



New proteomic developments to analyze protein isomerization and their biological significance in plants

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Résumé en anglais	<p>Spontaneous isoaspartyl formation from aspartyl dehydration or asparaginyl deamidation is a major source of modifications in protein structures. In cells, these conformational changes could be reverted by the protein l-isoaspartyl methyltransferase (PIMT) repair enzyme that converts the isoaspartyl residues into aspartyl. The physiological importance of this metabolism has been recently illustrated in plants. Recent developments allowing peptide isomer identification and quantification at the proteome scale are portrayed. The relevance of these new proteomic approaches based on 2-D electrophoresis or electron capture dissociation analysis methods was initially documented in mammals. Extended use to Arabidopsis model systems is promising for the discovery of controlling mechanisms induced by these particular post-translational modifications and their biological role in plants.</p>
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[1] [http://okina.univ-angers.fr/publications?f\[author\]=15605](http://okina.univ-angers.fr/publications?f[author]=15605)

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- [6] [http://okina.univ-angers.fr/publications?f\[author\]=15616](http://okina.univ-angers.fr/publications?f[author]=15616)
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