		学位論文要旨
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題	目	Molecular biological studies of the bHLH transcription factors, BES1/BZR1 homolog 1-4 in <i>Arabidopsis</i> and their involvement in brassinosteroid signaling (シロイヌナズナの bHLH 転写因子・BES1/BZR1 ホモログに関する分子生物 学的研究)

Brassinosteroids (BRs) are a class of growth promoting phytohormones, but they are also involved in response to various abiotic and biotic stressors and often confer stress tolerance to numerous crops, leading to the yield increase and market values as well, even in hostile environments. However, BRs have not yet been officially registered as plant growth regulators in Japan. BR action mechanisms, especially for BR signal transduction must be elucidated to utilize their functions effectively in agriculture.

BES1/BZR1 transcription factors are indispensable transcription factors acting in BR signaling pathway and construct a small family with four other BES1/BZR1 homologs (BEH) in Arabidopsis. This author molecularly characterized BEH proteins (and genes) to further elucidate the mechanisms underlying BR signaling and made the following findings. First, the author found that the expression of the four *BEH* genes were distinct with each other, regarding growth-stage dependence and organ specificity but exhibited some overlaps as well. Furthermore, their mRNA levels mostly remained unchanged responding to seven non-BR phytohormones. However, BEH1 and BEH2 were downregulated by BL, suggesting a close association with the BR function. Additionally, BEH4 was ubiquitously expressed throughout the life of the plant but displayed some expression preference. For instance, BEH4 expression was limited to guard cells and the adjacent pavement cells in the leaf epidermis and was induced during growth progression in very young seedlings, suggesting that *BEH4* is specifically regulated in certain contexts, although it is almost constitutively controlled. Moreover, the author proceeded the research on BEH2 that was downregulated by BL, and made the following findings. *BEH2* was expressed preferentially in the roots and leaf margins including serrations, which was quite different from another member BEH4, and that BRs downregulated BEH2 through a module containing GSK3-like kinases and BES1/BZR1 TFs, among which BES1, rather than BZR1, contributed to this process. In addition, BEH2 consistently existed in the nucleus, suggesting that its subcellular localization is not under BR-dependent nuclear-cytoplasmic shuttling control. Furthermore, gene ontology analysis on RNA-seq data indicated that BEH2 may be implicated in stress response and photosynthesis.

These findings might assist in the future elucidation of the molecular mechanisms underlying BR signaling, and hopefully help the future application of BRs to agriculture through their registration as plant growth regulators as well as the usage of BR-related genes in crop breeding.