H$_2$DCFDA, while prominent labeling appeared in bulges, short root hairs and apices

of long growing root hairs (Supplemental Figure S1A). Staining with CellRox Deep Red led

to detection of considerably lower signal in root epidermal cells, although the signal in bulges,

short root hairs and apices of long growing root hairs was still very high (Supplemental Figure

S1B). Unlike these two probes, staining with Amplex Red left root epidermal cells virtually

negative. However, short root hairs and apices of long growing root hairs were specifically

labeled (Supplemental Figure S1C). The first screening analysis thus revealed that the staining

pattern of these three ROS-selective probes may differ in *A. thaliana* root cells, and that root

hairs are worth to test these probes for detailed subcellular qualitative and quantitative ROS

distribution pattern.

ROS detection in bulges and root hairs

In developing bulges, staining with CM-H_2DCFDA revealed presence of relatively low signal,

distributed evenly in cytoplasm without any preference to particular subcellular compartments

(Figure 1A-F). At given frequency of image acquisition every 30 sec, it was possible to

capture bulge development and further root hair tip growth. Evaluation of images acquired at

three different time points (0 min, 5 min and 10 min from the beginning of imaging) revealed

no change in pattern of CM-H_2DCFDA signal distribution in developing bulge (Figure 1A-F;

Supplemental Movie S1). Overview of the root hair formation zone revealed a prominent

labeling pattern observed in apices of long growing root hairs (Supplemental Figure S1A).

Therefore, after documentation of signal intensity and distribution in bulges, we analyzed

„long" growing root hairs first, that reached the length of 200 μm or were longer at the time

of imaging. In these „long" root hairs, staining with CM-H_2DCFDA led to accumulation of

specific signal in cytoplasm, which was particularly prominent in root hair subapical zone

(Figure 1G-L). Analysis at time points 0 min, 5 min and 10 min from the beginning of

imaging showed that with root hair tip growth the zone with highest signal slightly enlarged

after staining with CM-H_2DCFDA (Figure 1G-L; Supplemental Movie S2). Analysis of signal

distribution after staining with CM-H_2DCFDA in „short" root hairs, annotated according their

length in the range of 10-200 μm at the time of imaging, revealed the same pattern

(Supplemental Figure S2).

After staining with CellRox Deep Red, resulting signal was localized in distinct oval

compartments in developing bulges. The size, number and cellular distribution of ROS-

positive compartments was not changed during bulge development, and this staining pattern

was stable over recorded time points (Figure 2A-F; Supplemental Movie S3). In „long"

growing root hairs stained with CellRox Deep Red these compartments were distributed in

cytoplasm within the subapical zone and around the vacuole, but were absent in clear zone (Figure 2G-L). The most prominent accumulation of these compartments was visible in root hair subapical zone (Figure 2G-L). From the analysis at 0 min, 5 min and 10 min time points from the beginning of imaging was apparent that number of ROS-positive compartments after staining with CellRox Deep Red in root hair subapical zone increases (Figure 2H,J,L; Supplemental Movie S4). The same localization pattern after staining with CellRox Deep Red was observed in „short" root hairs, reaching the length of 10-200 μm at the time of imaging (Supplemental Figure S3).

Specific staining pattern for root hairs after application of Amplex Red was apparent from overview imaging of the root hair formation zone (Supplemental Figure S1C). In higher resolution, developing bulges were outlined by strong Amplex Red-specific signal at the surface, suggesting the localization in apoplast (Figure 3A-F; Supplemental Movie S5). In the stage of „long" growing root hairs, the Amplex Red-specific signal also outlined root hairs at the surface (Figure 3G,I,K). Analysis of „short" root hairs, reaching the length of 10-200 μm at the time of imaging revealed the same localization pattern (Supplemental Figure S4). In addition, this peripheral signal was weaker at the apex, where typically cell wall is thin, and considerably stronger at the surface of subapical and shank regions where cell wall gets thicker (Figure 3H,J,L; Supplemental Movie S6), suggesting an apoplast localization. We decided to proof this localization pattern using transgenic line carrying GFP-RHD2, a GFP-tagged AtRBOHC/RHD2, which is localized in specialized vesicular compartments and apical plasma membrane in root hairs (Kuběnová et al., 2022). In root hairs, stained for ROS with Amplex Red before, plasmolysis using 300 mM Mannitol induced the protoplast visualized by GFP-RHD2 detachment from the apical cell wall (Figure 3M). Amplex Red-induced surface signal observed before at the apical and subapical regions of control non-plasmolyzed root hairs (Figure 3G-L) appeared at the remaining apoplast upon protoplast detachment after plasmolysis (Figure 3N,O). Interestingly, in addition of apoplastic signal localization, we observed also intracellular compartments positive to Amplex Red staining of ROS (Figure 3G,I,K). The internalization of Amplex Red and the presence of subcellular compartments positive to Amplex Red-based ROS detection was proved also by a pseudo-color-coded visualization of signal distribution (Figure 3H,J,L). The presence of intracellular compartments positive to Amplex Red-based ROS detection was confirmed also by a plasmolysis experiment (Figure 3N,O), indicating relatively high level of intracellular ROS levels detectable by Amplex Red in growing root hairs after plasmolysis.

 Semi-quantitative analysis of ROS distribution

We analyzed semi-quantitatively fluorescence signal distribution in apical parts of developing

bulges and growing root hairs after ROS staining with CM-H$_2$DCFDA, CellRox Deep Red

and Amplex Red probes. We characterized a mean fluorescence intensity distribution

measured along a line oriented longitudinally at the apex of bulges and root hairs that was 10

μm long and reached up to the apical cell wall (Supplemental Movie S7). We analyzed data

separately from bulges, as well as from „short" and „long" growing root hairs, and the mean

fluorescence intensities were measured and analyzed at three time points (0 min, 5 min and 10

min) of imaging. Mean fluorescence intensity distribution of CM-H$_2$DCFDA revealed no

differences among three recorded time points in bulges and growing root hairs (Figure 4A-C),

however, the fluorescence intensity gradually increased (Figure 4A-C) with the lowest level in

bulges and highest level in „long" root hairs (Figure 4D; Supplemental Movie S8,S9). This

analysis also revealed that CM-H$_2$DCFDA-specific signal was distributed equally in the

subapical region, however decreasing considerably in apical clear zone and vanishing at

apical plasma membrane and cell wall (Figure 4A-D; Supplemental Figure S5A). In bulges

and root hairs stained with CellRox Deep Red the mean fluorescence intensity distribution

showed rather an oscillating profile (Figure 4E-G), which followed ROS localization pattern

in distinct subcellular compartments (Figure 2). Due to active movement of ROS-positive

compartments, fluctuations in mean fluorescence intensities occurred and was obvious among

recorded time points at 0 min, 5 min and 10 min (Figure 4E-G). In comparison to bulges, the

mean fluorescence intensities considerably increased in growing root hairs (Figure 4H;

Supplemental Movie S10,S11). Similarly to CM-H$_2$DCFDA-staining pattern, the signal

intensity after CellRox Deep Red staining decreased in the apical clear zone and was

considerably low at apical plasma membrane and cell wall (Figure 4E-H; Supplemental

Figure S5B). Mean fluorescence intensity distribution within the apex of bulges and growing

root hairs after staining with Amplex Red was analyzed in the distance of 10 μm

longitudinally from the apical cell wall (Figure 5A) and transversally in 8 μm long profile

located in a distance of 5 μm from the apical cell wall (Figure 5B). Both fluorescence

intensity measurements revealed prominent signal located at the apical cell wall

(longitudinally) and lateral cell wall at the subapical region. At the apex, it was apparent in

bulges (Figure 5C), „short" (Figure 5D) and „long" (Figure 5E) growing root hairs, and there

were no differences found among three time points (0 min, 5 min and 10 min) of imaging

(Figure 5C-E). However, mean fluorescence intensity was lowest in bulges and higher in

„short" and „long" growing root hairs (Figure 5F; Supplemental Movie S12,S13). Lateral cell

wall measured at the subapical region in a distance of 5 μm from the apex, provided the trend

which was very similar, showing strong peak at the cell wall in „short" (Figure 5G) and

„long" (Figure 5H) growing root hairs, while in „short" growing root hairs the peak was more

prominent (Figure 5I). Consistently with data presented in profiles (Figure 5), the average

data of signal intensity after Amplex Red staining corroborated localized high cell wall

staining pattern in bulges and growing root hairs (Supplemental Figure S5C).

ROS detection in root hair mutants

To reveal the relationship between subcellular sources of ROS generation and mechanism of

root hair tip growth, we analyzed root hair mutants with phenotype of short root hairs (bulges)

that are unable to elongate by tip growth. First one bears a loss-of-function mutations in the

AtRBOHC/RHD2 locus (*rhd2-1* mutant) resulting in missing tip-focused ROS and Ca^{2+}

gradients (Schiefelbein and Somerville, 1990; Foreman et al., 2003). The second one, *der1-3*

mutant, bears a single-point mutation in the *ACTIN2* gene and is typical by an impairment of

root hair elongation after bulge establishment (Ringli et al., 2002). Distribution of ROS in

bulges of *rhd2-1* mutant after staining with CM-H_2DCFDA revealed very low signal in the

cytoplasm that remained unchanged in recorded time points at 0 min, 5 min and 10 min of

imaging (Figure 6A-F; Supplemental Movie S14). Unlike this situation, in bulges of *der1-3*

mutant the fluorescence signal after staining with CM-H_2DCFDA was considerably stronger

(Figure 6G,I,K; Supplemental Movie S15) and exhibited visual increase in recorded time

points at 0 min, 5 min and 10 min of imaging (Figure 6H,J,L). Comparison of differences in

mean fluorescence intensities after CM-H_2DCFDA staining, measured along a 10 μm line

oriented longitudinally at the central part of bulges among *rhd2-1* and *der1-3* mutants, and in

respective Col-0 and C24 wild-types revealed normal level of ROS signal intensity in *der1-3*

mutant, which was considerable reduced in *rhd2-1* mutant (Figure 6M). Differences in mean

fluorescence intensities after CM-H_2DCFDA staining in Col-0 and C24 wild-types were

negligible in „short" root hairs and higher level of mean fluorescence intensity in C24 was

found in „long" root hairs (Supplemental Figure S6A,B). Staining of ROS with CellRox Deep

Red in mutants showed similar pattern as observed in bulges of wild-type. CellRox Deep Red-

dependent ROS localization in distinct compartments moving in the cytoplasm was observed

in bulges of both *rhd2-1* (Figure 7A-F; Supplemental Movie S16) and *der1-3* (Figure 7G-L;

Supplemental Movie S17) mutants. Analysis of mean fluorescence intensities after CellRox

Deep Red staining, measured along a 10 μm line oriented longitudinally at the central part of

bulges, revealed a scattered pattern, among which data from *rhd2-1* and *der1-3* mutants

fluctuated similarly as in respective Col-0 and C24 wild-types (Figure 6M). In „short" root

hairs CellRox Deep Red staining did not show any differences between Col-0 and C24 wild-

types, while in „long" root hairs higher level of mean fluorescence intensity was found in C24

(Supplemental Figure S6C,D). Staining root hair bulges with Amplex Red provided almost

negative results in *rhd2-1* mutant (Figure 8A-F; Supplemental Movie S18), while in *der1-3*

mutant showed signal strongly outlining the surface of bulges (Figure 8G-L; Supplemental

Movie S19). Mean fluorescence intensities after Amplex Red staining, measured along a 10

µm line oriented longitudinally at the central part of bulges, revealed that signal intensity in

peripheral cell wall was strong in *der1-3* mutant and its related C24 wild-type, while Col-0

wild type expressed lower cell wall staining (Figure 8M). Importantly, *rhd2-1* mutant

contained only negligible amount of ROS detectable by Amplex Red in cell wall of bulges

(Figure 8M). In growing root hairs, cell wall-localized ROS signal after Amplex Red staining

was more or less uniform in Col-0 and C24 wild-types (Supplemental Figure S6E,F).

Subcellular identity of ROS-positive compartments in root hairs

Localization of ROS in subcellular compartments after CellRox Deep Red and Amplex Red

staining prompted us to define their nature by a colocalization analysis with known

subcellular molecular markers. We used transgenic lines carrying i) GFP-RHD2, a GFP-

tagged AtRBOHC/RHD2 (Kuběnová et al., 2022), ii) GFP-RabA1d marker for early

endosomal/TGN compartments (Ovečka et al., 2010; Berson et al., 2014; von Wangenheim et

al., 2016), iii) RabF2a-YFP marker of late endosomes (von Wangenheim et al., 2016), and iv)

GFP-tagged mitochondria-targeting sequence of the N terminus of the F1-ATPase g-subunit

(Niwa et al., 1999). ROS-positive compartments after CellRox Deep Red staining were

distributed in whole root hairs in exception of the clear zone (Figure 9A,D,G,J). GFP-RHD2

locates to vesicular compartments belonging to early endosomes/TGN and to apical plasma

membrane in root hairs (Figure 9A). Detailed view did not revealed a colocalization between

ROS-positive compartments and GFP-RHD2 (Figure 9B), which was confirmed by a

fluorescence intensity profile measurement through the compartments (Figure 9C). GFP-

RabA1d was located in early endosomal/TGN compartments accumulated in the apical and

subapical regions of root hairs (Figure 9D) and detailed analysis showed no colocalization

with ROS-positive compartments (Figure 9E,F). RabF2a-YFP decorated larger late

endosomes located mainly away of the apical and subapical regions of root hairs (Figure 9G).

Higher magnification (Figure 9H) and a semi-quantitative profile measurement of

fluorescence signal intensities (Figure 9I) revealed no colocalization with ROS-positive compartments. On the other hand, mitochondria identified by a mitochondrial GFP marker showed the same size, shape and distribution pattern as ROS-positive compartments after CellRox Deep Red staining (Figure 9J). A high degree of their colocalization was revealed by both high magnification visualization (Figure 9K) and fluorescence intensity profile measurements (Figure 9L).

Staining of root hairs with Amplex Red resulted in strong signal accumulation in cell wall (Figure 3,5), but there was also obvious internalization of the probe and localization of ROS by Amplex Red intracellularly (Figure 3H,L,N,O). To characterize the nature of intracellular ROS-positive compartments after Amplex Red staining, we used the same colocalization analysis. GFP-RHD2 in moving vesicular compartments (Figure 10A) did not colocalize with ROS-positive compartments (Figure 10B,C). Early endosomal/TGN compartments marked by GFP-RabA1d (Figure 10D) did not show the colocalization with ROS-positive compartments as well (Figure 10E,F). The same results we received after colocalization of late endosomes marked by RabF2a-YFP (Figure 10G) with ROS-positive compartments, it was negative (Figure 10H,I). Importantly, a mitochondrial GFP marker identifying mitochondria (Figure 10J) showed overlapping distribution pattern with ROS-positive compartments after Amplex Red staining (Figure 10K), which was proved by fluorescence intensity profile measurements (Figure 10L). Colocalization analysis thus revealed that distinct compartments in developing bulges and growing root hairs, highly positive to ROS after CellRox Deep Red staining are mitochondria, and unique intracellular ROS-positive compartments after Amplex Red staining, which is specific probe for ROS detection in apolpast, are indeed mitochondria as well.

Discussion

Production, accumulation and localization of ROS in plant cells can be documented by different methods. Popular are small-molecule fluorescent probes that are able to assess ROS produced within cells, or even those that are released from cells. Because ROS represent a range of chemical oxygen species with different properties, investigating ROS in biological systems should selectively concern a particular ROS of interest. It is obvious that most of the ROS probes do not capture quantitatively intracellular ROS formed under investigation. In addition, specific reaction of the probe with the ROS generated in cells may interfere with

redox state in cells and indeed, affect experimental results (Murphy et al., 2022). Small-molecule fluorescent probes are thus frequently used for ROS documentation, however, some of their limitations such as selectivity, ability to quantify, linearity in response or some possible artefacts should be considered (Kalyanaraman et al., 2012). Fluorescent probe 2',7'-dichlorodihydrofluorescein (DCFH), its diacetate form (CM-H_2DCFDA), rapidly enters living cells, and is used as an indicator of ROS in living cells. After its passive diffusion into the cytoplasm, its acetate groups are cleaved by esterases and chloromethyl groups react with glutathione and other thiols. It is subsequently oxidized to highly fluorescent product 2',7'-dichlorofluorescein (DCF), which is entrapped inside the cell. This allows long-term observation (Eruslanov and Kusmartsev, 2010). It is often used as a probe for the indirect detection of H_2O_2 and oxidative stress (Kalyanaraman et al., 2012; Winterbourn, 2014). However, oxidation to the fluorescent 2',7'-dichlorofluorescein could be catalyzed by several ROS, and thus this probe is not always considered as specific for any particular ROS (Murphy et al., 2022). It is very important to assess physiologically relevant conditions for cells before ROS are going to be detected, visualized and measured. In our system, undisturbed tip growth of root hairs, reflected by speed of growth and root hair morphology, secured biologically relevant conditions in our experiments. A slight increase in ROS levels during imaging of growing root hairs could be induced by the energy of lasers used in long-term observation (Khan et al., 2015). Light is absorbed by organic molecules such as flavins and they degrade in reaction with oxygen (Gorgidze et al., 1998; Hockberger et al., 1999; Rösner et al., 2016). This process then produces ROS, mainly superoxide and hydroxyl radicals (Icha et al., 2017), which cause the formation of DCF (Eruslanov and Kusmartsev, 2010) and the subsequent increase in fluorescence intensity. However, the increasing amount of ROS during root hair elongation is indeed typical for the course of their tip growth. Generation of ROS is important for the import of Ca^{2+} ions, which are required for apical cell expansion (Foreman et al., 2003; Carrol et al., 2005).

Level of H_2O_2 in the apoplast can be determined by oxidizing substrates for peroxidases, such as frequently used Amplex Red. In addition of H_2O_2 content created in the apoplast, this probe can be sensitive to H_2O_2 released from cell, since H_2O_2 is able to cross plasma membranes, directly or via aquaporins. Importantly, the measurement could be a real balance between H_2O_2 being produced, or removed by intracellular enzymes, and it may reflect the rate of diffusion not only inside, but also outside of the cell. Therefore, Amplex Red with horseradish

peroxidase can be used for detection of H_2O_2 release from cells if other reducing agents or peroxidase substrates are absent (Murphy et al., 2022).

Process of ROS production in cells, in relation to their subcellular source, reflects either a passive production, where ROS are generated as by-products of metabolic pathways during photosynthesis and respiration, or active production by oxidases for signaling, such as RBOHs, respiratory burst oxidase homologues. The cellular sources of ROS production for signaling can thus be defined as extrinsic (in apoplast and/or cell wall), cytoplasmic and nuclear, or organellar (in chloroplasts, mitochondria, or peroxisomes) (Yao et al., 2002; Datt et al., 2003; Mittler et al., 2022). The NADPH oxidases are plasma membrane proteins and for their activity they accept electrons from NADPH. This happens at the cytosolic side of the plasma membrane with the formation of molecular oxygen at the outer side, leading to the production of apoplastic superoxide (Mittler, 2017; Smirnoff and Arnaud, 2019). Fluorescent probe 2',7'-dichlorodihydrofluorescein-diacetate (H_2DCFDA) that is particularly sensitive to H_2O_2, was used for time course of production and intracellular localization of ROS in Arabidopsis root tips exposed to salt stress. The fact that non-fluorescent H_2DCFDA became entrapped by the surrounding membrane once hydrolyzed by the intracellular esterases to H_2DCF, which after reaction with H_2O_2 produced fluorescent dichlorofluorescein (DCF), was utilized for ROS localization in endosomes (Leshem et al., 2007). In Arabidopsis it was established that phosphatidylinositol 3-phosphate (PtdIns(3)P) and phosphatidylinositol 3-kinase (PI3K) as important factors for normal root hair growth. Essential processes such as vesicle trafficking and ROS formation, were compromised in the presence of LY294002, a PI3K-specific inhibitor. ROS generation inside of endosomes and endocytosis were indispensable for tip growth. Preincubation of seedlings with LY294002 considerably reduced ROS levels in the root hairs, as estimated using the dye 2',7'-dichlorodihydrofluorescein-diacetate (Lee et al., 2008). The use of the CellRox Deep Red, on the other hand, revealed that the signal was excluded from the apex of growing pollen tube. Instead, it was distributed throughout the body of the pollen tube. This analysis suggested that the tip-localized ROS signal does not represent superoxide or hydroxyl radicals, but H_2O_2 in growing pollen tubes. Such results indicate that ROS generated from mitochondria are not major contributors to specific spatial distribution of H_2O_2 in the apex of growing pollen tubes (Do et al., 2019).

Root hair tip growth is regulated to secure correct shape and size of bulges and elongating root hairs. Factors such as Ca^{2+}, pH and ROS play an important role in this process (Mangano et al., 2016). In growing root hairs, ROS are produced by RHD2 (ROOT HAIR DEFECTIVE

2), which is a plasma membrane-resident NADPH oxidase. ROS regulate polar root hair

expansion through activation of calcium channels allowing Ca^{2+} uptake. Mutants *rhd2-1* are

defective in Ca^{2+} uptake, have impaired cell expansion, causing a phenotype of very short root

hairs (Foreman et al., 2003). Our results show that the *rhd2-1* mutant line possess a

considerably lower amount of ROS in the bulge as analyzed by a CM-H_2DCFDA

fluorescence. These results are not surprising, as a mutation of the *RHD2* gene targets the

NADPH oxidase AtRBOHC/RHD2, responsible for the production of ROS in root hairs

(Foreman et al., 2003). It proofs previous results that intracellular ROS levels in short root

hairs of the *rhd2* mutant, detected using 2',7'-dichlorodihydrofluorescein-diacetate, were

below the detection limit at pH 5 (Lee et al., 2008). Activity of AtRBOHC/RHD2 leads to

generation of apoplastic $O_2^{\bullet-}$, from which H_2O_2 is subsequently produced by a reaction

catalyzed by superoxide dismutase (SOD; Mangano et al., 2016). Our data show a dramatic

reduction in the formation of apoplastic ROS, particularly H_2O_2, that has been clearly

documented by Amplex Red staining. In turn, a reduction in the formation of apoplastic ROS

can also result in reduced levels of H_2O_2 in the cytoplasm, reflected by lowering in

fluorescence intensity after CM-H_2DCFDA staining. The actin cytoskeleton participates in the

polar elongation of cells, and is indispensable also for determining the tip growth in root hairs

(Zheng et al., 2009; Wang et al., 2010; Pei et al., 2012). Together with actin, indispensable is

the activity of actin-binding proteins. Actin-depolymerization factor (ADF) and profilin are

accumulated in the bulge and in the growing tips of root hairs, where they are responsible for

the dynamic remodeling of the filamentous actin network (Staiger et al., 1997, Braun et al.,

1999). A high degree of actin dynamics in the bulge selectively concentrates endomembranes

and leads to the direction of vesicular transport preferentially to this subcellular domain

(Baluška et al., 2000). Mutagenesis of the *ACTIN2* gene led to the isolation of *der1-3*

(*deformed root hairs*) mutant line, which shows a phenotype of very short root hairs not able

to elongate after a bulge formation (Ringli et al., 2002; Vaškebová et al., 2018).

Determination of ROS related to bulge stage during the root hair formation process revealed,

however, that ROS levels selectively detected by CM-H_2DCFDA and Amplex Red staining

were not altered in *der1-3* mutant. It clearly shows that inability of root hairs to elongate in

rhd2-1 and *der1-3* mutants have principally different relationship to spatiotemporal

distribution, production, delivery and utilization of ROS.

In conclusion, our high-resolution live-cell imaging provide a dynamic mapping of ROS in

cytoplasm, mitochondria and apoplast, highlighting subcellular location of the production and

dynamics in tip-growth root hairs (Figure 11). This study also establish currently used fluorescent ROS probes, CM-H$_2$DCFDA, CellRox Deep Red and Amplex Red, for functional characterization of spatiotemporal mode of ROS production, delivery and utilization in Arabidopsis bulges and root hairs.

Materials and methods

Plant material and cultivation in vitro

Experiments were performed with plants of *Arabidopsis thaliana* wild types of the Col-0 and C24 ecotypes, *rhd2-1* mutant (Foreman *et al*., 2003) and *der1-3* mutant (Ringli *et al*., 2002) and stably transformed Arabidopsis lines carrying construct GFP-RHD2 for NADPH oxidase type C (Takeda *et al*., 2008), GFP-RabA1d for early endosomes/TGN (Ovečka *et al*., 2010; Berson et al., 2014; von Wangenheim et al., 2016), RabF2a-YFP fore late endosomes (von Wangenheim et al., 2016), and the GFP-tagged mitochondria-targeting sequence of the N terminus of the F1-ATPase g-subunit (Niwa et al., 1999). After surface-sterilization, the seeds of control, mutant and transgenic lines were planted on half-strength Murasige and Skoog (MS) medium (Murashige and Skoog, 1962) without vitamins, solidified with 0.6% (w/v) gellan gum (Alfa Aesar, Thermo Fisher Scientific, Heysham, UK). To synchronize seed germination, Petri dishes were stratified for 3 days at 4°C and then cultivated vertically in an environmental chamber at 21°C, 70% humidity, and 16-h/8-h light/dark cycle. The illumination intensity was 130 µmol m^{-2}s^{-1}.

Application of fluorescent probes for ROS detection

CM-H$_2$DCFDA, CellROX™ Deep Red and Amplex™ Red reagents (Thermo Fisher Scientific, Waltham, MA, USA) were used as vital probes for ROS detection in growing root hairs. At least in five independent plants per treatment, CM-H$_2$DCFDA (5 µmol.L^{-1}), CellROX ™ Deep Red (10 µmol.L^{-1}), and Amplex™ Red (1 µmol.L^{-1}) in modified liquid MS medium (Ovečka et al. 2014) were individually applied by perfusion directly to plantlets in the microscopic chamber. In total, 60 µL of the modified liquid MS medium with CM-H$_2$DCFDA, CellROX™ Deep Red, or Amplex™ Red was applied in 6 separate steps of 10 µL each. Plants were then observed using a spinning disk microscope. The root hairs were scanned at different times after perfusion of the probes. Several hairs were usually scanned consecutively, with at least 10 min pauses between scans to avoid induction of fluorescence caused by overloaded laser exposure.

 Plasmolysis of root hairs

Transgenic plants carrying GFP-RHD2, 2- to 3-day-old were transferred to microscopic
chambers containing liquid modified MS medium according to Ovečka *et al.* (2005, 2014).
After manipulation with plants during sample preparation, the subsequent stabilization period
for 24 h allowed undisturbed growth of the root and the formation of new root hairs. The
plasmolysis was induced with 300 mmol.L^{-1} solution of mannitol (Sigma-Aldrich, St Louis,
MO, USA) by perfusion methods. Amplex™ Red Reagent (1 µmol.L^{-1}) was added to the
mannitol solution. Total volume of solution was 100 µl divided into 10 steps of 10 µl
applications. Plasmolysed root hairs were immediately observed by Airyscan microscope.

Epifluorescence microscopy

Plantlets of Col-0 plants (prepared in the microscopic chambers) were observed using an
epifluorescence microscope Axio Imager M2 equipped with DIC optics and epifluorescence
metal halide source illuminator HXP 120 V (Zeiss, Oberkochen, Germany), and analyzed
using Zeiss ZEN 2012 Blue software (Zeiss, Germany). Root tips were labelled with
fluorescent probes for ROS detection (CM-H$_2$DCFDA, CellROX ™ Deep Red and Amplex™
Red). Imaging was performed with N-Achroplan 5x/0.15 NA dry objective and documented
with a Zeiss AxioCam ICm1 camera. A filter set providing a wavelength of 450-490 nm for
the excitation and 515-565 nm for the emission at 200 ms exposure time was used to visualize
the CM-H$_2$DCFDA signal. For the CellROX ™ Deep Red and Amplex™ Red, the filter set
provided an excitation wavelength of 533-558 nm and an emission wavelength of 570-640
nm. The exposure time was set up to 1 s for both probes. The image scaling for all signals was
0.93 × 0.93 µm in x × y dimensions, and 15.12 µm in the z dimension. Final images were
processed by orthogonal projection with weighted average function.

Spinning disk (SD) microscopy

Samples were prepared according to Ovečka *et al.* (2005, 2014), by transferring 2- to 3-d-old
plants to microscopic chambers containing liquid modified MS medium. As the root hairs are
very sensitive to stress during the manipulation, overnight cultivation for plant stabilization
and undisturbed growth of the root and the formation of new root hairs was necessary. For
quantitative and colocalization analyses a Cell Observer SD Axio Observer Z1 spinning disk
microscope (Carl Zeiss,Germany) was used, equipped with alpha Plan-Apochromat
100×/1.57 NA DIC Korr oil immersion objective (Carl Zeiss, Germany). The samples were

imaged using an excitation laser line of 488 nm and emission filter BP525/50 for CM-
H$_2$DCFDA and GFP signal detection, excitation laser line of 514 nm, and emission filter
BP535/30 for YFP signal detection, excitation laser line of 639 nm and emission filter
BP690/50 for CellROX[TM] Deep Red signal detection, and excitation laser line of 561 nm and
emission filter BP629/62 for the Amplex[TM] Red signal detection. The excitation laser power
level for all lasers used was set up to 50%, and the image scaling for all channels was 0.133 ×
0.133 µm in x × y dimensions, and with the z dimension 0.63 µm for the GFP and CM-
H$_2$DCFDA signal, 0.66 µm for the YFP channel, 0.75 µm for the CellROX[TM] Deep Red and
Amplex[TM] Red signal. Images were acquired sequentially or simultaneously with two Evolve
512 EMCCD cameras (Photometrics) with an exposure time of 700 ms. The samples were
scanned with 700 ms of exposure time for GFP, YFP and CM-H$_2$DCFDA signal, with 50 ms
of exposure time for CellROX[TM] Deep Red signal, and with 500 ms of exposure time for
Amplex[TM] Red signal (for quantitative analysis) or using a camera-streaming mode (for
colocalization studies).

Airyscan confocal laser scanning microscopy (Airyscan CLSM)

Root hairs for ROS staining after plasmolysis were observed using a confocal laser scanning
microscope LSM880 equipped with Airyscan (Carl Zeiss, Germany). Image acquisition was
performed with a 20×/0.8 NA dry Plan-Apochromat objective (Carl Zeiss, Germany). The
samples were imaged with an excitation laser line of 488 nm and BP420-480 + BP495-550
emission filters for GFP detection and an excitation laser line of 561 nm and BP420-480 +
BP600-650 emission filters for Amplex[TM] Red detection. The laser power did not exceed 2%
for GFP and 1% for Amplex[TM] Red of the available laser intensity range. The samples were
scanned with 700 ms of exposure time for both signals using a 32 GaAsP detector. Pixel dwell
time was set up to 1.6 µs, and with default settings of the gain level the image scaling was set
up to 0.07 × 0.07 µm (x × y).

Data analysis and measurements

The signal intensity was analyzed using a spinning disk microscope. The root hairs were
scanned for 10 min at 30 s intervals and sorted into groups according to developmental stages.
For Col-0 and C24 lines at the stages of bulge, short root hair (10-200 µm) and long root hair
(200+ µm), in *der1-3* and *rhd2-1* mutant lines at the bulge stage. Zen 3.3 blue edition
software (Carl Zeiss, Germany) was used to obtain profiles for quantitative signal intensity

distribution of different fluorescent probes in growing root hairs. Intensities were measured in single optical plane, in a 10 µm segment leading from the centre of the root hair to its tip (Schematics, Supplemental Movie S7), always at the start of the scanning (0 min), in the middle of the scanning (5 min) and at the end of the scanning (10 min).

Acquired data were processed in Microsoft Excel. Individually, the mean background intensities were subtracted from the intensities in the segment. Root hairs with abnormal intensities (exceeding double intensity over the average) were discarded from the statistics. All charts were done in Microsoft Excel software and statistical analyses were obtained using STATISTICA 13.4 (StatSoft) software using analysis of variance (ANOVA) and subsequent Fisher's LSD tests ($P < 0.05$). The colocalization studies of fluorescence signals were analyzed using a spinning disk microscope by simultaneous signal acquisition with two independent Evolve 512 EMCCD cameras. The colocalization was analyzed in transgenic lines GFP-RHD2, mito-GFP, GFP-RabA1d, and RabF2a-YFP in combination with the fluorescent probes for ROS detection described above. Profiles for colocalization were generated using Zen Blue 2014 software (Carl Zeiss, Germany) and graphically edited in Microsoft Excel.

Supplemental Data

Supplemental Figure S1. Overview of ROS staining pattern in root hair formation zone using different fluorescent probes.

Supplemental Figure S2. Distribution of ROS in root hairs after staining with CM-H_2DCFDA.

Supplemental Figure S3. Distribution of ROS in root hairs after staining with CellRox Deep Red.

Supplemental Figure S4. Distribution of ROS in root hairs after staining with Amplex Red.

Supplemental Figure S5. Average of fluorescence intensities in apical parts of bulges and root hairs after ROS staining with CM-H_2DCFDA, CellRox Deep Red and Amplex Red.

Supplemental Figure S6. Fluorescence intensity profiles in apical parts of root hairs after
ROS staining with CM-H$_2$DCFDA, CellRox Deep Red and Amplex Red in wild-type Col-0
and C24 lines.

Supplemental Movie S1. Developing bulge of Col-0 wild-type imaged with CM-H$_2$DCFDA.

Supplemental Movie S2. Growing root hair of Col-0 wild-type imaged with CM-H$_2$DCFDA.

Supplemental Movie S3. Developing bulge of Col-0 wild-type imaged with CellRox Deep
Red.

Supplemental Movie S4. Growing root hair of Col-0 wild-type imaged with CellRox Deep
Red.

Supplemental Movie S5. Developing bulge of Col-0 wild-type imaged with Amplex Red.

Supplemental Movie S6. Growing root hair of Col-0 wild-type imaged with Amplex Red.

Supplemental Movie S7. Principle of semi-quantitative fluorescence signal intensity
measurement in profiles of 10 µm long from the center of the root hair to its tip.

Supplemental Movie S8. Semi-quantitative fluorescence signal intensity measurement in
bulge of Col-0 wild-type imaged with CM-H$_2$DCFDA.

Supplemental Movie S9. Semi-quantitative fluorescence signal intensity measurement in
root hair of Col-0 wild-type imaged with CM-H$_2$DCFDA.

Supplemental Movie S10. Semi-quantitative fluorescence signal intensity measurement in
bulge of Col-0 wild-type imaged with CellRox Deep Red.

Supplemental Movie S11. Semi-quantitative fluorescence signal intensity measurement in
root hair of Col-0 wild-type imaged with CellRox Deep Red.

Supplemental Movie S12. Semi-quantitative fluorescence signal intensity measurement in
bulge of Col-0 wild-type imaged with Amplex Red.

Supplemental Movie S13. Semi-quantitative fluorescence signal intensity measurement in
root hair of Col-0 wild-type imaged with Amplex Red.

Supplemental Movie S14. Semi-quantitative fluorescence signal intensity measurement in
bulge of *rhd2-1* mutant imaged with CM-H$_2$DCFDA.

Supplemental Movie S15. Semi-quantitative fluorescence signal intensity measurement in
bulge of *der1-3* mutant imaged with CM-H$_2$DCFDA.

Supplemental Movie S16. Semi-quantitative fluorescence signal intensity measurement in
bulge of *rhd2-1* mutant imaged with CellRox Deep Red.

Supplemental Movie S17. Semi-quantitative fluorescence signal intensity measurement in
bulge of *der1-3* mutant imaged with CellRox Deep Red.

Supplemental Movie S18. Semi-quantitative fluorescence signal intensity measurement in
bulge of *rhd2-1* mutant imaged with Amplex Red.

Supplemental Movie S19. Semi-quantitative fluorescence signal intensity measurement in
bulge of *der1-3* mutant imaged with Amplex Red.

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Authors' contributions

577 LK and JH performed experiments, microscopic data acquisition and analysis, semi-
578 quantitative evaluation and statistical analyses. PD analyzed data from fluorescent probe
579 labeling. JŠ and MO contributed to the experimental plan and data interpretation. MO wrote
580 the manuscript with input from all co-authors. JŠ provided infrastructure and secured funding.

Conflicts of interest

582 The authors declare that they have no conflict of interest.

Data Availability

Data that support the findings of this study are available from the corresponding author upon reasonable request.

Figure legends

Figure 1. Distribution of ROS in bulges and root hairs after staining with CM-H$_2$DCFDA. A-F. Developing bulge imaged at time points of 0 min **(A,D)**, 5 min **(B,E)** and 10 min **(C,F)** of growth. **G-L.** Growing root hairs imaged at time points of 0 min **(G,H)**, 5 min **(I,J)** and 10 min **(K,L)**. Semi-quantitative fluorescence intensity distribution **(D-F,H-L)** is visualized in a pseudo-color-coded scale, where dark blue represents minimal intensity and pale red represents maximum intensity **(**insets in **D** and **H)**. Growing root hairs were annotated as „long", reaching the length of 200 μm and more at the time of imaging. Image acquisition at the time point 0 min started 110 min and 154 min after probe application in bulge **(A-F)** and „long" root hair (G-L), respectively. Scale bar = 10 μm **(A-L)**.

Figure 2. Distribution of ROS in bulges and root hairs after staining with CellRox Deep Red. A-F. Developing bulge imaged at time points of 0 min **(A,D)**, 5 min **(B,E)** and 10 min **(C,F)** of growth. **G-L.** Growing root hairs imaged at time points of 0 min **(G,H)**, 5 min **(I,J)** and 10 min **(K,L)**. Semi-quantitative fluorescence intensity distribution **(D-F,H-L)** is visualized in a pseudo-color-coded scale, where dark blue represents minimal intensity and pale red represents maximum intensity **(**insets in **D** and **H)**. Growing root hairs were annotated as „long", reaching the length of 200 μm and more at the time of imaging. Image acquisition at the time point 0 min started 37 min and 47 min after probe application in bulge **(A-F)** and „long" root hair **(G-L)**, respectively. Scale bar = 10 μm **(A-L)**.

Figure 3. Distribution of ROS in bulges and root hairs after staining with Amplex Red. A-F. Developing bulge imaged at time points of 0 min **(A,D)**, 5 min **(B,E)** and 10 min **(C,F)** of growth. **G-L.** Growing root hairs imaged at time points of 0 min **(G,H)**, 5 min **(I,J)** and 10 min **(K,L)**. Semi-quantitative fluorescence intensity distribution **(D-F,H-L)** is visualized in a pseudo-color-coded scale, where dark blue represents minimal intensity and pale red represents maximum intensity **(**insets in **D** and **H)**. Growing root hairs were annotated as „long", reaching the length of 200 μm and more at the time of imaging. Image acquisition at the time point 0 min started 28 min and 47 min after probe application in bulge **(A-F)** and „long" root hair **(G-L)**, respectively. **M-O.** Root hair of transgenic line carrying GFP-RHD2 plasmolyzed by 300 mM mannitol **(M)** that was before stained with Amplex Red **(N)**, shown in merged image **(O)**. Scale bar = 10 μm **(A-O)**.

Figure 4. Fluorescence intensity profiles in apical parts of bulges and root hairs after ROS staining with CM-H$_2$DCFDA and CellRox Deep Red. A-D. Mean fluorescence intensity distribution of CM-H$_2$DCFDA measured along a 10 μm line oriented longitudinally at the central part, reaching the apical cell wall (schematically illustrated in Materials and Methods) in bulges **(A)** „short" **(B)** and „long" **(C)** growing root hairs. Mean fluorescence intensities were measured at 0 min, 5 min and 10 min of imaging **(A-C)**. **D.** Differences in

mean fluorescence intensities of CM-H$_2$DCFDA measured during root hair development from
bulges to „long" root hairs. **E-H.** Mean fluorescence intensity distribution of CellRox Deep
Red measured along a 10 µm line oriented longitudinally at the central part, reaching the
apical cell wall in bulges **(E)**, „short" **(F)** and „long" **(G)** growing root hairs. Mean
fluorescence intensities were measured at 0 min, 5 min and 10 min of imaging **(E-G)**. **H.**
Differences in mean fluorescence intensities of CellRox Deep Red measured during root hair
development from bulges to „long" root hairs.

Figure 5. Fluorescence intensity profiles in apical parts of bulges and root hairs after
ROS staining with Amplex Red. A-B. Location of a profile 10 µm long for fluorescence
intensity measurement in the longitudinal direction **(A)** and a profile 8 µm long in a distance
of 5 µm from the apical cell wall for fluorescence intensity measurement in the transversal
direction **(B)**. **C-F.** Mean fluorescence intensity distribution of Amplex Red measured along a
10 µm line oriented longitudinally at the central part, reaching the apical cell wall **(**according
to **A)** in bulges **(C)**, „short" **(D)** and „long" **(E)** growing root hairs. **F.** Differences in mean
fluorescence intensities of Amplex Red measured in longitudinal direction during root hair
development from bulges to „long" root hairs. **G-I.** Mean fluorescence intensity distribution
of Amplex Red measured transversally **(**according to **B)** in „short" **(G)** and „long" **(H)**
growing root hairs. **I.** Differences in mean fluorescence intensities of Amplex Red measured
in transversal direction between „short" and „long" root hairs. Mean fluorescence intensities
were measured at 0 min, 5 min and 10 min of imaging. Scale bar = 10 µm **(A,B)**.

Figure 6. Distribution of ROS after staining with CM-H$_2$DCFDA in bulges of *rhd2-1* and
***der1-3* mutants. A-F.** Bulge in *rhd2-1* mutant illustrated at time points of 0 min **(A,B)**, 5 min
(C,D) and 10 min **(E,F)** of imaging. **G-L.** Bulge in *der1-3* mutant illustrated at time points of
0 min **(G,H)**, 5 min **(I,J)** and 10 min **(K,L)** of imaging. Semi-quantitative fluorescence
intensity distribution in *rhd2-1* mutant **(B,D,F)** and *der1-3* mutant **(H,J,L)** is visualized in a
pseudo-color-coded scale, where dark blue represents minimal intensity and pale red
represents maximum intensity **(**insets in **B** and **H)**. Image acquisition at the time point 0 min
started 101 min and 49 min after probe application in *rhd2-1* mutant and *der1-3* mutant,
respectively. M. Differences in mean fluorescence intensities of CM-H$_2$DCFDA in *rhd2-1* and
der1-3 mutants, and respective Col-0 and C24 wild-types, measured along a 10 µm line
oriented longitudinally at the central part of bulges. Scale bar = 10 µm **(A-L)**.

Figure 7. Distribution of ROS after staining with CellRox Deep Red in bulges of *rhd2-1*
and *der1-3* mutants. A-F. Bulge in *rhd2-1* mutant illustrated at time points of 0 min **(A,B)**, 5
min **(C,D)** and 10 min **(E,F)** of imaging. **G-L.** Bulge in *der1-3* mutant illustrated at time
points of 0 min **(G,H)**, 5 min **(I,J)** and 10 min **(K,L)** of imaging. Semi-quantitative
fluorescence intensity distribution in *rhd2-1* mutant **(B,D,F)** and *der1-3* mutant **(H,J,L)** is
visualized in a pseudo-color-coded scale, where dark blue represents minimal intensity and
pale red represents maximum intensity **(**insets in **B** and **H)**. Image acquisition at the time point
0 min started 74 min and 7 min after probe application in *rhd2-1* mutant and *der1-3* mutant,
respectively. **M.** Differences in mean fluorescence intensities of CellRox Deep Red in *rhd2-1*
and *der1-3* mutants, and respective Col-0 and C24 wild-types, measured along a 10 µm line
oriented longitudinally at the central part of bulges. Scale bar = 10 µm **(A-L)**.

Figure 8. Distribution of ROS after staining with Amplex Red in bulges of *rhd2-1* and *der1-3* mutants. A-F. Bulge in *rhd2-1* mutant illustrated at time points of 0 min **(A,B)**, 5 min **(C,D)** and 10 min **(E,F)** of imaging. **G-L.** Bulge in *der1-3* mutant illustrated at time points of 0 min **(G,H)**, 5 min **(I,J)** and 10 min **(K,L)** of imaging. Semi-quantitative fluorescence intensity distribution in *rhd2-1* mutant **(B,D,F)** and *der1-3* mutant **(H,J,L)** is visualized in a pseudo-color-coded scale, where dark blue represents minimal intensity and pale red represents maximum intensity **(**insets in **B** and **H)**. Image acquisition at the time point 0 min started 5 min and 29 min after probe application in *rhd2-1* mutant and *der1-3* mutant, respectively. **M.** Differences in mean fluorescence intensities of Amplex Red in *rhd2-1* and *der1-3* mutants, and respective Col-0 and C24 wild-types, measured along a 10 µm line oriented longitudinally at the central part of bulges. Scale bar = 10 µm **(A-L)**.

Figure 9. Colocalization analysis of subcellular molecular markers in root hairs with compartments accumulating ROS after staining with CellRox Deep Red. A-C. Colocalization with transgenic line for visualization of vesicular compartments containing GFP-RHD2, a GFP-tagged AtRBOHC/RHD2. **D-F.** Colocalization with transgenic line carrying early endosomal marker GFP-RabA1d. **G-I.** Colocalization with transgenic line carrying late endosomal marker RabF2a-YFP. **J-L.** Colocalization with transgenic line carrying GFP-tagged mitochondria. Overview of root hairs carrying molecular markers (in green) and ROS-accumulating compartments (in magenta) after CellRox Deep Red staining **(A,D,G,J)**. Detailed images of compartments containing carrying molecular markers and ROS **(B,E,H,K)** from the white boxes shown in **(A,D,G,J)**. Fluorescence intensity profiles **(C,F,I,L)** of fluorescence signals of molecular markers (green lines) and ROS-containing compartments (magenta lines) along the interrupted white lines shown in **(B,E,H,K)**. Arrows in **(B,C,E,F,H,I,K,L)** indicate the position of the compartments. Scale bar = 5 µm **(A,D,G,J)**, 1 µm **(B,E,H,K)**.

Figure 10. Colocalization analysis of subcellular molecular markers in root hairs with compartments accumulating ROS after staining with Amplex Red. A-C. Colocalization with transgenic line for visualization of vesicular compartments containing GFP-RHD2, a GFP-tagged AtRBOHC/RHD2. **D-F.** Colocalization with transgenic line carrying early endosomal marker GFP-RabA1d. **G-I.** Colocalization with transgenic line carrying late endosomal marker RabF2a-YFP. **J-L.** Colocalization with transgenic line carrying GFP-tagged mitochondria. Overview of root hairs carrying molecular markers (in green) and ROS-accumulating compartments (in magenta) after Amplex Red staining **(A,D,G,J)**. Detailed images of compartments containing carrying molecular markers and ROS **(B,E,H,K)** from the white boxes shown in **(A,D,G,J)**. Fluorescence intensity profiles **(C,F,I,L)** of fluorescence signals of molecular markers (green lines) and ROS-containing compartments (magenta lines) along the interrupted white lines shown in **(B,E,H,K)**. Arrows in **(B,C,E,F,H,I,K,L)** indicate the position of the compartments. Scale bar = 5 µm **(A,D,G,J)**, 0.5 µm **(B,E,H,K)**.

Figure 11. Model of subcellular ROS localization in root hairs with CM-H$_2$DCFDA, CellRox Deep Red and Amplex Red. CM-H$_2$DCFDA represents a sensitive probe for ROS (mainly H$_2$O$_2$) in the cytoplasm. CellRox Deep Red localizes specifically ROS in mitochondria. Amplex Red serves as a highly sensitive marker for root hair-specific

apoplastic ROS (mainly H_2O_2). In addition, root hairs are able to internalize Amplex Red, which sensitively detects H_2O_2 in mitochondria.

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Figure 1. Distribution of ROS in bulges and root hairs after staining with CM-H$_2$DCFDA. A-F. Developing bulge imaged at time points of 0 min **(A,D)**, 5 min **(B,E)** and 10 min **(C,F)** of growth. **G-L.** Growing root hairs imaged at time points of 0 min **(G,H)**, 5 min **(I,J)** and 10 min **(K,L)**. Semi-quantitative fluorescence intensity distribution **(D-F,H-L)** is visualized in a pseudo-color-coded scale, where dark blue represents minimal intensity and pale red represents maximum intensity (insets in **D** and **H**). Growing root hairs were annotated as „long", reaching the length of 200 μm and more at the time of imaging. Image acquisition at the time point 0 min started 110 min and 154 min after probe application in bulge **(A-F)** and „long" root hair **(G-L)**, respectively. Scale bar = 10 μm **(A-L)**.

Figure 2. Distribution of ROS in bulges and root hairs after staining with CellRox Deep Red. A-F. Developing bulge imaged at time points of 0 min **(A,D)**, 5 min **(B,E)** and 10 min **(C,F)** of growth. **G-L.** Growing root hairs imaged at time points of 0 min **(G,H)**, 5 min **(I,J)** and 10 min **(K,L)**. Semi-quantitative fluorescence intensity distribution **(D-F,H-L)** is visualized in a pseudo-color-coded scale, where dark blue represents minimal intensity and pale red represents maximum intensity (insets in **D** and **H**). Growing root hairs were annotated as „long", reaching the length of 200 μm and more at the time of imaging. Image acquisition at the time point 0 min started 37 min and 47 min after probe application in bulge **(A-F)** and „long" root hair **(G-L)**, respectively. Scale bar = 10 μm **(A-L)**.

Figure 3. Distribution of ROS in bulges and root hairs after staining with Amplex Red. A-F. Developing bulge imaged at time points of 0 min **(A,D)**, 5 min **(B,E)** and 10 min **(C,F)** of growth. **G-L.** Growing root hairs imaged at time points of 0 min **(G,H)**, 5 min **(I,J)** and 10 min **(K,L)**. Semi-quantitative fluorescence intensity distribution **(D-F,H-L)** is visualized in a pseudo-color-coded scale, where dark blue represents minimal intensity and pale red represents maximum intensity (insets in **D** and **H**). Growing root hairs were annotated as „long", reaching the length of 200 µm and more at the time of imaging. Image acquisition at the time point 0 min started 28 min and 47 min after probe application in bulge **(A-F)** and „long" root hair **(G-L)**, respectively. **M-O.** Root hair of transgenic line carrying GFP-RHD2 plasmolyzed by 300 mM mannitol **(M)** that was before stained with Amplex Red **(N)**, shown in merged image **(O)**. Scale bar = 10 µm **(A-O)**.

Figure 4. Fluorescence intensity profiles in apical parts of bulges and root hairs after ROS staining with CM-H$_2$DCFDA and CellRox Deep Red. A-D. Mean fluorescence intensity distribution of CM-H$_2$DCFDA measured along a 10 μm line oriented longitudinally at the central part, reaching the apical cell wall (schematically illustrated in Materials and Methods) in bulges **(A)**, „short" **(B)** and „long" **(C)** growing root hairs. Mean fluorescence intensities were measured at 0 min, 5 min and 10 min of imaging **(A-C)**. **D.** Differences in mean fluorescence intensities of CM-H$_2$DCFDA measured during root hair development from bulges to „long" root hairs. **E-H.** Mean fluorescence intensity distribution of CellRox Deep Red measured along a 10 μm line oriented longitudinally at the central part, reaching the apical cell wall in bulges **(E)** „short" **(F)** and „long" **(G)** growing root hairs. Mean fluorescence intensities were measured at 0 min, 5 min and 10 min of imaging **(E-G)**. **H.** Differences in mean fluorescence intensities of CellRox Deep Red measured during root hair development from bulges to „long" root hairs.

Figure 5. Fluorescence intensity profiles in apical parts of bulges and root hairs after ROS staining with Amplex Red. A-B. Location of a profile 10 μm long for fluorescence intensity measurement in the longitudinal direction **(A)** and a profile 8 μm long in a distance of 5 μm from the apical cell wall for fluorescence intensity measurement in the transversal direction **(B)**. **C-F.** Mean fluorescence intensity distribution of Amplex Red measured along a 10 μm line oriented longitudinally at the central part, reaching the apical cell wall (according to **A**) in bulges **(C)**, „short" **(D)** and „long" **(E)** growing root hairs. **F.** Differences in mean fluorescence intensities of Amplex Red measured in longitudinal direction during root hair development from bulges to „long" root hairs. **G-I.** Mean fluorescence intensity distribution of Amplex Red measured transversally (according to **B**) in „short" **(G)** and „long" **(H)** growing root hairs. **I.** Differences in mean fluorescence intensities of Amplex Red measured in transversal direction between „short" and „long" root hairs. Mean fluorescence intensities were measured at 0 min, 5 min and 10 min of imaging. Scale bar = 10 μm **(A,B)**.

Figure 6. Distribution of ROS after staining with CM-H₂DCFDA in bulges of *rhd2-1* and *der1-3* mutants. A-F. Bulge in *rhd2-1* mutant illustrated at time points of 0 min **(A,B)**, 5 min **(C,D)** and 10 min **(E,F)** of imaging. **G-L.** Bulge in *der1-3* mutant illustrated at time points of 0 min **(G,H)**, 5 min **(I,J)** and 10 min **(K,L)** of imaging. Semi-quantitative fluorescence intensity distribution in *rhd2-1* mutant **(B,D,F)** and *der1-3* mutant **(H,J,L)** is visualized in a pseudo-color-coded scale, where dark blue represents minimal intensity and pale red represents maximum intensity (insets in **B** and **H**). Image acquisition at the time point 0 min started 101 min and 49 min after probe application in *rhd2-1* mutant and *der1-3* mutant, respectively. **M.** Differences in mean fluorescence intensities of CM-H₂DCFDA in *rhd2-1* and *der1-3* mutants, and respective Col-0 and C24 wild-types, measured along a 10 μm line oriented longitudinally at the central part of bulges. Scale bar = 10 μm **(A-L)**.

Figure 7. Distribution of ROS after staining with CellRox Deep Red in bulges of *rhd2-1* and *der1-3* mutants. A-F. Bulge in *rhd2-1* mutant illustrated at time points of 0 min **(A,B)**, 5 min **(C,D)** and 10 min **(E,F)** of imaging. **G-L.** Bulge in *der1-3* mutant illustrated at time points of 0 min **(G,H)**, 5 min **(I,J)** and 10 min **(K,L)** of imaging. Semi-quantitative fluorescence intensity distribution in *rhd2-1* mutant **(B,D,F)** and *der1-3* mutant **(H,J,L)** is visualized in a pseudo-color-coded scale, where dark blue represents minimal intensity and pale red represents maximum intensity (insets in **B** and **H**). Image acquisition at the time point 0 min started 74 min and 7 min after probe application in *rhd2-1* mutant and *der1-3* mutant, respectively. **M.** Differences in mean fluorescence intensities of CellRox Deep Red in *rhd2-1* and *der1-3* mutants, and respective Col-0 and C24 wild-types, measured along a 10 μm line oriented longitudinally at the central part of bulges. Scale bar = 10 μm **(A-L)**.

Figure 8. Distribution of ROS after staining with Amplex Red in bulges of *rhd2-1* and *der1-3* mutants.
A-F. Bulge in *rhd2-1* mutant illustrated at time points of 0 min **(A,B)**, 5 min **(C,D)** and 10 min **(E,F)** of imaging. **G-L.** Bulge in *der1-3* mutant illustrated at time points of 0 min **(G,H)**, 5 min **(I,J)** and 10 min **(K,L)** of imaging. Semi-quantitative fluorescence intensity distribution in *rhd2-1* mutant **(B,D,F)** and *der1-3* mutant **(H,J,L)** is visualized in a pseudo-color-coded scale, where dark blue represents minimal intensity and pale red represents maximum intensity (insets in **B** and **H**). Image acquisition at the time point 0 min started 5 min and 29 min after probe application in *rhd2-1* mutant and *der1-3* mutant, respectively. **M.** Differences in mean fluorescence intensities of Amplex Red in *rhd2-1* and *der1-3* mutants, and respective Col-0 and C24 wild-types, measured along a 10 μm line oriented longitudinally at the central part of bulges. Scale bar = 10 μm **(A-L)**.

Figure 9. Colocalization analysis of subcellular molecular markers in root hairs with compartments accumulating ROS after staining with CellRox Deep Red. A-C. Colocalization with transgenic line for visualization of vesicular compartments containing GFP-RHD2, a GFP-tagged AtRBOHC/RHD2. **D-F.** Colocalization with transgenic line carrying early endosomal marker GFP-RabA1d. **G-I.** Colocalization with transgenic line carrying late endosomal marker RabF2a-YFP. **J-L.** Colocalization with transgenic line carrying GFP-tagged mitochondria. Overview of root hairs carrying molecular markers (in green) and ROS-accumulating compartments (in magenta) after CellRox Deep Red staining **(A,D,G,J)**. Detailed images of compartments containing carrying molecular markers and ROS **(B,E,H,K)** from the white boxes shown in **(A,D,G,J)**. Fluorescence intensity profiles **(C,F,I,L)** of fluorescence signals of molecular markers (green lines) and ROS-containing compartments (magenta lines) along the interrupted white lines shown in **(B,E,H,K)**. Arrows in **(B,C,E,F,H,I,K,L)** indicate the position of the compartments. Scale bar = 5 µm **(A,D,G,J),** 1 µm **(B,E,H,K)**.

Figure 10. Colocalization analysis of subcellular molecular markers in root hairs with compartments accumulating ROS after staining with Amplex Red. A-C. Colocalization with transgenic line for visualization of vesicular compartments containing GFP-RHD2, a GFP-tagged AtRBOHC/RHD2. **D-F.** Colocalization with transgenic line carrying early endosomal marker GFP-RabA1d. **G-I.** Colocalization with transgenic line carrying late endosomal marker RabF2a-YFP. **J-L.** Colocalization with transgenic line carrying GFP-tagged mitochondria. Overview of root hairs carrying molecular markers (in green) and ROS-accumulating compartments (in magenta) after Amplex Red staining **(A,D,G,J)**. Detailed images of compartments containing carrying molecular markers and ROS **(B,E,H,K)** from the white boxes shown in **(A,D,G,J)**. Fluorescence intensity profiles **(C,F,I,L)** of fluorescence signals of molecular markers (green lines) and ROS-containing compartments (magenta lines) along the interrupted white lines shown in **(B,E,H,K)**. Arrows in **(B,C,E,F,H,I,K,L)** indicate the position of the compartments. Scale bar = 5 µm **(A,D,G,J),** 0.5 µm **(B,E,H,K)**.

Figure 11. Model of subcellular ROS localization in root hairs with CM-H$_2$DCFDA, CellRox Deep Red and Amplex Red. CM-H$_2$DCFDA represents a sensitive probe for ROS (mainly H$_2$O$_2$) in the cytoplasm. CellRox Deep Red localizes specifically ROS in mitochondria. Amplex Red serves as a highly sensitive marker for root hair-specific apoplastic ROS (mainly H$_2$O$_2$). In addition, root hairs are able to internalize Amplex Red, which sensitively detects H$_2$O$_2$ in mitochondria.

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