Research progress of aldehyde oxidases in plants

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Plant aldehyde oxidases (AOs) are multi-functional enzymes, and they could oxidize abscisic aldehyde into ABA (abscisic acid) or indole acetaldehyde into IAA (indoleacetic acid) as the last step, respectively. AOs can be divided into four groups based on their biochemical and physiological functions. In this review, we summarized the recent studies about AOs in plants including the motif information, biochemical, and physiological functions. Besides their role in phytohormones biosynthesis and stress response, AOs could also involve in reactive oxygen species homeostasis, aldehyde detoxification and stress tolerance.

1 **Research progress of aldehyde oxidases in plants**

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10 **Abstract**

11   Plant aldehyde oxidases (AOs) are multi-functional enzymes, and they could oxidize

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13 as the last step, respectively. AOs can be divided into four groups based on their biochemical and

14 physiological functions. In this review, we summarized the recent studies about AOs in plants

15 including the motif information, biochemical, and physiological functions. Besides their role in

16 phytohormones biosynthesis and stress response, AOs could also involve in reactive oxygen

17 species homeostasis, aldehyde detoxification and stress tolerance.

18 **Keywords:** aldehyde oxidases, abscisic acid, indoleacetic acid, stress

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Introduction

32   Abscisic acid (ABA) acts as a ubiquitous signal that regulates diverse processes and plant

33   responses, including seed maturation/germination, dormancy, leaf senescence, stomatal aperture,

34   apical dominance, and the regulation of phototropic and gravitropic behaviour, as well as

35   adaptation to a variety of environmental stresses, such as drought and salinity (Verslues et al.,

36   2005; Normanly et al., 1995; Merlot and Giraudat, 1997; Srivastava et al., 2017).

37   ABA biosynthetic genes and enzymes have been identified in various plants species (Taylor

38   et al, 2000; Milborrow, 2001; Seo and Koshiba, 2002; Nambara and Marion-Poll, 2005). ABA

39   synthesis starts from C40 epoxycarotenoids that derived from isopentenyl diphosphate in

40   methylerythritol phosphate pathway. Zeaxanthin epoxidase (ZEP) is responsible for catalyzing

41   the two-step epoxidation of all-trans-zeaxanthin to all-trans-violaxanthin (Finkelstein et al., 2013;

42   Marin et al., 1996; Audran et al., 1998, 2001; Xiong et al., 2002). The latter is then converted

43   into the cis-isomers of neoxanthin and violaxanthin, which are cleaved by a 9-cis-

44   epoxycarotenoid dioxygenase (NCED) to its direct precursor, xanthoxin (Schwartz et al., 1997;

45   Qin et al., 1999), and this oxidative cleavage process is a key rate-limiting step for ABA

46   biosynthesis (Estrada-Melo et al., 2015). Conversion of xanthoxin to abscisic aldehyde is

47   catalyzed by a short-chain dehydrogenase/reductase (SDR) (Cheng et al.,2002; González-

48   Guzmán et al.,2002), and aldehyde oxidases (AOs; EC 1.2.3.1) oxidize abscisic aldehyde into

49   ABA as the final step (Seo et al., 2000 a, b; Barrero et al., 2006; Melhorn et al., 2008; Ando et al.,

50   2006). Pathway for ABA biosynthesis was summarized in Figure 1A.

51   AOs are widespread cytosolic molybdo-iron-flavo enzymes that oxidize a variety of

52   aldehydes to their corresponding carboxylic acids (Koshiba et al., 1996; Ori et al., 1997; Seo et

53   al., 1998, 2000a, 2000b; Garattini et al., 2008; Zdunek-Zastocka, 2008). Except involved in ABA

54   synthesis, AO enzyme could also oxidize indole acetaldehyde into indoleacetic acid (IAA, most

55   important form of auxin). Though the tryptophan (Trp)-independent pathway has been proposed

56   for IAA biosynthesis alternatively, Trp-dependent pathway is the main one including four

58   proposed pathways for IAA biosynthesis in plants: (I) indole-3-acetaldoxime (IAOx) pathway,

59   (II) the indole-3-pyruvic acid (IPA) pathway, (III) tryptamine (TAM) pathway, and (IV) the

60   indole-3-acetamide (IAM) pathway. Based on evolutionarily conserved core mechanisms, it is

61   thought that the pathway via IAM or IPA are the major route(s) to IAA in plants (Mano et al.,

62   2012). AO is responsible for the final step of IPA pathway in auxin biosynthesis (Figure 1B).

63   Auxin is deeply implicated in most aspects of plant growth and development, and the detail of

64   AO in IAA production will discuss in the part of aldehyde oxidase 1 later.

65   The nucleotide and amino acid of the AO multigene family shares high similarity with

66   xanthine dehydrogenase (XDH), and AO is likely derived from XDH by gene duplication and

67   neofunctionalization, though their function could be divergent. Both AO and XDH comprise

68   FAD, Fe-S, and molybdenum cofactor (Moco) as prosthetic groups (Koshiba et al., 1996; Hille et

69   al. 2011). However, different physiological electron acceptors distinguish AO and XDH enzymes:

70   AO enzymes does not contain NAD-binding site, and AO can exclusively use molecular oxygen

71   as a physiological electron acceptor and XDH use NAD^+ as the final electron acceptor (Nishino,

72   1989; Turner et al., 1995).

73   Plants AOs catalyze the oxidation a variety of different aromatic and aliphatic aldehydes

74   (Zdunek et al., 2004). The conversion of abscisic aldehyde to ABA and indole acetaldehyde into

75   indoleacetic acid by AOs, respectively, may constitute important regulatory element; however,

76   its regulatory role is still being debated and we summarize the biochemical and physiological

77   function of AO1, AO2, AO3, and AO4.

78   **Survey Methodology**

79   Primary and secondary literature relevant to the topic of this paper was assessed using Web

80   of Science (Clarivate Analytics). Key words such as "aldehyde oxidase," "abscisic acid,"

81   "indoleacetic acid," "plants" and "stress," were searched between 1 March and 31 October, 2021.

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83   The information of stress induced genes, interaction proteins and function predictions were

84   generated with the interaction viewer at bar.utoronto.ca/eplant by Waese et al. 2017. The detail

85   experiment information can be found on this website. Take AO1 gene (AT5G20960) in

86   *Arabidopsis* as an example, search the gene number, and choose Abiotic Stress II eFP, and we

87   could find the total RNA and polysomal mRNA upregulated after hypoxia stress.

Biochemical and physiological function of AO1

89   Plant AOs have been studied from several sources, including oat (*Avena sativa*) coleoptiles

90   (Rajagopal, 1971), potato tubers (Rothe, 1974), cucumber (*Cucumis sativus*) seedlings (Bower et

91   al., 1978), pea seedlings (Miyata et al., 1981; Zdunek-Zastocka, 2010), and maize (*Zea mays* L.)

92   coleoptiles (Koshiba et al., 1996). Both animal and plant AOs possess relatively wide substrate

93   specificity and can oxidize a number of different aldehydes, and this trait indicates that AOs have

94   different biological roles (Koshiba et al., 1996; Ori et al., 1997; Akaba et al., 1999; Omarov et al.,

95   1999; Koiwai et al., 2000, 2004; Seo et al., 2000a; Ibdah et al., 2009). AO isoforms have been

96   largely characterized in *Arabidopsis*, and the AO gene family consists of at least four aldehyde

97   oxidase genes, AO1–AO4 by forming homodimers and heterodimers (Akaba et al., 1999; Koiwai

98   et al., 2000, 2004; Seo et al., 2000a; Zdunek-Zastocka et al., 2004).

99   In *Arabidopsis* AOα (homodimers of AAO1) showed a relatively high efficiency for indole-

100   3-acetaldehyde, a precursor of IAA and it indicates AOα is a possible candidate aldehyde

101   oxidase for IAA biosynthesis, and this activity is higher in IAA-overproducing *sur1* mutant

102   seedlings (Akaba et al., 1999; Seo et al., 1998). The study of AO in maize also confirms its role

103   in IAA biosynthesis (Koshiba et al., 1996; Sekimoto et al., 1997). Fedorova et al (2005)

104   proposed that the local synthesis of IAA in the root nodule meristem and the modulation of AO

105   expression and activity are involved in the regulation of *Lupinus albus* and *Medicago truncatula*

106   nodule development. Two isoforms, BrAO-a, and BrAO-d, were suggested to be involved in

107   auxin overproduction during clubroot development induced by pathogen infection in Chinese

108   cabbage (Ando et al., 2006). In *Arabidopsis*, the expression patterns of AO1 are tissue specific

109   and are expressed predominantly in seedlings, roots, and seeds.

110   Based on the publicly available microarray data (http://bar.utoronto.ca/eplant/, Kilian et al.,

111   2007), we can predict AO1 might be involved in hypoxia response in *Arabidopsis* because it was

112   induced significantly by hypoxia stress. Waterlogging or flooding is one of the main abiotic

113   stresses that limit crops production and deficiency of oxygen is the main reason responsible for

114   the damages caused by waterlogging or flooding stress, and according to the extent of lack of

115   oxygen, it can be divided into anoxia (nearly no oxygen) or hypoxia (low oxygen). In most cases,

116   waterlogging or flooding stress cause hypoxia conditions and it is detrimental to plants due to the

117   energy crisis caused by aerobic respiration to anaerobic respiration and the accumulation of toxic

118   substances (Xu et al., 2020).

119   **Biochemical and physiological function of AO2**

120   AO2 is highly expressed in hypocotyls, seedlings, roots and senescing leaves. In

121   *Arabidopsis*, AO2 homodimers have a strong preference for 1-naphthaldehyde as a substrate,

122   which is oxidized to 1-naphthyl acetic acid, whereas the AO1/AO2 heterodimer has a preference

123   for indole-3-acetaldehyde and 1-naphthyl acetic acid (Akaba et al., 1999). The deduced amino

124   acid sequence of aldehyde oxidase 2 (AhAO2) in *Arachis hypogaea* L. showed high similarity

125   with other plant AOs. *AhAO2* was dominantly expressed in leaves, and its transcript level was

126   greatly increased under exogenous ABA application; overexpression of *AhAO2* in *Arabidopsis*

127   led to improved ABA levels and drought tolerance after drought treatment (Yang et al., 2011).

128   ZmAO-2 in maize was expressed at a higher level in coleoptiles than in roots (Sekimoto et al.,

129   1997).

130   From the prediction of the website, AtAO2 in *Arabidopsis* (AT3G43600) could interact

131   with two proteins (gene number: AT1G19730 and AT5G42980) which are belong to thioredoxin

132   superfamily and it indicates AO2 might involve in redox reaction.

133   **Biochemical and physiological function of AO3**

134   Among the AOs, AO3 has gained great attention owing to its possible involvement in ABA

135   biosynthesis and its importance under normal and stress conditions (Seo et al., 2000a, 2000b;

136   González-Guzmán et al., 2004). The AO3 gene can efficiently catalyse the final step in ABA

137   synthesis in *Arabidopsis* leaves (Seo et al., 2000b) and seeds (González Guzmán et al., 2004), in

138   barley roots (Omarov et al., 2003), and in pea plant leaves and roots (Zdunek-Zastocka et al.,

139   2004).

140   AO3 is mainly localized in vegetative organs such as the vascular tissues of roots,

141   hypocotyls as well as leaves and is also slightly expressed within guard cells and surrounding

142   cells (Koiwai et al., 2004; Nambara et al., 2005). Rice *OsAO3* was expressed in germinated seeds,

143   roots, leaves, and floral organs, particularly in vascular tissues and guard cells, and its expression

144   was significantly induced by exogenous ABA and mannitol treatment. The *osao3* mutant

145   accumulated less ABA and exhibited earlier seed germination, increased seedling growth and

146   grain yield, and decreased drought tolerance than the wild-type, and *OsAO3*-overexpressing lines

147   exhibited the opposite phenotype. Mutation and overexpression of OsAO3 increased and

148   decreased grain yield, respectively, by affecting panicle number per plant, spikelet number per

149   panicle, and spikelet fertility (Shi et al., 2021).

150   In *Arabidopsis*, AO3 mRNA is mainly expressed and most AOd enzyme activity is detected

151   in rosette leaves. The *ao3-1* mutant exhibited a wilted phenotype under normal conditions,

152   reduced ABA levels accompanied by excessive water loss and retarded vegetative growth and

153   reduced stress tolerance, but this mutant showed a less prominent dormancy-associated

154   phenotype in seeds compared with *aba3-2*, with impaired function of all AOs due to the

155   dysfunction of Moco (Seo et al., 2000b; González-Guzmán et al., 2004). These findings

156   indicated that AOd is involved in ABA biosynthesis in leaves and that other aldehyde oxidases

157   are involved in ABA biosynthesis in other organs, such as roots, silique, and seeds (Seo et al.,

158   2004). Consistently, mutations in AO1 or AO4 in the *AO3* mutant background aggravated ABA

159   deficiency in seeds, demonstrating that both gene products contribute partially to ABA

160   biosynthesis and act as a 'back-up system' to AO3 in the AO3 mutant background, while this

161   effect might be negligible in wild-type *Arabidopsis*. Absence of AAO3 oxidation activity (rather

162   than the lower ABA) and its associated function is responsible for the earlier senescence

163   symptoms in aao3 mutant. *Arabidopsis* AAO3 knockout mutant aao3 exhibited earlier

164   senescence compared with wild-type during normal growth or upon application of UV-C

165   irradiation. Different aldehydes accumulated prominently in aao3 mutants compared with WT

166   leaves under normal growth conditions, upon UV-C irradiation and after exogenous aldehydes

167   application (Nurbekova et al., 2021).

168   AO3 can be slightly induced by stresses; for example, an increase in abscisic aldehyde

169   oxidizing activity was observed for the PsAO isoform in the leaves and roots of pea plants

170   exposed to salinity or ammonium treatments (Zdunek-Zastocka et al., 2004). Drought stress

171   increases AO3 transcript levels and the activity of AOd (Seo et al., 2000b; Bittner et al., 2001)

172   and high AO3 expression was sufficient to induce stomatal closure (Melhorn et al., 2008).

173   **Biochemical and physiological function of AO4**

174   A study on *Arabidopsis* AO4 knockout mutants and overexpressing lines demonstrated that

175   AO4 plays a critical role in delaying senescence and protecting silique against toxic aldehydes

176   (Ibdah et al., 2009). Single loss-of-function mutants for AO4 failed to show significant changes

177   in endogenous ABA levels in seeds compared with wild type. Plants produce toxic aldehydes

178   under normal and stress conditions (Mano, 2012; Srivastava et al., 2017) and excess aldehydes

179   may lead to reactive oxygen species (ROS) accumulation that could damage proteins, lipids and

180   other molecular compounds (Bartels, 2001; Kotchoni et al., 2006; Zhang et al., 2012; Biswas et

181   al., 2015). AO4 was expressed most abundantly in developing silique, and AO4 was involved in

182   the oxidation of benzaldehyde (BA) in silique, contributing to the synthesis of the benzoic acid

183   (BA) pool in seed capsules (Ibdah et al., 2009). The AO4 mutant seeds showed significant

184   reductions in the total contents of BA and 4-benzoyloxybutylglucosinolate, as well as a slight

185   reductions in the levels of 3-benzoyloxypropylglucosinolate (Ibdah et al., 2009).

186   AO4 can oxidize various aromatic and aliphatic aldehydes and it differentially generates

187   superoxide (O^{2-}) and hydrogen peroxide (H_2O_2) in an aldehyde-dependent manner. In addition,

188   AO4 transcript levels and activity in silique were induced by H_2O_2 application, indicating that

189   the ROS generated by the activity of AO4 can self-amplify, enabling further detoxification of

190   toxic aldehydes and delaying silique senescence of *Arabidopsis* plants (Srivastava et al., 2017).

191 **Summary and Prospect**

192   Phylogenic tree showed at least two conserved clades for AO enzymes involved in the

193 biosynthesis of ABA and auxin synthesis (Abu-Zaitoon et al., 2014) and it supports the proposed

194 function of ABA and auxin biosynthesis. Studies about AOs are quite scant; however, AOs are

195 very import enzymes merit better understandings due to two reasons. Firstly, they may involve in

196 biosynthesis of important phytohormones, and it may be a potential target for genetic control in

197 agriculture as genes like GA20-oxidase in green revolution. Phytohormones are vital substances

198 regulates multifaced function of plants and mutants in the early steps of biosynthetic pathway

199 could be lethal and useful tools in scientific researches while mutation in late nodes could be

200 important regulating points and easier for genetic manipulation in agriculture. Secondly, AOs

201 could have multifaced functions due to their wide substrate of AOs, thus pathway or traits

202 influenced by AOs also deserve further studies. In this review, we summarized the recent studies

203 about AO in plants including the motif information, biochemical, and physiological functions

204 which may provide useful information for botanist and biologist and it is also beneficial for

205 agriculture.

206   AO may be involved in metabolic processes not only phytohormone synthesis but also

207 cellular ROS homeostasis under normal and stress conditions (Wendehene et al., 2014; Gilroy et

208 al., 2014). Recombinantly expressed *Arabidopsis* AO1 and AO3 in the methylotrophic yeast

209 *Pichia pastoris* are capable of producing not only H_2O_2 but also O^{2-} during oxidation of

210 aldehydes (Zarepour et al., 2012). In addition to their aldehyde oxidation activity, AO1 and AO3

211 were found to exhibit NADH oxidase activity (Yergaliyeva et al., 2016; Brikis et al., 2018;

212 Zhong et al., 2010; Hesberg et al., 2004; Diallianas et al., 1997; Yesbergenova et al., 2005). In

213 this respect, conditions such as natural senescence and stress-induced stomatal movement, which

214 both require simultaneously elevated levels of abscisic acid and hydrogen peroxide/superoxide,

215 are likely to benefit from AOs by formation of abscisic acid and ROS.

216   As mentioned above, Moco is an important component of several enzymes including nitrate

217 reductase, AOs, XDH. The activity of AO enzymes requires a sulfurated Moco, which is

218   converted from the desulfo- to the sulfo-form by the Moco sulfurase ABA3 (Xiong et al., 2001;

219   Bittner et al., 2001). Deficiency in the biosynthesis of Moco might result in pleiotropic effect or

220   even lethal consequences for the respective organisms (Mendel, 2013). For example, Moco

221   deficient mutants of barley *Az34* (Walker et al., 1989), tobacco (Leydecker et al., 1995), tomato

222   *flacca* and *sitiens1* (Marin et al., 1997; Sagi et al. 2002), and *Arabidopsis aba3* (Akaba et al.,

223   1999, Bittner et al., 2001) had severely impaired ABA production.

224   The availability of Moco and its sulfuration may therefore represent a potential point of

225   interaction between cytokinin, ABA and IAA metabolism in plants to control phytohormone

226   balance, which may determine the stress tolerance of plants (Cowan et al., 2001). In addition, the

227   plant Moco-pool size (enzymes with Moco) varies under different nutritional and environmental

228   conditions (Sagi et al., 1997; Sagi et al., 1998). Thus, increased activity of Mo-hydroxylases (i.e.

229   AO and XDH) in response to salt stress and ammonium treatment could be one mechanism for

230   stress adaptation, which could include enhanced activity of the Moco-containing enzymes

231   responsible for ABA synthesis (Sagi et al., 1998). When XDH activity or nitrate assimilation is

232   reduced or inhibited, more Moco might therefore be available for sulfuration (Sagi et al., 1999,

233   2002; Bittner et al., 2001) and thus AOs enzymes were more activated. One the other hand, when

234   nitrate reductase has been induced by its substrate, the AO activity and ABA content in plants

235   were reduced (Omarov et al.,1998). Molybdenum as one of the trace essential elements for plants,

236   and the effect of external sources molybdenum on AO, XDH, and other enzymes as well as

237   phytohormone biosynthesis could be a promising research direction.

238   In addition, AO1 was predict to involve in hypoxia stress of *Arabidopsis* and AO2 was

239   assumed to interact with proteins belong to thioredoxin superfamily. We can speculate AOs

240   might regulate the abiotic stress of plants including drought, and osmotic, stress. The study about

241   AO enzymes thrived around 20 years ago, and they need further study for possible manipulation

242   in agriculture for suitable phytohormone biosynthesis, ROS homeostasis, stress tolerance,

243   development, and aldehyde detoxification.

244

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246 the database. MS and WZ analyzed database. LX and YX prepared the figures and/or tables. JW,

247 BMS, WZ, YX, and LX wrote the original draft. YX, and LX revised the manuscript.

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250 **Reference**

251 **Abu-Zaitoon YM**. **2014.** Phylogenetic analysis of putative genes involved in the tryptophan-dependent
252 pathway of auxin biosynthesis in rice. *Applied Biochemistry and Biotechnology* **172(5)**: 2480-2495 DOI
253 10.1007/s12010-013-0710-4.

254 **Akaba S, Seo M, Dohmae N, Takio K, Sekimoto H, Kamiya Y, Furuya N, Romano T, Koshiba T. 1999.**
255 Production of homo- and hetero-dimeric isozymes from two aldehyde oxidase genes of *Arabidopsis*
256 *thaliana*. *The Journal of Biochemistry* **126 (2)**: 395–401 DOI 10.1093/oxfordjournals.jbchem.a022463.

257 **Ando S, Tsushima S, Tagili A, Kamachi S, Konagaya K, Hagio T, Tabei Y. 2006**. Increase in BrAO1 gene
258 expression and aldehyde oxidase activity during clubroot development in Chinese cabbage (*Brassica rapa*
259 L.). *Molecular Plant Biology* **7(4)**: 223-234 DOI 10.1111/j.1364-3703.2006.00333.x.

260 **Audran C, Borel C, Frey A, Sotta B, Meyer C, Simonneau T, Marion-Poll A. 1998**. Expression Studies of
261 the Zeaxanthin Epoxidase Gene in *Nicotiana plumbaginifolia*. *Plant Physiology* **118(3)**: 1021–1028 DOI
262 10.1104/pp.118.3.1021.

263 **Audran C, Liotenberg S, Gonneau M, North H, Frey A, Tap-Waksman K, Vartanian N, Marion-Poll A.**
264 **2001**. Localisation and expression of zeaxanthin epoxidase mRNA in *Arabidopsis* in response to drought
265 stress and during seed development. *Australian Journal of Plant Physiology* **28(12)**: 1161-1173 DOI
266 10.1071/pp00134.

267 **Barrero JM, RODRÍGUEZ PL, Quesada V, Piqueras P, Ponse MR, Micol JL. 2006**. Both abscisic acid
268 (ABA)-dependent and ABA-independent pathways govern the induction of NCED3, AAO3 and ABA1 in
269 response to salt stress. *Plant Cell and Environment* **29(10)**: 2000-2008 DOI 10.1111/j.1365-
270 3040.2006.01576.x.

271 **Bartels D. 2001**. Targeting detoxification pathways: an efficient approach to obtain plants with multiple stress
272 tolerance? *Trends Plant Sciences* **6(7):** 284–286 DOI 10.1016/S1360-1385(01)01983-5.

273 **Biswas MS, Mano JI. 2015**. Lipid peroxide-derived short-chain carbonyls mediate hydrogen peroxide-
274 induced and salt-induced programmed cell death in plants. *Plant Physiology* **168(3):** 885–898 DOI
275 10.1104/pp.115.256834.

276 **Bittner F, Oreb M, Mendel RR. 2001**. ABA3 Is a molybdenum cofactor sulfurase required for activation of
277 aldehyde oxidase and xanthine dehydrogenase in *Arabidopsis thaliana*. *The Journal of `Biological
278 Chemistry* **276(44)**: 40381–40384 DOI 10.1074/jbc.C100472200.

279 **Böttcher C, Chapman A, Fellermeier F, Choudhary M, Scheel D, Glawischnig, E. 2014.** The biosynthetic
280 pathway of indole-3-carbaldehyde and indole-3-carboxylic acid derivatives in arabidopsis**.** *Plant
281 Physiology*. **165:** 841–853 DOI 10.1104/pp.114.235630.

282 **Bower PJ, Brown HM, Purves WK. 1978**. Cucumber seedling indoleacetaldehyde oxidase. *Plant Physiology*
283 **61(1)**: 107-110 DOI 10.1104/pp.61.1.107.

284 **Brikis CJ, Zarei A, Chiu GZ, Deyman KL, Liu JL, Trobacher CP, Hoover GJ, Subedi S, DeEll JR,**
285   **Bozzo GG, Shelp BJ. 2018**. Targeted quantitative profiling of metabolites and gene transcripts associated
286   with 4-aminobutyrate (GABA) in apple fruit stored under multiple abiotic stresses. *Horticulture Research*
287   **61(5):** 1-18 DOI 10.1038/s41438-018-0069-3.

288 **Cheng WH, Endo A, Zhou L, Penney J, Chen HC, Arroyo A, Leon P, Nambara E, Asami T, Seo M,**
289   **Koshiba T, Sheen J. 2002**. A unique short-chain dehydrogenase/reductase in *Arabidopsis* glucose
290   signaling and abscisic acid biosynthesis and functions. *The Plant Cell* **14(11)**: 2723-2743 DOI
291   10.1105/tpc.006494.

292 **Colasuonno P, Marcotuli I, Lozito ML, Simeone R, Blanco A, Gadaleta A. 2017.**
293   Characterization of aldehyde oxidase (ao) genes involved in the accumulation of carotenoid pigments in
294   wheat grain. *Frontiers in Plant Science* **8**:863 I DOI 10.3389/fpls.2017.00863

295 **Cowan K, Tayor N. 2001.** Plant hormone homeostasis and the control of avocado fruit size. *Plant Growth*
296   *Regulation* **35(3)**: 247-255 DOI 10.1023/A:1014463300850.

297 **Dejonghe W, Okamoto M, Cutler S R. 2018.** Small molecule probes of ABA biosynthesis and signaling.
298   *Plant Cell and Physiology* **59(8):** 1490-1499 DOI 10.1093/pcp/pcy126.

299 **Diallinas G, Pateraki I, Sanmartin M, Scossa A, Stilianou E, Panopoulos NJ, Kanellis AK. 1997.** Melon
300   ascorbate oxidase: cloning of a multigene family, induction during fruit development and repression by
301   wounding. *Plant Molecular Biology* **34(5):** 759–770 DOI 10.1023/A:1005851527227.

302 **Estrada-Melo AC, Chao, Reid MS, Jiang, Cai-Zhong. 2015**. Overexpression of an ABA biosynthesis gene
303   using a stress-inducible promoter enhances drought resistance in petunia. *Horticulture Research* **2015(2)**:
304   p. 15013 DOI10.1038/hortres.2015.13.

305 **Fedorova E, Redondo FJ, Koshiba T, Pueyo JJ, Rosario de Felipe M, Lucas MM. 2005**. Aldehyde oxidase
306   (ao) in the root nodules of lupinus albus and medicago truncatula: identification of ao in meristematic and
307   infection zones. *The American Phytopathological Society* **18(5):** 405–413 DOI 10.1094/MPMI-18-0405.

308 **Finkelstein R. 2013.** Abscisic Acid Synthesis and Response. *Arabidopsis Book* **11(e0166):** e0166-e0166 DOI
309   10.1199/tab.0166.

310 **Garattini E, Fratelli M, Terao M. 2008**. Mammalian aldehyde oxidases: genetics, evolution and
311   biochemistry. *Cellular and Molecular Life Sciences* **65(7-8):** 1019–1048 DOI 10.1007/s00018-007-7398-
312   y.

313 **Gilroy S, Suzuki N, Miller G, Choi WG, Toyota M, Devireddy AR, Mittler R. 2014**. A tidal wave of
314   signals: calcium and ROS at the forefront of rapid systemic signaling. *Trends in Plant Science* **19(10):**
315   623-630 DOI 10.1016/j.tplants.2014.06.013.

316 **González-Guzmán M, Abia D, Salinas J, Serrano R, Rodríguez PL. 2004**. Two new alleles of the abscisic
317   aldehyde oxidase 3 gene reveal its role in abscisic acid biosynthesis in seeds. *Plant Physiology* **135 (1)**:
318   325–333 DOI 10.1104/pp.103.036590.

319 **González-Guzmán M, Apostolova N, Bellés JM, Barrero JM, Piqueras P, Ponce MR, Micol JL, Serrano**
320   **R, Rodríguez PL. 2002**. The short-chain alcohol dehydrogenase aba2 catalyzes the conversion of
321   xanthoxin to abscisic aldehyde. *The Plant Ccell* **14(8):** 1833–1846 DOI 10.1105/tpc.002477.

322 **Hesberg C, Hänsch R, Mendel RR, Bittner F. 2004**. Tandem orientation of duplicated xanthine
323   dehydrogenase genes from *Arabidopsis thaliana* differential gene expression and enzyme activities.
324   *Journal of Bilogical Chemistry* **279(14):** 13547-13554 DOI 10.1074/jbc.M312929200.

325 **Hille R, Nishinoab T, Bittner F. 2011**. Molybdenum enzymes in higher organisms. *Coordination Chemistry*
326 *Reviews* **255 (9-10)**: 1179-1205 DOI 10.1016/j.ccr.2010.11.034.

327 **Ibdah M, Chen YT, Wilkerson CG, Pichersky E. 2009**. An aldehyde oxidase in developing seeds of
328 *Arabidopsis* converts benzaldehyde to benzoic acid. *Plant physiology Physiology* **150(1):** 416-423 DOI
329 10.1104/pp.109.135848.

330 **Kasahara H. 2016.** Current aspects of auxin biosynthesis in plants. *Bioscience Biotechnology and*
331 *Biochemistry* 80(1): 34-42 DOI 10.1080/09168451.2015.1086259.

332 **Kilian, J., Whitehead, D., Horak, J., Wanke, D., Weinl, S., Batistic, O., D'Angelo, C., Bornberg-Bauer,**
333 **E., Kudla, J., Harter, K. (2007).** The AtGenExpress global stress expression data set: protocols,
334 evaluation and model data analysis of UV-B light, drought and cold stress responses. *Plant Journal*.
335 50(2):347–363. DOI: 10.1111/j.1365-313X.2007.03052.x

336 **Koiwai H, Akaba S, Seo M, Komano T, Koshiba T. 2000**. Functional expression of two *Arabidopsis*
337 aldehyde oxidases in the yeast *Pichia pastoris*. *The Journal of Biochemistry* **127(4):** 659–664 DOI
338 10.1093/oxfordjournals.jbchem.a022654.

339 **Koiwai H, Nakaminami K, Seo M, Mitsuhashi W, Koshiba TT. 2004**. Tissue-specific localization of an
340 abscisic acid biosynthetic enzyme, aao3, in *Arabidopsis*. *Plant Physiology* **134(4)**: 1697-1707 DOI
341 10.2307/4281702.

342 **Koshiba T, Saito E, Ono N, Yamamoto N, Sato M. 1996.** Purification and properties of flavin—and
343 molybdenum- containing aldehyde oxidase from coleoptiles of maize. *Plant Physiology* **110(3)**: 781-789
344 DOI 10.1104/pp.110.3.781.

345 **Kotchoni SO, Kuhns C, Ditzer A, Kirch HH, Bartels D. 2006**. Over-expression of different aldehyde
346 dehydrogenase genes in *Arabidopsis thaliana* confers tolerance to abiotic stress and protects plants
347 against lipid peroxidation and oxidative stress. *Plant Cell Environment* **29(6):** 1033-1048 DOI
348 10.1111/j.1365-3040.2005.01458.x.

349 **Leydecker MT, Moureaux T, Kraepiel Y, Schnorr K, Caboche M. 1995**. Molybdenum cofactor mutants,
350 specifically impaired in xanthine dehydrogenase activity and abscisic acid biosynthesis, simultaneously
351 overexpress nitrate reductase. *Plant Physiology* **107(4):** 1427–1431 DOI 10.1104/pp.107.4.1427.

352 **Mano J. 2012**. Reactive carbonyl species: their production from lipid peroxides, action in environmental stress,
353 and the detoxification mechanism. *Plant Physiology Biochemistry* **59(1)**: 90–97 DOI
354 10.1016/j.plaphy.2012.03.010.

355 **Mano Yoshihiro, Nemoto, Keiichirou. 2012.** The pathway of auxin biosynthesis in plants, . *Journal of*
356 *Experimental Botany* **63(8)**: 2853–2872 DOI 10.1093/jxb/ers091.

357 **Marin E, Marion-poll A. 1997**. Tomato *flacca* mutant is impaired in ABA aldehyde oxidase and xanthine
358 dehydrogenase activities. *Plant physiology and biochemistry* **35(5)**: 369-372

359 **Marin E, Nussaume L, Quesada A, Gonneau M, Sotta B, Hugueney P, Frey A, Marion-Poll A. 1996**.
360 Molecular identification of zeaxanthin epoxidase of Nicotiana plumbaginifolia, a gene involved in
361 abscisic acid biosynthesis and corresponding to the ABA locus of *Arabidopsis thaliana*. *EMBO Journal*
362 **15(10)**: 2331-2342 DOI 10.1002/j.1460-2075.1996.tb00589.x.

363 **Melhorn V, Matsumi K, Koiwai H, Ikegami K, Okamoto M, Nambara E, Bittner F, Koshiba T. 2008**.
364 Transient expression of AtNCED3 and AAO3 genes in guard cells causes stomatal closure in Vicia faba.

365   *Journal of plant research* **121(1)**: 125–131 DOI 10.1007/s10265-007-0127-7.

366   **Mendel RR. 2013**. The Molybdenum Cofactor. *The Journal of Biological Chemistry* **288(19):** 13165–13172
367   DOI 10.1074/jbc.R113.455311.

368   **Merlot S, Giraudat J. 1997**. Genetic analysis of abscisic acid signal transduction. *Plant Physiology* **114(3)**:
369   751-757 DOI 10.1104/pp.114.3.751.

370   **Milborrow BV. 2001**. The pathway of biosynthesis of abscisic acid in vascular plants: a review of the present
371   state of knowledge of ABA biosynthesis. *Journal of Experimental Botany* **52(359)**: 1143-1164 DOI
372   10.1093/jexbot/52.359.1145.

373   **Miyata S, Suzuki Y, Kamisaka S, Masuda Y. 1981**. Indole-3-acetaldehyde oxidase of pea seedlings.
374   *Physiologia Plantarum* **51(4):** 402-406 DOI 10.1111/j.1399-3054.1981.tb05577.x.

375   **Nambara E, Marion-Poll A. 2005**. Abscisic acid biosynthesis and catabolism. *Annual Review of Plant*
376   *Biology* **56(1)**: 165-185 DOI 10.1146/annurev.arplant.56.032604.144046.

377   **Nishino T, Nishino T. 1989**. The nicotinamide adenine dinucleotide-binding site of chicken liver xanthine
378   dehydrogenase: evidence for alteration of the redox potential of the flavin by NAD binding or
379   modification of the NAD-binding site and isolation of a modified peptide. *Journal of Biology Chemistry*
380   **264(10)**: 5468-5473 DOI 10.1016/0167-4838(89)90081-2.

381   **Normanly J, Slovin JP, Cohen JD. 1995**. Rethinking auxin biosynthesis and metabolism. *Plant*
382   *Physiology* **107(2)**: 323-329 DOI 10.1104/pp.107.2.323.

383   **Nurbekova Z, Srivastava S, Standing D, Kurmanbayeva A, Bekturova A, Soltabayeva A, Oshanova D,**
384   **Tureckova V, Strand M, Biswas MS, Mano J, Sagi M. 2021.** Arabidopsis aldehyde oxidase 3, known
385   to oxidize abscisic aldehyde to abscisic acid, protects leaves from aldehyde toxicity. *The Plant Journal*
386   **108(5):** 1439-1455 DOI 10.1111/tpj.15521.

387   **Omarov R, Dräger D, Tischner R, Lips H. 2003**. Aldehyde oxidase isoforms and subunit composition in
388   roots of barley as affected by ammonium and nitrate. *Physiologia Plantarum* **117(3)**: 337–342 DOI
389   10.1034/j.1399-3054.2003.00043.x.

390   **Omarov RT, Sagi M, Lips SH. 1998**. Regulation of aldehyde oxidase and nitrate reductase in roots of barley
391   (*Hordeum vulgare* L.) by nitrogen source and salinity. *Journal of Experimental Botany* **49(322):** 897–902
392   DOI 10.1093/jxb/49.322.897.

393   **Omarov RT, Shuichi A, Tomokazu K, Herman LS. 1999**. Aldehyde oxidase in roots, leaves and seeds of
394   barley (*Hordeum vulgare* L.). *The Journal of Experimental Botany* **50(330)**: 63–69 DOI
395   10.1093/jexbot/50.330.63.

396   **Ori N, Eshed Y, Paran I, Zamir D, Fluhr R. 1997**. TAO1, a representative of the molybdenum cofactor
397   containing hydroxylases from tomato. *Journal of Biological Chemistry* **272(2)**: 1019-1025 DOI
398   10.1074/jbc.272.2.1019.

399   **Qin X, Zeevaart JAD. 1999**. The 9-cis-epoxycarotenoid cleavage reaction is the key regulatory step of
400   abscisic acid biosynthesis in water-stressed bean. *Proceedings of the National Academy of Sciences of*
401   *the United States of America.* **96(26)**:15354-15361 DOI 10.1073/pnas.96.26.15354.

402   **Rajagopal R. 1971**. Metabolism of Indole-3-acetaldehyde. III. Some characteristics of the aldehyde oxidase of
403   avena coleoptiles. *Physiologia Plantarum* **24(2)**: 272-281 DOI 10.1111/j.1399-3054.1971.tb03491.x.

404   **Rothe GM. 1974**. Aldehyde oxidase isoenzymes (E.C. 1.2.3.1) in potato tubers (*Solanum tuberosum*). *Plant*
405   *and Cell Physiology* **15(3)**: 493–499 DOI 10.1103/PhysRevD.7.3821.3.

406 **Sagi M, Dovrat A, Kipnis T, Lips H. 1997.** Ionic balance, biomass production, and organic nitrogen as
407   affected by salinity and nitrogen source in annual ryegrass. *Journal of Plant Nutrition* **20(10)**: 1291-1316
408   DOI 10.1080/01904169709365336.

409 **Sagi M, Fluhr R, Lips SH. 1999.** Aldehyde oxidase and xanthine dehydrogenase in a flacca tomato mutant
410   with deficient abscisic acid and wilty phenotype. *Plant Physiology* **121(2)**:315-315 DOI
411   10.1104/pp.120.2.571.

412 **Sagi M, Omarov RT, Lips SH. 1998.** The Mo-hydroxylases xanthine dehydrogenase and aldehyde oxidase in
413   ryegrass as affected by nitrogen and salinity. *Plant Science* **135(2)**:125-135 DOI 10.1016/S0168-
414   9452(98)00075-2.

415 **Sagi M, Scazzocchio C, Fluhr R. 2002.** The absence of molybdenum cofactor sulfuration is the primary cause
416   of the *flacca* phenotype in tomato plants. *The Plant Journal* **31(3)**:305-317 DOI 10.1046/j.1365-
417   313x.2002.01363.x.

418 **Schwartz SH, Tan BC, Gage DA, Zeevaart JAD, and Mccarty DA. 1997**. Specific oxidative cleavage of
419   carotenoids by VP14 of maize. *Science* **276(5320)**:1872-1874 DOI 10.1126/science.276.5320.1872.

420 **Sekimoto H, Seo M, Dohmae N, Takio K, Kamiya Y, Koshiba T. 1997**. cloning and molecular
421   characterization of plant aldehyde oxidase. *Journal of Biological Chemistry* **272(24)**: 15280-15285 DOI
422   10.1074/jbc.272.24.15280.

423 **Seo M, Akaba S, Oritani T, Delarue M, Bellini C, Caboche M, Koshiba T. 1998**. Higher activity of an
424   aldehyde oxidase in the auxin-overproducing *superroot1* mutant of *Arabidopsis thaliana*. *Plant*
425   *Physiology* **116(2)**: 687–693 DOI 10.1104/pp.116.2.687.

426 **Seo M, Aoki H, Koiwai H, Kamiya Y, Nambara E, Koshiba T. 2004**. Comparative studies on the
427   *Arabidopsis* aldehyde oxidase (AAO) gene family revealed a major role of AAO3 in ABA biosynthesis in
428   seeds. *Plant Cell Physiology* **45(11)**:1694-1703 DOI 10.1093/pcp/pch198.

429 **Seo M, Koiwai H, Akaba S, Komano T, Oritani T, Kamiya Y, Koshiba T. 2000a.** Abscisic aldehyde
430   oxidase in leaves of *Arabidopsis thaliana*. *The Plant Journal* **23(4):** 481-488 DOI 10.1046/j.1365-
431   313x.2000.00812.x.

432 **Seo M, Koshiba T. 2002**. Complex regulation of ABA biosynthesis in plants. *Trends in Plant Science* **7(1)**:
433   41-48 DOI 10.1016/s1360-1385(01)02187-2.

434 **Seo M, Peeters AJM, Koiwai H, Oritani T, Marion-Poll A, Zeevaart JAD, Koornneef M, Kamiya Y,**
435   **Koshiba T, Koshiba T. 2000b**. The *Arabidopsis* aldehyde oxidase 3 (AAO3) gene product catalyzes the
436   final step in abscisic acid biosynthesis in leaves. *Proceedlings of the National Academy of Sciences of the*
437   *United States of America* **97(23):** 12908-12913 DOI 10.1073/pnas.220426197.

438 **Shi X, Tian Q, Deng P, Zhang W, Jing W. 2021.** The rice aldehyde oxidase osao3 gene regulates plant
439   growth, grain yield, and drought tolerance by participating in aba biosynthesis. *Biochemical and*
440   *Biophysical Research Communications* **548(9):** 189-195 DOI 10.1016/j.bbrc.2021.02.047.

441 **Song SQ, Liu J, Tang CF, Zhang WH, Xu HH, Zhang Q, Gao JD. 2020.** Metabolism and signaling of
442   auxins and their roles in regulating seed dormancy and germination (in Chinese). *Chin Sci Bull*
443   65(34):3924-3943 DOI 10.1360/TB-2020-0509.

444 **Song SQ, Liu J, Xu HH, Xu L, Hui H. 2020.** ABA metabolism and signaling and their molecular mechanism
445   regulating seed dormancy and germination. *Scientia Agricultura Sinica* **53(5):** 857-873 DOI
446   10.3864/j.issn.0578-1752.2020.05.001.

447 **Srivastava S, Brychkova G, Yarmolinsky D, Soltabayeva A, Samani T, Sagi M. 2017**. Aldehyde oxidase 4
448   plays a critical role in delaying silique senescence by catalyzing aldehyde detoxification. *Plany Plant*
449   *Physiology* **173(4)**: 1977-1997 DOI 10.1104/pp.16.01939.

450 **Taylor IB, Burbidge A, Thompson AJ. 2000**. Control of abscisic acid synthesis. *Journal of Experimental*
451   *Botany* **51(350)**: 1563-1574 DOI 10.1590/S0103-97332006000700029.

452 **Turner RJ, Weiner JH, Tayior DE. 1995.** The tellurite-resistance determinants tehAtehB and klaAklaBtelB
453   have different biochemical requirements. *Microbiology* **141 (Pt 12)**: 3133-3140 DOI 10.1099/13500872-
454   141-12-3133.

455 **Verslues PE, Zhu JK. 2005**. Before and beyond ABA: upstream sensing and internal signals that determine
456   ABA accumulation and response under abiotic stress. *Biochemical Society Transactions* **33 (Pt 2)**: 375-
457   379 DOI 10.1042/BST0330375.

458 **Waese J, Fan J, Pasha A, Yu H, Geoffrey Fucile G, Shi R, Cumming M, Kelley LA, Sternberg**
459   **MJ, Krishnakumar V, Ferlanti E, Miller J, Town C, Stuerzlinger W, Provart NJ. 2017.** ePlant:
460   visualizing and exploring multiple levels of data for hypothesis generation in plant biology. *The Plant*
461   *Cell*. **29(8)**: 1806–1821 DOI: 10.1105/tpc.17.00073.

462 **Walker SM, Kudrna DA, Warner RL. 1989**. Reduced accumulation of ABA during water stress in a
463   molybdenum cofactor mutant of barley. *Plant Physiology* **90(2):** 728-733 DOI 10.1104/pp.90.2.728.

464 **Wendehenne D, Gao QM, Kachroo A, Kachroo P. 2014**. Free radical-mediated systemic immunity in plants
465   Author links open overlay panel. *Current Opinion in Plant Biology* **20:** 127-134 DOI
466   10.1016/j.pbi.2014.05.012.

467 **Xiong L, Ishitani M, Lee H, Zhu JK. 2001**. The *Arabidopsis* LOS5/ABA3 locus encodes a molybdenum
468   cofactor sulfurase and modulates cold stress– and osmotic stress–responsive gene expression. *The Plant Cell*
469   **13(9)**: 2063–2083 DOI 10.1105/tpc.13.9.2063.

470 **Xiong L, Schumaker KS, Jian-Kang Z. 2002**. Cell signaling during cold, drought, and salt stress. *The Plant*
471   *Cell* **14(S)**: S165-S183 DOI 10.1105/tpc.000596.

472 **Xu L, Pan R, Zhang W**. 2020. Membrane lipids are involved in plant response to oxygen deprivation. *Plant*
473   *Signaling & Behavi*or. **15:**7 DOI 10.1080/15592324.2020.1771938.

474 **Yang J, Worley E, Udvardi M. 2014.** A nap-aao3 regulatory module promotes chlorophyll degradation via
475   ABA biosynthesis in Arabidopsis leaves. *The Plant Cell* **26(12)**: 4862-4874 DOI 10.1105/tpc.114.133769.

476 **Yang L, Liang J, Zhou W, Su L, Zhang B, Li L. 2011.** Isolation and Characterization of the Aldehyde
477   Oxidase2 Gene from Arachis hypogaea L. *Plant Molecular Biology* **29(3):** 544-553 DOI 10.1007/s11105-
478   010-0259-0.

479 **Yergaliyeva TM, Nurbekova Z, Mukiyanova G, Akbassova A, Omarov RT. 2016**. The involvement of
480   ROS producing aldehyde oxidase in plant response to Tombusvirus infection. *Plant Physiology and*
481   *Biochemistry* **109:** 36-44 DOI 10.1016/j.plaphy.2016.09.001.

482 **Yesbergenova Z, Yang G, Oron E, Soffer D, Fluhr R, Sagi M. 2005**. The plant Mo-hydroxylases aldehyde
483   oxidase and xanthine dehydrogenase have distinct reactive oxygen species signatures and are induced by
484   drought and abscisic acid. *Plant Journal* **42(6):** 862–876 DOI 10.1111/j.1365-313X.2005.02422.x.

485 **Zarepour M, Simon K, Wilch M, Nieländer U, Koshiba T, Seo M, Lindel T, Bittner F. 2012.**
486   Identification of superoxide production by *Arabidopsis thaliana* aldehyde oxidases AAO1 and AAO3.
487   *Plant Molecular Biology* **80(6):** 671-671 DOI 10.1007/s11103-012-9975-1.

488 **Zdunek E, Lips HS. 2001**. Transport and accumulation rates of abscisic acid and aldehyde oxidase activity in
489   *pisum sativum* L. in response to suboptimal growth conditions. *Journal of Experimental Botany* **359(52):**
490   1269-1276 DOI 10.1093/jexbot/52.359.1269.
491 **Zdunek-Zastocka E, Omarov RT, Koshiba T, Lips HS. 2004**. Activity and protein level of AO isoforms in
492   pea plants (*Pisum sativum* L.) during vegetative development and in response to stress conditions. *Journal*
493   *of Experimental Botany* **55(401)**: 1361–1369 DOI 10.1093/jxb/erh134.
494 **Zdunek-Zastocka E. 2008**. Molecular cloning, characterization and expression analysis of three aldehyde
495   oxidase genes from Pisum sativum L. *Plant Physiology and Biochemistry* **46(1):** 19-28 DOI
496   10.1016/j.plaphy.2007.09.011.
497 **Zdunek-Zastocka E. 2010**. The activity pattern and gene expression profile of aldehyde oxidase during the
498   development of *Pisum sativum* seeds. *Plant Science* **179(5):** 543-548 DOI 10.1016/j.plantsci.2010.08.005.
499 **Zhang Y, Mao L, Wang H, Brocker C, Yin X, Vasiliou V, Fei Z, Wang X, Blazquez MA. 2012**. Genome-
500   wide identification and analysis of grape aldehyde dehydrogenase (ALDH) gene superfamily. *PloS ONE*
501   **7(2):** e32153 DOI 10.1371/journal.pone.0032153.
502 **Zhong R, Thompson J, Ottesen E, Lamppa GK. 2010.** A forward genetic screen to explore chloroplast
503   protein import in vivo identifies *Moco* sulfurase, pivotal for ABA and IAA biosynthesis and purine
504   turnover. *The Plant Journal* **63(1):** 44–59 DOI 10.1111/j.1365-313X.2010.04220.x.
505

506 **Figure legend**
507 Figure 1. The ABA and IAA synthesis pathway
508 A: ABA precursor is synthesized from the methylerythritol phosphate (MEP) pathway. Enzymes are shown in
509 red colour. BCH1/BCH2: β-carotene hydroxylases; ZEP: Zeaxanthin epoxidase; NSY: Neoxanthin synthase;
510 NCED: 9-cis-epoxycarotenoid dioxygenase; XD: Xanthoxin dehydrogenase; ABAO: Abscisic aldehyde
511 oxidase; CYP707A: ABA 8'-hydroxylase; ABH1: Phaseic acid reductase 1; ABAGT: ABA glucosyltransferase;
512 βG: β-glucosidase; VDE: violaxanthin de-epoxidase, AOs: aldehyde oxidases were indicated with "*".
513 Adapted from Dejonghe et al., 2018; Song et al., 2020; Finkelstein et al; 2013.
514 B: ANT, anthranilate; IAA, indole-3-acetic acid; IAAld, indole-3-acetaldehyde; IAN, indole-3-acetonitrile;
515 IGP, indole-3-glycerol phosphate; IND, indole; AAO, aldehydeoxidase; CYP79B2/3, cytochrome P450
516 monooxygenases2/3; IMI, amidase; INS, indole synthase; NIT, nitrilase; TAA, tryptophan aminotransferase;
517 TRP3/TSA1, Trp synthase α-subunit; TRP2/TSB1, Trp synthase β-subunit; VAS1, pyridoxal phosphate-
518 dependentaminotransferase1; YUC, YUCCA flavin-containing monooxygenase. Adapted from Kasahara et al.,
519 2016; Song et al., 2020.
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521
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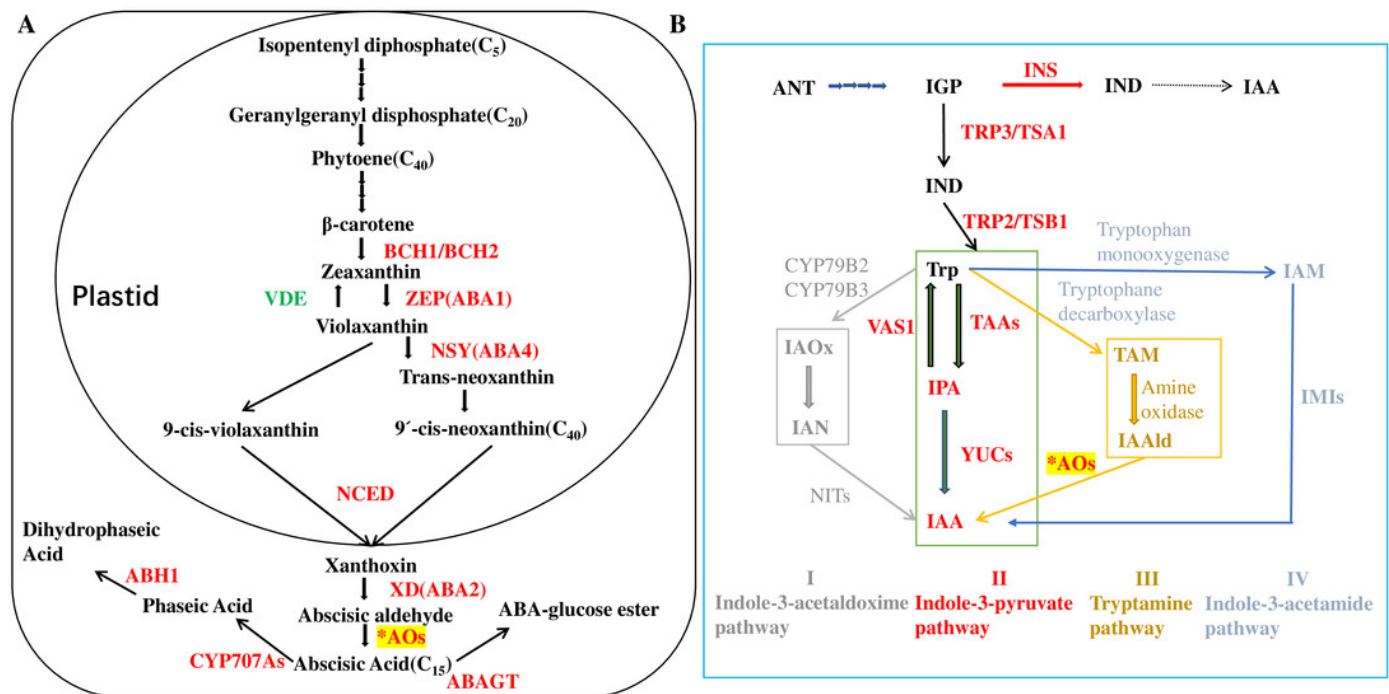
Figure 1

ABA and IAA biosynthesis

Aldehyde oxidase in plants

1 **Table 1. Function of aldehyde oxidase in plant**

Species	Substrate/localization	Protein	Function	Reference
Cucumber	Benzaldehyde, Phenylacetaldehyde Indole-3-acetaldehyde (major)	AO1	IAA biosynthesis	Bower et al., 1978 [1]
Pea	Indole-3-acetaldehyde	AO1	IAA biosyntesis	Miyata et al., 1981 [2]
Pea	Indole-3-aldehyde	AO3	AO activity and ABA induced by suboptimal conditions	Zdunek et al., 2001 [3]
Maize	Indole-3-acetaldehyde/apical region of coleoptiles	AO1	IAA production	Koshiba et al., 1996 [4]
Barley	indole-3-aldehyde, acetaldehyde, heptaldehyde, benzaldehyde	AOs		Omarov et al., 1999 [5]
Oat	indoleacetaldehyde		IAA biosynthesis	Rajagopal et al., 1971 [6]
Arabidopsis	Indole-3-aldehyde	AO1	ABA biosyntesis	Seo et al., 1998; Böttcher et al., 2014 [7、8]
Arabidopsis	Abscisic aldehyde/ rosette leaves	AO3	ABA production	González-Guzmán et al., 2004 [9]
Arabidopsis	Abscisic aldehyde	AO3	ABA and ROS production, drought and water stress	Yesbergenova et al., 2005 [10]
Arabidopsis	Aromatic and aliphatic aldehydes/silique	AO4	Aldehyde detoxification	Srivastava et al., 2017 [11]
Arabidopsis	Abscisic aldehyde, hexanal, and acetaldehyde	AO3	ABA production, Aldehyde detoxification	Nurbekova et al., 2021 [12]
Arabidopsis	Abscisic aldehyde/ leaves	AO3	ABA biosyntesis	Seo et al., 2000a [13]
Arabidopsis	Abscisic aldehyde/seeds	AO3	ABA biosyntesis	Seo et al., 2004 [14]
Arabidopsis	Benzaldehyde/sillique	AO4	Benzoic acid	Ibdah et al., 2009 [15]

wheat	Abscisic aldehyde	AO3	carotenoid pigments accumulation	Colasuonno et al., 2017 [16]
Rice	Abscisic aldehyde/ germinated seeds, roots, leaves, floral organs, vascular tissues, guard cells	AO3	ABA production, drought stress	Shi et al., 2021 [17]

3 **[1]. Bower PJ, Brown HM, Purves WK. 1978**. Cucumber seedling indoleacetaldehyde oxidase. *Plant Physiology* **61(1)**: 107-110 DOI
4   10.1104/pp.61.1.107.

5 **[2]. Miyata S, Suzuki Y, Kamisaka S, Masuda Y. 1981**. Indole-3-acetaldehyde oxidase of pea seedlings. *Physiologia Plantarum* **51(4):** 402-406
6   DOI10.1111/j.1399-3054.1981.tb05577.x.

7 **[3]. Zdunek E, Lips HS. 2001**. Transport and accumulation rates of abscisic acid and aldehyde oxidase activity in *pisum sativum* L. in response to
8   suboptimal growth conditions. *Journal of Experimental Botany* **359(52):** 1269-1276 DOI 10.1093/jexbot/52.359.1269.

9 **[4]. Koshiba T, Saito E, Ono N, Yamamoto N, Sato M. 1996.** Purification and properties of flavin—and molybdenum- containing aldehyde oxidase
10   from coleoptiles of maize. *Plant Physiology* **110(3)**: 781-789 DOI 10.1104/pp.110.3.781.

11 **[5]. Omarov RT, Shuichi A, Tomokazu K, Herman LS. 1999**. Aldehyde oxidase in roots, leaves and seeds of barley (*Hordeum vulgare* L.). *The*
12   *Journal of Experimental Botany* **50(330)**: 63–69 DOI 10.1093/jexbot/50.330.63.

13 **[6]. Rajagopal R. 1971**. Metabolism of Indole-3-acetaldehyde. III. Some characteristics of the aldehyde oxidase of avena coleoptiles. *Physiologia*
14   *Plantarum* **24(2)**: 272-281 DOI 10.1111/j.1399-3054.1971.tb03491.x.

15 **[7]. Seo M, Akaba S, Oritani T, Delarue M, Bellini C, Caboche M, Koshiba T. 1998**. Higher activity of an aldehyde oxidase in the auxin-
16   overproducing *superroot1* mutant of *Arabidopsis thaliana*. *Plant Physiology* **116(2)**: 687–693 DOI 10.1104/pp.116.2.687.

17 **[8]. Böttcher C, Chapman A, Fellermeier F, Choudhary M, Scheel D. Glawischnig E. 2014.** The biosynthetic pathway of indole-3-carbaldehyde and
18   indole-3-carboxylic acid derivatives in arabidopsis**.** *Plant Physiology* **165:** 841–853 DOI 10.1104/pp.114.235630.

19 **[9]. González-Guzmán M, Abia D, Salinas J, Serrano R, Rodríguez PL. 2004**. Two new alleles of the abscisic aldehyde oxidase 3 gene reveal its role
20   in abscisic acid biosynthesis in seeds. *Plant Physiology* **135 (1)**: 325–333 DOI 10.1104/pp.103.036590.

21 **[10]. Yesbergenova Z, Yang G, Oron E, Soffer D, Fluhr R, Sagi M. 2005**. The plant Mo-hydroxylases aldehyde oxidase and xanthine dehydrogenase
22   have distinct reactive oxygen species signatures and are induced by drought and abscisic acid. *Plant Journal* **42(6):** 862–876 DOI 10.1111/j.1365-
23   313X.2005.02422.x.

24 **[11]. Srivastava S, Brychkova G, Yarmolinsky D, Soltabayeva A, Samani T, Sagi M. 2017**. Aldehyde oxidase 4 plays a critical role in delaying
25   silique senescence by catalyzing aldehyde detoxification. *Plany Plant Physiology* **173(4)**: 1977-1997 DOI 10.1104/pp.16.01939.

26 **[12]. Nurbekova Z, Srivastava S, Standing D, Kurmanbayeva A, Bekturova A, Soltabayeva A, Oshanova D, Tureckova V, Strand M, Biswas MS,**

27   **Mano J, Sagi M. 2021.** Arabidopsis aldehyde oxidase 3, known to oxidize abscisic aldehyde to abscisic acid, protects leaves from aldehyde toxicity.
28   *The Plant Journal* **108(5):** 1439-1455 DOI 10.1111/tpj.15521.
29   **[13]. Seo M, Koiwai H, Akaba S, Komano T, Oritani T, Kamiya Y, Koshiba T. 2000a.** Abscisic aldehyde oxidase in leaves of *Arabidopsis thaliana*.
30   *The Plant Journal* **23(4):** 481-488 DOI 10.1046/j.1365-313x.2000.00812.x.
31   **[14]. Seo M, Aoki H, Koiwai H, Kamiya Y, Nambara E, Koshiba T. 2004**. Comparative studies on the *Arabidopsis* aldehyde oxidase (AAO) gene
32   family revealed a major role of AAO3 in ABA biosynthesis in seeds. *Plant Cell Physiology* **45(11)**:1694-1703 DOI 10.1093/pcp/pch198.
33   **[15]. Ibdah M, Chen YT, Wilkerson CG, Pichersky E. 2009**. An aldehyde oxidase in developing seeds of *Arabidopsis* converts benzaldehyde to
34   benzoic acid. *Plant physiology Physiology* **150(1):** 416-423 DOI 10.1104/pp.109.135848.
35   **[16]. Colasuonno P, Lozito ML, Marcotuli I, Nigro D, Giancaspro A, Mangini G, De VP, Mastrangelo AM, Pecchioni N, Houston K, Simeone R,**
36   **Gadaleta A, Blanco A. 2017.** The carotenoid biosynthetic and catabolic genes in wheat and their association with yellow pigments. *BMC Genomics*
37   **18(1):**2-18 DOI 10.1186/s12864-016-3395-6.
38   **[17]. Shi X, Tian Q, Deng P, Zhang W, Jing W. 2021.** The rice aldehyde oxidase osao3 gene regulates plant growth, grain yield, and drought tolerance
39   by participating in aba biosynthesis. *Biochemical and Biophysical Research Communications* **548(9):** 189-195 DOI 10.1016/j.bbrc.2021.02.047.