Demethylation Promotes Rhizoid and Root Hair Development in Ceratopteris richardii

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Global agricultural sustainability is currently threatened by the inefficient use of chemical fertilizers, which often leach into ecosystems as pollutants rather than being absorbed by crops. To address this challenge and enhance crop resiliency, this research investigates DNA methylation, a critical epigenetic regulatory mechanism that plays a role in controlling root architecture. This study tests the hypothesis that DNA demethylation affects rhizoid and root hair development in the vascular model Ceratopteris richardii. Experimental procedures involved treating C. richardii spores with zebularine, a DNA methyltransferase inhibitor. Transient 40 μM exposure significantly promoted the elongation of both gametophytic rhizoids and sporophytic root hairs compared to controls. Furthermore, continuous exposure revealed a dose-dependent response: low concentrations (1 μM) enhanced growth, while higher concentrations (20 μM) induced developmental retardation. Crucially, this study identified a C. richardii orthologue of Root Hair Defective 3 (CrRHD3), a master regulator of root hair formation. Semi-quantitative RT-PCR analysis confirmed that DNA demethylation via zebularine modulates the expression profile of CrRHD3 in C. richardii. Data showed that CrRHD3 is progressively upregulated throughout development, and demethylation significantly enhances its transcriptional activity, driving the observed phenotypic improvements. By leveraging epigenetic engineering to precisely modulate root architecture through the CrRHD3 pathway, this research offers a scalable, sustainable strategy to maximize nutrient uptake efficiency. This biotechnological solution reduces the global ecological footprint of modern agriculture while securing food resources for a growing population.

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Fourth Award of $600