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Virus-induced down-regulation of soybean farnesyltransferase genes enhances the stomatal response to abscisic acid and drought resistance in soybean

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Drought is a major constraint to the soybean growth and production in the world. The limited transformation potential and polypoid nature of soybean have hampered functional validation of soybean genes. Functional analysis of candidate genes for increased drought resistance identified in model plants such as *Arabidopsis thaliana* could provide gene resources for breeding varieties of non-model staple crops, such as soybean, that can withstand drought conditions. Former research has indicated that *Arabidopsis ERA1*(*Enhanced Response to Abscisic acid 1*) gene encoding β-subunit of protein farnesyltransferase plays an important role in plant's response to abscisic acid (ABA) and drought tolerance. Repression of ERA1 has been shown to enhance drought resistance in Arabidopsis, canola, wheat, and rice. Thus, ERA1 homologs represent promising candidate genes for improving drought resistance in soybean. Here, we identified two soybean *ERA1* homologs of Arabidopsis ERA1, *GmERA1A* and *GmERA1B*, and evaluate *GmERA1s* as potential targets for increasing drought resistance in soybean using *Apple latent spherical virus* (ALSV)-mediated virus-induced gene silencing (VIGS) system. Soybean plants (cultivar Williams 82) inoculated with recombinant ALSVs harboring a partial sequence of *GmERA1* showed down-regulation of *GmERA1s* compared to that in control plants. The isolated leaves of the *GmERA1s*-down-regulated soybean exhibited an increased stomatal closure response to ABA and reduced water loss and gas exchange. In addition, the whole plants of *GmERA1*-down-regulated soybean exhibited better survival ratio under the dehydration stress than did the vector control plants in terms of wilting. These results suggest that *GmERA1*s act as negative regulators of ABA signaling in soybean under dehydration conditions, and *GmERA1*s are useful target genes for enhancing drought resistance in soybean. Furthermore, our study provides the evidence that the ALSV-VIGS system is a useful tool for evaluating candidate drought-resistance genes in soybean easily and rapidly without the need to generate transgenic soybean.