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► **To cite this version:**

Xiaoyun Cui, Avilien Dard, Jean-Philippe Reichheld, Dao-Xiu Zhou. Multifaceted functions of histone deacetylases in stress response. *Trends in Plant Science*, In press, 10.1016/j.tplants.2023.06.006 . hal-04155434

HAL Id: hal-04155434

<https://hal.science/hal-04155434>

Submitted on 7 Jul 2023

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1 Multifaceted functions of histone deacetylases in stress response

2 Xiaoyun Cui¹, Avilien Dard², Jean-Philippe Reichheld², and Dao-Xiu Zhou^{1,3*}

3 ¹Institute of Plant Sciences Paris-Saclay, CNRS, INRA, Université Paris-Saclay, 91405
4 Orsay, France

5 ²Laboratoire Génome et Développement des Plantes, CNRS, Université Perpignan Via
6 Domitia, 66860 Perpignan, France

7 ³National Key Laboratory of Crop Genetic Improvement, Hubei Hongshan Laboratory,
8 Huazhong Agricultural University, 430070 Wuhan, China

9

10 Authors contacts:

11 Xiaoyun Cui (cxyuiaon@hotmail.com) ORCID: 0000-0001-5238-5780

12 Avilien Dard (avilien.dard@psb.vib-ugent.be) ORCID: 0000-0003-0420-7642. Present address:
13 VIB-UGent Center for Plant Systems Biology. Ghent University. Technologiepark-Zwijnaarde 71
14 - 9052 Ghent - Belgium

15 Jean-Philippe Reichheld (jpr@univ-perp.fr) ORCID: 0000-0001-6884-0602

16 *Corresponding author: Dao-Xiu Zhou (dao-xiu.zhou@universite-paris-saclay.fr) ORCID: 0000-
17 0002-1540-0598

18 **Keywords:** Histone deacetylase; Protein lysine acetylation/acylation, Metabolic enzymes,
19 transcription factors, stress granules

20 Glossary

21 **Histone acetylation and deacetylation** are the processes by which histone lysine residues at
22 the N-terminal tail are acetylated or acetylated lysine residues are deacetylated. Lysine
23 acetylation (Kac) is the process where an acetyl group is transferred from the donor molecule
24 acetyl coenzyme A (acetyl-CoA) to a lysine residue. Deacetylation is the reverse reaction where
25 an acetyl group is removed from an acetylated lysine residue generating acetate. These
26 reactions are catalyzed by "histone acetyltransferase" (HAT) and "histone deacetylase" (HDAC)
27 activity, respectively. Histone acetylation marks relaxed chromatin regions and represents an
28 epigenetic mark for gene activation.

29 **Chromatin remodeling** is the dynamic modification of chromatin architecture by ATP-
30 dependent chromatin remodeling proteins complexes. These complexes recognize chromatin
31 modifications such histone acetylation, control chromatin states between relaxation and
32 condensation, and thus regulate gene activity.

33 **Histone lysine acylations** mirror acetylation, but entail histone acylation of histone lysine
34 residues with either short-chain fatty acids, such as malonylation (Kmal), propionylation (Kpr),
35 butyrylation (Kbu), crotonylation (Kcr), β -hydroxybutyrylation (Kbhb), 2-hydroxyisobutyrylation
36 (Khib), or dicarboxylic acids such as succinylation (Ksu). HAT and HDAC are involved in lysine
37 acylation and deacylation.

38 **Post-translational modification (PTM)** is the covalent modification of proteins following protein
39 biosynthesis by ribosomes. As an example, phosphorylation is adding a phosphate to a hydroxyl
40 group of an amino acid residue. Among other types of PTMs are ubiquitination, acetylation or S-
41 nitrosylation. PTMs usually respond to cell signaling and regulate the modified protein function.

42 **Stress granules** are dense aggregations composed of proteins and RNAs that can appear in
43 different cell compartments when the cell is under stress.

44

45 **Abstract**

46 Histone deacetylases (HDAC) are important chromatin regulators essential for plant
47 tolerance to adverse environments. Plants use HDACs as part of diverse strategies to
48 respond to different stresses. In addition to histone deacetylation and epigenetic
49 regulation, HDACs deacetylate non-histone proteins and thereby regulate multiple
50 pathways. Like other post-translational modifications, acetylation/deacetylation is a
51 reversible switch regulating different cellular processes in plants. Here, by focusing on
52 results obtained in arabidopsis and rice plants, we analyze the different aspects of
53 HDAC functions and the underlying regulatory mechanisms in modulating plant
54 responses to stress. We hypothesize that, in addition to epigenetic regulation of gene
55 expression, HDACs can also control plant tolerance to stress by regulating transcription,
56 translation, and metabolic activities and possibly assembly-disassembly of stress
57 granules through lysine deacetylation of non-histone proteins.

58

59 ***HDAC functions beyond histone deacetylation***

60

61 **Histone lysine acetylation (Glossary)** is an important chromatin modification that
62 promotes chromatin decondensation by neutralizing the positive charges of histones.
63 Thus, it weakens histone interactions with the negatively charged DNA, and recruits
64 **chromatin remodeling complexes** to alter chromatin structure [1,2]. **Histone**
65 **acetyltransferases** and **deacetylases (HDAC)** control the dynamic equilibrium of
66 histone acetylation levels, affecting chromatin structures and gene activity [1]. Therefore,
67 like phosphatases/kinases or reductases/oxidases, HDACs/HATs constitute a reversible
68 pair of enzymes regulating post-translational modifications (PTMs) of histone proteins. In
69 addition to acetylation, **histone lysine acylation** involves the addition of diverse short-
70 chain fatty acids as histone marks, which can compete with acetylation and potentially
71 affect gene expression patterns [2]. The different types of acyl-CoA used for histone
72 acylation are derived from multiple primary metabolic pathways [3], which vary greatly in
73 different cell types or in response to adverse environmental conditions. HDAC-regulated
74 histone deacetylation is essential for epigenetic regulation of plant response to diverse
75 environmental stress, which has been reviewed in several papers (e.g. [4-7]). On the
76 other hand, HDACs can also remove the acyl groups from histones and play a role in
77 regulating chromatin structure and gene expression [2]. Recent results indicated that
78 HDACs are involved in multiple stress-responses and that different classes of HDACs
79 may have opposite functions in controlling plant tolerance to stresses by epigenetic
80 regulation of different sets of genes. HDACs were shown to interact with diverse
81 chromatin and transcription factors, or with signaling proteins to target specific genomic
82 loci. In addition, HDAC functions could be regulated by dynamic subcellular localization
83 and posttranslational modifications. Furthermore, function of HDAC-mediated histone
84 deacylation in gene regulation has been documented. Importantly, besides histones,
85 increasing numbers of non-histone proteins have been recognized as substrates for
86 HDACs. In plants, proteomics analysis uncovered hundreds of lysine acetylated proteins
87 that are involved in diverse pathways and processes, and exhibiting different subcellular
88 localizations [8,9]. In this opinion paper, we analyze these new facets of HDAC
89 functioning in arabidopsis (*Arabidopsis thaliana*) and rice (*Oryza sativa*) and discuss the
90 function of HDAC-mediated deacetylation of actors involved in transcription, translation,

91 and metabolic pathways as well as in cellular organization by modulating membrane-
92 less organelles.

93

94 ***Diverse functions of HDACs in stress responses***

95

96 HDACs are highly conserved enzymes in eukaryotes. In arabidopsis, 18 HDACs have
97 been identified, of which 12 belong to the Reduced Potassium Dependency3
98 (RPD3/HDA1) subfamily, 4 belong to the plant-specific HD2 subfamily, and 2 belong to
99 the SIR2 subfamily [10]. The RPD3/HDA1-like HDACs, which are Zn²⁺-dependent, are
100 further divided into three classes (I, II and IV) [11]. All HDAC subfamilies are involved in
101 plant response to diverse stress [4-7], but display agonistic or antagonistic functions in
102 specific stress-responses (**Table 1**). For instance, arabidopsis RPD3/HDA1-like class I
103 and class II HDACs oppositely control plant response to salt stress. Class I *hda19* (or
104 *athd1*) and *hda9* mutants are more tolerant than the wild type to salt stress, whereas
105 class II quadruple mutants (*hda5, 14, 15, 18*) are hypersensitive to salt stress [12-14].
106 HDA9 negatively regulates stress-tolerance by inhibiting DNA-binding activity of
107 WRKY53 that functions as a higher hierarchy transcription activator of stress-responsive
108 genes [14]. An opposite role in drought stress was also detected for class I and class II
109 HDACs. For instance, class II *hda15* mutants displayed a reduced ABA sensitivity and
110 were susceptible to drought stress [15], while class I *hda6* mutants showed a strong
111 drought tolerance [16]. HDA15 suppresses negative regulators of ABA signaling to
112 enhance plant tolerance to drought [15], whereas HDA6 regulates metabolic gene
113 expression for drought stress response [16] (see below). Similarly, class I *hda19* and
114 *hda9* mutants displayed a warm temperature-insensitive phenotype, which is opposite to
115 what observed in class II *hda15* mutants [17]. Likely, the opposite functions between
116 class I and class II HDACs in stress tolerance are based on regulation of distinct cellular
117 pathways and different sets of stress-responsive genes, which may help to balance
118 cellular response to stress. This is supported by the comparative transcriptomic analysis
119 showing that HDA9, HDA19, and HDA15 control a distinct gene expression programs in

120 seedling response to warm (27°C) temperature [17]. HDA15 represses plant response to
121 warm temperature by deacetylating and repressing thermal responsive marker genes,
122 whereas HDA9 and HDA19 promote plant response to elevated temperature likely
123 through repression of metabolic and stress-induced genes, respectively [17]. The
124 opposite functions of class I and II HDACs in plant response to stresses may also
125 involve their distinct stress-sensing mechanisms and specific modes of action (see
126 below).

127
128 In addition to directly regulating stress-responsive genes, HDAC-mediated stress
129 responses may also implicate the regulation of metabolic flux by epigenetic regulation of
130 metabolic gene expression. For instance, HDA15 is shown to repress many primary
131 metabolic genes in response to elevated temperature [17]. Under normal conditions,
132 HDA6 directly bound to and repressed acetate biosynthetic pathway genes encoding
133 pyruvate decarboxylase and acetaldehyde dehydrogenase. However, under drought
134 stress, HDA6 dissociated from the acetate biosynthetic genes, leading to a metabolic
135 flux conversion from glycolysis into acetate synthesis [16], which can be recycled to
136 produce acetyl-CoA, and to support histone acetylation of jasmonate-dependent stress-
137 responsive genes. Moreover, it was shown that SRT1-controlled plant stress response
138 regulated glycolysis through epigenetic repression of several glycolytic genes [18,19]. In
139 addition to histone deacetylation, a few HDACs were also shown to remove different
140 histone acylation marks. For instance, rice SRT2 selectively catalyzes decrotonylation
141 [20], while Arabidopsis HDA6 and HDA9 catalyze histone 2-hydroxyisobutyrylation [21].
142 However, whether HDAC-mediated histone deacylation responds to different metabolic
143 levels and affects histone acetylation and gene expression in stress response remains
144 unclear. The mechanism underlying the selective deacylation by individual HDACs is
145 presently obscure.

146

147 ***Controlling HDAC function in stress response***

148

149 As with most chromatin regulators, HDACs do not have DNA-binding activity. Although
150 the mechanism by which HDACs target to specific genomic loci to undertake histone

151 modification is generally unclear, accumulating results showed that interaction with
152 DNA-binding transcription factors or chromatin regulators appears to be the principal
153 manner for HDAC targeting to downstream genes (**Figure 1**). For instance, class I HDA9
154 interacts with several stress-related transcription factors such as PWR [22], WRKY53
155 [14]; HOS15 [23], HY5 [24], and ABI4 [25]. HDA6 has been shown to interact with
156 diverse proteins including BIN2, FLD, MET1, SUVH, AS1, HSI2, transposase, as well as
157 HD2C [26-31]. Recent results indicated that HD2 proteins are histone chaperones and
158 are present in complexes with RPD3-like HDACs, increasing their histone deacetylation
159 activities by bringing histones and HDACs together [27,32,33]. HDA19 (or AtHD1) was
160 shown to form conserved SIN3-type transcriptional repressor complexes with other
161 proteins to regulate plant response to abiotic stress through histone deacetylation at
162 specific target genes [34,35]. In addition, HDA19 interacts with WRKY38 and WRKY62
163 transcription factors to negatively regulate plant basal response to biotic stress [36].
164 Class II HDA15 was shown to interact with diverse transcription factors (PIF1/3, NF-
165 YCs, HY5, HFR1 and MYB86) to control plant response to stress [17,37-40]. AtSRT1
166 interacts with AtMBP-1 to repress glycolysis and stress tolerance [18]. AtSRT1 and
167 AtSRT2 interact with ENAP1 to negatively regulate ethylene-responsive genes [41]. The
168 diverse interacting protein partners of individual HDACs indicate the versatility of their
169 recruitment to genomic targets and suggest different mechanisms or regulatory
170 networks of the HDAC proteins in controlling stress responses.

171
172 Most plant HDAC proteins are localized in the nucleus, while several HDACs are
173 detected in the cytoplasm, mitochondria, or chloroplasts [42-45] (**Figure 1**). In addition,
174 arabidopsis HD2 members and HDA15 also function in the nucleolus [46,47]. Some
175 HDACs show both cytoplasmic and nuclear localization, the partitioning between the two
176 compartments is likely a regulated process. Dynamic subcellular localization appears to
177 regulate HDAC function or activity. For instance, HDA9 localizes in both cytoplasm and
178 nucleus, but is enriched in the nucleus under heat stress at 37 °C, where the zinc-finger
179 transcription factor YY1 helps to recruit it to target genes and to regulate gene
180 expression by histone deacetylation [48]. HDA15 localizes in the nucleus in the light and
181 in the cytosol in the dark [38], but another study showed that HDA15 is sequestered by

182 PIF3 to repress photosynthesis-related genes [37]. HDA5 was previously reported to
183 reside in the cytoplasm when transiently expressed as a HDA5-YFP fusion protein in
184 arabidopsis cells [43]. However, another report showed that HDA5 could interact with
185 FLD and FVE (or MSI4) in the nucleus [49]. Furthermore, the recent characterization of
186 HDA5 subcellular localization using stable 35S:HDA5-GFP plants revealed its presence
187 in both the nucleus and cytoplasm [50]. A recent study indicated that HDA6 could be
188 exported to the cytoplasm by exportin XPO1A, as the *xpo1a* mutation increased nuclear
189 retention of HDA6, resulting in reduced histone acetylation and enhanced transgene
190 silencing [51]. Furthermore, the analysis of transient expression in tobacco
191 demonstrated that HDA14 exhibits dual localization in both mitochondria and
192 chloroplasts [8]. Thus, subcellular partitioning that can be stress-responsive may control
193 HDAC activities in gene regulation and other cellular pathways.

194
195 As with many cellular proteins, HDAC proteins can be subjected to **post-translational**
196 **modifications (PTMs) (Figure 1)**. It has been shown that HDAC PTMs affect their
197 activity or function and can be regulated by stress. For instance, HDA9 is
198 phosphorylated by an unknown mechanism. Under heat stress, the phosphatase
199 PP2AB β dephosphorylates HDA9 which prevents HDA9 from 26S proteasome-
200 mediated degradation, leading to HDA9 translocating to the nucleus [48]. The
201 phosphorylation status of HDA15 affects its sub-nuclear localization and enzymatic
202 activity [47]. Phosphorylation/dephosphorylation of rice HDT701 that negatively regulate
203 rice immunity is switched in response to *Xanthomonas oryzae pv.oryzae* (*Xoo*) infection
204 [52-54]. S-nitrosylation is an important PTM that affects protein activity. Proteomic data
205 have identified arabidopsis HD2B and HD2C as targets of S-nitrosylation, which might
206 affect their activity [55]. Recently, HDA19 was shown to be modified by S-nitrosylation
207 which is enhanced under stress and promotes its deacetylase activity [56]. However,
208 nitric oxide (NO) treatment increases histone acetylation in the plant [57,58], suggesting
209 that S-nitrosylation is inhibitory for most HDACs catalytic activity. Moreover, HDACs can
210 be subjected to ubiquitination and proteasome degradation, suggesting a regulation of
211 their turnover. For instance, cold induces HD2C degradation mediated by the CULLIN4
212 (CUL4)-based E3 ubiquitin ligase complex [59]. In addition, several rice HDAC proteins

213 are found to be acetylated [60], but the effect of acetylation on the protein activity is not
214 yet studied. Currently, the importance of PTMs as mechanisms to regulate HDAC
215 subcellular localization, catalytic activity, and turnover in response to stress is
216 underestimated.

217

218 ***HDAC functions in deacetylation of non-histone proteins***

219 In addition to its occurrence on histones, lysine acetylation (Kac) is a widespread post-
220 translational modification occurring at a large number of proteins of diverse biological
221 functions in various organisms [1,61]. Kac is modulated by acetyl-CoA availability in the
222 cell and is suggested to have a function in protein activity and/or quality control. In
223 particular, most enzymes of energy metabolism such as glycolysis, tricarboxylic acid
224 (TCA) cycle and photosynthesis, are modified by Kac, and their acetylation status
225 affects enzymatic activities and metabolic flux (e.g. [60,62-64]. Because Kac requires
226 the primary metabolite acetyl-coA, Kac appears to be an additional cellular responsive
227 mechanism that allows plants to acclimate metabolic and cellular activities to the
228 environment. Consistently, recent analysis in arabidopsis roots revealed an alteration of
229 protein lysine acetylation in response to osmotic and salt stress [65]. Homeostasis of
230 non-histone protein Kac that can occur autonomously in cells with high acetyl-CoA
231 levels is also regulated by HATs and HDACs. Several plant HDACs were shown to
232 regulate Kac and activity of proteins involved in diverse cellular pathways including
233 transcription, translation and metabolism (**Figure 1**).

234 **Controlling transcription factor and signaling proteins by lysine deacetylation:**

235 Evidence for HDAC-mediated lysine deacetylation of transcription and signaling proteins
236 is emerging in plants. For instance, HDA6 can deacetylate BIN2 (a repressor of
237 brassinosteroid signaling) at lysine 189 to repress its kinase activity in arabidopsis [29].
238 HDA9 deacetylates and impairs DNA-binding of WRKY53, a stress-responsive
239 transcription factor [14]. In contrast, arabidopsis SRT1 deacetylates and enhances the
240 stability of AtMBP-1, a transcriptional repressor of stress tolerance and glycolytic genes
241 [18]. Similarly, rice SRT1 could deacetylate glyceraldehyde-3-phosphate dehydrogenase
242 (GAPDH) and inhibit its nuclear localization and moonlighting function as a
243 transcriptional activator of glycolytic genes under oxidative stress [19]. Thus, controlling

244 transcription factors activity by lysine deacetylation may represent an additional layer of
245 HDAC-dependent stress-responsive gene regulation. How HDAC senses cellular signals
246 to deacetylate and regulate activity of transcription factors and signal proteins remains
247 unclear.

248 **Controlling metabolic and translational activities by lysine deacetylation:** Kac may
249 affect enzymatic activities and metabolic flux [64], but its effect on most modified
250 proteins is unclear. It appears that KAc inhibits activities of Rubisco, phosphoglycerate
251 kinase and GAPDH in *in vitro* assays [64]. Several plant HDACs have been shown to
252 regulate Kac of metabolic enzymes. Arabidopsis HDA14 located in the chloroplasts,
253 deacetylates many proteins having functions in photosynthesis [8]. In addition, HDA14
254 can deacetylate α -tubulin, associate with α/β -tubulin and is retained on GTP/taxol-
255 stabilized microtubules [44]. Arabidopsis SRT2 was shown to deacetylate inner
256 mitochondrial membrane protein complexes to participate in energy metabolism and
257 metabolite transport [42]. Rice HDA714 and HDA706 function redundantly to maintain
258 Kac homeostasis of a large number of rice proteins, many of which are metabolic
259 enzymes [60]. HDA714 is closely related to Arabidopsis HDA14 but is mainly found in
260 the cytoplasm [60]. Mutation of HDA714 increased Kac of glycolytic and TCA enzymes
261 as well as chloroplast proteins, suggesting a conserved function between HDA714 and
262 AtHDA14. *HDA714* mutants showed lower activity of glycolysis [60], corroborating
263 previous results showing that Kac represses GAPDH enzymatic activity [65]. HDA714-
264 mediated lysine deacetylation of metabolic enzymes may be related to stress tolerance,
265 since the *hda714* mutation reduced rice plant tolerance to submergence stress [60].

266 Interestingly, many ribosomal (r-proteins) and translation proteins are extensively
267 acetylated in rice and many other eukaryotes [60], suggesting that r-protein Kac may be
268 modulated by intracellular acetyl-CoA levels, which provides a possible link between
269 translational regulation and cellular metabolic activity. As cellular acetyl-CoA levels are
270 sensitive to stress, r-protein Kac could connect translational activities to stress
271 response. HDA714 was found to deacetylate r-proteins in rice plants [60]. HDA714 loss-
272 of function increases Kac levels but reduces abundance of r-proteins. Further analysis
273 indicated that the increased Kac of translational proteins resulted in increased ribosome

274 stalling frequency and impaired translation. Thus, HDA714 appears to control
275 translational activity by regulating r-protein stability and ribosome function through lysine
276 deacetylation. Whether HDA714-controlled r-protein Kac is involved in stress response
277 needs further investigation. Nevertheless, the results extend the role of Kac
278 homeostasis mediated by HDACs in gene expression to protein translational regulation,
279 These examples illustrate that HDAC may regulate diverse cellular pathways by
280 deacetylating non-histone proteins. How HDAC activities towards non-histone protein
281 are controlled await further investigation.

282

283 ***Do plant HDACs function in Stress Granules?***

284 **Stress granules** (SGs) are inducible and reversible membraneless biomolecular
285 condensates and are assembled via liquid-liquid phase separation (LLPS) upon
286 induction by a variety of endogenous and exogenous stresses [66-68]. In general, SGs
287 are disassembled during the recovery from the stress condition, allowing the restoration
288 of active translation [67]. Consistently, SGs contain translationally stalled mRNA,
289 translation inhibition factors, and RNA binding proteins (RBPs), but also HSPs and other
290 stress-related proteins [69,70]. In plants, SGs form in response to diverse stress
291 including heat, hypoxia, high salt, and darkness as well as hormone treatment or
292 metabolic inhibition [71-74]. Several RBPs have been identified as integral components
293 of plant SGs [70], and undergo phase separation to promote plant survival in response
294 to heat stress [75]. While SG has been largely documented in the cytosol, recent works
295 described formation of chloroplastic SG (cpSG) under heat stress, in which RNA-binding
296 proteins, ATPases, chaperones, as well as a magnesium chelatase complex, involved in
297 photosynthetic acclimation to stress was found [76].

298 LLPS is often triggered by proteins with intrinsically disordered regions (IDRs) and/or
299 prion-like domains that induce the aggregation of complex proteins or protein-RNA
300 networks, such as SGs. According to the "stickers-and-spacers" model, oligomerization
301 and condensation is promoted by protein domains called stickers which serve as
302 adhesion drivers, while the spacers that connect the stickers dictate solvent/protein

303 interactions [77]. PTMs like phosphorylation, can alter the phase separation threshold of
304 IDRs by changing the charge and hydrophobicity of amino acids, and thus are
305 recognized as important regulators for condensate formation [78]. For example, Gle1, a
306 crucial regulator of translation during stress, undergoes phosphorylation by MAPKs and
307 GSK3. When Gle1 is phosphorylated, it hinders the assembly of SGs and facilitates their
308 disassembly [79]. Recently, phase separation has been shown to be regulated by
309 oxidoreduction. In arabidopsis, cysteine residues within the TERMINATING FLOWER
310 (TMF) transcription factor sense cellular redox to form disulfide bonds that concatenate
311 multiple TMF molecules and elevate the amount of intrinsically disordered regions to
312 drive phase separation. This enables TMF to bind and sequester the promoter of a floral
313 identity gene *ANANTHA* to repress its expression [79]. Among all PTMs, most of lysine
314 acetylations has a negative effect on phase separation, and appears to play a pivotal
315 role in inhibiting stress granules assembly [80]. During the dynamics of stress granules
316 (SGs), the modification of lysine 376 residue in the RNA-binding domain of G3BP1 is
317 under the regulation of HDAC6 and CBP/p300. When G3BP1 undergoes acetylation, it
318 negatively affects its ability to bind RNA and interact with other components, thereby
319 promoting the disassembly of SG [81]. It was shown that the mammalian histone
320 deacetylase HDAC6 participates in and is required for the formation of SGs during
321 stress response [82]. Additionally, acetylation of IDR inhibits protein phase separation
322 and SGs assembly and HDAC6 deacetylates IDRs, promoting SG assembly [83]. The
323 acetylation of the intrinsically disordered region (IDR) of DDX3X, which is a component
324 of SGs, hinders the formation of SGs [82] [83]. Plant homologs of G3BP-1 and DDX3
325 are shown to function in SGs, although no evidence of lysine acetylation has been
326 explored yet [84,85].

327 Interestingly, many plant cytosolic or chloroplastic SG proteins show lysine acetylation
328 (**Table 2 and 3**), suggesting that this PTM may also play an important role in SGs in
329 plant cells. For instance, a HDAC-dependent partitioning of ethylene metabolic proteins
330 into stress granules might contribute to balance growth and stress responses. No plant
331 HDAC has been identified yet in SG. However, several plant HDACs localize in the
332 cytoplasm and in chloroplasts and contain IDRs [11]. Among them, class II HDA14 and

333 HDA15, the closest Arabidopsis homologs of HsHDAC6, and class I HDA6, 7, 9 and 19
334 harbor IDR both at N- and C-terminal ends. Particularly, the C-terminal IDR is conserved
335 in the green lineage [11] and is also present in mammalian HDAC2 in which it induces
336 phase separation *in vitro* [86]. Therefore, HDACs may be potentially implicated in plant
337 SG formation under stress (**Figure 1**). This is particularly compelling for rice HDA714, as
338 it targets many translational initiation/elongation proteins, r-proteins, and HSPs as well
339 as metabolic enzymes for deacetylation in the cytoplasm [60]. Whether HDA714 is
340 involved in SG dynamics awaits further investigation.

341

342 ***Concluding remarks and future perspectives***

343

344 Accumulating evidence indicates that HDACs are essential regulators of plant response
345 and adaption to adverse environmental conditions. Although HDACs act primarily
346 through epigenetic regulation of stress-responsive genes by mediating histone
347 acetylation/deacetylation, increasing data indicate that HDACs are also implicated in the
348 control of additional cellular processes including metabolism, hormone signaling,
349 microtubule, transcription, ribosomal biogenesis, and translation to modulate plant stress
350 tolerance. It appears that some HDACs are specialized to control lysine acetylation of
351 non-histone proteins in the cytoplasm and/or organelles, while others have a more
352 polyvalent function in both cytoplasm and nucleus. Several HDACs are involved in
353 multiple stress pathways and some HDACs respond to and regulate plant response to
354 the same stress, sometimes with opposing functions. This functional versatility of
355 HDACs in plant stress responses is mysterious. Whether or how the function of different
356 HDACs is coordinated in the nucleus and/or in the cytoplasm awaits further investigation
357 (**Outstanding Questions**). Although HDAC gene expression *per se* may be responsive
358 to stress, posttranslational modification, protein interaction and subcellular partitioning
359 are likely the principal way to control HDAC activity in plant response to stress. Whether
360 and how stress signals regulate HDAC PTMs, protein interaction and/or subcellular
361 localization remains largely unclear. Stress can trigger metabolic flux conversions, while

362 metabolic activity controls plant adaptation to stress, which partly relies on epigenetic
363 regulation of gene expression. How HDACs sense metabolic changes and precisely
364 coordinate metabolic activity to gene expression in specific cell types are challenging
365 questions to be answered in the future. The function of HDAC in SG dynamics in plant
366 cells remains to be studied. Several HDACs (e.g., HDA6, HDA9, HDA19, SRT1 as well
367 as HD2 members) negatively regulate plant immunity and tolerance to heat/salt stress.
368 Engineering these HDACs or identifying natural inhibitory products targeting specifically
369 these HDACs would represent an alternative approach to enhance plant/crop stress
370 tolerance in the global warming era.

371

372 **Acknowledgements**

373 This work was supported by the French Agence Nationale de la recherche (ANR-19-CE12-0027-
374 01).

375

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581 **Figure legend**

582 **Figure 1.** Multiple modes of action of HDACs in regulating plant stress responses. HDACs
583 localize in the different cellular compartments. Subcellular partitioning and/or posttranslational
584 modifications (such as phosphorylation in red and S-nitrosylation in blue) of HDACs can be
585 regulated by diverse stresses (arrows). In the nucleus, members of all HDAC families
586 HDA5/HDA15; HDA6/HDA9/HDA19; HD2A/HD2C/HD2D; HDA701/HDA710 and SRT1/OsSRT2)
587 can be recruited to chromatin by interacting with transcription factors (TFs) and/or chromatin
588 proteins to deacetylate histones for gene repression. In addition, some HDACs (such as HDA6
589 and OsSRT2) also remove acyl groups from histones. Besides the histone
590 deacetylation/deacylation function, HDACs can also deacetylate non-histone proteins such as
591 TFs and signaling proteins. (i.e. HDA6 deacetylates BIN2, HDA9 deacetylates WRKY53, and
592 SRT1 deacetylates GAPDH and AtMBP-1). In the cytoplasm, HDACs regulate lysine acetylation
593 of glycolytic enzymes, microtubules, ribosomal and translational proteins in the cytosol,
594 photosynthetic proteins in chloroplasts, and tricarboxylic acid cycle (TCA) enzymes and
595 membrane proteins in mitochondria. A function of HDACs in stress granule assembly and
596 disassembly is highly possible.

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601 Table 1. Stress functions of HDACs in arabidopsis and rice.

Classes	Arabidopsis Gene	ID	Rice Gene	ID	Functions in stress
Class I RPD3/HDA1 homologs	AtHDA6	At5g63110	OsHDA705	Os08g25570	<i>Athda6</i> mutant is drought tolerant [16], but shows impaired tolerance to heat stress [87]; AtHDA6 regulates scrotomorphogenesis [29]
	AtHDA7	At5g35600			
	AtHDA9	At3g44680	OsHDA711	Os04g33480	<i>Athda9</i> mutant is insensitive to NaCl and polyethylene glycol (PEG) [13]; <i>Athda9</i> mutant shows impaired warm temperature-response [17]; AtHDA9 represses thermotolerance responses [48]
	AtHDA19	At4g38130	OsHDA702 OsHDA703 OsHDA710	Os06g38470 Os02g12350 Os02g12380	<i>Athda19</i> mutant is insensitive to NaCl and polyethylene glycol (PEG); <i>Athda19</i> mutant is salt stress tolerant [12]; <i>hda19</i> mutant shows impaired warm temperature-response [17]; AtHDA19 negatively regulates plant basal defense responses [36] OsHDA710 is required for salt stress tolerance and ABA signaling in rice[88]
			OsHDA701	Os01g40400	OsHDA701 reduces defense gene activation [89]
	AtHDA10	At3g44660			
	AtHDA17	At3g44490			
Class II RPD3/HDA1 homologs	AtHDA5	At5g61060	OsHDA713	Os07g41090	<i>hda5 hda14 hda15 hda18</i> quadruple mutant is hypersensitive to salt stress [12]
	AtHDA8	At1g08460	OsHDA712 OsHDA716	Os05g36920	
	AtHDA14	At4g33470	OsHDA714	Os05g36930 Os12g08220	OsHDA714 represses glycolysis under stress. <i>Oshda714</i> mutant seed germination rates is reduced under water (submergence) stress [60]
	AtHDA15	At3g18520	OsHDA704	Os07g06980	<i>Athda15</i> mutant is insensitive to ABA, susceptible to drought stress but hyposensitive to salinity during seed germination [15] and [90] Tu et al 2022; AtHDA15 overexpression confers salt stress resistance [91]. <i>Athda15</i> mutant shows enhanced warm temperature-response [17]; AtHDA15 regulates responses to light [39]. HDA15 is involved in FR light-regulated hypocotyl elongation [92].
	AtHDA18	At5g61070			
Class III Sir2 homologs	AtSRT1	At5g55760	OsSRT1	Os04g20270	AtSIRT1 has negative function in salt stress and exogenous ABA response [18]; OsSIRT1 is regulates oxidative stress adaptation and represses glycolysis in rice [93,19]
	AtSRT2	At5g09230	OsSRT2	Os12g07950	OsSRT2 is involved in the removal of Kcr.[20]

Class VI RPD3/HDA1 homologs	AtHDA2	At5g26040	OsHDA706	Os06g37420	HDA706 deacetylates non-histone proteins [60]
Plant-specific HD2	AtHD2A	At3g44750	OsHDT1	Os05g51830	OsHDT1 controls plant immunity [52]
	AtHD2B	At5g22649			
	AtHD2C	At5g03740			AtHD2C is involved in drought stress [94] and heat stress responses [95]; cold induces AtHD2C degradation [96,59]
	AtHD2D	At2g27840			AtHD2D is involved in drought stress response [97,96]

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605 Table 2. List of arabidopsis cytosol SG proteins with lysine-acetylation identified.

Protein ID	Name	Function	Localization	Acetylated Lysine	Putative IDR
AT1G09780	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	Metabolism	cytosol	236,238,402, 463	1-15
AT1G12010	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily	Ethylene Metabolism	peroxisome	63	307-320
AT1G62380	ACO2, ATACO2 ACC oxidase 2	Ethylene Metabolism	golgi	68	308-320
AT1G62390	Phox2 Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein	Other	nucleus	80, 160,328	1-35, 183-285, 442, 626-676, 751
AT1G63000	NRS/ER, UER1 nucleotide-rhamnose synthase/epimerase-reductase	Rhamnose metabolism	cytosol	179, 263	1-12
AT1G78570	RHM1, ROL1, ATRHM1 rhamnose biosynthesis 1	Rhamnose metabolism	cytosol	49, 290, 551	354-379
AT2G01520	MLP328 MLP-like protein 328	Lipid Binding [putative]	cytosol	15, 136	-
AT2G23350	PAB4, PABP4 poly(A) binding protein 4	RNA	cytosol	130, 131, 139, 216, 334	1-42, 120-133, 253, 302-323, 456, 634-662
AT2G25450	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	Glucosinolate Metabolism	golgi	23,322	-
AT2G42520	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Other	nucleus	390	1-140, 556-600
AT2G45220	Plant invertase/pectin methyl esterase inhibitor superfamily	Pathogen Response	extracellular	373	1-26
AT3G01290	SPFH/Band 7/PHB domain-containing membrane-associated protein family	Pathogen Response	plasma membrane	78, 178	-
AT3G26450	Polyketide cyclase/dehydrase and lipid transport superfamily	Lipid Binding [putative]	cytosol	15, 117	-
AT3G45640	ATMPK3, MPK3, ATMAPK3 mitogen-activated protein kinase 3	Signaling/Regulation	cytosol	69	1-14
AT3G48750	CDKA;1, CDC2AAT, CDK2, CDC, CDC2A, CDKA1 cell division control 2	Signaling/Regulation	cytosol	32, 66	-
AT4G23670	Polyketide cyclase/dehydrase and lipid transport superfamily protein	Lipid Binding [putative]	cytosol	15, 74, 78, 116, 139	-
AT4G23680	Polyketide cyclase/dehydrase and lipid transport superfamily protein	Lipid Binding [putative]	cytosol	116, 136, 139	-
AT4G27500	PPI1 proton pump interactor 1	Transport	endoplasmic reticulum	57, 148, 356, 428, 442	1-70, 154-176, 612
AT4G34110	PAB2, PABP2, ATPAB2 poly(A) binding protein 2	RNA	cytosol	324	1-33, 116-135, 251, 291-313, 354, 615-629
AT4G34870	ROC5, ATCYP1 rotamase cyclophilin 5	Protein Folding	cytosol	49, 78, 96, 142, 147, 151	-
AT4G39520	GTP-binding protein-related	Signaling/Regulation	cytosol	49	44-56
AT5G19510	Translation elongation factor EF1B/ribosomal protein S6 family protein	Translation	cytosol	132	88-131
AT5G20890	TCP-1/cpn60 chaperonin family protein	Protein Folding	cytosol	145	518-527
AT5G59420	ORP3C OSBP (oxysterol binding protein)-related protein 3C	Lipid Binding [putative]	cytosol	369	1-62, 429-439
AT3G44890	Ribosomal protein L9	Translation	cytosol	98, 158	1-34
AT4G01310	Ribosomal L5P family protein	Translation	cytosol	67, 76, 111, 114	1-47, 245-262
AT3G25920	Ribosomal protein L15	Translation	cytosol	217, 247, 254, 260	1-74, 240-277
AT3G54210	Ribosomal protein L17 family protein	Translation	cytosol	118, 125	1-63
AT3G59400	Protein GENOMES UNCOUPLED 4	Signaling	cytosol	248	1-74, 233-260
AT5G55280	Homolog of bacterial cytokinesis Z-ring protein FTSZ 1-1	Protein binding	cytosol	416	1-66, 385-433
AT5G64050	Glutamate tRNA synthetase	Protein/tRNA binding	cytosol	211, 215, 356, 378, 485, 494	1-51, 557-570
AT2G42220	Rhodanese/Cell cycle control phosphatase superfamily protein	Metabolism	cytosol	73, 123, 129	1-38
AT4G31500	Cytochrome P450, family 83, subfamily B, polypeptide 1	Pathogen response	endoplasmic reticulum	190, 489	1-23, 257-270
AT1G78370	Glutathione S-transferase TAU 20	Glutathione metabolism	cytosol, nucleus	25, 47, 118, 125, 193	-

606 Data of lysine-acetylated proteins were retrieved from [98] and the list of SGs-proteins was from
 607 [70]. IDR prediction were performed using DISOPRED3 [99]. <http://bioinf.cs.ucl.ac.uk/psipred/>

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609 Table 3. List of arabidopsis plastidial SG proteins with lysine-acetylation identified.

Protein ID	Name	Function	Localization	Acetylated Lysine	Putative IDR
AT1G08520	ALBINA 1	Chlorophyll metabolism	chloroplast	487, 692	1-76, 402-497
AT1G74470	Pyridine nucleotide-disulfide oxidoreductase family protein	Chlorophyll metabolism	chloroplast	137, 383, 423	1-52, 460-467
AT5G55220	trigger factor type chaperone family protein	RNA	chloroplast	162, 221, 254, 382, 476, 532	1-49
AT4G18480	P-loop containing nucleoside triphosphate hydrolases superfamily	Chlorophyll metabolism	chloroplast	122, 308, 374	1-81
AT1G56050	GTP-binding protein-like protein	Metabolism	chloroplast, nucleus	131, 216	1-46
AT2G37660	NAD(P)-binding Rossmann-fold superfamily protein	Rhamnose metabolism	chloroplast	246, 252, 303, 306	1-74
AT5G46580	Pentatricopeptide (PPR) repeat-containing protein	rRNA processing	chloroplast	634	-
AT4G28750	Photosystem I reaction centre subunit IV / PsaE protein	Photosynthesis	chloroplast, plastid	67, 93, 98, 99, 111	1-83
AT5G23020	2-isopropylmalate synthase 2	Glucosinolate Metabolism	chloroplast	217	1-66, 493-503
AT1G76080	Chloroplastic drought-induced stress protein of 32 kD	Pathogen response, heat acclimation	chloroplast	78, 147, 150	1-68
AT4G15560	Deoxyxylulose-5-phosphate synthase	Protein binding	chloroplast	166	1-55
AT1G78630	Ribosomal protein L13 family protein	mRNA binding	plastid	197	1-51
AT5G47890	NADH-ubiquinone oxidoreductase B8 subunit	Unknown	plastid	5, 85	-

610 Data of lysine-acetylated proteins were retrieved from [98] and the list of SGs-proteins was from
 611 [76]. IDR prediction were performed using DISOPRED3 [99]. <http://bioinf.cs.ucl.ac.uk/psipred/>

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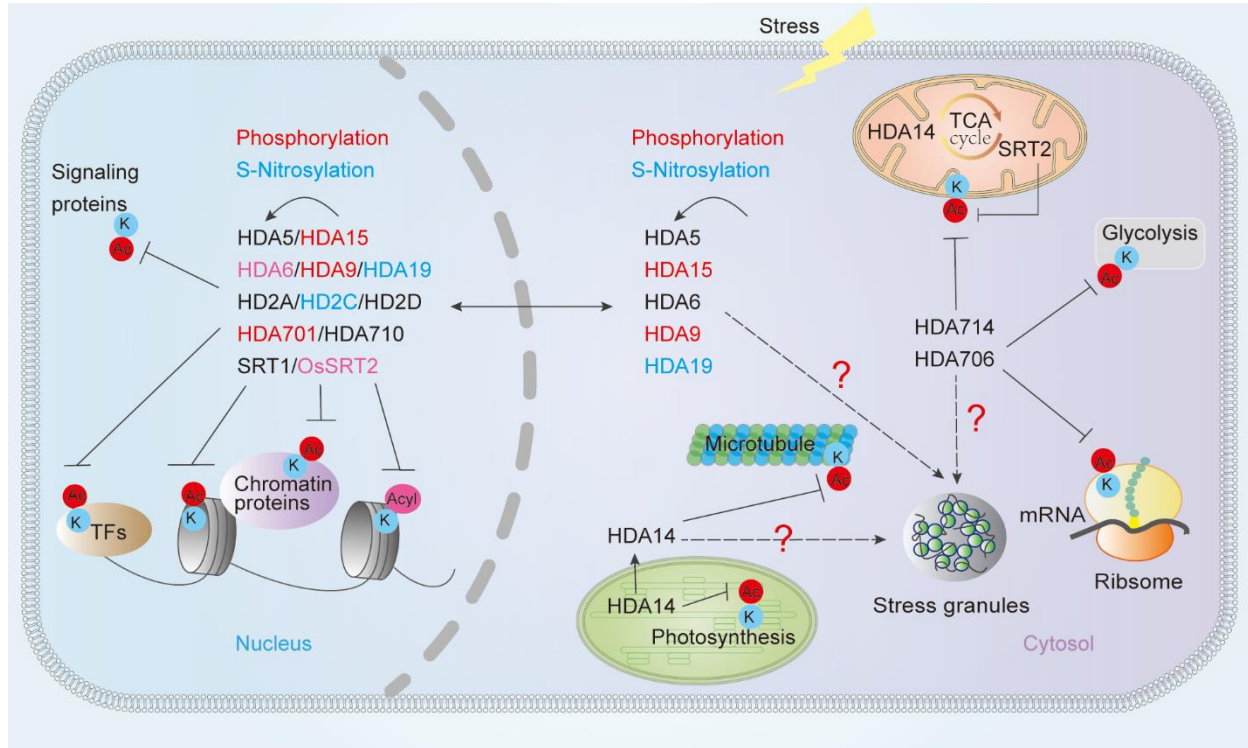
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622 Figure 1

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