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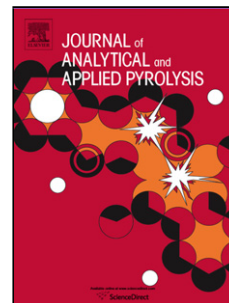
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Analytical pyrolysis to gain insights into the protein structure.

The case of ovalbumin

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Highlights

- Ovalbumin structure was modified to obtain β -sheets and intermolecular aggregates
- Ovalbumin structure was modified to obtain covalent cross-links
- Aggregation and cross-linking increase the thermal stability of OVA
- Aggregation and cross-linking significantly affect pyrolytic profile a of OVA
- Analytical pyrolysis gives insights into the protein structure at the molecular level

Abstract

We report a novel study based on analytical pyrolysis coupled with mass spectrometry to investigate, at the molecular level, the formation of aggregates and cross-linked structures in ovalbumin (OVA). For this scope, OVA was dissolved in water at different concentrations and temperatures (up to 80°C), and was added with 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide hydrochloride (EDC). The formation of β -sheets and intermolecular aggregates, which are stabilized by weak hydrophobic and hydrogen bonds, is favoured in OVA by higher protein concentration and temperatures. The cross-linker (EDC) gives the formation of covalent bonds randomly distributed in the protein, inducing significant portions of random coil structures in OVA. FTIR-ATR spectroscopy was employed to study the protein conformation. Evolved gas analysis coupled with mass spectrometry (EGA-MS) and pyrolysis coupled with gas chromatography mass spectrometry (Py-GC-MS) were used to characterise the gaseous compounds evolved during pyrolysis at the different temperatures. Aggregation and cross-linking increase the thermal stability of OVA and significantly affect its pyrolytic profile.

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