

Structural characterization and stability of proteins in solid forms

P-02.4-13

A. Bolje¹, S. Gobec¹

¹University of Ljubljana, Faculty of Pharmacy, Ljubljana, Slovenia

Protein therapeutics are becoming increasingly important as an alternative treatment for a variety of diseases. For better stability, proteins are often formulated as solid dosage forms, the most common of which are lyophilizates. Their stability depends on the preservation of the native structure during lyophilization, as well as in the lyophilizates. During lyophilization cycle, proteins are exposed to various stress factors that, in combination with the excipients, can affect the protein structure in the final solid form. If the native structure of the protein is not maintained during lyophilization, this may be reflected in an unstable final pharmaceutical product and consequently in its quality, safety and efficiency. Characterization of proteins in solid form is less established, as most methods evaluate critical properties in solution, which is not necessarily indicative of adequate stabilization in the solid phase and thus long-term stability of the pharmaceutical form. Characterization of proteins in solid form can be used to evaluate both secondary and tertiary structure during formulation development. In addition to structural characterization, monitoring protein aggregation is very important. Together with denaturation and surface adsorption, aggregation can affect the activity and stability of lyophilized proteins. Only formulations that retain their structure in the solid state are included in stability studies, which are of particular importance for the development of protein drugs.¹ In this work, the study of protein structure and stability in solid dosage forms using analytical methods such as FTIR, NIR, Raman, solid-state fluorescence, UV-Vis and NMR spectroscopy, as well as circular dichroism, DSC and X-ray powder diffraction is presented. Aggregation phenomena were also studied by size exclusion chromatography and dynamic light scattering.²

1. Bolje, A.; Gobec, S. (2021) (under peer-review).

2. Bolje, A. et al. (2021) (unpublished results).