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Comparative acetylome analysis of wild-type and fuzzless-lintless mutant of upland cotton (*Gossypium hirsutum* cv. Xuzhou 142) unveils metabolic rearrangement during the fiber development

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Protein acetylation emerged as a crucial post-translational modification and play a crucial role in the regulation of growth and development in various organisms. Unfortunately related studies inadequately available in angiosperms and to date, there is no report providing insight on the role of KAC on fiber development in cotton plant. Therefore, we first compared the lysine-acetylation proteome (acetylome) of ovule of upland cotton (*Gossypium hirsutum* cv. Xuzhou 142) by using wild-type (Xuzhou 142) as well as its fuzzless-lintless mutant (Xuzhou 142M) with an aim to identify the differentially acetylated proteins to uncover the fiber development. Out of 1696 proteins with 2754 acetylation sites, 1358 proteins with 2104 acetylation sites were quantified by using Tandem Mass Tag (TMT) labeling and acetylation enrichment coupled with high-resolution liquid chromatography-mass spectrometry (LC-MS). 101 acetylation sites were upregulated in the Xu142M-0D/Xu142M-1D comparison group in the quantified acetylation site, in the group of Xu142-0D/Xu142-1D, the modification level of 250 acetylation sites were up-regulated, and 9 sites were down-regulated. While, in the group of Xu142-0D/ Xu142M-0D, the modification of 31 loci were up-regulated and 72 loci were down-regulated, the modification of 20 loci in Xu142-1d/Xu142M-1D was up-regulated, and the modification of 201 loci was down-regulated. Furthermore, a systemic bioinformatics analysis of proteins containing quantitative information, including protein annotation, functional classification, functional enrichment, and functional enrichment based clustering analysis was also performed to gain better understanding of acetylome data. Strangely a huge proportion of differentially expressed acetylation sites largely fitting to non-histone proteins belonging to the metabolic pathways such as respiration, photosynthesis, lipid and protein biosynthesis pathway, posttranslational modification machinery, antioxidative defence system proteins and regulatory pathway such as ROS signaling and transcription factors were up-regulated in Xu142. However, the acetylation sites in histone proteins fitting to chromatin assembly or de-assembly, nucleosomal packaging and assembly and protein-DNA complexes mostly up-regulated in Xu142M. To our knowledge this is first report of comparative acetylome analysis in cotton to uncover the fiber development event and may serve as an important resource to decode the developmental clues in other crops too.

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