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Distinctive roles of E2F transcription factors during plant replicative stress response

(collaboration with Masaki Ito at Kanazawa University)

Abstract

Survival of living organism is fully dependent on the maintenance of genome integrity. Due to their sessile lifestyle, plants are constantly exposed to biotic and abiotic stresses, that could lead to DNA damage. Studies show that compared to animals, plants have both shared and unique mechanisms that control the DNA Damage Responses (DDR). One central integrator of the plant DDR is the SOG1 transcription factor, but there is accumulating evidence that other pathways function independently of SOG1, notably in the context of replicative stress. Replicative stress is one of the most common threats to genome integrity as it occurs in all proliferating cells. Core cell cycle regulators, that are highly expressed in proliferating cells, are thus good candidates to contribute to the signaling pathways activated by replicative stress. Among those, the E2F transcription factors, are well characterized for their role at the G1/S transition, and one of them, EF2a has been recently shown to contribute to the cellular response to double strand breaks. However, there are still loopholes that require extensive study to clearly understand the role of E2Fs in the plant DDR signaling pathways. In order to test the involvement of E2Fs in replicative stress response in plants, we used genetic approaches, taking advantage of a mutant deficient for a replicative DNA polymerase, that displays constitutive replicative stress. Our results indicate that E2Fb may function in parallel of SOG1 in replicative stress response, providing evidence for the existence of a novel pathway in plants' DDR signaling, and suggesting that the two closely-related transcription factors E2Fa and E2Fb may play distinctive roles in this process.