Errata

Metabolic Regulation in Developing Barley Seeds – Novel Insights from Transcriptome Analyses.

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Paper III, page 1, abstract:

It says:
“Meta-data analysis identified pericarp and endosperm as primary locations of heat stress responses, indicating that short-term heat stress impacts storage activities more strongly than embryo development, at least initially.”
It should say:
“Metadata analysis identified embryo and endosperm as primary locations of heat stress responses, indicating a strong impact of short-term heat stress on central developmental functions of the caryopsis.”¨

Paper III page 15, paragraph heading:

It says:
“Meta data analysis identifies the pericarp as the predominant location of HSR”
It should say:
“Meta data analysis identifies embryo and endosperm as predominant locations of HSR”

Paper III pages 15, second paragraph:

It says:
“Among the pericarp-specific genes… adaptations upon heat stress exposure.”
It should say:
Among the predominantly pericarp-expressed genes described by Mangelsen *et al.* (2010), a total of 192 genes (6.2%) responded to the heat treatment. Amongst endosperm and embryo-specific genes, 7.1% (141 genes) and 9.6% (28 genes) were heat-responsive, respectively. These observations suggest that embryo and endosperm tissues are the predominant locations for heat stress responses, whereas genes predominantly expressed in the pericarp are less affected by high temperature stress. Considering their central role in the development of the caryopsis, we speculate that embryo and endosperm tissues possess a higher transcriptional and metabolic activity under control-conditions. Hence, in comparison to the pericarp, the genes specifically expressed in these suborgans may require more pronounced adaptations upon heat stress exposure. Interestingly, our findings contradict observations by Abebe *et al.* (2009), who found that drought stress mainly affects the outer, green organs of the caryopsis. It remains by now elusive whether this discrepancy is due to different physiological effects of heat and drought stress in investigated suborgans or whether it is due to the different criteria for selecting stress-responsive genes.