
Physical pre-treatments of pigeon pea seeds: impact on the conformation and functionality of proteins extracted by aqueous fractionation

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Pigeon pea (*Cajanus cajan*) is a pulse crop native to countries in South America, Africa and Asia. Its high protein content (18-28%) makes it a high potential source for the development of new food ingredients. Seed pre-treatments, such as soaking and boiling, have been shown to be effective at reducing anti-nutritional compounds and improving pigeon pea proteins' digestibility. However, the effects of these pre-treatments on the protein functionality still need to be investigated. The aim of this study was to evaluate the influence of seed soaking and boiling pre-treatments on the protein conformation and functionality in pigeon pea protein concentrates. Three treatments were performed: control (without pre-treatment), soaking in water for 24 h, and soaking for 24 h + boiling for 30 min. After pre-treatments, the seeds were dried at 60 °C, milled, and the flour was dispersed in water. The pH was adjusted to 12.0 and the solution was centrifuged. The supernatant was collected, adjusted to pH 4.0, and centrifuged again. The resulting pellet was collected, redispersed in distilled water and freeze-dried. The composition of protein concentrates showed average values of proteins, carbohydrates, lipids, ash, and moisture of 77, 12, 0.5, 6.7, and 4 wt.%, respectively. To evaluate the effect of pre-treatments on protein composition and conformation, sodium dodecyl-sulfate polyacrylamide gel electrophoresis (SDS-PAGE), fluorescence spectroscopy, and Fourier-transform infrared spectroscopy (FTIR) were used. Two bands were identified in the SDS-PAGE, one between 37-50 kDa and the other between 50-75 kDa, probably related to the globulin fraction. The fluorescence emission peak of the proteins for the sample that was subjected to boiling showed a slight shift compared to the other samples. This may indicate partial unfolding of the protein structure. Deconvolution of the amide I region in the FTIR spectrum showed that the boiling treatment caused a decrease in β -sheet and β -helix structures and an increase in disordered structures, such as random coils. Only soaking did not affect the protein conformation, whereas the soaking + boiling treatment resulted in partial denaturation of the proteins and impacted their functionality, especially for the emulsifying, foaming, and gelation properties.