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Physicochemical and Some Functional Properties of Melon (*Cucumeropsis mannii*) Protein Isolate in Comparison With Pea (*Pisum sativum*) Protein

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ABSTRACT

The increase in the world population has necessitated the search for newer sources of plant protein, such as *Cucumeropsis mannii* (melon). In this study, *Cucumeropsis mannii* protein isolate (MPI) was extracted and characterized in comparison to the pea protein isolate (PPI). The methionine content of the *Cucumeropsis mannii* protein isolate (4.93 g/100 g protein) was about four times that of the pea protein. Arginine and glutamic acid were the major amino acids in the melon protein. The β-sheet secondary structure was the dominant structure in the proteins. Melon protein isolate contains an acidic legumin subunit. Fluorescence and hydrophobicity data suggested a folded structure for the *Cucumeropsis mannii* protein isolate when compared to the pea protein. Gel electrophoresis indicated six polypeptide bands (35, 70, 80, 120, 130, and 170 kDa) in the melon protein isolates. In contrast to the pea protein, melon protein had a maximum of 85% protein solubility at pH 3. The emulsifying stability of the proteins significantly differed ($p < 0.05$) at pH 7. Higher emulsifying capacity and stability were observed in melon than in pea proteins under acidic and alkaline media. MPI displayed a higher solubility profile than PPI at all pHs. Weaker gel formation was observed in the melon protein. It could be concluded that melon protein isolate would be a potential functional ingredient in the food system sequel to the highlighted properties.

1 | Introduction

Research into plant-based protein continues to experience progressive growth as consumers' demand for more economically, ethically, and environmentally sustainable alternatives to animal proteins is on the increase. Pea (*Pisum sativum*) belongs to the pulse family, and it is a very popular seed; its protein is known for its nutritionally balanced amino acid profile and high branched-chain amino acid (Krentz et al. 2022). Branched-chain amino acids have been rated as a very valuable group of amino acids owing to their ability to be involved in muscle synthesis and expansion (Babault et al. 2015). Higher sulfur amino acids and nutritional value have been reported in pea protein isolates compared with the storage protein globulin and gluten of soybeans. Pea protein, like soybean, has gained ground in food applications as a nutritional and functional ingredient.

Even though research into and application of plant proteins is becoming more popular, their industrial applications are still limited to the conventional ones such as soybean, pea, and a few others. However, many of the indigenous plant proteins are not utilized beyond their inherited household use. They have not been found applicable as food ingredients in the food industry despite their documented nutritional composition. Among these indigenous food crops is melon (*Cucumeropsis mannii*); the white seed-coated variety.

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Melon (*Cucumeropsis mannii*), also known as white melon, belongs to the *Cucurbitaceae* family; it is a legume crop generally cultivated in Nigeria, especially in the southwestern part of the country (Ogunbusola et al. 2022). It is an oil-rich seed grown as a soup ingredient where it serves as a thickener in local soup delicacies and is also roasted with the seed coat and eaten as a snack. Moreover, it is used in making fermented condiments (Ogiri) in local soup and can also be wet-milled, rolled into balls, and fried to produce indigenous snacks (robo) popularly eaten in many regions of Nigeria. In our earlier findings, high essential amino acids, especially arginine, biological values, protein efficiency ratio, and in vitro protein digestibility were documented in white melon protein isolates and concentrates (Ogunbusola et al. 2022, 2013), suggesting the potentiality of the seed's proteins as nutritional ingredients. Arginine has been reported to enhance protein solubility due to its ability to cause interaction between hydrophobic amino acid groups (Alabi et al. 2023). The Authors also reported that arginine increases protein solubility due to its synergetic effect with glutamic acid. Beyond the basic nutritional quality of protein, of utmost importance for industrial application are the structural and physicochemical characteristics. Differences in the structure of proteins have been noted to affect their structural behavior in the food system (Klost and Drusch 2019). For instance, the suitability of casein as a good emulsifier has been linked to the absence of tertiary structure and its unfolding tendency at the interface (Zayas 1997).

Therefore, to advance the quest for the application of melon protein in the food system, it becomes imperative to research their structural, rheological, and physicochemical characteristics as they may have a great influence on their behavior and functionality. It is also necessary to compare the characteristics of melon protein isolates with a relatively well-traded plant protein (pea protein isolates) to ascertain its usability; thus, the need for this work. Furthermore, the findings from the current study will offer important knowledge on the use of white melon protein isolates in comparison to pea protein. This will offer up new opportunities for the creation of novel foods like dietary supplements and imitation meats and will ultimately widen the scope of its use in a variety of food products with a variety of desirable characteristics.

2 | Materials and Methods

2.1 | Materials

Melon (*Cucumeropsisi mannii*) seeds (unshelled) were purchased from the King's market, Omuo Ekiti, Southwestern Nigeria. Commercial pea protein isolate (PPI) was used. The melon seed and pea protein isolate were stored in the cold room at 4°C. All chemicals used were of analytical grade and supplied by Sigma-Aldrich (St Louis, MO, USA).

2.2 | Preparation of the Melon Seeds

The melon seeds were manually shelled, washed in water, drained, and dried in an Air Oven (GRANDETOP, China) at 50°C for 2 h. The seeds were ground using a Marlex Electroline grinding machine MRC (SM-450) and sieved through a 250 μm mesh size. The melon flour obtained was defatted using *n*-hexane following the method described in our previous study (Ogunbusola et al. 2022).

2.3 | Preparation of the Protein Isolates From Melon Flour

Protein was isolated from the defatted melon flour using the modified procedure of (Busu and Amonsou 2019). The seed flour was dispersed in 100 mM Tris–HCl containing 0.2 M NaCl; the pH was adjusted to 8.0 with 2 M HCl (Ohaus pH meter (Starter 2100)), and a flour to solvent ratio of 1:20 w/v was used. The dispersion was stirred continuously on a magnetic stirrer (Stuart CB162) for 2 h at 3000 rpm. The dispersion was centrifuged with a Thermoscientific centrifuge (Multifuge ×3FR) at 10,000 × g and a temperature of 4°C for 20 min. The supernatant was dialyzed (10 KDa cut off) against deionized water for 24 h at 4°C with the water changed at intervals of 6 h. This was freeze-dried (CHRIST, ALPHA1-2LSCBASIC) and kept in an air-tight plastic bottle at −18°C until use.

2.4 | Determination of Protein Content

This was carried out using the Lowry method. The protein isolate was dissolved for the measurement. The melon seed protein isolate was soluble. The protein content of the melon protein isolate was determined using the modified Lowry method (Markwell et al. 1978). Briefly, the protein was solubilized in 0.1 M NaOH solution (10 mg/mL). A 20 mL melon protein isolate solution was prepared by adding 1 mL of protein solution to 19 mL of distilled water. This was serially diluted to a sample volume of 1 mL containing 20 to 100 μg protein. Stock solutions of reagent A (2.0% $NaCO_3$, 0.4% NaOH, 0.16% sodium tartrate, and 1% SDS) and reagent B (4% $CuSO_4$. $5H_2O$) were prepared, respectively. Reagent C was prepared by adding 100 parts of reagent A to 1 part of reagent B. Reagent D (Folin–Ciocalteu phenol reagent diluted 1: 1 with distilled water). A 3 mL of reagent C was added to the serially prepared melon protein solution and incubated at room temperature for 60 min. The samples were mixed vigorously with 0.3 mL of the reagent D and incubated for 45 min at room temperature. The absorbance was read at 660 nm on a Thermo Scientific Orion-Aquamate AQ7100 VIS spectrophotometer (Waltham, Massachusetts). Bovine serum albumin was used to generate the standard curve and was prepared similarly to the sample. The experiment was carried out in triplicate.

The protein content of the melon protein isolate was recorded to be 94.82%, while that of the pea protein isolate was 85%. Recovery and yield for the melon protein isolate were recorded to be 17.58% and 12.08%, respectively.

2.5 | Amino Acid Determination

The amino acid composition of the protein isolates extracted from melon and pea was determined using the HPLC method previously documented in the work of Ogunbusola and coworkers, 2022 (Ogunbusola et al. 2022). Briefly, the samples were hydrolyzed with 6 M HCl at 116°C for 24 h. The methionine

contents were determined after performic acid oxidation. The digests were separated on a cationic column (4.6×150 mm) using a gradient of sodium citrate buffers (pH 3.45 and pH 10.85) at a flow rate of 0.45 mL/min. The experiment was carried out in duplicate.

2.6 | SDS-PAGE Gel Electrophoresis

The gel electrophoresis of the protein isolates was done with or without mercaptoethanol (reducing or non-reducing respectively) following the procedure of Laemmli (1970) with little adjustment. The protein isolate (1 mg/mL) was dispersed in tris–HCl buffer at pH 8.0. The sample was then treated with sample buffer containing SDS (10% w/v) under non-reducing conditions, and with SDS plus β-mercaptoethanol (10% v/v) under reducing conditions. The mixture was heated in a water bath at 95°C for 10 min, cooled, and centrifuged for 5 min at 8000×g (Benchtop microcentrifuge-Sanjeev Scientific U dyog SSU-227). A 15 µL aliquot was loaded on 4%–12% gradient gels and electrophoresis was done with a mini-PROTEAN. A protein marker (MW 12–260 KDa) was used, and Coomassie brilliant blue was used to stain the gels.

2.7 | FTIR Determination and Deconvolution

Fourier transform infrared spectrophotometer (630 FTIR, Agilent Cary, CA, USA) was used to record the FTIR spectra of the protein isolate powder samples (4000–600 cm^{-1}). For the secondary structure of the protein in the samples, the data in the range of 1700–1600 cm^{-1} known as the amide I region was deconvoluted. The FTIR data were evaluated using second derivative analyses of FTIR spectra. The percentage of each component was then estimated from the relative area under the fitted curves of the amide I region.

2.8 | Surface Hydrophobicity

The surface hydrophobicity (S_O) of melon (MPI) and pea protein isolates (PPI) was determined using a Cary Eclipse fluorescence spectrophotometer (Agilent Technologies, Santa Clara, CA, USA) as previously described by Alabi and coworkers 2020 (Alabi et al. 2020). A serial dilution of 0.0009–0.015 mg/mL protein solution was prepared from the stock protein solution (10 mg/mL) prepared in 0.1 M Na_2PO_4 buffer (pH 3, 7, and 9). 8-anilino-1-naphthalene sulfonic acid (ANS) 8 mM was used. Absorbance was read at excitation and emission wavelengths of 390 nm and 470 nm, respectively. The absorbance was plotted against the protein concentration, and the slope was taken as the hydrophobicity.

2.9 | Intrinsic Fluorescence Intensity

A spectrofluorometer (JASCO FP-6300, Tokyo Japan) with a 1.0 cm path cuvette and set at 25°C was used to measure the intrinsic fluorescence spectra of the protein isolate samples (Alabi et al. 2020). A 0.002 mg/mL solution was prepared from the protein stock solution prepared above, and the absorbance was measured at 275 nm excitation wavelength (tyrosine and tryptophan) and at 280–450 nm (emission wavelength).

2.10 | Particle Size Determination

The particle size of the protein isolates was measured using Zetasizer (dynamic light scattering DLS, Nano ZS, Anton Paar, Newcastle, Delaware). The dispersion of a 2 mg/mL sample was prepared at pH 7.0 and hydrated for 1 h prior to filtering with a HA Millipore membrane (0.45 µm). The measurement was taken at an angle of 90° and at a temperature of 25°C.

2.11 | Protein Solubility

Solubility test was carried out on the protein isolates by the procedure documented by Alabi and others 2020 (Alabi et al. 2020). Briefly, a 10 mg/mL suspension of the sample was made in 0.1 M phosphate buffer at pH 2–9, centrifuged for 15 min at 8000×g The supernatant was analyzed for the protein content following the method of Lowry (Markwell et al. 1978). For the total protein content, a 10 mg sample was extracted with 1.0 mL sodium hydroxide solution (0.1 M). The percentage ratio of the protein in the supernatant to the total protein content gives the protein solubility.

2.12 | Emulsifying Activity and Stability

Protein isolates of melon and pea were tested for their emulsifying activity and stability according to the procedure of Alabi and coworkers 2020 (Alabi et al. 2020) with slight modification. A 20 mg/mL protein dispersion was prepared with 5 mL of 0.1 M phosphate buffer (pH 3, 7 and 9). To this, 5 mL of canola oil (pure) was added, and the mixture was homogenized for 2 min at 15,000 rpm using a polytron homogenizer (PT 210: Fisher Scientific, Water side, UK). The emulsified layer was read. The emulsifying activity was expressed as the percentage of the emulsified layer to the total volume, while the emulsifying activity after 1 h of standing was used to express the stability.

$$\text{Emulsifying activity}\,(\%) = \frac{\text{Length of emulsified layer}}{\text{Length of total volume}} \times 100$$

2.13 | Rheological Properties of the Proteins

The rheological properties of the protein dispersion (18%) were performed using a rheometer (MCR102 Rheometer, Anton Paar, Austria) equipped with parallel plate geometry (diameter of 50 mm and 1 mm gap) (Ruzengwe et al. 2020). The solutions were put on the parallel plate. A time-sweep analysis was carried out at a shear frequency of 1 Hz and a strain of 0.5% to ensure measurements were being performed within the linear viscoelastic region (LVR). The temperature was raised from 25°C to 95°C (2°C/min), maintained at that temperature for 20 min, and cooled from 95°C to 25°C at the same rate as before (2°C/min). All samples were covered by a thin layer of paraffin oil to minimize evaporation during measurements. The dynamic rheological parameters used to

evaluate the gel network were the storage modulus (G′) and loss modulus (G″).

2.14 | Statistical Analysis

All experiments were carried out in triplicate, except as otherwise stated. Means were compared using a two-sample *t* test analysis ($p < 0.05$).

3 | Results and Discussion

3.1 | The Amino Acid Composition of White Melon and Pea Protein Isolates

Glutamic acid was the most abundant amino acid in melon and pea proteins (Table 1). A high content of Arginine was recorded for melon protein. A high content of both glutamic acid and arginine has been reported to enhance solubility synergistically (Shukla and Trout 2011). Increased solubility in chicken myosin due to conformational and charge changes induced by L-arginine and L-lysine have also been reported (Li et al. 2019). High arginine and lysine content has been linked to improved gel formation (Wang et al. 2021). High arginine and lysine content has also been linked to improved emulsion stability (Zhu et al. 2019). Higher positively charged amino acids present in the melon protein isolates might indicate the protein is a better functional ingredient in food applications compared with the pea protein. Melon protein contains a higher amount of methionine. Methionine is a limiting amino acid in most legumes.

TABLE 1 | Amino acid composition (g/100 g protein) of white melon and pea protein isolates.

Amino acid	MPI	PPI
His	2.14	1.96
Arg	13.29	6.61
Ser	3.35	3.90
Gly	3.79	3.12
Asp	6.70	8.91
Glu	14.05	13.20
Thr	2.66	2.81
Ala	2.66	3.30
Pro	2.52	3.41
Lys	6.60	5.71
Tyr	1.63	0.70
Met	4.93	0.80
Val	3.18	3.86
Ile	2.77	3.70
Leu	5.17	6.40
Phe	5.54	4.23
Trp	1.65	0.70
Total aromatic amino acid	8.82	5.63
Total hydrophobic amino acid	32.21	29.52
Total branched chain amino acid	11.12	13.96
Total negatively charged amino acid	19.59	17.43
Total positively charged amino acid	22.03	14.28

Note: $n = 2$. Values with different superscripts in the same row differed significantly.

3.2 | SPS PAGE Of Melon and Pea Protein Isolates

Under nonreducing conditions, melon protein isolates showed six bands (35, 70, 80, 120, 130, and 170 kDa), whereas pea protein isolates had four bands (40, 130, 160, and 180 kDa) (Figure 1). The very pronounced bands in both melon and pea protein isolates at approximate weight bands of 170 and 180 kDa are attributable to the trimeric structure of vicilin (Diedericks et al. 2019). The bands at 70 and 80 kDa that appeared in the melon protein isolate (MPI) were not seen in the pea protein isolate (PPI). These bands were attributed to the subunit of vicilin, convicilin. The low molecular weight band at ~35 and 40 kDa in MPI and PPI, respectively, corresponds to the α-legumin subunit in protein. Under reducing conditions, the disappearance of the convicilin band at 70 and 80 kDa in MPI was observed. This might be due to the dissociation of the disulfide bonds. The band linked to the convicilin (~70 kDa) was not observed in pea protein under reducing and non-reducing conditions, contrary to the report of Hansen and coworkers (Hansen et al. 2022).

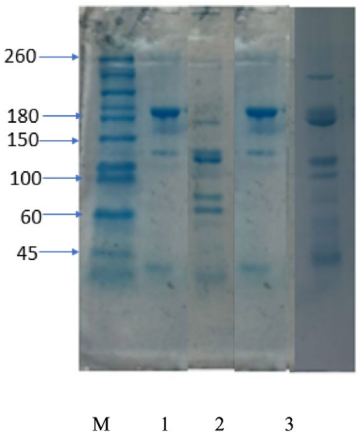


FIGURE 1 | SDS PAGE of white melon and pea protein isolates under reducing and nonreducing. M: Marker; Lane 1: PPI (NR); Lane 2: MPI (NR); Lane 3: PPI (R); Lane 4: MPI (R). MPI = melon protein isolate; PPI = pea protein isolate.

3.3 | Fourier Transform Infrared Spectrophotometer

Secondary structures of the isolates are obtained from the approximate wavelength of 1629–1632 cm^{-1} and 1670–1694 cm^{-1} for β-sheet, 1648–1660 cm^{-1} for α-helix, 1662–1684 cm for β-turns, and 1640–1650 cm^{-1} for random coil. The β-sheet structure was observed to be the dominant secondary structure in the melon and pea proteins (Table 2). MPI contains more α-helix structure but lacks β-turn structure compared with the

PPI. A preponderance of β-sheet structure in yellow pea protein isolate has earlier been reported (Cui et al. 2020).

3.4 | Surface Hydrophobicity

The surface hydrophobicity of melon and pea protein isolates is depicted in Figure 2. MPI exhibited lower surface hydrophobicity under the examined pHs of 3, 7, and 9 in comparison to PPI. Differences in the hydrophobicity of the proteins might be due to the variation in the protein conformation (Mir et al. 2021). Both MPI and PPI showed the highest surface hydrophobicity at pH 3 (acidic region) compared with the neutral and alkaline regions. This may be attributed to the exposure of more hydrophobic amino acids to the surface at the acidic region because of protein denaturation (Alabi et al. 2023). The values recorded for melon and pea isolates were higher at pH 7 compared with the value reported for sesame globulin (Idowu et al. 2021). This might be due to the interactions between polar amino acid residues leading to electrostatic repulsions that unfold the proteins and thus expose more hydrophobic amino acids at the surface.

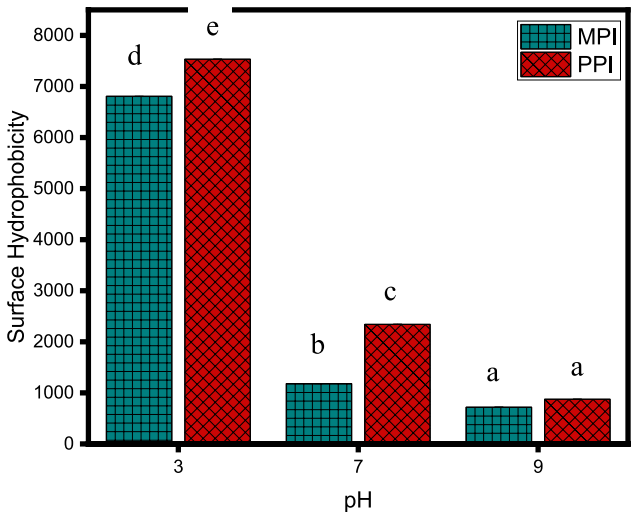


FIGURE 2 | Surface hydrophobicity of white melon and pea protein isolates. MPI = melon protein isolate; PPI = pea protein isolate.

3.5 | Fluorescence Intensity

The conformational changes in the proteins are shown in the spectra of the fluorescence intensity at pH 3, 7, and 9 (Figure 3). The maximum fluorescence intensity of 344 nm observed for the proteins suggested the dormancy of tryptophan in the protein isolates. Maximum intrinsic fluorescence intensity was observed for the protein isolates at 330 nm (Idowu et al. 2021) and at 344 nm (He et al. 2021) at all studied pHs. MPI has a higher maximum fluorescence intensity than PPI at all the examined pH levels, indicating a folded protein. This may be linked to the variation in the amino acid composition of melon and pea protein, as shown in Table 1 and their structural conformation (Alabi et al. 2020; Cheng and Cui 2021). Higher intermolecular interaction among the molecules of protein has also been implicated in lower emission spectra (He et al. 2021).

3.6 | Particle Size of White Melon and Pea Protein Isolates

The particle size distribution of MPI is typical of a bimodal pattern with a surface mean diameter of 0.005 and 0.1 μm, whilst PPI displayed an unimodal pattern with a surface mean diameter of 0.04 μm (Figure 4). An unimodal pattern has been

TABLE 2 | The secondary structure of melon and pea protein isolates.

Samples	β-sheet (%)	Random coil (%)	α-helix (%)	β-turns (%)
Melon protein	61.31 ± 0.53^{a}	—	37.63 ± 0.38^{b}	—
Pea protein	67.13 ± 0.09^{b}	—	27.97 ± 0.00^{a}	4.86 ± 0.07

Note: $n = 3$. Values with different superscripts in the same row differed significantly.

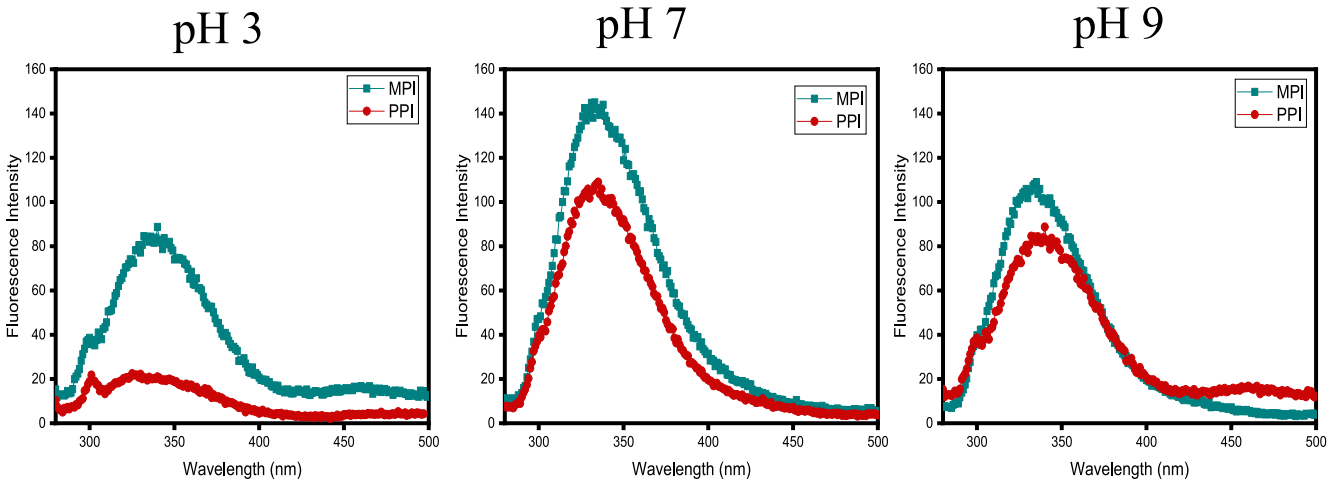


FIGURE 3 | Fluorescence intensity of white melon and pea protein isolates at varying pH. MPI = melon protein isolate; PPI = pea protein isolate.

documented for soy protein isolate (Damodaran et al. 2008). The particle size of proteins has been reported to influence solubility (John et al. 2018). Proteins with smaller particle sizes have higher differential concentration, thinner diffusion layers, and increased surface area that result in higher interfacial solubility.

Particle size is affected by processing and has also been reported to influence flow properties and the ability to reconstitute in solution (Wu et al. 2019).

3.7 | Emulsifying Properties of Melon and Pea Protein Isolates

The emulsifying activity and stability of MPI and PPI as affected by the pH is depicted in Figure 5. Emulsion capacity and stability of MPI were higher than those of PPI at both acidic and alkaline regions. However, at a neutral pH of 7, PPI showed higher emulsion capacity and relatively the same emulsion stability as MPI. Higher emulsifying properties at pH 3 may be attributed to the higher hydrophobicity of these protein isolates at this pH (Figures 2 and 6). Hydrophobic-hydrophilic balance has been documented to be enhanced by high hydrophobicity (Laval and Pak 1995). This is because the strong interfacial membrane needed for stabilization at the oil–water interface requires hydrophobic-hydrophilic balance (Laval and Pak 1995). This study suggests that white melon protein isolate may be a better functional ingredient than pea protein in oil–water emulsions such as homogenized milk and mayonnaise.

3.8 | Protein Solubility

Percentage solubility of melon and pea protein isolates at different pH is shown in Figure 6. MPI has higher protein solubility

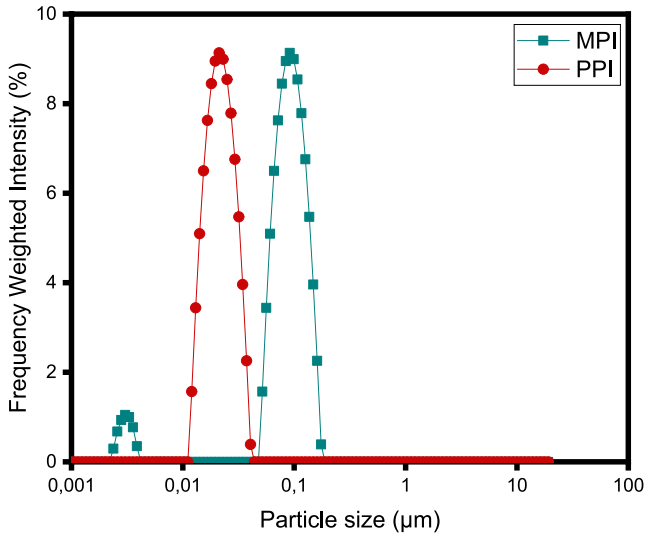


FIGURE 4 | Particle size of white melon and pea protein isolates. MPI = melon protein isolate; PPI = pea protein isolate.

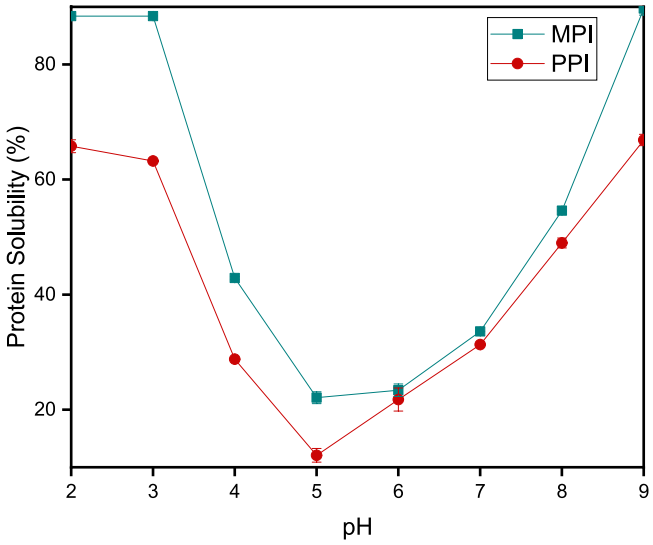


FIGURE 6 | Protein solubility of white melon and pea protein isolates. MPI = melon protein isolate; PPI = pea protein isolate.

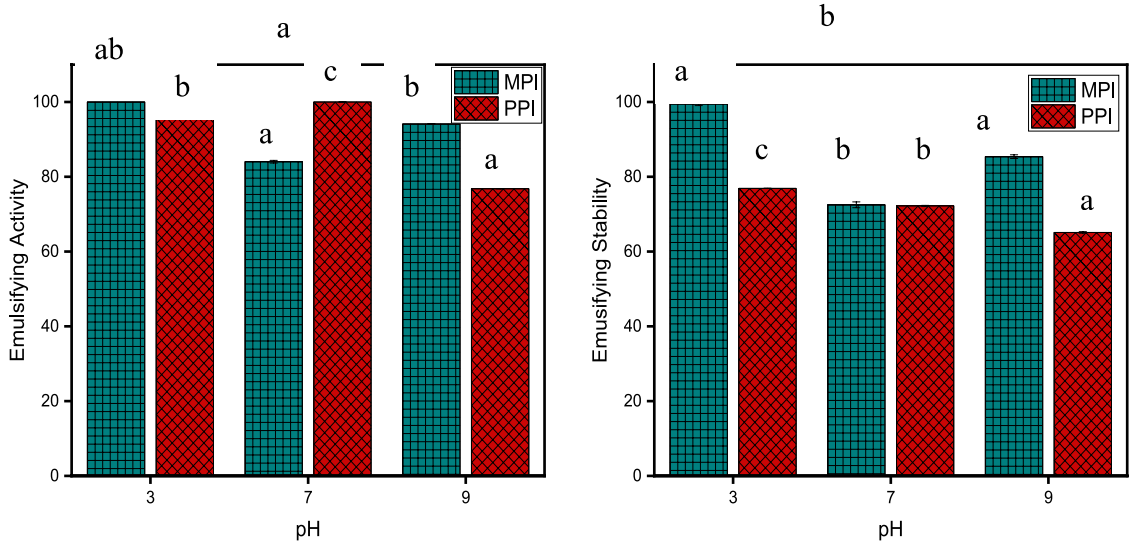


FIGURE 5 | Emulsifying properties of white melon and pea protein isolates. a: Emulsifying activity; b: Emulsifying stability. MPI = melon protein isolate; PPI = pea protein isolate.

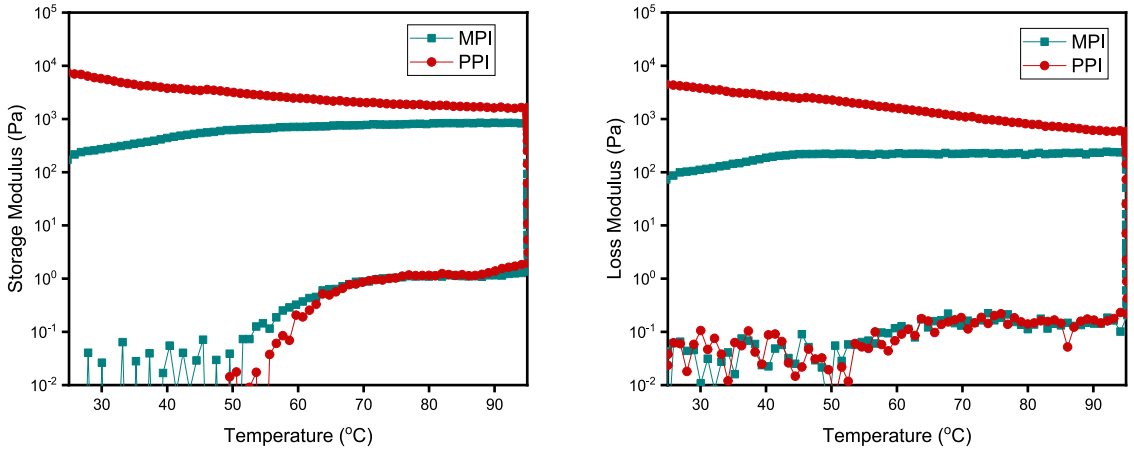


FIGURE 7 | Temperature ramp of storage modulus and loss modulus of white melon and pea protein isolates. MPI = melon protein isolate; PPI = pea protein isolate.

than PPI at all the pHs examined. This might be attributed to the synergetic impact of higher content of arginine and glutamic acid present in MPI compared to PPI (Table 1). MPI and PPI showed the least solubility at the same pH 5. Solubility of the isolates increased with increased acidity or alkalinity. This is because of the net protein charges on the isolates. MPI showed higher solubility at pH 3 compared to soybean (20%) and flaxweed (5%) (Lam and Nickerson 2013). Contrary to PPI, MPI showed high solubility at pH 3. This study suggests that melon protein isolate may be a potential food ingredient in acidic beverages compared with pea protein.

3.9 | Temperature Ramp Analysis

The comparison of the gelation process of melon and pea protein (Figure 6) reflects the unfolding of the protein chains leading to the conformational changes and exposure of reactive sites; and the formation of a gel network through protein–protein interaction. The storage modulus (G′) and loss modulus (G″) as affected by temperature during heating and cooling steps are depicted in Figure 7. There was an increase in G′ and G″ of both MPI and PPI during the heating step. As the temperature increased from about 50°C to around 80°C, the G′ and G″ of MPI increased similarly to PPI. This behavior has been linked to protein denaturation during heating, leading to the exposure of hydrophobic and hydrogen bonds otherwise buried in the molecules and thus resulting in the association of protein peptides and gel network formation (Ngo and Shahidi 2021). Upon cooling, G′ of MPI remained constant at about 1000 Pa up to 50°C and thereafter decreased as the protein isolate cooled to 20°C. The weaker gelling attribute displayed by MPI in this study may be attributable to the destruction of the three-dimensional gel network due to shear stress and the oscillatory frequency applied during the rheology experiment (Mir et al. 2021). This observation is similar to the report on quinoa protein (Tan et al. 2014) and those on album (*Chenopodium album*) and quinoa (*Chenopodium quinoa*) seed proteins (Mir et al. 2021).

4 | Conclusion

The physicochemical properties of melon protein were compared to those of pea protein. Melon protein isolates are considerably higher in arginine and methionine than pea protein. The β sheet secondary structure was the dominant structure in the proteins. Melon protein contains an acidic legumin subunit. Melon protein isolate exhibited a folded structure compared to the pea protein, as revealed by the surface hydrophobicity and fluorescence intensity data. Higher emulsifying capacity and stability were observed in melon than in pea proteins under acidic and alkaline media. MPI displayed a higher solubility profile than PPI at all pHs. MPI displayed weaker gelling attributes. It could be concluded that melon protein isolate would be a potential functional ingredient in food systems due to the highlighted properties.

Author Contributions

Eunice M. Ogunbusola: conceptualization, investigation, writing – original draft. **Opeyemi O. Alabi:** conceptualization, writing – review and editing. **Eric O. Amonsou:** resources, conceptualization.

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Ethics Statement

The authors have nothing to report.

Consent

The authors have nothing to report.

Conflicts of Interest

The authors declare no conflicts of interest.

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