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Editorial

Developments In Plant Nitric Oxide Signaling And Metabolism.

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EDITORIAL

The Web of Science database contains more than 15,000 scholarly publications about RNSaction or detection in different plant materials that have been published since the late 1950s [1]. As a key gaseous signaling molecule, nitric oxide (NO) may play a role in a number of physiological processes in plants, from seed germination to root formation to seedling growth. It may also play a role in how plants react to abiotic stressors such as drought, low temperature, heat, high salinity, ozone, and heavy metal stress [2]. Enzymatic and nonenzymatic reaction pathways are the two ways that plants produce NO [3]. Generally speaking, oxidation and reduction pathways are the primary sources of endogenous NO production [4]. Nitric oxide synthase (NOS)-like enzymes catalyze the oxidation pathway's generation of NO from L-arginine, while nitrate reductase (NR) converts nitrites in the reduction pathway.Furthermore, endogenous NO is also stimulated by abiotic circumstances. Other enzymes, in addition to NR and NOS, catalyze the synthesis of NO. Naturally, we won't go into much more detail here.

Numerous significant problems about NO's role in postharvest fruit senescence still need to be investigated and resolved. For example, it is still unknown which precise molecular processes are triggered during NO-regulated fruit ripening and which signal transduction pathways allow NO to interact via transcription or translation with other signaling molecules. According to Li et al.'s research, there are eight primary reasons why appropriate NO concentrations reduce senescence in postharvest fruit: (1) ethylene biosynthesis; (2) the antioxidant system; (3) polyamine metabolism and γ-aminobutyric acid (GABA) shunt; (4) cell wall metabolism; (5) sugar metabolism; (6) energy metabolism; (7) the CRT/DRE-binding factor (CBF) pathway; and (8) S-nitrosylation [5].Zhu et al. also summed up how an exogenous NO donor delays postharvest senescence in horticultural crops by controlling a number of metabolisms, such as energy metabolism, reactive oxygen species (ROS) metabolism, cell wall metabolism, respiratory metabolism, and ethylene biosynthesis [6]. Qian et al. recently found that by preserving the integrity of the mitochondrial ultrastructure and enhancing mitochondrial energy metabolism, NO prevented quality degradation and increased the postharvest life of water bamboo shoots [7]. Furthermore, a thorough investigation of the mechanisms underlying RNS (NO)-induced seed dormancy relief has been conducted. Furthermore, in seed germination, reactive oxygen metabolism may function as a dormancy-breaking agent [1].The response to abiotic stressors continues to be the primary focus of NO research hotspots in recent years. NO may increase a plant's resilience to cadmium (Cd) stress and lessen its toxicity. The buildup of NO brought on by Cd stress may also make plants more susceptible to Cd poisoning. Nonetheless, there is disagreement in the literature about the connection between NO and Cd stress. The fact that NO generation has many origins and functional features could be the primary cause of these contradictory findings [8]. Undoubtedly, more research is still required to fully understand the intricate web of NO regulation mechanisms in response to Cd stress. In order to reduce salt toxicity in tomato seedlings, Wei et al. found that NO, a common gas signaling molecule, improved photosynthetic capability and controlled endogenous hormonal balance [9].

In soybeans, overexpression of phytoglobin GmPgb1 reduced ROS-induced damage and foliar Na^+ buildup in salt-stressed leaf tissue [10]. Under drought and salt stress, Chammakhi et al. discovered that NO was accumulated in the faba bean

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(Vicia faba L.) nodules [11]. To create a primary NO signaling pathway for salt resistance, research should integrate the currently fragmented pathways, as Shang et al. detailed [12]. The molecular mechanism of NO's reaction to plant salt tolerance was then investigated further, including the identification of target proteins that are S-nitrosylated and the impact of trans- and de-nitrosylation on plant salt tolerance. According to Zafari et al., NtAOX overexpression reduced NO levels under normoxia, however AOX overexpressors showed higher NO and S-nitrosylation levels than knockdowns under hypoxia [13].Additionally, in terms of plant NO biology, transcriptome sequencing technology is a crucial approach to investigate. Transcriptome results revealed that improved tomato resistance in NO treatment and decreased tomato yellow leaf curl virus burden were primarily caused by increased peptidase inhibitor gene expression [14]. NO signaling is involved in both photoprotection and photosynthesis in plants.In tomato plants, elevated NO levels accelerated the breakdown of the LONG HYPOCOTYL 5 (HY5) protein and further inhibited the transcription of genes encoding the enzymes phytoene synthase 2 (PSY2) and protochlorophyllide oxidoreductase C (PORC), which catalyze the rate-limiting processes in the biosynthesis of carotenoid and chlorophyll. This work offers fresh understanding of how NO signaling regulates the transcriptional level of HY5-mediated photosynthetic pigment biosynthesis [15]. Furthermore, NO plays a crucial role in the signal transduction mechanism of Arabidopsis stomatal closure brought on by darkness.

By inhibiting FT, TSF, and SOC1 expression levels, COP1 transduced H_2O_2 signaling and encouraged NO buildup in guard cells, which ultimately resulted in stomatal closure in darkness [16]. These results provide fresh understanding of the processes behind stomatal closure brought on by darkness.

The identification of a thorough regulatory network at the molecular level is currently what we lack most, since much research has been done to clarify the most evident physiological events in NO response to plant growth and development and adverse stress. To have a clear regulatory network of NO signaling and metabolism in plants, there is obviously still a lot to learn.

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