work is not critical when considering present computation facilities.

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Registry No. K, 7440-09-7; Mg, 7439-95-4; Ca, 7440-70-2; aspartic acid, 56-84-8; glutamic acid, 56-86-0; asparagine, 70-47-3; glutamine, 56-85-9; serine, 56-45-1; threonine, 72-19-5; glycine, 56-40-6; alanine, 56-41-7; arginine, 74-79-3; γ-aminobutyric acid, 56-12-2; proline, 147-85-3; valine, 72-18-4; methionine, 63-68-3; ornithine, 70-26-8; lysine, 56-87-1; histidine, 71-00-1; isocitric acid, 320-77-4; citric acid, 77-92-9; sucrose, 57-50-1; glucose, 50-99-7; fructose, 57-48-7.

Supplementary Material Available: Raw data of White and Navel oranges (4 pages). Ordering information is given on any current masthead page.

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Characterization of the Kinetics of Breakdown of Protein Stabilized Oil in Water Emulsions

Robert L. Jackman,* Rickey Y. Yada, and Allan T. Paulson

The breakdown of oil in water emulsions, after initial formation, in the presence of 0.1% (w/v) whey, potato, pea, or soy proteins at pH 4–8 was monitored by measuring the absorbance at 500 nm of emulsions diluted in 0.1% (w/v) SDS after various time periods. Emulsion breakdown/absorbance decay was asymptotic, decreasing to an equilibrium value that was pH and protein dependent. Application of nonlinear modeling techniques revealed breakdown of protein-stabilized emulsions to follow first-order kinetics ($p < 0.001$). Use of a two-phase first-order model to characterize emulsion breakdown is also discussed. Results from this study emphasize the need to use appropriate statistical techniques to analyze replicated emulsion breakdown data; failure to do so could lead to biased estimates of kinetic parameters.

The ability of a protein to stabilize an oil in water emulsion is one of the most important functional properties with respect to application in food products such as finely comminuted meats, soups, cakes, and salad dressings. The dispersion of oil into water greatly increases the interfacial area and thus, also, the free energy of the interface between the two phases. As a result, a thermodynamically unfavorable environment is created, and this is reflected in an unstable emulsion. Due to their amphoteric nature and relatively large molecular weights, proteins are capable of adsorbing at the oil/water interface, thereby decreasing the interfacial tension between the two phases (Stainsby, 1986). The surface-active properties of proteins serve to lower the free energy of the oil/water interface and thus provide for a more thermodynamically stable system.

Department of Food Science, University of Guelph, Guelph, Ontario N1G 2W1, Canada (R.L.J., R.Y.Y.), and Department of Food Science and Technology, Technical University of Nova Scotia, P.O. Box 1000, Halifax, Nova Scotia B3J 2X4, Canada (A.T.P.).

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Once formed, an emulsion may break down via creaming (movement of dispersed droplets under the influence of gravity), flocculation (clustering of droplets), and/or coalescence (merging of smaller droplets into larger ones). These processes are not independent of one other (Halling, 1981; Stainsby, 1986) and are influenced by numerous factors (Kinsella, 1976; Pearce and Kinsella, 1978; Cante et al., 1979; Halling, 1981; Nakai, 1983; Voutsinas et al., 1983; Paulson and Tung, 1988). Using turbidimetry to monitor changes in particle/droplet size as a function of time, Reddy and Fogler (1981a,b) were able to delineate the different particle loss mechanisms (i.e., creaming, flocculation, coalescence) contributing to the breakdown of model paraffin oil in water emulsions by taking account of particle/droplet size distribution, surface potential, concentration, density difference, temperature, and ionic strength in their kinetic analyses.

In a rather extensive investigation of the emulsification properties of succinylated canola protein, Paulson and Tung (1988) recently demonstrated that the breakdown of emulsions measured using the turbidimetric method of Pearce and Kinsella (1978) was primarily due to creaming. The separation of aqueous phase from oil phase under the influence of gravity was controlled mainly by drainage (Paulson and Tung, 1988). Since drainage of foams has been shown to follow first-order kinetics (Mita et al., 1977; Waniska and Kinsella, 1979), by analogy, so should emulsion breakdown measured using turbidimetric methods.

Pearce and Kinsella (1978) described the breakdown of various protein-stabilized oil in water emulsions as "approximately first order", while Dagorn-Scaviner et al. (1987) recently described the separation of aqueous phase from pea globulin stabilized oil in water emulsions to occur via two successive first-order processes. In neither case, nor in subsequent studies, was supporting evidence provided for their kinetic analyses. The present study was therefore carried out to investigate and characterize the kinetics of breakdown of oil in water emulsions stabilized by whey, potato, pea, or soy proteins.

MATERIALS AND METHODS

Reagents. All chemicals and reagents used in this investigation were purchased from Fisher Scientific Co. (Fair Lawn, NJ), unless otherwise indicated. Chemicals and reagents were of reagent grade.

Sample Preparation. Acid whey protein was prepared by acidifying a 10% (w/v) solution of low-fat, low-temperature processed skim milk powder (Stacey Brothers Ltd., Mitchell, ON) to pH 4.6 with 0.1 M HCl and centrifuging at 10000*g* for 15 min to remove caseins.

Potato protein was extracted and isolated from potatoes (cv. Simcoe) by homogenizing peeled tissue in a Waring Blendor with 3 volumes of 0.025 M phosphate buffer (pH 7.0) containing 0.1% (w/v) sodium bisulfite, 0.1% (w/v) ethylenediaminetetraacetic acid (EDTA), and 0.1% (w/v) polyvinylpyrrolidone (PVP) (Sigma Chemical Co., St. Louis, MO), filtering through Miracloth (Calbiochem-Behring Corp., LaJolla, CA), and centrifuging the resulting filtrate at 10000*g* for 30 min (Paiva et al., 1982).

Air-classified pea (*Pisum sativum*) protein (53.8% protein, 27.5% carbohydrate, 8.2% moisture, 4.9% ash) was the generous gift of Y. J. Osuwu-Ansah (POS Pilot Plant Corp., Saskatoon, SK). A pea protein dispersion was prepared by mixing 2% (w/v) pea protein concentrate in 0.025 M phosphate buffer (pH 7.0) for 30 min, followed by centrifugation at 10000*g* for 30 min to remove starch and other insoluble material (Patel and Grant, 1982).

A dispersion of soy protein isolate (82.0% protein, 2.8% carbohydrate, 6.5% moisture, 4.2% ash) (Ardex F Dispersible, Frank E. Dempsey & Sons Ltd., Toronto, ON) was prepared by mixing 2% (w/v) isolate in 0.025 M phosphate buffer (pH 7.0) and centrifuging for 30 min at 10000*g*.

After gravity filtering, the whey, potato, pea, and soy protein supernatants were each dialyzed against 0.025 M phosphate buffer (pH 7.0) containing 0.02% (w/v) sodium azide for 3–5 days at 4 °C with at least five changes of buffer. The dialysates were each lyophilized and stored in a desiccator until required.

Protein Determination. All protein determinations were carried out with use of the method of Lowry et al. (1951), with bovine serum albumin (BSA) as the reference protein.

Emulsifying Activity. Protein dispersions (0.1% w/v) were prepared with acetate (sodium acetate–acetic acid; pH 4.0 and 5.0) and phosphate (sodium phosphate monobasic–sodium phosphate dibasic; pH 6.0, 7.0, and 8.0) buffers such that the ionic strength was held constant at 0.1. Protein was dispersed using an Ultra-Turrax homogenizer (Hansen & Co.) at 5000 rpm for 30 s at 20 °C, followed by equilibration for a minimum of 1 h.

Emulsifying properties of proteins were determined according to the turbidimetric method of Pearce and Kinsella (1978), with modifications. Mixtures of 4.0 mL of corn oil (Best Foods, Canada Starch Co. Inc., Toronto, ON) and 4.0 mL of 0.1% (w/v) protein dispersion were homogenized at 12000 rpm for 1 min at 20 °C on an Ultra-Turrax homogenizer. At various times (i.e., 0, 0.5, 1, 1.5, 2, 3, 4, 5, 6, 8, and 10 min) after homogenization, 0.05-mL aliquots of emulsion were carefully drawn from the test tube bottom and diluted in 10 mL of 0.1% (w/v) sodium dodecyl sulfate (SDS) in phosphate buffer (pH 7.0). The absorbance (A) of diluted emulsions was measured in duplicate against a buffer blank at 500 nm on a UV–visible recording spectrophotometer (Model UV-260, Shimadzu Corp., Kyoto, Japan). The absorbance readings were used as a measure of emulsifying activity.

Emulsion Breakdown. The rate law for emulsion breakdown/absorbance decay can be expressed as

$$-dA/dt = kA^n \tag{1}$$

where A is the absorbance at 500 nm, t is the time, n is the reaction order, and k is the rate constant. By integrating eq 1, eq 2 and 3 were derived, where A_0 is the initial absorbance at 500 nm (i.e., the absorbance at time $t = 0$ min).

$$A = A_0e^{-kt} \qquad n = 1 \tag{2}$$

$$A^{1-n} = A_0^{1-n} + (n-1)kt \qquad n \neq 1 \tag{3}$$

The denaturation/coagulation of proteins that occurs upon their adsorption at the oil/water interface (MacRitchie and Owens, 1969; Henson et al., 1970) is generally an irreversible process (MacRitchie, 1978). Desorption of such protein from the oil/water interface into the aqueous (i.e., drainage) phase will result in a suspension, or dispersion, of insoluble/coagulated protein that may contribute significantly to the absorbance of diluted emulsions measured at any given time. In addition, a portion of the dispersed oil phase may be present as very fine globules that do not cream but contribute to an equilibrium absorbance. A correction for this contribution may be made by incorporating an equilibrium term into eq 2 and 3, which leads to

$$A - A_e = (A_0 - A_e)e^{-kt} \qquad n = 1 \tag{4}$$

and

$$(A - A_e)^{1-n} = (A_0 - A_e)^{1-n} + (n-1)kt \qquad n \neq 1 \tag{5}$$

where A_e is the equilibrium absorbance at time $t = t_e$ (i.e., $A = A_e$ at $t \leq t_e$).

Dagorn-Scaviner et al. (1987) reported emulsion breakdown as a succession of first-order processes where each kinetic phase was characterized by its rate constant (k_i), its initial activity (i.e., A_i), and its duration (Δt_i, where $\Delta t_1 = t_1$ and $\Delta t_2 = t_e - t_1$), for $i = 1, 2$. The two-phase first-order decay model, corrected for equilibrium absorbance, may be defined by

$$A - A_e = (A_1 - A_e)e^{-k_1t} \qquad t < t_1 \tag{6}$$

$$A - A_e = (A_2 - A_e)e^{-k_2t} \qquad t_1 < t < t_e \tag{7}$$

where t_1 is the time at which eq 6 and 7 are equal.

Data Analysis. The NLIN procedure of the Statistical Analysis System (SAS) package was used to generate least-squares estimates of the parameters of the nonlinear models described

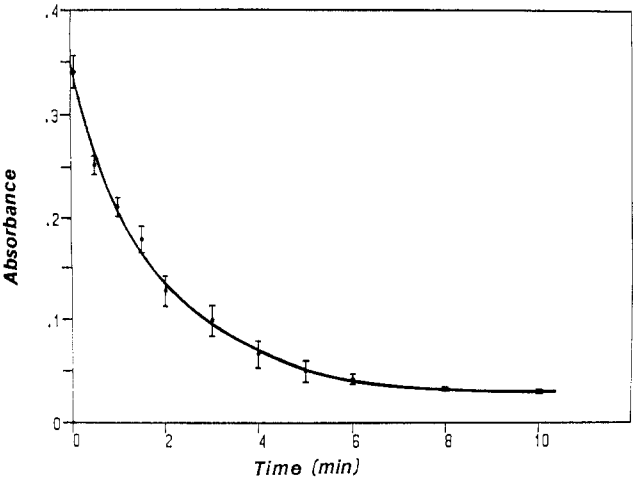

Figure 1. Typical asymptotic breakdown/decay of protein stabilized oil in water emulsions. Absorbance of diluted oil in water emulsion stabilized by 0.1% (w/v) potato protein at pH 8 was measured at 500 nm. Plotted points and associated error bars represent means and standard deviations calculated from three replicates at each time.

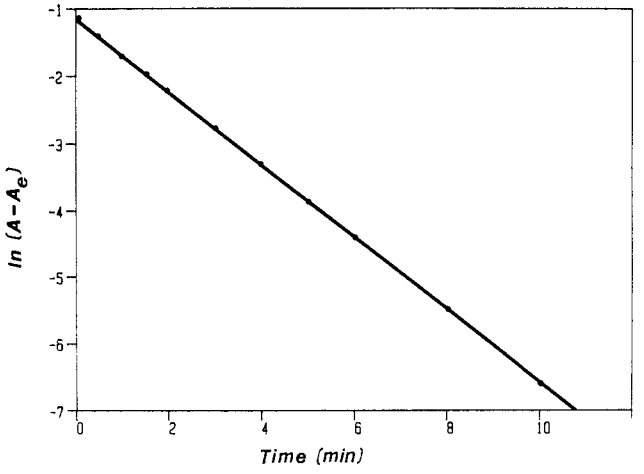

Figure 2. First-order kinetic interpretation of experimental emulsion breakdown data depicted in Figure 1. Absorbance of diluted oil in water emulsions stabilized by 0.1% (w/v) potato protein at pH 8 was measured at 500 nm. Plotted points at each time are means from three replicates (cf. Table I); $A_0 = 0.346$, $A_e = 0.030$, $k = -0.542$ min^{-1}.

first by eq 4 and 5 and then by eq 6 and 7, using the following initial starting values: $A_0 = A_1 = 0.400$, $A_2 = 0.200$, $A_e = 0.005$, $k = k_1 = -0.010$ min^{-1}, $k_2 = -0.001$ min^{-1}, and $n = 2.0$. In the NLIN procedure, the starting values specified for the parameters were first examined, and then, by applying the iterative method of Marquardt, residuals were regressed onto the partial derivatives of each of the models with respect to parameters, until successive iterations converged (SAS Institute Inc., 1985). The maximum number of iterations was arbitrarily set at 50. Absorbance data within 10% of estimated A_e were omitted from the analyses.

Three separate replicates of the experiment were carried out, except for whey protein, which was replicated six times at each combination of pH and time.

RESULTS AND DISCUSSION

Absorbance data for each of whey, potato, pea, and soy protein stabilized oil in water emulsions at pH 4–8 are provided in Table I. Asymptotic decay of absorbance, or emulsifying activity (Pearce and Kinsella, 1978), was observed for all protein–pH combinations examined (e.g., Figure 1). Such decay is typically described by a first (i.e., eq 2 and 4) or higher order model (i.e., eq 3 and 5). All protein-stabilized oil in water emulsions examined in this

Table I. Absorbance[a] of Oil in Water Emulsions Stabilized by Whey, Potato, Pea, and Soy Proteins at pH 4–8 after Various Time Periods[b]

protein	pH	time, min										
		0	0.5	1	1.5	2	3	4	5	6	8	10
whey	4	0.270 (0.015)	0.233 (0.019)	0.206 (0.016)	0.185 (0.015)	0.178 (0.015)	0.111 (0.015)	0.079 (0.011)	0.066 (0.015)	0.053 (0.015)	0.025 (0.011)	0.018 (0.004)
	5	0.355 (0.013)	0.331 (0.014)	0.317 (0.013)	0.293 (0.012)	0.263 (0.013)	0.180 (0.012)	0.169 (0.020)	0.150 (0.019)	0.141 (0.020)	0.071 (0.013)	0.068 (0.011)
	6	0.479 (0.009)	0.482 (0.010)	0.448 (0.013)	0.428 (0.012)	0.420 (0.014)	0.353 (0.017)	0.337 (0.013)	0.328 (0.016)	0.327 (0.018)	0.203 (0.012)	0.171 (0.016)
	7	0.530 (0.020)	0.529 (0.017)	0.493 (0.018)	0.483 (0.019)	0.482 (0.020)	0.405 (0.020)	0.389 (0.023)	0.382 (0.019)	0.390 (0.019)	0.267 (0.024)	0.223 (0.021)
	8	0.571 (0.020)	0.584 (0.023)	0.558 (0.026)	0.546 (0.030)	0.554 (0.030)	0.484 (0.033)	0.468 (0.031)	0.470 (0.031)	0.474 (0.029)	0.357 (0.031)	0.344 (0.035)
potato	4	0.289 (0.011)	0.244 (0.013)	0.208 (0.015)	0.167 (0.016)	0.159 (0.021)	0.070 (0.021)	0.056 (0.014)	0.048 (0.016)	0.026 (0.011)	0.009 (0.001)	0.008 (0.000)
	5	0.235 (0.014)	0.175 (0.023)	0.124 (0.016)	0.093 (0.020)	0.080 (0.016)	0.049 (0.011)	0.025 (0.003)	0.019 (0.001)	0.017 (0.001)	0.015 (0.002)	0.015 (0.001)
	6	0.322 (0.008)	0.287 (0.013)	0.231 (0.014)	0.184 (0.011)	0.177 (0.015)	0.079 (0.015)	0.067 (0.015)	0.044 (0.008)	0.041 (0.008)	0.023 (0.003)	0.025 (0.003)
	7	0.326 (0.013)	0.273 (0.013)	0.214 (0.011)	0.198 (0.006)	0.161 (0.014)	0.082 (0.012)	0.074 (0.011)	0.058 (0.010)	0.041 (0.004)	0.037 (0.002)	0.037 (0.005)
	8	0.342 (0.016)	0.251 (0.010)	0.211 (0.010)	0.178 (0.014)	0.128 (0.015)	0.100 (0.015)	0.065 (0.014)	0.050 (0.011)	0.042 (0.005)	0.032 (0.002)	0.031 (0.002)
pea	4	0.245 (0.021)	0.204 (0.015)	0.186 (0.008)	0.150 (0.011)	0.146 (0.006)	0.077 (0.008)	0.066 (0.014)	0.046 (0.003)	0.036 (0.001)	0.032 (0.001)	0.030 (0.001)
	5	0.127 (0.005)	0.043 (0.008)	0.019 (0.003)	0.013 (0.002)	0.012 (0.002)	0.009 (0.001)	0.005 (0.001)	0.006 (0.001)	0.006 (0.001)	0.005 (0.001)	0.006 (0.001)
	6	0.219 (0.013)	0.174 (0.016)	0.133 (0.024)	0.106 (0.016)	0.072 (0.014)	0.030 (0.006)	0.019 (0.003)	0.016 (0.001)	0.016 (0.003)	0.013 (0.001)	0.013 (0.001)
	7	0.284 (0.005)	0.240 (0.010)	0.181 (0.008)	0.168 (0.008)	0.160 (0.012)	0.067 (0.021)	0.036 (0.008)	0.036 (0.008)	0.039 (0.008)	0.023 (0.001)	0.023 (0.002)
	8	0.301 (0.011)	0.256 (0.018)	0.185 (0.025)	0.168 (0.014)	0.163 (0.018)	0.092 (0.013)	0.066 (0.015)	0.060 (0.014)	0.055 (0.014)	0.032 (0.003)	0.036 (0.006)
soy	4	0.067 (0.011)	0.015 (0.002)	0.014 (0.001)	0.013 (0.001)	0.012 (0.001)	0.011 (0.001)	0.010 (0.001)	0.009 (0.001)	0.008 (0.001)	0.008 (0.001)	0.007 (0.001)
	5	0.097 (0.012)	0.019 (0.002)	0.020 (0.005)	0.016 (0.001)	0.013 (0.001)	0.011 (0.001)	0.008 (0.001)	0.009 (0.001)	0.009 (0.001)	0.006 (0.000)	0.006 (0.001)
	6	0.372 (0.014)	0.375 (0.014)	0.350 (0.015)	0.332 (0.016)	0.336 (0.015)	0.268 (0.017)	0.255 (0.027)	0.237 (0.030)	0.227 (0.029)	0.126 (0.018)	0.130 (0.022)
	7	0.423 (0.008)	0.439 (0.008)	0.418 (0.019)	0.402 (0.013)	0.405 (0.014)	0.335 (0.014)	0.306 (0.025)	0.261 (0.027)	0.309 (0.021)	0.150 (0.009)	0.152 (0.022)
	8	0.469 (0.010)	0.484 (0.009)	0.460 (0.006)	0.456 (0.010)	0.444 (0.010)	0.391 (0.007)	0.349 (0.013)	0.368 (0.018)	0.349 (0.008)	0.235 (0.026)	0.284 (0.015)

[a] Absorbance of emulsions diluted 1:200 in 0.1% (w/v) SDS (pH 7) was measured at 500 nm. [b] Tabulated values represent means where $n = 3$, except whey proteins where $n = 6$. Values in parentheses represent standard deviations of respective means.

Table II. Coefficient of Multiple Determination (R^2) and F Statistic Associated with Fitting of Emulsion Breakdown Data to First-Order and Two-Phase First-Order Models

		first-order		two-phase first-order	
protein	pH	R^2	F	R^2	F
whey	4	0.771	451.7	0.768	446.9
	5	0.757	666.6	0.757	496.0
	6	0.850	2616.7	0.849	1939.2
	7	0.716	1584.1	–[a]	–
	8	0.527	1111.4	0.232	394.5
potato	4	0.888	417.9	0.887	418.4
	5	0.859	280.8	0.859	280.8
	6	0.933	757.6	0.935	457.7
	7	0.942	1004.9	0.943	1010.8
	8	0.931	777.4	0.926	731.5
pea	4	0.900	622.1	0.900	622.1
	5	0.954	620.7	–[a]	–
	6	0.860	277.9	0.861	278.0
	7	0.922	649.1	0.927	402.9
	8	0.864	421.7	0.864	311.5
soy	4	0.956	814.8	0.974	1018.7
	5	0.903	299.1	0.293	23.6
	6	0.831	828.9	–[a]	–
	7	0.867	1207.8	0.887	825.8
	8	0.893	2988.6	0.892	2195.5

[a] The residual sums of squares failed to converge after 50 iterations.

study displayed a first-order decay in absorbance (i.e., $n = 1$, $p < 0.001$), as exemplified in Figure 2 for potato protein at pH 8; i.e., plots of ln $(A - A_e)$ versus time resulted in straight lines of slope $-k$ and intercepts on the ordinate of ln $(A_0 - A_e)$.

With the exception of soy protein at pH 5 and whey protein at pH 8, fitting the absorbance data to the two-phase first-order model (eq 6 and 7) was also found to be highly significant ($p < 0.001$), as indicated by large coefficients of multiple determination (R^2) and F statistics (Table II). The observed R^2 values associated with the first-order and two-phase first-order models for each protein–pH combination, with the exception of the above, were effectively the same. The values for the F statistic generously exceeded 4 times their corresponding critical F ratios, thereby allowing the fitted models/equations to be used as predictors (Draper and Smith, 1981). Values of the F statistic were generally greater for emulsions modeled by "simple" first-order kinetics than by two-phase first-order kinetics (Table II).

In general, the first-order and two-phase first-order models explained the variability in the data set equally well. This suggests, however, that the two-phase model is overparameterized (Draper and Smith, 1981); i.e., a break in absorbance decay, which would indicate a change in breakdown mechanism, is not significant. The presence of a break may be artefactual, dependent upon the experimental conditions employed, i.e., the time periods chosen. The first-order model is therefore proposed as the most appropriate for interpretation of emulsion breakdown/absorbance decay in this study: It has fewer parameters to be estimated and is easiest to explain. Use of the first-order model is consistent with previous empirical observations (Pearce and Kinsella, 1978).

The mechanisms responsible for oil in water emulsion breakdown (i.e., creaming, flocculation, coalescence) are interdependent and are influenced by such factors as protein concentration, viscosity of the continuous phase, oil droplet size distribution, and surface charge of dispersed droplets (Halling, 1981; Dickinson and Stainsby, 1982; Paulson and Tung, 1988). The rate of creaming is governed by Stokes law (Halling, 1981; Paulson and Tung, 1988) and generally increases as both the droplet size distribution and the density difference between dispersed and aqueous phases increase and as the apparent viscosity of the continuous phase decreases. The formation of very small droplets during emulsification increases the effective viscosity of the continuous phase and reduces the effective density difference between dispersed and continuous phases (Stainsby, 1986). Very small droplets formed during emulsification have little influence on creaming rate, relative to larger droplets, since creaming rate is also proportional to the square of the radius of dispersed droplets.

The droplet size distribution in a given emulsion may affect flocculation and coalescence as a result of collisions between fast-moving larger droplets and slow-moving small droplets. The occurrence of flocculation and/or coalescence tends to enhance creaming rate since flocculation increases effective droplet size and coalescence increases the actual droplet size (Paulson and Tung, 1988).

If relative droplet size is small upon emulsification, and flocculation and/or coalescence is sufficiently delayed, a lag in (the rate of) absorbance decay may be observed. (A lag period of up to 1.5 min was observed for whey and soy proteins at pH 6–8 in the present study; Table I.) In addition, Pearce and Kinsella (1978) demonstrated that as the concentration of a particular protein increased, emulsion droplet size decreased, thereby enhancing stability with respect to creaming. In these cases emulsion breakdown/absorbance decay exhibits sigmoidal behavior. The two-phase first-order model may be more appropriate for the kinetic interpretation of such emulsion breakdown behavior, the lag period being represented by the first of the two phases. If relative droplet size is large upon emulsification, absorbance decay may be initially very rapid, until the size distribution of dispersed oil droplets becomes more homogeneous. The two-phase first-order model may then be more appropriate in describing the breakdown of these emulsions.

Under the test conditions of this investigation (i.e., 0.1% (w/v) protein concentration, initial volume fraction of dispersed phase, $\phi = 0.5$), the breakdown of oil in water emulsions stabilized by whey, potato, pea, or soy proteins was characterized in terms of the first-order rate constant (k) and the initial absorbance of diluted emulsions (A_0) at 500 nm. The initial absorbance is equivalent to the emulsifying activity index (EAI) defined by Pearce and Kinsella (1978), and emulsion stability (ES) has traditionally and conveniently been expressed as the half-life of EAI, i.e., ES = ln $(0.5)/k$, assuming that emulsion breakdown/absorbance decay follows first-order kinetics (Pearce and Kinsella, 1978). In the event that the two-phase first-order model best describes the emulsion breakdown data, ES would be a function of both phases of the biphasic plot defined by eq 6 and 7. These emulsification parameters (i.e., EAI and ES) are rapid and simple to obtain, and their derivation is based on theoretically sound principles.

The parameters obtained using turbidimetric methods do not solely reflect the functionality of the protein per se, but rather they are a reflection of the whole system (Stainsby, 1986). Without knowledge of the various factors characterizing the given test system (e.g., droplet size distribution, surface charge, pH, etc.), delineation of the mechanisms responsible for emulsion breakdown is not possible (Reddy and Fogler, 1981a). However, to assess the relative emulsification behavior of a protein for its potential application in a given food system, delineation of breakdown mechanisms is secondary. Of greater im-

portance is the ability to quantify this behavior so that relative comparisons to other proteins can be made, thus improving the efficiency of protein selection/application.

The turbidimetric method of Pearce and Kinsella (1978) provides a rapid and simple means by which to quantitate the emulsification behavior of proteins under fairly well defined conditions, through first-order (or two-phase first-order) kinetic interpretation of emulsion breakdown/absorbance decay. Choice of the appropriate kinetic model can often be made through simple visual examination of trends in the raw data. It should be pointed out, however, that without appropriate/adequate replication biased estimates of the emulsification parameters (i.e., EAI and ES) will result. The kinetics of emulsion breakdown have rarely, if ever, been statistically examined. However, the use of statistical analyses in the evaluation and interpretation of emulsion breakdown data is imperative if the empirical nature of protein functionality methodology is to be avoided.

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