

Role of autophagy during sulfur limitation

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Autophagy, an important cellular degradation system plays an important role in plant growth, development and response to environmental stresses. In stress conditions it protects plant cells from the oxidative stress by degrading oxidized proteins and it recovers valuable substances from the degraded cellular components. On the other hand selective degradation of certain cellular targets (such as transcription factors or other regulatory proteins) by the plant autophagy machinery might be an effective strategy of reprogramming the cellular metabolism during shortage of nutrients. The role of selective autophagy and the selective autophagy cargo receptors is quite well characterized in mammals. Plants also possess selective autophagy cargo receptors, of similar to mammalian proteins domain architecture, named, depending on the plant species, NBR1 (*Arabidopsis*) or Joka2 (tobacco, potato). Through binding to ATG8s proteins NBR1/Joka2 deliver cargo to autophagosomes. However, their other partners, such as upstream regulators and degradation targets are not yet sufficiently investigated. Therefore, one of the focus of our work is identification of the protein partners of NBR1/Joka2 in normal and sulfur-deficiency conditions.

Moreover, plants with increased level of selective cargo receptors have been obtained in our laboratory and characterized in various growth conditions. Phenotypic differences between the wild type plants and the lines with the changed level of NBR1/Joka2 were rather subtle in normal growth conditions, however suggested that NBR1/Joka2 might be involved in nutrients deficiency response. Comparison of the transcriptomic profiles in shoots (rosette leaves) and roots of the wild type and the NBR1 overexpressing *Arabidopsis* revealed that NBR1 might be involved in certain processes related to abiotic stress response, such as cold or heat acclimation, regulation of circadian rhythm, flowering and ribosome biogenesis. Interestingly, increased level of NBR1 protein seems to affect the expression of numerous transcription factors. Involvement of NBR1 in processes and stresses concluded from the transcriptomic analysis is currently under investigation.

Acknowledgments: The research in the laboratory is supported by National Science Centre (grant No 2014/15/B/NZ3/04854).

Bearbeitet von/ Compiled by:

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**25th International Symposium of the Scientific
Centre for Fertilizers “Significance of Sulfur in
High-Input Cropping Systems”
Groningen (Netherlands), September 5-8, 2017**

¹Julius Kühn-Institut (JKI), Bundesforschungsinstitut für Kulturpflanzen
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Julius Kühn-Institut, Bundesforschungsinstitut für Kulturpflanzen, Braunschweig, Deutschland
Julius Kühn Institute, Federal Research Centre for Cultivated Plants, Braunschweig, Germany

Vertrieb

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Telefon +49 (0)5374 6576
Telefax +49 (0)5374 6577

ISSN 1866-590X

DOI 10.5073/berjki.2017.191.000



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