Study of protein aggregation and enzymatic activity after exposure to dielectric barrier plasma jet in helium

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Molecular mechanisms of action in living organisms exposed to the direct action of plasmas are not clearly understood. Efforts have been made to understand the effects of plasma on DNA molecules, leading to advanced knowledge on plasma induced DNA damage [1,2]. However structural effects of plasma on other biological macromolecules as well very important for living organisms, i.e. proteins, are not reported in the literature, excepting proteins destruction by high power plasmas at low or atmospheric pressure [3]. For low power, non thermal plasma sources, operating at atmospheric pressure it is interesting to study the possible structural effects on proteins architecture. This can affect the functional properties of proteins, making this study a subject of interest for plasma medicine.
We report here results on protein structure and function after exposure to a dielectric barrier plasma jet in helium. As model proteins we used the bovine serum albumin (BSA) and pepsin. The plasma is generated in helium using the principle of dielectric barrier discharge. The protein powder was exposed 1 min to the action of plasma jet, in a microtiter plate. Various parameters of plasma (e.g. amplitude and width of driving voltage pulse, frequency) can be modified in order to understand the relationship between plasma properties and the structural effects on proteins. Spectroscopic studies were carried out on plasma modified proteins to probe structural modifications during plasma actions and to study theirs functional properties.
From all used methods for protein structure determination, we obtained the same result: a fraction of protein powder is destroyed during plasma exposure, a fraction remains unaltered and third fraction suffers structural modifications. In the case of plasma modified pepsin, we have found differences in the thermal denaturation temperature in comparison with native molecules. This is related to possible unfolding events induced during plasma exposure. This was verified also by extrinsic fluorescence spectroscopy studies using 1,8-ANS marker for hydrophobic proteins domains.
Plasma modified protein aggregation and adsorption on standard polymer surfaces was investigated using Rayleigh scattering in UV range and quartz crystal microbalance (QCM). Differences were found for the modified proteins aggregation kinetics as function of plsma treatment conditions. QCM adsorption of proteins on polystyrene coated electrodes showed that plasma treated proteins injection gives a lower vibration frequency than native proteins, corresponding to a lower adsorbed mass. Enzymatic activity of pepsin tested with BSA as substrate, shows a lower capacity of plasma treated enzyme to digest its substrate.
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References

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