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指導教員 承認印	模計	(III)	(P)

2018年 12月 10日 Year Month Day

学位(博士)論文要旨

(Doctoral thesis abstract)

	生物システム応用科学	学府 生物核	能システム科学	_専攻			
論文提出者	博士後期課程 資源生物創製科学		_専修/グループ(De	専修/グループ(Department Course)			
Ph. D.	平成 <u>27</u> 年度入学(Your Entrance Fiscal Year)						
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Name		Name		Name			
	定量プロテオミクスによる陸上植物のアブシジン酸シグナル伝達ネットワークの						
論文題目	大規模解析						
Title	Analysis of protein phosphorylation networks of abscisic acid based on quantitative						
	proteomics in Arabidopsis thaliana seeds and Physcomitrella patens						

論文要旨(和文要旨(2000字程度)または英文要旨(500words))

※欧文・和文どちらでもよい。但し、和文の場合は英訳を付すこと。

Write a summary in Japanese (2000 characters) or in English (500words).

If the abstract is written in Japanese, needed to translate into English.

The plant hormone abscisic acid (ABA) have important role in regulating seed maturation, dormancy, and germination. We use phosphoproteomic analysis in *Arabidopsis thaliana* dry seeds that was storage for one month to elucidate the unique ABA signaling network in seeds. We identify 308 phosphopeptides from Arabidopsis wild type and *ahg1agh3abi1*, a disturuptant of group A 2C-type phosphatase (PP2C). We could not identified any ABA responsive phosphopepeides that has been studied by other researchers. From this results, dry seeds that were storage for month might reduce their ABA sensitivity.

Abscisic acid (ABA) and its signaling system are also important for land plants to survive in terrestrial conditions. Here, we took a phosphoproteomic approach to elucidate the ABA signaling network in Physcomitrella patens, a model species of basal land plants. Our phosphoproteomics analysis detected 4,630 phosphopeptides from P. patens wild-type and two ABA responsive mutants, a disturuptant of group A 2C-type protein phosphatase (PP2C) (ppabila/b) and AR7, defective mutant in ARK identified as an upstream regulator of SnRK2. A quantitative analysis detected 143 ABA-responsive phosphopeptides in P. patens. The analysis indicated that SnRK2-meditated phosphorylation and target motifs were partially conserved in bryophytes. Our data demonstrate that the PpSnRK2B and AREB/ABF-type transcription factors are phosphorylated in vivo in response to ABA under the control of ARK. On the other hand, our data also revealed the following: 1) the entire ABA-responsive phosphoproteome in P. patens is quite diverse, 2) P. patens PP2C affects additional pathways other than the known ABA signaling, and 3) ARK is mainly involved in ABA signaling. Taken together, we propose that the core ABA signaling pathway is essential in all land plants; however, some ABA-responsive phosphosignaling uniquely developed in bryophytes during the evolutionally process.

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