

Exploration of the Selenium-Enrichment Mechanism in Paper Mulberry

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Abstract: Paper mulberry (*Broussonetia papyrifera*) is recognized for its fast growth, wide adaptability, and high protein content capacity, making it a valuable feed resource. This study investigates the mechanisms of Se tolerance and accumulation in *B. papyrifera* through foliar application of sodium selenite and selenate. Results indicated that both Se forms significantly increased total Se content, with sodium selenite treatment yielding a higher proportion of organic Se. Additionally, exogenous Se enhanced soluble sugar, phenolic acid, flavonoid contents, and antioxidant enzyme activities. RNA-seq revealed 644 and 1,804 differentially expressed genes in selenite and selenate treatments, respectively. Pathway enrichment analysis identified significant upregulation of sulfur assimilation genes under selenite treatment, while Se conjugation and transporter genes (e.g., SBP1, PCS, GSTs, ABCs, GPX) were induced by selenate. Weighted-gene co-expression network analysis highlighted the crucial roles of sulfur assimilation, conjugation, and transporter genes in Se metabolism and tolerance. A Se metabolism model in *B. papyrifera* was proposed based on these findings. Focusing on the synthesis of selenomethionine (SeMet), the primary Se form in *B. papyrifera*, we further identified three homocysteine S-methyltransferase (BpHMT) genes, with *BpHMT2* being a key gene linked to Se tolerance. Phylogenetic analysis placed BpHMT2 in the Class 2-D subfamily, indicating fundamental evolutionary functions. Subcellular localization confirmed BpHMT2 targeting in the nucleus, cell membrane, and chloroplasts. Overexpression of *BpHMT2* in *Arabidopsis thaliana* enhanced Se tolerance and SeMet accumulation, underscoring its role in Se metabolism. These insights into the molecular mechanisms of Se metabolism in *B. papyrifera* enhance its potential as a selenium-enriched feed resource, improving its nutritional value.