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Linear and Non-Linear Kinetics in the Synthesis and Degradation of Acrylamide in Foods and Model Systems

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Isothermal acrylamide formation in foods and asparagine-glucose model systems has ubiquitous features. On a time scale of about 60 min, at temperatures in the approximate range of 120−160°C, the acrylamide concentration-time curve has a characteristic sigmoid shape whose asymptotic level and steepness increases with temperature while the time that corresponds to the inflection point decreases. In the approximate range of 160−200°C, the curve has a clear peak, whose onset, height, width and degree of asymmetry depend on the system's composition and temperature. The synthesis-degradation of acrylamide in model systems has been recently described by traditional kinetic models. They account for the intermediate stages of the process and the fate of reactants involved at different levels of scrutiny. The resulting models have 2–6 rate constants, accounting for both the generation and elimination of the acrylamide. Their temperature dependence has been assumed to obey the Arrhenius equation, i.e., each step in the reaction was considered as having a fixed energy of activation. A proposed alternative is constructing the concentration curve by superimposing a Fermian decay term on a logistic growth function. The resulting model, which is not unique, has five parameters: a hypothetical uninterrupted generation-level, two steepness parameters; of the concentration climbs and fall and two time characteristics; of the acrylamide synthesis and elimination. According to this model, peak concentration is observed only when the two time constants are comparable. The peak's shape and height are determined by the gap between the two time constants and the relative magnitudes of the two "rate" parameters. The concept can be extended to create models of non-isothermal acrylamide formation. The basic assumption, which is yet to be verified experimentally, is that the momentary rate of the acrylamide synthesis or degradation is the isothermal rate at the momentary temperature, at a time that corresponds to its momentary concentration. The theoretical capabilities of a model of this kind are demonstrated with computer simulations. If the described model is correct, then by controlling temperature history, it is possible to reduce the acrylamide while still accomplishing much of the desirable effects of a heat process.

Keywords acrylamide, non-linear kinetics, non-isothermal reactions, Logistic-Fermi model, mathematical modeling, food safety, fried foods

INTRODUCTION

Acrylamide formation is one of the chemical consequences of the exposure of foods to high temperatures, like those that exist in frying or baking. Since the acrylamide presence has been identified as a potential health risk, the chemistry and kinetics of its synthesis have received considerable attention in recent years (Friedman, 2003; Taeymans et al., 2004; Friedman and Mottran, 2005; Claeys et al., 2005a). A comprehensive list of references covering the various aspects of acrylamide formation in foods can be found in the web page http://www.foodrisk.org/acrylamide_form_reduction.cfm. Recently, the relationship between dietary acrylamide and colon and rectal cancer in Swedish women has been challenged (Mucci et al., 2006). But since the topic of this communication is the acrylamide formation kinetics and not its toxicology, this should not concern us here.

It has been early established that acrylamide is the product of a set of complex reactions between carbonyl groups available in foods through starch and sugars, primarily glucose and

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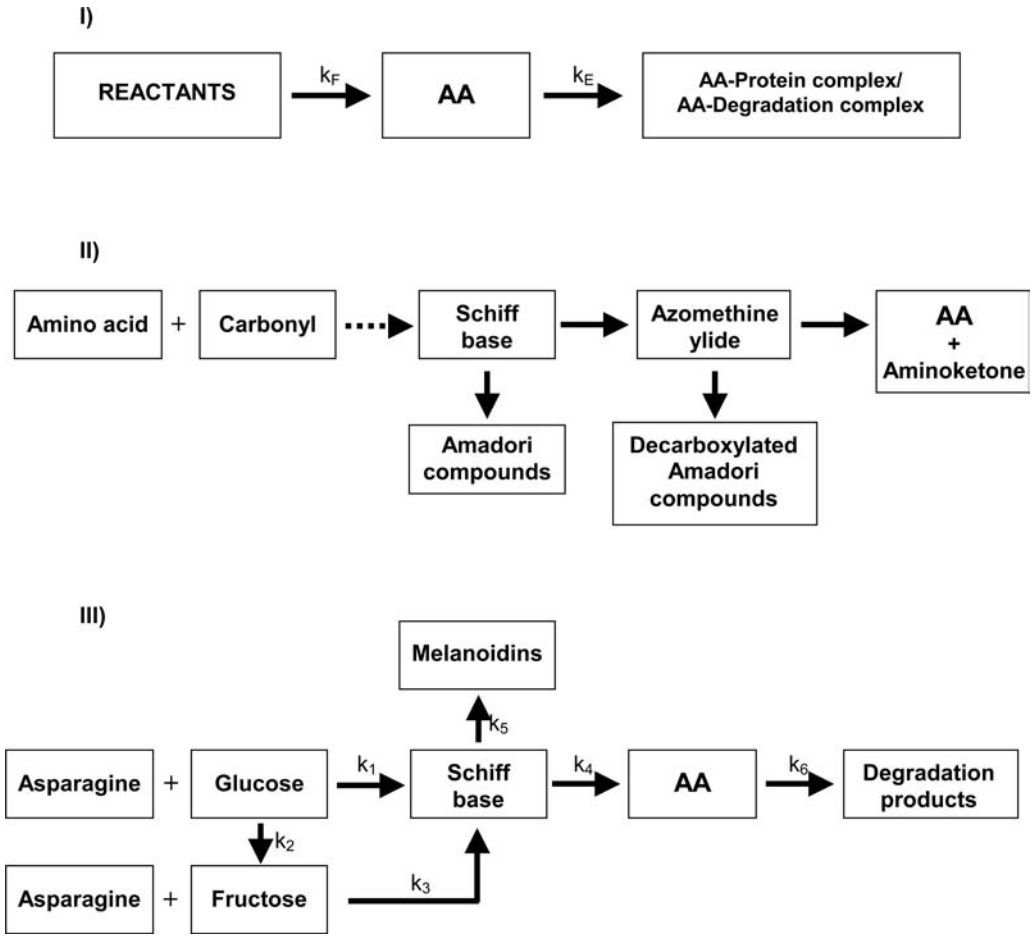

Figure 1 Schematic view of the different mechanisms that generate and eliminate acrylamide in foods and model systems. I – according to Claeys et al. (2005b), II – according to Stadler et al. (2004) and III – according to Knol et al. (2005).

fructose, and proteins, notably through the amino acid asparagine (Fig.1). Other pathways have also been proposed (Mottram et al., 2002; Becalski et al., 2003, Wedzicha et al., 2005) and these may be responsible for at least some of the acrylamide synthesis in foods. Measurable amounts of acrylamide are only formed in foods exposed to temperatures above about 120 °C. However, at temperatures above about 160 °C, the formed acrylamide is eliminated and its residual amount depends on the temperature and the exposure duration (Fig.2). In both real foods and model systems, the acrylamide's formation can follow several, sometimes interactive pathways that involve the synthesis and degradation of intermediate compounds. The kinetics of the acrylamide formation and elimination has been described by several different mathematical models of different degrees of complexity. These models were derived from dynamic mass balance considerations or a reactions network approach. Almost invariably, the models have been based on the assumption that all the intermediate reactions follow the first order kinetics and therefore have characteristic rate constants. It has also been assumed that the temperature dependence of these rate constraints follows the Arrhenius model (e.g., Knol et al., 2005; Claeys et al., 2005b). The kinetic models based on these assumptions indeed capture the essence of the acrylamide concentration's rise and, at very high temperatures, rise and eventual fall. Hence, they serve as an excellent conceptual framework to understanding the process of acrylamide formation and elimination. They also explain the synthesis and degradation of intermediate compounds and the generation of melanoidins, which are usually the final product of the Maillard reaction at high temperatures.

The assumption that each and every intermediate reaction in the acrylamide synthesis and degradation can be characterized by a single rate constant, although convenient and attractive, is yet to be validated by independent tests. The same can be said about the idea that all these rate constants are only temperature but not time dependent. Although these two assumptions are probably justified for simple model systems, where the number of pathways is limited, this might not be the case in real foods. One can argue that because of the complex character and interactive nature of the molecular mechanisms, even the isothermal logarithmic rates of the acrylamide concentration synthesis and degradation, as well as those of at least some of the

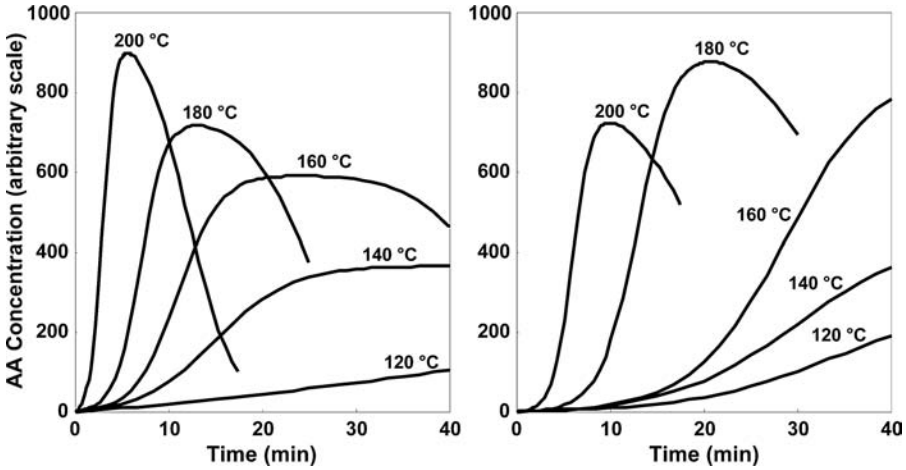

Figure 2 Schematic view of two kinds of typical acrylamide's isothermal concentration-time curves as reported in the literature. Notice that the peak at 200 °C can be either higher or lower than that at 180 °C, left and right, respectively, and that at the same temperature (e.g., 160 °C) a peak concentration can or cannot be observed within the experiment duration.

intermediate compounds, are temperature *and* time dependent – see below. Hence, it would be very *unlikely* that most, let alone all the intermediate reactions that are involved in acrylamide formation, have a fixed energy of activation as presently assumed. Or in other words, if the momentary synthesis and degradation rates of the acrylamide in a given environment are functions of the reaction's *temperature history*, there would be no reason to assume that they must be produced by a combination of reaction rates that are themselves only temperature dependent as required by the Arrhenius equation. Had the Arrhenius equation been a valid model for complex chemical systems, the exponential rate of acrylamide formation, or degradation at the final step of the reaction, at 150 °C let us say, would have to be exactly the same if the food had been kept at 200 °C for 30 min prior to reaching this temperature or left at room temperature for about the same time before reaching 150 °C in two minutes, for example. It is unknown to us whether the traditional approach to kinetic modeling in food chemistry has ever been validated in this manner. Had this been done, we would be surprised if it had passed the test, especially in reactions that occur in fried or baked foods. We suspect that history of independent rates would be a very unlikely characteristic of complex chemical and biochemical reactions in general (Peleg et al., 2004) and not only in acrylamide synthesis. The often overlooked the deficiency of the Arrhenius model, when used for complex reactions, is that time does not appear in the equation as an independent variable. Consequently, the logarithmic rate of any given reaction according to this model is determined by the momentary temperature alone. The Arrhenius model was originally developed for reactions between gases under low pressure. In these, except during their brief interaction, the molecules remain chemically unchanged, *regardless of temperature*. In contrast, the reactants and the products of the Amadori and Maillard reactions that are responsible for the acrylamide molecules formation in foods are continuously changing. Moreover, for the Arrhenius model application, the range of 100−200 °C, or 373−473 °K, where the acrylamide formation changes from marginal to peak production followed by a sharp decline, is converted into the unimpressive $0.0027-0.0021\,^{\circ}K^{-1}$ range for no apparent reason. Similarly, the logarithmic conversion of the intermediate reactions' "rates," the k's of the traditional first order kinetics model, even if they were uniquely defined, might not serve any useful purpose if their magnitudes do not change by several orders of magnitude within the pertinent temperature range. In light of the above, and because the evidence that all the intermediate reactions must follow the first order kinetics is less than conclusive, there can be room for trying a different approach to modeling acrylamide formation in foods and model systems which does not require any of the traditional assumptions (Peleg et al., 2004).

The objectives of this article are to present such a modeling approach and to explore its potential application to the kinetics of acrylamide synthesis and degradation under isothermal and non isothermal conditions. It should be stated from the outset that the presented alternative models are not intended to replace or displace the mechanistic models constructed on the basis of insight into the complex chemistry of the processes involved. The proposed models only provide a complementary picture of the acrylamide formation kinetics when viewed from a different angle. These models are based on the admission that knowledge of the intermediate steps of the reaction might be incomplete. Their acknowledged weakness is that they do not explain why or how the process proceeds. But we believe, and will try to demonstrate, that such models can be useful in quantitative characterization acrylamide formation patterns in foods and the interpretation of experimental data. And, although yet to be validated experimentally, models of the proposed kind might be also used to simulate and predict *non-isothermal* generation of acrylamide, in foods on the basis of isothermal data, gathered in the laboratory.

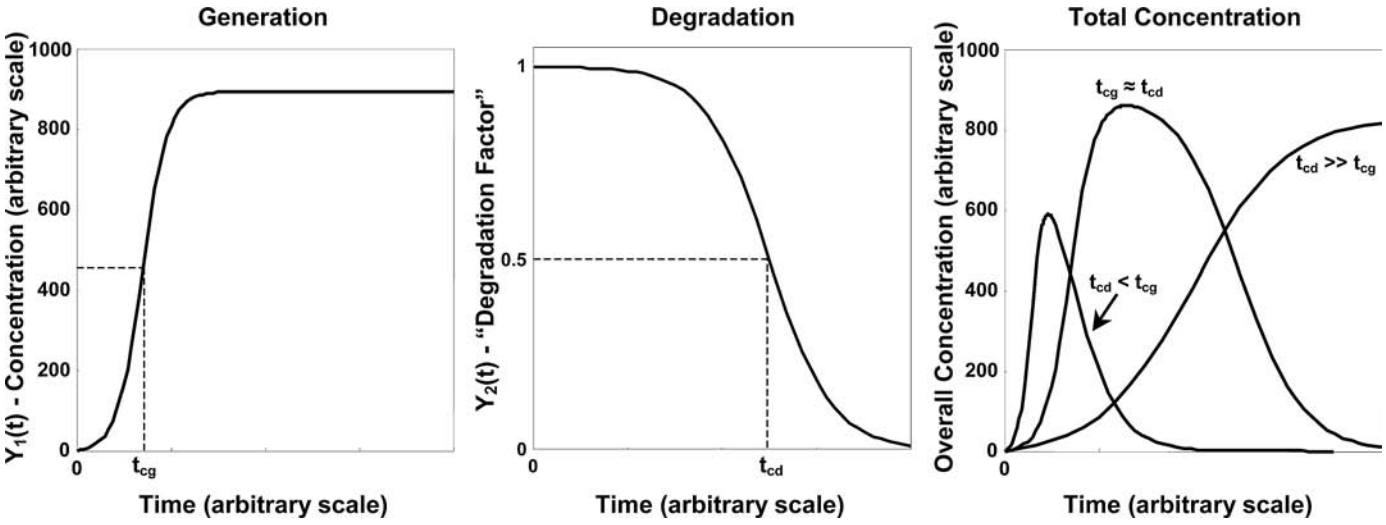

Figure 3 Schematic view of the construction of the Logistic-Fermi model. Notice that all three patterns; narrow peak, wide asymmetric peak and a sigmoid growth, can be produced by a single model (in this case, Eq. 4).

ISOTHERMAL FORMATION AND DEGRADATION

Isothermal Generation of Acrylamide

Published results on the formation of acrylamide in both foods and model systems (e.g., Eldmore et al., 2005; Knol et al., 2005) indicate that depending on the temperature, the acrylamide content can follow any of the patterns shown schematically in Fig. 2. At temperatures below about 100−120 °C acrylamide is not formed in any measurable amounts on a time scale of 30–60 min. At temperatures between about 100 °C to about 160 °C, the curves depicting the acrylamide concentration's growth have a characteristic sigmoid shape. Above this temperature, the curves have a clearly discernible peak, which becomes sharper and shifted more to the right (to shorter time that is) as the temperature rises to the neighborhood of 200 °C. This consistent observation—see below—suggests that regardless of its detailed reaction kinetics, the rate of the acrylamide production increases with temperature, but at the same time so does its degradation rate. Unless there is a compelling reason to think otherwise, neither the synthesis nor the degradation process has to follow any particular kinetics or reaction order universally. Consequently, it would be safer to describe them by empirical models that capture their main features. The choice of a particular model should be guided solely by mathematical simplicity considerations and the possibility to assign intuitive meaning to the resulting expression's parameters.

Here is an example of such a model. Consider that the uninterrupted isothermal formation of the acrylamide, $Y_1(t)$, follows the shifted logistic function (Peleg, 1996; 2006; Corradini and Peleg, 2005; 2006a):

$$Y_1(t) = \frac{a(T)}{1+\exp\{k_g(T)[t_{cg}(T)-t]\}} - \frac{a(T)}{1+\exp\left[k_g(T)\,t_{cg}(T)\right]} \tag{1}$$

where a(T), k_g(T) and t_{cg}(T) are temperature dependent coefficients. (The subscript 'g' stands for "generation" or "growth".) As shown schematically in Fig. 3-left, the location of the concentration growth curve's inflection point is determined by t_{cg}(T) and the steepness of its climb around it by k_g(T). The rationale of introducing the second term at the right side of the equation is that it forces the model to satisfy the condition that $Y_1(0) = 0$, thus avoiding the need of truncation and the introduction of an "If statement" into the model's equation.

Also consider that the degradation of the formed acrylamide is regulated by a "degradation factor," $Y_2(t)$, in the form of a Fermian term. The Fermi distribution function is the mirror image of the logistic function, see Fig.3-middle. Or mathematically:

$$Y_2(t) = \frac{1}{1+\exp\{k_d(T)[t-t_{cd}(T)]\}} \tag{2}$$

where k_d(T) and t_{cd}(T) are temperature dependent coefficients. (The subscript "d" stands for "degradation" or "decay".) As before, the inflection point of $Y_2(t)$ is marked by t_{cd}(T) and the curve's steepness around it is characterized by k_d(T).

The acrylamide isothermal concentration curve C(t) vs. t, at any given temperature T, would be the product of $Y_1(t)$ and $Y_2(t)$, i.e. (Peleg, 1996),

$$C(t) = Y_1(t)\cdot Y_2(t) \tag{3}$$

or:

$$C(t) = \left[\frac{a(T)}{1+\exp\{k_g(T)[t_{cg}(T)-t]\}} - \frac{a(T)}{1+\exp[k_g(T)t_d(T)]}\right]\cdot\frac{1}{1+\exp[k_d(T)[t-t_{cd}(T)]\}} \tag{4}$$

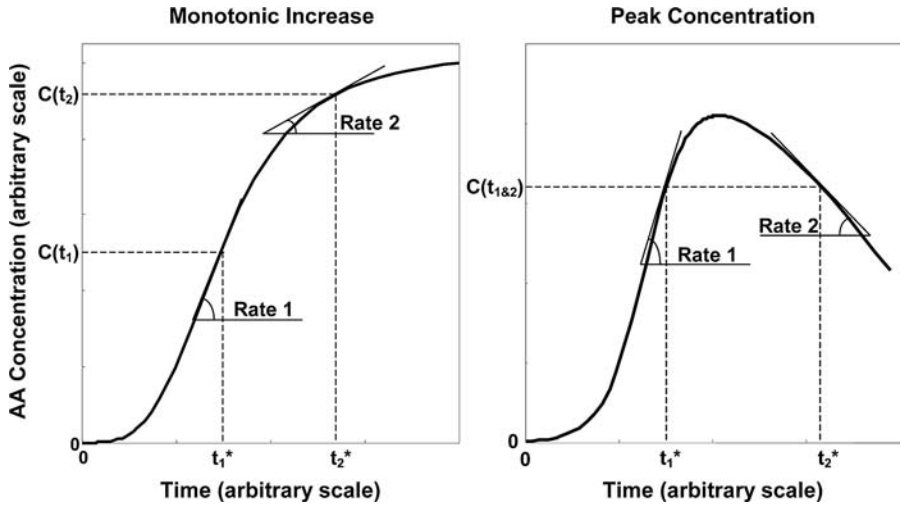

Figure 4 Schematic view of the changing isothermal rates of acrylamide formation in foods. Notice that when the concentration curve has a peak within the experimental heat treatment duration (right plot), not only does the curve's slope change direction but also the same concentration is reached at two different times.

According to this model, see Fig. 3-right, the acrylamide's concentration level is primarily (but not solely) determined by a(T) which serves as a "scale factor". The steepness of the concentration's buildup is primarily regulated by $k_g(T)$ and of its degradation, whenever it is observable within the experiment's duration, by $k_d(T)$. The overall shape of the curve is primarily determined by the relationship between $t_{cg}(T)$ and $t_{cd}(T)$ as shown in the figure. If $t_{cd}(T) \gg t_{cg}(T)$, the curve will appear sigmoid for a considerable time. But if $t_{cg}(T) \sim t_{cd}(T)$, a true peak concentration would appear, whose height, width and degree of symmetry (or asymmetry-see Fig. 4) would depend on the ratio between $k_g(T)$ and $k_d(T)$ and the actual gap between $t_{cg}(T)$ and $t_{cd}(T)$ as shown in Fig. 3-right. [Notice that the model allows for $t_{cg}(T) < t_{cd}(T)$ in which case the concentration peak will be relatively small.

Since the model's five parameters, namely, $a(T)$, $k_g(T)$, $t_{cg}(T)$, $k_d(T)$ and $t_{cd}(T)$ are all temperature dependent, a transition from one formation pattern to another in a given medium is regulated by how the temperature affects their absolute and relative magnitudes. The temperature influence, however, can only be determined experimentally and it might vary, depending on the food. In case of a model system, the temperature role might also depend on the reactants composition, their overall concentration, factors such as pH, and the like. Nevertheless, one can expect that in the range of 100−200 °C, a(T) will always increase monotonically with temperature and so will $k_g(T)$, and $k_d(T)$ where relevant. But at the same time, $t_{cg}(T)$, and $t_{cd}(T)$ where relevant, will both decrease with temperature. Or in other words, the acrylamide's production level and rate are both stimulated by the temperature elevation. However, the rate of the processes that cause the acrylamide's degradation also increases with temperature and their effect becomes noticeable after a progressively shorter time, as the temperature reaches a sufficiently high level. Clearly, a model of the kind expressed by Eqs.1–4 does not account for the specific molecular mechanisms that regulate the process. But it does quantify their overall manifestation in the acrylamide's changing concentration, regardless of the details. Consequently, the kinetics of the events that take place at the molecular level need not be known or even assumed in order to construct this model. Its formulation is solely based on the acrylamide's measured concentrations at various times. As far as kinetics is concerned, all that the model states, is that there are two competing processes, of synthesis and degradation, and that they can operate simultaneously, especially at elevated temperatures. And, as will be demonstrated below, the terms assigned to the two processes need not be unique, let alone universal. For example, Eq. 2 implies that as $t \to \infty$, $Y_2(t) \to 0$ and hence $C(t) \to 0$ as well. But sometimes, whether this will actually happen might not be always clear from the data, the temperature elevation can raise the prospect of a residual acrylamide concentration even after a very long time. In such a case, an alternative model that allows for a residual concentration would have an equal or even better fit to the experimental data. If a_R is the "residual" portion ($0 < a_R \leq 1$), then Eq. 2 will become:

$$Y_2(t) = a_R + \frac{1 - a_R}{1 + \exp\{k_d(T)\,[t - t_{cd}(T)]\}} \tag{5}$$

The combined model will remain $Y_1(t) \cdot Y_2(t)$, except that $Y_2(t)$ will be represented by Eq. 5 instead of Eq. 2. Similarly, if the post peak part of the concentration curve has a prominent upward concavity, $Y_2(t)$ can still be represented by the original Eq. 2, but t_c might be negative. This can be avoided by expressing the decay by an exponential term, e.g.:

$$Y_2(t) = \exp\left(-\frac{t}{\tau}\right) \tag{6}$$

where τ is a characteristic time. Again, the concentration curve will be expressed by the product $Y_1(t) \cdot Y_2(t)$, except that this

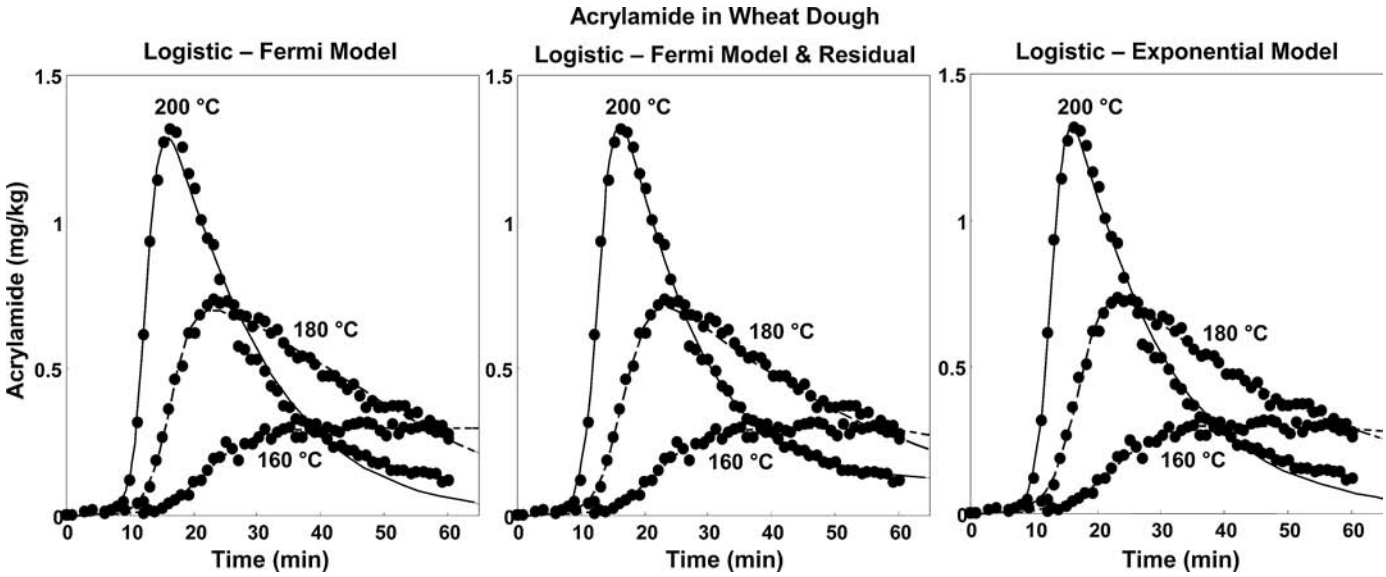

Figure 5 Isothermal acrylamide concentration vs. time relationships of wheat dough, fitted with the Logistic-Fermi, Logistic-Fermi and a Residual and Logistic-Exponential models. The original data are from Cook and Taylor (2005).

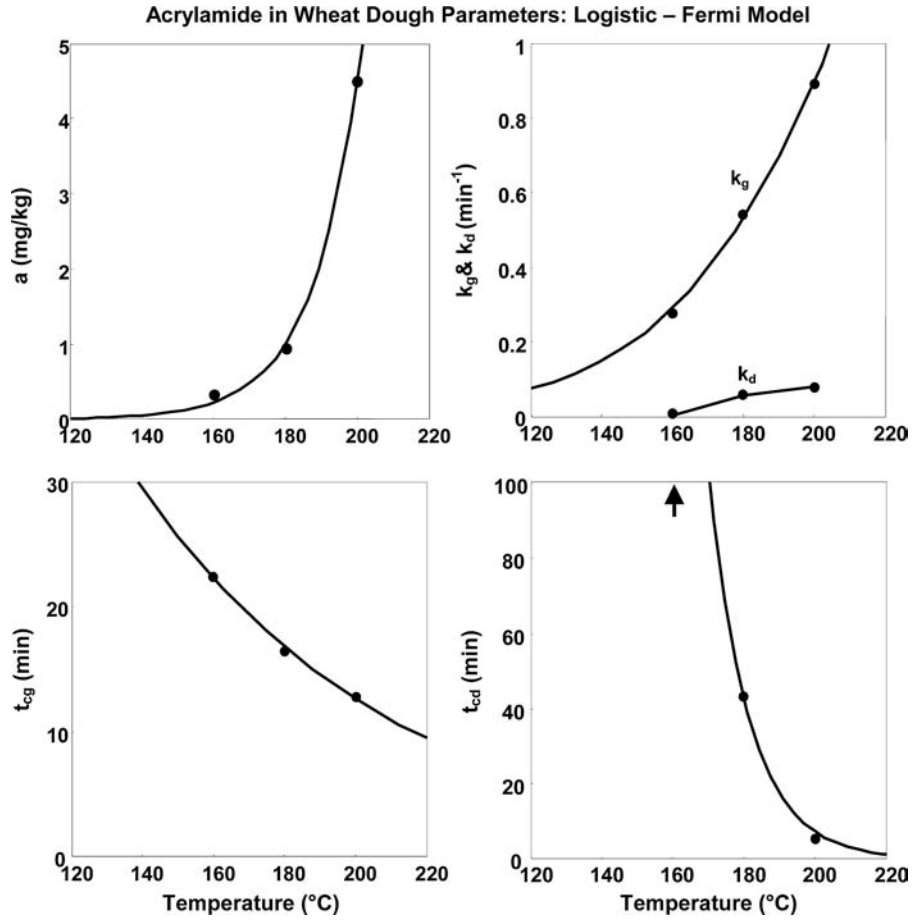

Figure 6 The temperature dependence of the Logistic-Fermi model's parameters when applied to acrylamide formation in wheat dough. The fit of the model is itself shown in Fig. 5.

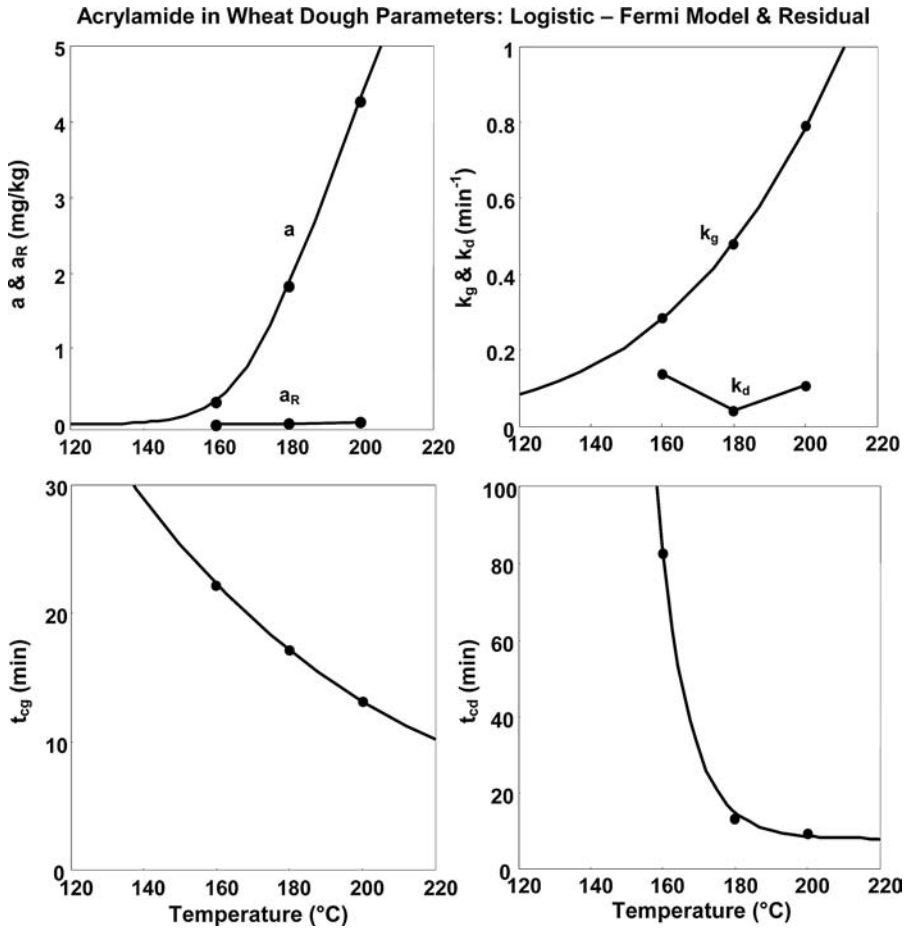

Figure 7 The temperature dependence of the Logistic-Fermi and a Residual model's parameters when applied to acrylamide formation in wheat dough. The fit of the model is itself shown in Fig. 5.

time $Y_2(t)$ will be presented by Eq. 6, instead of Eq. 2 or 5. We'll call the three combined models: Logistic – Fermi, Logistic – Fermi & a Residual and Logistic–Exponential – see below.

ISOTHEMAL ACRYLAMIDE FORMATION IN FOODS

Published measurements of acrylamide formation in actual foods have been rarely intended to confirm any kinetic model, let alone to establish the temperature dependence of its parameters. Nevertheless, the published experimental concentration – time curves can still be used to test the fit of the proposed models (combinations of Eq. 1 and Eqs. 2, 5, or 6) and to demonstrate the temperature effect on their parameters at least qualitatively. The following examples show the actual fit of the three versions of the synthesis-degradation model, namely the Logistic – Fermi combination (Eq. 4), the Logistic – Fermi & a Residual (where $Y_2(t)$ is specified by Eq. 5) and the Logistic – Exponential combination (where $Y_2(t)$ is defined by Eq. 6). The purpose of showing all three is to demonstrate that none of them is inherently superior to the other two as far as fit is concerned and that they all give more or less the same picture of the relative weight of the acrylamide's competing processes of synthesis and degradation. We will also show that the same data can be fitted with a totally different *four*-parameter model whose main advantage is in the formulation of a non-isothermal rate model. In all the demonstrations, tabulated and graphed, the acrylamide concentration is presented in the units reported by the original authors.

Wheat and Rye Doughs

The data of acrylamide formation in wheat dough at 160, 180 and 200 °C published by Cook and Taylor (2005) are shown in Fig. 5. It demonstrates that all three models have such a comparable fit that the fitted curves are practically indistinguishable. The temperature dependence of the coefficients is shown in Figs. 6–8. Admittedly, three points are barely sufficient to establish a trend. Yet all three models showed very similar increase in the hypothetical "uninterrupted formation level," a(T), and the "synthesis rate parameter," $k_g(T)$. The first two figures (Figs. 6 and 7) show that the "degradation rate parameter," $k_d(T)$, was

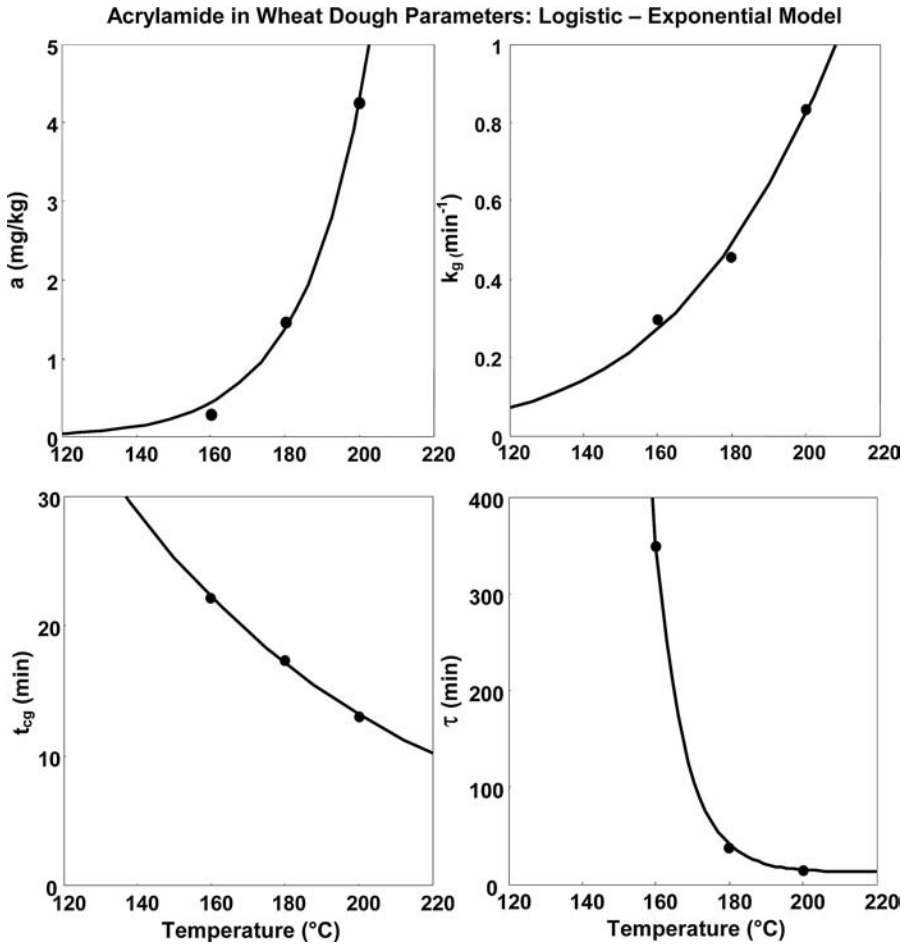

Figure 8 The temperature dependence of the Logistic-Exponential model's parameters when applied to acrylamide formation in wheat dough. The fit of the model is itself shown in Fig. 5.

much smaller than $k_g(T)$, at all three temperatures. This was quite expected since the range of $Y_1(t)$ is from zero to a(T) while that of $Y_2(t)$ from zero to one only. The figures also show, as expected, that $t_{cg}(T)$ was about the same, regardless of its calculation method. In addition, they demonstrate that the time scale of the degradation processes, represented by $t_{cd}(T)$, by far exceeded the experiment duration at 160°C and hence that the degradation effect itself was minor if not negligible at that temperature.

The analysis of the rye dough data, reported by the same authors (Fig. 9), yielded the same qualitative results. Again, the fit of all three models was identical for all practical purposes as can be seen in the figure. The temperature effect on the models' parameters was also very similar to that observed in the wheat dough as Figs. 10–12 show. Nevertheless, there was a considerable difference in the total amount of acrylamide formed in the two doughs. At the same temperature and time, there was about twice as much acrylamide formed in the rye dough than in the wheat's, except for the first ten minutes or so, where no significant amount of the compound was detected in either.

Potato Flakes

The data on acrylamide formation in potato flakes, reported by Cook and Taylor (2005) are shown in Fig. 13. As in the case of the two doughs, they could be fitted successfully by all three versions of the model—see figure. The concentration-time curves had the same shape as those of the wheat and rye doughs, except that the overall level of the acrylamide was about twice that found in the rye dough and about four times that found in the wheat dough. This was primarily reflected in the magnitude of the parameter a(T), which, as previously stated, serves as a "scale factor." Otherwise, there was relatively little difference in the magnitudes of the other parameters and their ratios—see Figs. 14–16. The same can be said about the onset of the reaction. Like in the two doughs, a measurable concentration of acrylamide could only be found after about 8–12 min, depending on the temperature. That the time scales were comparable but not the concentrations suggests that the reactants in the potato flakes were more readily available for the reaction than those in the two doughs. However, confirmation of this hypothesis will require a follow up of the intermediate products,

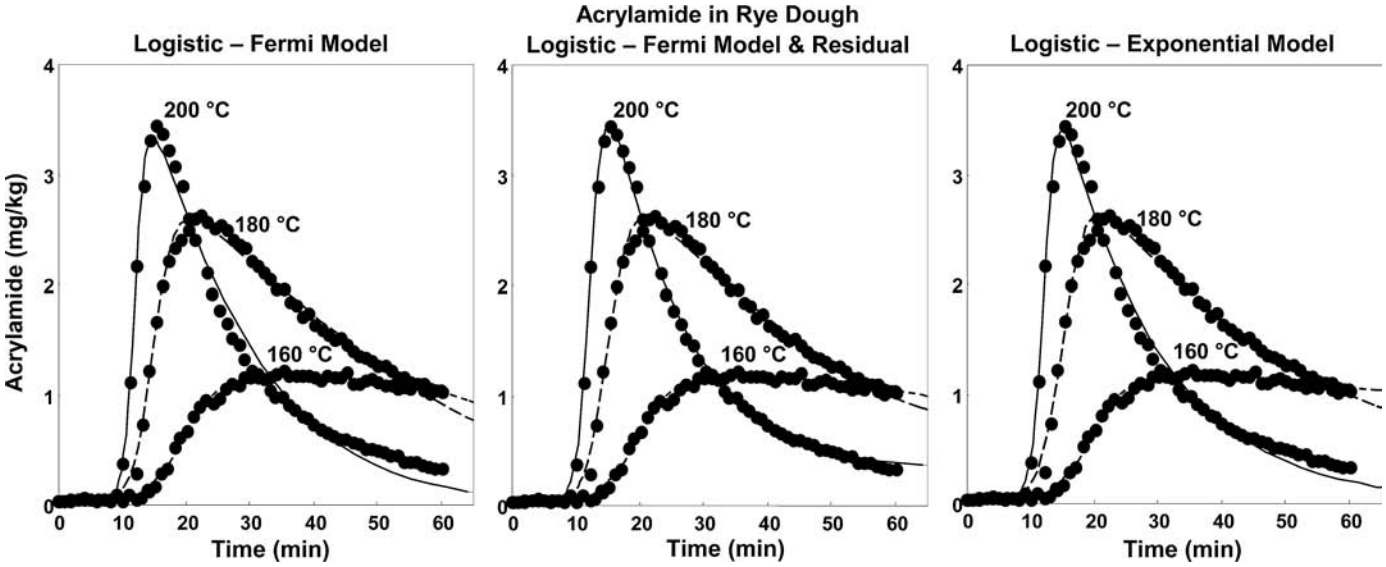

Figure 9 Isothermal acrylamide concentration vs. time relationships of rye dough fitted with the Logistic-Fermi, Logistic-Fermi and a Residual and Logistic-Exponential models. The original data are from Cook and Taylor (2005).

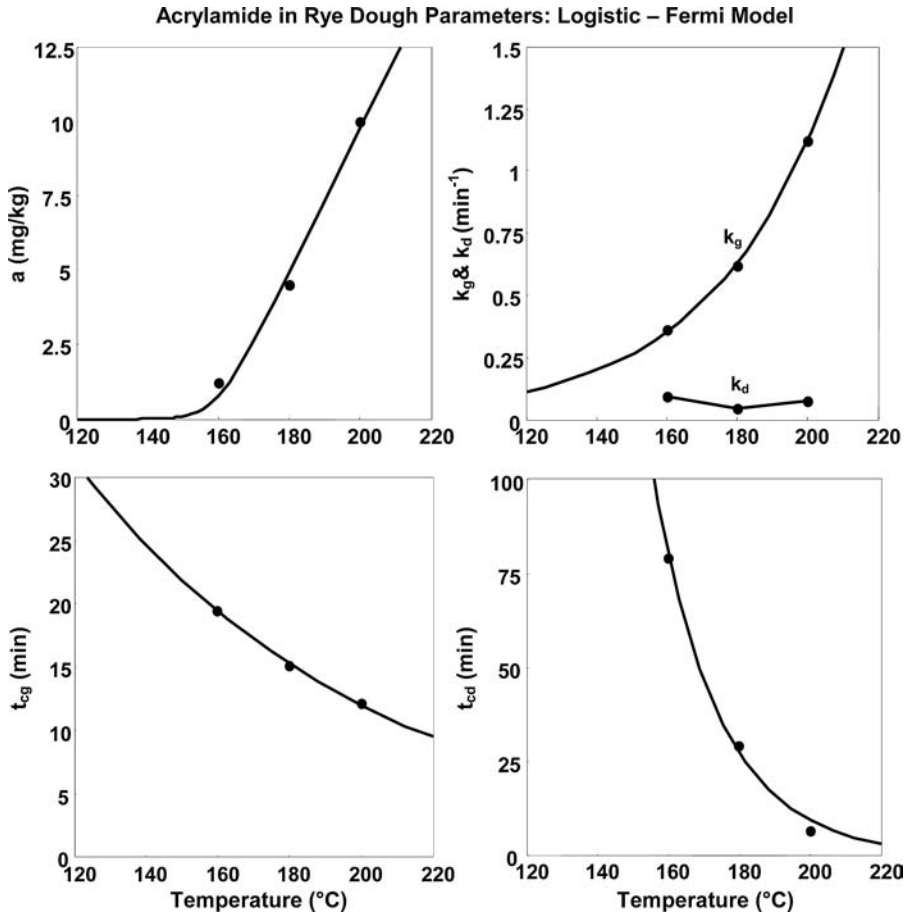

Figure 10 The temperature dependence of the Logistic-Fermi model's parameters when applied to acrylamide formation in rye dough. The fit of the model is shown in Fig. 9.

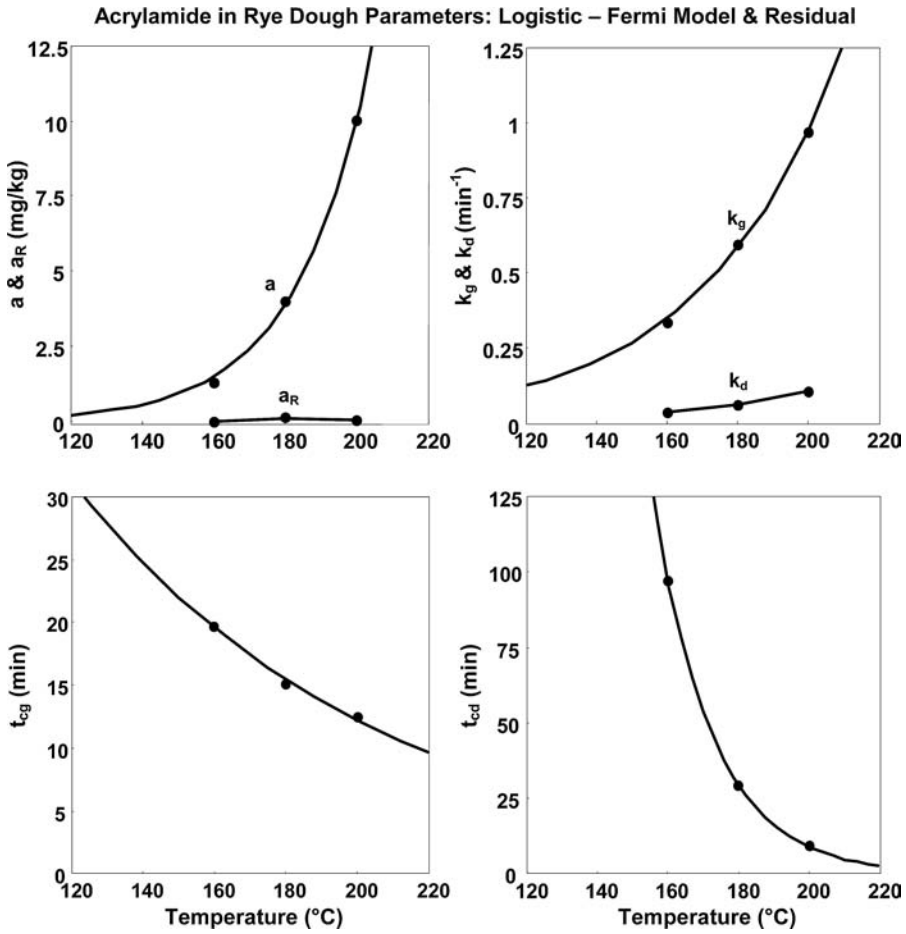

Figure 11 The dependence of the Logistic-Fermi and a Residual model's parameters when applied to acrylamide formation in rye dough. The fit of the model is itself shown in Fig. 9.

whose concentrations and fates were not reported in the original publication.

Coffee, Potato Chips and Wheat Flour

Incomplete data sets of acrylamide formation in coffee, fried potato chips and wheat flour reported by Gökmena & Senyuvab (2006) are shown in Figs. 17–19. By themselves, the plots would be insufficient to demonstrate the combined model's fit because of the too few data points. The only reason for the plots inclusion here is to show that the same general patterns that had been observed in the two doughs and potato flakes are most likely present in these three foods too. But in contrast with the three previous examples, calculation of the Logistic-Fermi and Logistic-Exponential models' parameters, although technically possible, can not give unambiguous results. This is primarily because without enough data points around the peak concentration, the magnitude of a(T), which sets the scale of the whole curve, could only be guessed rather than determined. Surprisingly, once "force-fitted" with the Logistic-Fermi equation and the Logistic-Exponential version of the model, the respective calculated model parameters were fairly similar to those found in the three former foods. All this suggests that the generation–degradation kinetics of acrylamide follows the same patterns in different foods and that these patterns are affected by temperature in basically the same way. The differences seem to be in the overall acrylamide level, which is most probably determined by the availability of the reactants. This, as has been shown by previous investigators, is revealed by the analysis of model systems, where the reactants, their concentration, and the chemical environment (e.g., the pH) can be chosen and controlled—see below.

ACRYLAMIDE FORMATION IN MODEL SYSTEMS

Studies of acrylamide formation in model systems have been specifically aimed at revealing the process's kinetics and determining the reactants rate constants. We will reanalyze two data sets; the one reported by Knol et al. (2005) and Claeys et al. (2005b). The first deals with the glucose-asparagine reaction system in isolation (Fig.1-bottom) and the second (Fig.1-top) in the presence of various amino acids. Although the three schematic presentations shown in Fig. 1 look different, they are

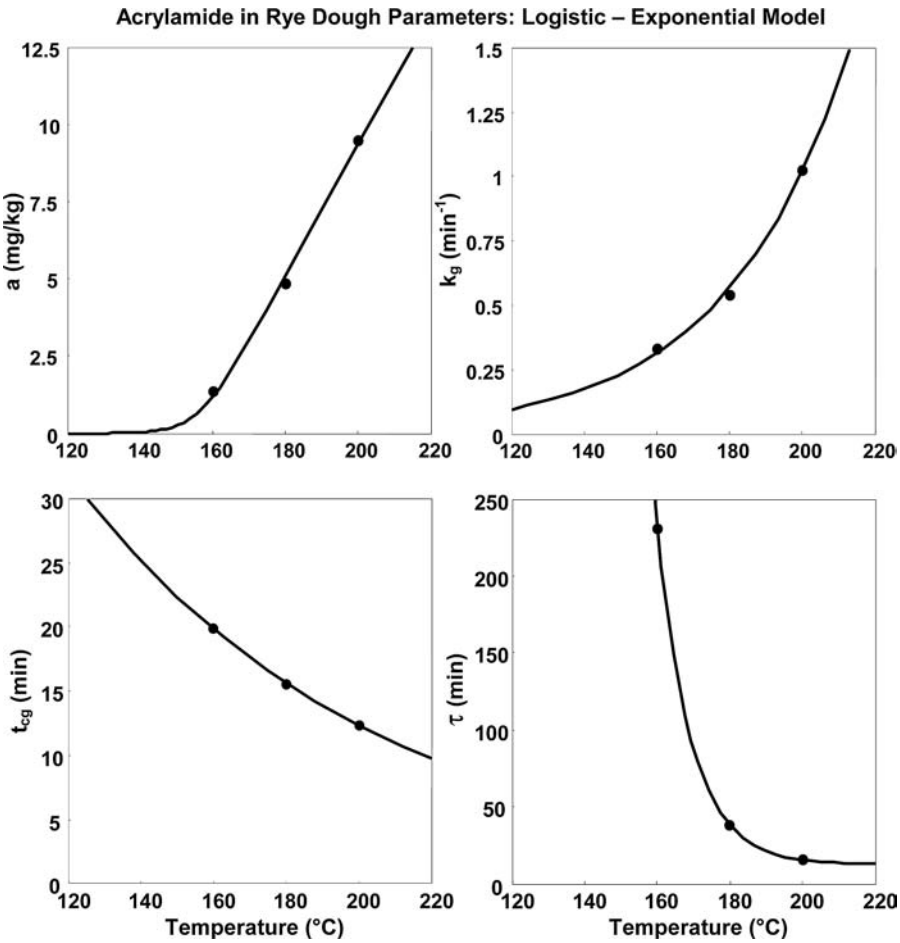

Figure 12 The temperature dependence of the Logistic-Exponential model's parameters when applied to acrylamide formation in rye dough. The fit of the model itself is shown in Fig. 9.

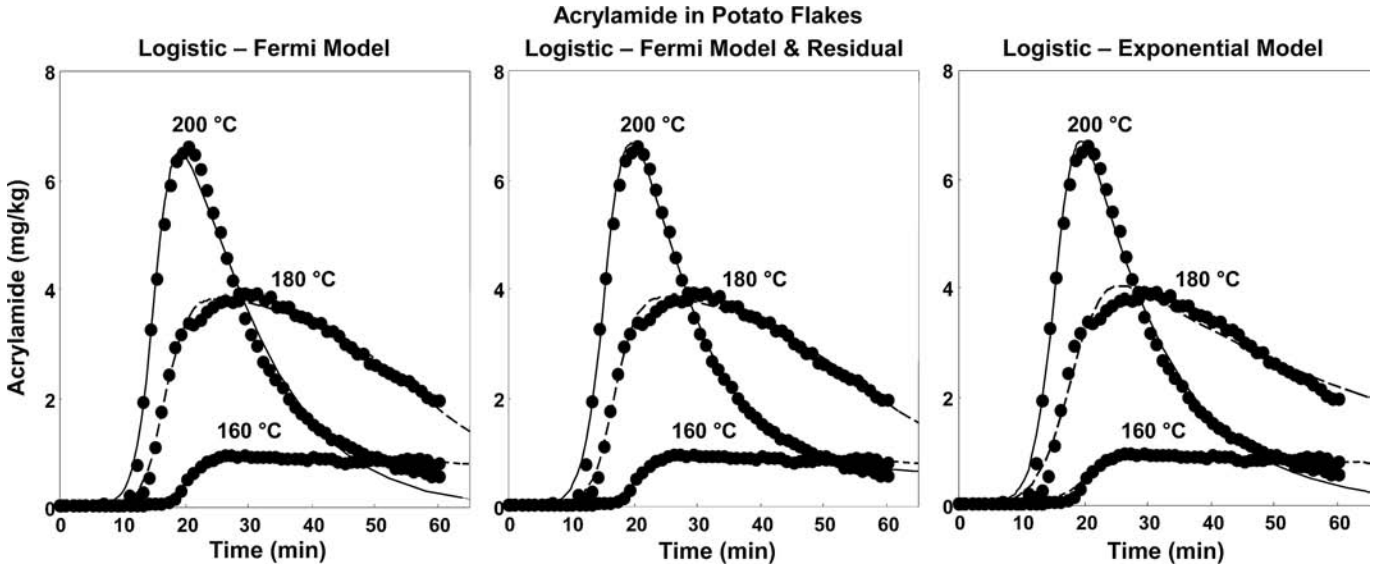

Figure 13 Isothermal acrylamide concentration vs. time relationships of potato flakes, fitted with the Logistic-Fermi, Logistic-Fermi and a Residual and Logistic-Exponential models. The original data are from Cook and Taylor (2005).

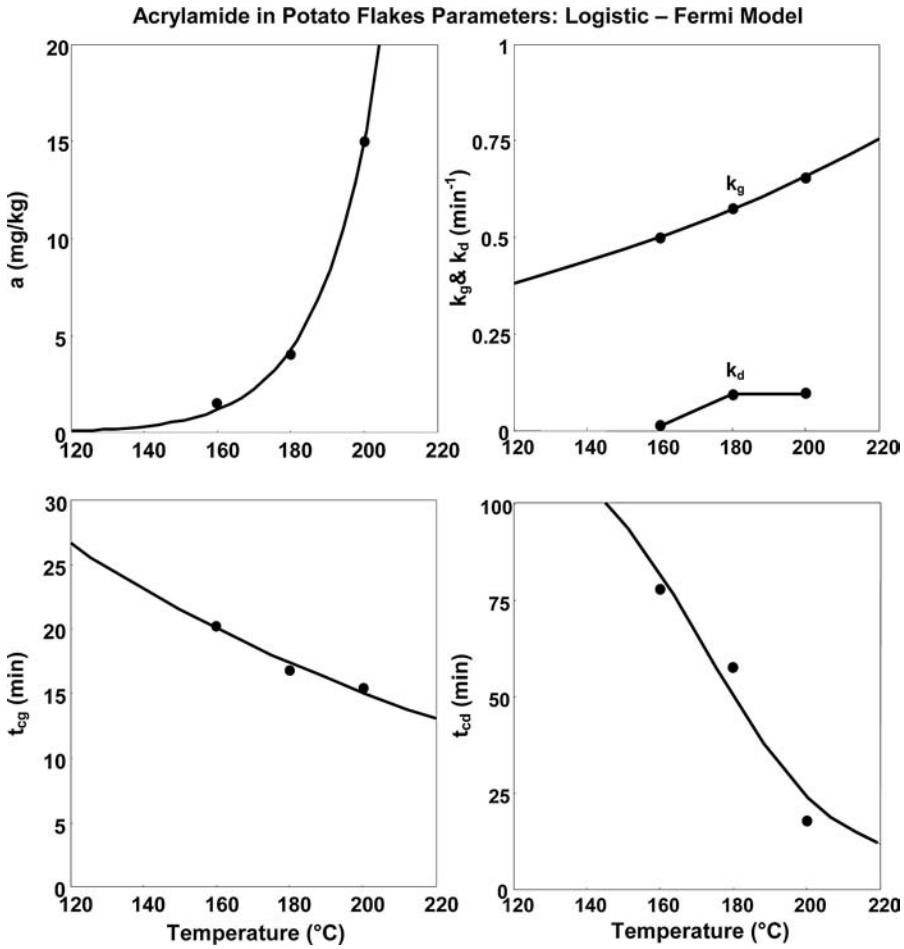

Figure 14 The temperature dependence of the Logistic-Fermi model's parameters when applied to acrylamide formation in potato flakes. The fit of the model is itself shown in Fig. 13.

basically a description of the same reaction, addressed at different levels of detail. In the first work, the intermediate reactants were identified and their transformation followed, while in the second publication, only the acrylamide concentration vs. time relationships are reported in the original.

The Glucose–Asparagine Reaction

The acrylamide formation in aqueous solutions of glucose and asparagine at five temperatures, reported by Knol et al. (2005) are shown in Fig. 20. Also shown in the figure is the fit of the three versions of the generation-degradation model. Like in the real foods data, the fit of the three models is extremely close, again showing that the same data can be described by different mathematical expressions. The temperature dependence of the Logistic-Fermi models' parameters is shown in Figs. 21–23. In this case there were *five* temperatures represented and hence, the trends could be clearly identified. Interestingly, despite the scatter in the original concentration vs. time data from which the models had been derived, the temperature dependencies of the respective parameters were remarkably smooth. As expected, the addition of a residual, a_R, to the Fermian term in the combined model's equation had hardly affected the principal parameters, i.e., a(T), k_g(T) and t_{cg}(T). Qualitatively, the temperature effect on these kinetic parameters was of the same kind observed in the real foods (see previous section). This confirms the notion that temperature accelerates the formation of acrylamide and at the same time shortens the time for the reaction's product to reach a measurable concentration. Yet, at the same time, the temperature elevation also shortens the time scale of the degradation reactions. Thus, as the temperature increases, the degradation's role becomes noticeable after a progressively shorter time, as is evident in the dramatic decrease of t_{cd}(T).

The Effect of Amino Acids Presence

Claeys et al. (2005b) investigated the effect of the presence of amino acids on the acrylamide formation by the glucose-asparagine reaction (Fig.1-top). They monitored the

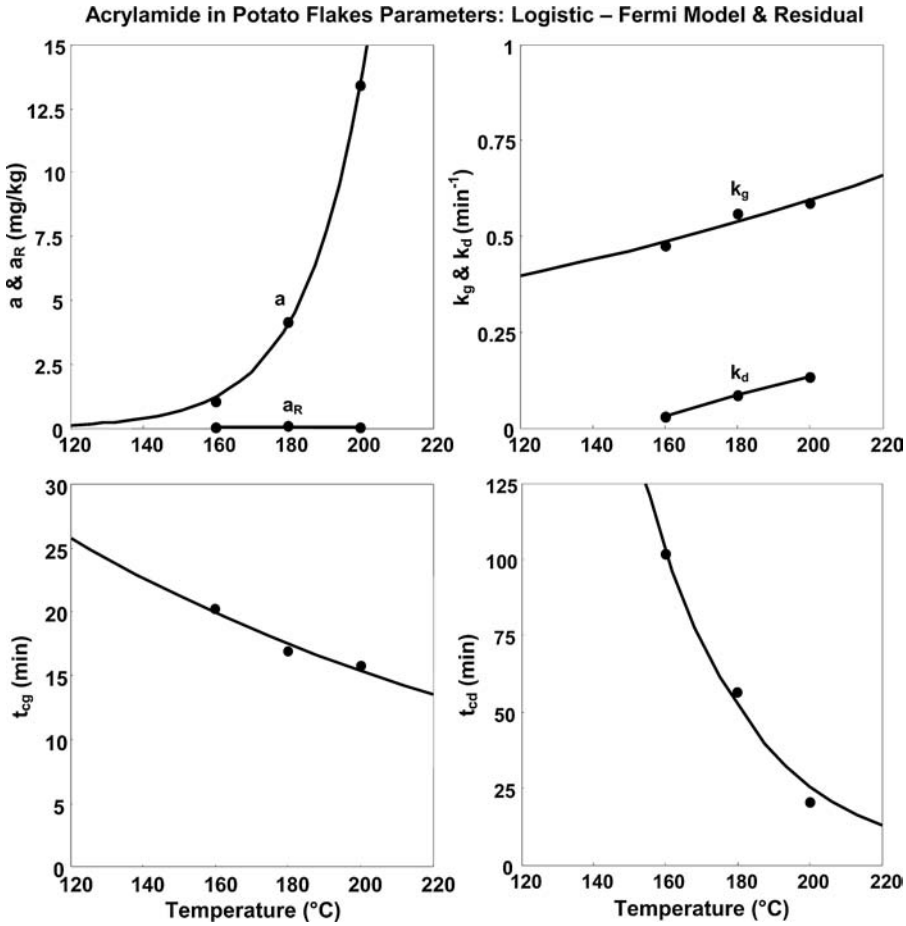

Figure 15 The temperature dependence of the Logistic-Fermi and a Residual model's parameters when applied to acrylamide formation in potato flakes. The fit of the model is itself shown in Fig. 13.

acrylamide formation at four temperatures, 140, 160, 180, and 200 °C, with and without the presence of alanine, cysteine, glutamine, or lysine. [The glucose-asparagine base was 0.01M (equimolar) at pH 6 and each amino acid added also had 0.01M concentration.] The control data, i.e., those on the acrylamide formation from glucose and asparagine only, fitted with the Logistic-Fermi and Logistic-Exponential model are shown in Fig. 23. As before, the same data could be fitted by more than one version of the model, demonstrating once more that the model is not unique. The temperature dependence of the Logistic-Fermi model parameters are shown in Fig. 24. [For space consideration, we do not show the corresponding relationships obtained by the other model's versions.] Qualitatively, the plots shown in the figure are very similar to those obtained in real foods and the ones derived from the results of Knol et al. (2005)—see previous section. The fit of the Logistic-Fermi model (Eq. 4) to the model food systems that contained the four added amino acids is shown in Fig. 25. As in all the previously discussed systems, the temperature dependence of the models' parameters exhibited the same general pattern, except that their absolute magnitudes differed to various extents as shown in Fig. 26. This was probably due to a slightly modified kinetics in the presence of different amino acids as Table 2 also indicates.

The effect of the added amino acids on the reaction was quantified by Claeys et al. (2005b) in terms of the formation and extinction rate constants, k_F and k_E respectively (see Fig. 1) at 160 °C, which served as a reference temperature, and by the corresponding "energies of activation" E_{aF} and E_{aE} calculated with the Arrhenius model. These authors also tabulated the ratios of the acrylamide formed in the presence of the four amino acids at the four temperatures and graphed them as a function of time also at 160 °C (see below).

Comparison of the Three Models (Claeys et al., 2005b; Knol et al., 2005 and the Logistic-Fermi Combination)

The kinetic parameters of the glucose-asparagine model systems, calculated by the three models are listed in Table 1. The kinetic model of Claeys et al. (2005b), see Fig. 1-top, is in the

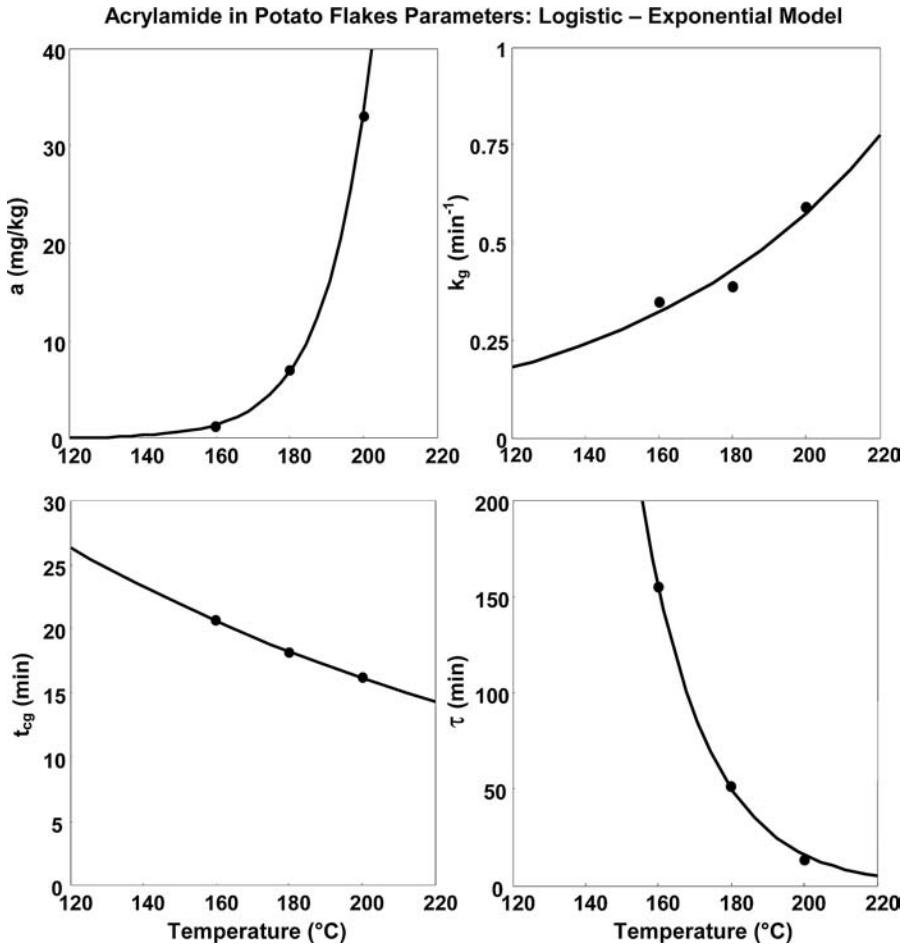

Figure 16 The temperature dependence of the Logistic-Exponential model's parameters when applied to acrylamide formation in potato flakes. The fit of the model is itself shown in Fig. 13.

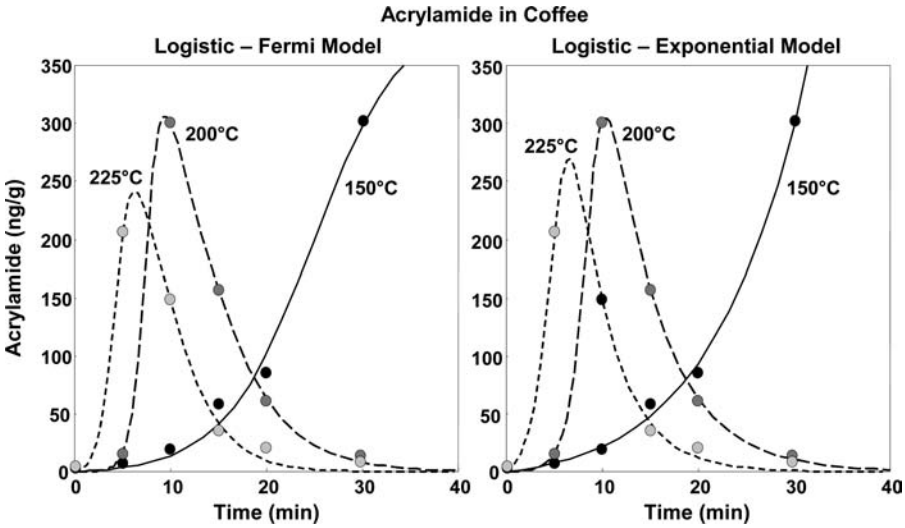

Figure 17 Isothermal concentration vs. time relationships of acrylamide in coffee fitted with the Logistic-Fermi and Logistic-Exponential models. Notice that despite the experimental data can be "forced fitted" with these models, they are insufficient to derive reliable kinetic parameters and to determine their temperature dependence. The original data are from Gökmena and Senyuvab (2006).

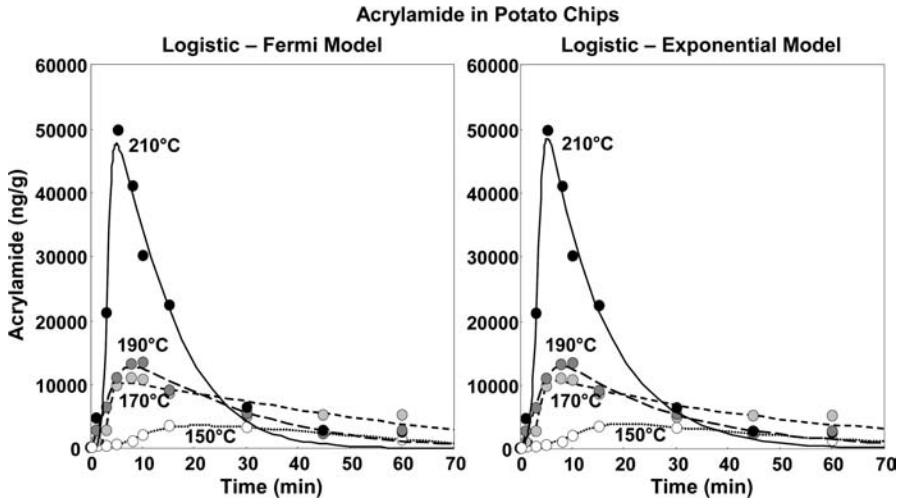

Figure 18 Isothermal concentration vs. time relationships of acrylamide in potato chips, fitted with the Logistic-Fermi and Logistic-Exponential models. Notice that despite that the exponential data can be "forced fitted" with these models they are insufficient to derive reliable kinetic parameters and to determine their temperature dependence. The original data are from Gökmena and Senyuvab (2006).

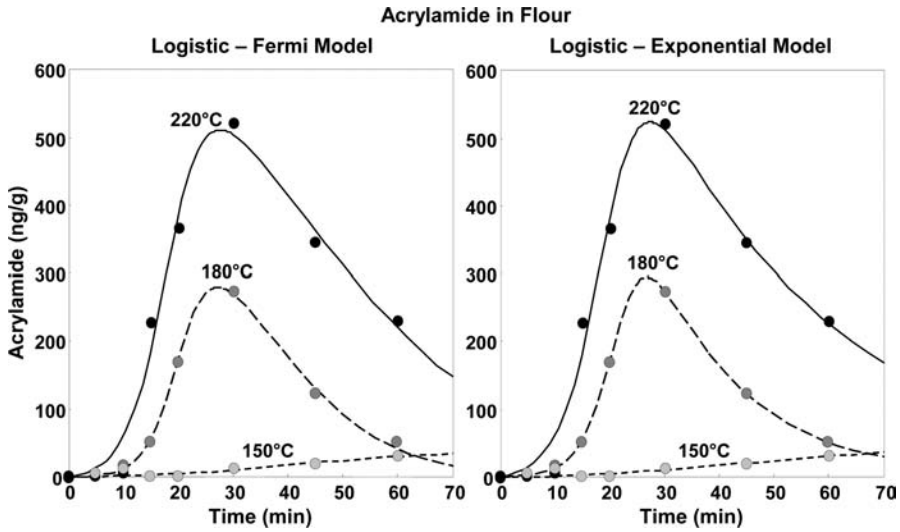

Figure 19 Isothermal concentration vs. time relationships of acrylamide in flour fitted with the Logistic-Fermi and Logistic-Exponential models. Notice that despite the exponential data can be "forced fitted" with these models they are insufficient to derive reliable kinetic parameters and to determine their temperature dependence. The original data are from Gökmena and Senyuvab (2006).

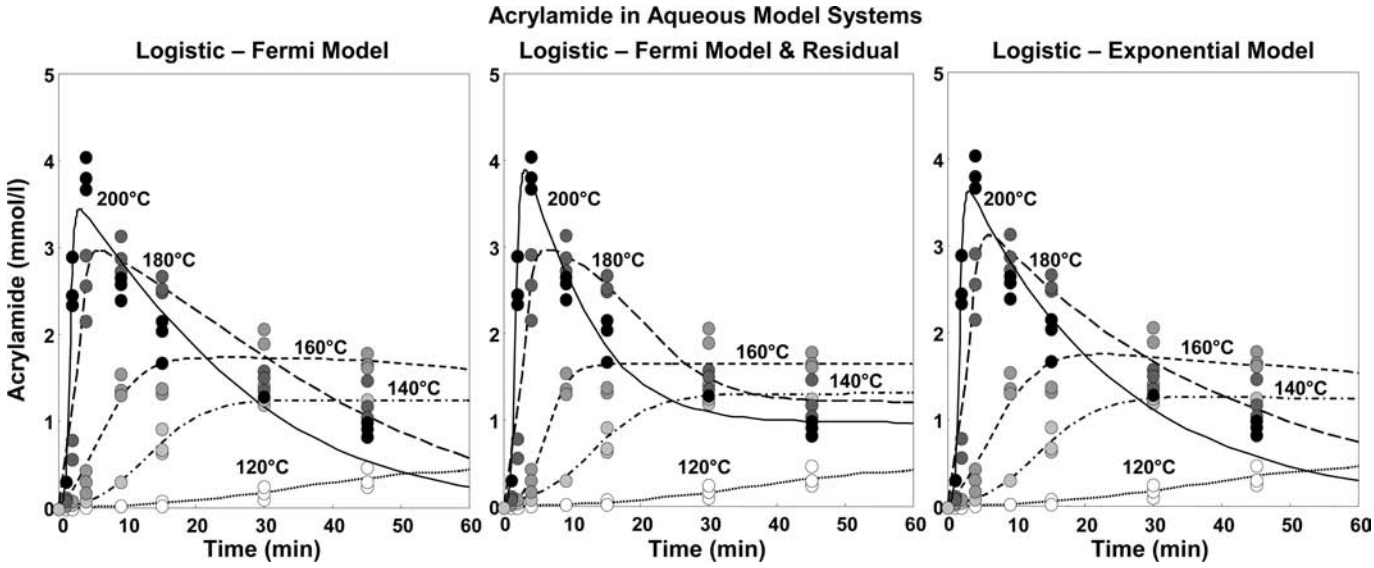

Figure 20 Isothermal acrylamide concentration vs. time relationships of an asparagine-glucose model system. The original data are from Knol et al. (2005).

Table 1 Kinetic parameters of acrylamide formation and degradation in model asparagine – glucose systems[1)]

	Based on data from Claeys et al. (2005b)							Based on data from Knol et al. (2005)								
	Reported		Logistic-Fermi model (Eq. 4)					Reported				Logistic-Fermi model (Eq. 4)				
Temp (°C)	k_F (10^{-3} min^{-1})	k_E (10^{-3} min^{-1})	a (ppm)	k_g (min^{-1})	t_{cg} (min)	k_d (min^{-1})	t_{cd} (min)	k_1 (10^{-3} min^{-1})	k_3 (10^{-3} min^{-1})	k_4 (10^{-3} min^{-1})	k_6 (10^{-3} min^{-1})	a (mmol l^{-1})	k_g (min^{-1})	t_{cg} (min)	k_d (min^{-1})	t_{cd} (min)
120	-	-	-	-	-	-	-	0.1	0.1	0.2	8	0.5	0.09	34.4	0.007	5000
140	0.047	12	1.8	0.05	37.6	0.008	5000	0.3	0.4	0.7	28	1.3	0.25	13.2	0.004	1000
160	0.45	110	2.7	0.25	17.5	0.006	750	0.7	1.5	2.5	88	2	0.34	5.8	0.075	91.9
180	3.5	860	3.1	0.45	8.9	0.215	40.9	1.4	5.0	8.1	250	4.5	1.43	2.9	0.049	20.9
200	23	5600	3.0	0.73	5.9	0.221	28.4	2.6	16	23	650	7.5	3.36	1.7	0.057	0.67
"E_a" (kJ/mol)	170	170	–	–	–	–	–	58	102	94	85	–	–	–	–	–

[1)] All the values are rounded. Schematic views of the models are given in Figs. 1 and 3.

following form:

$$\frac{dC_R(t)}{dt} = -k_F C_R(t) \tag{7}$$

$$\frac{dC_{AA}(t)}{dt} = k_F C_R(t) - k_E C_{AA}(t) \tag{8}$$

and

$$\frac{dC_D(t)}{dt} = k_E C_{AA}(t) \tag{9}$$

where the $C_R(t)$, $C_{AA}(t)$ and $C_D(t)$ are the momentary concentrations of the reactants (R), the acrylamide (AA), and its final

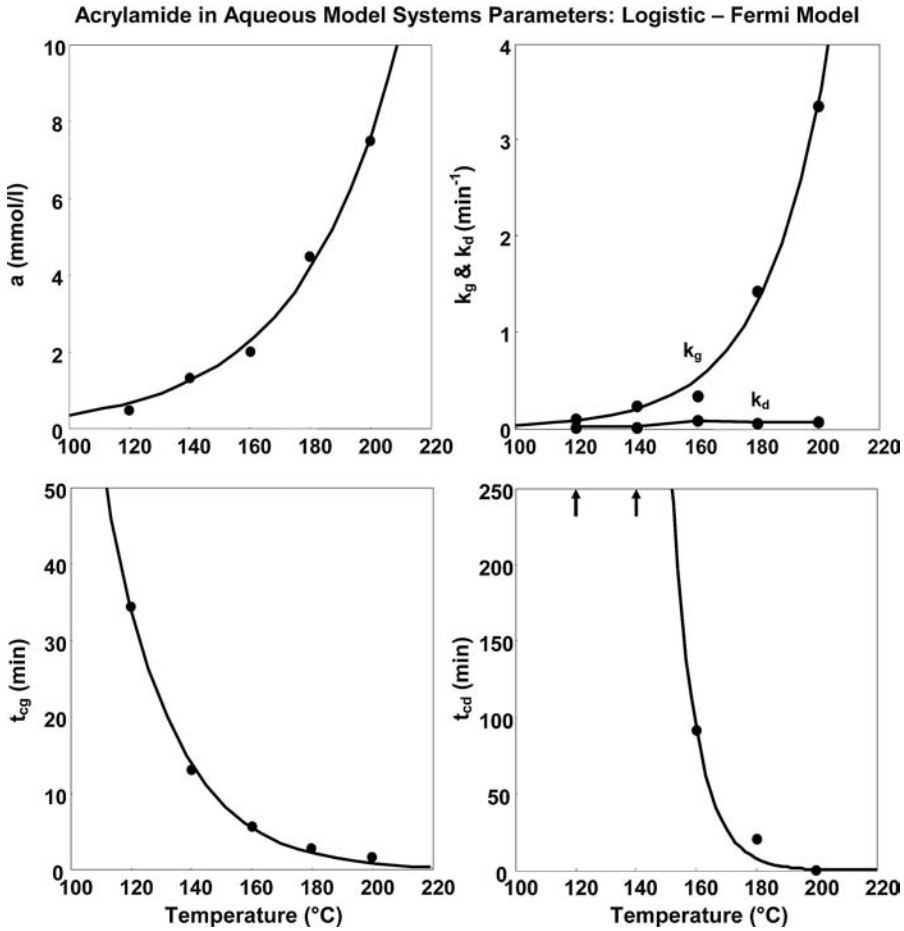

Figure 21 The temperature dependence of the Logistic-Fermi model's parameters when applied to acrylamide formation in an asparagine-glucose model system. The fit of the model itself is shown in Fig. 20. The original data are from Knol et al. (2005).

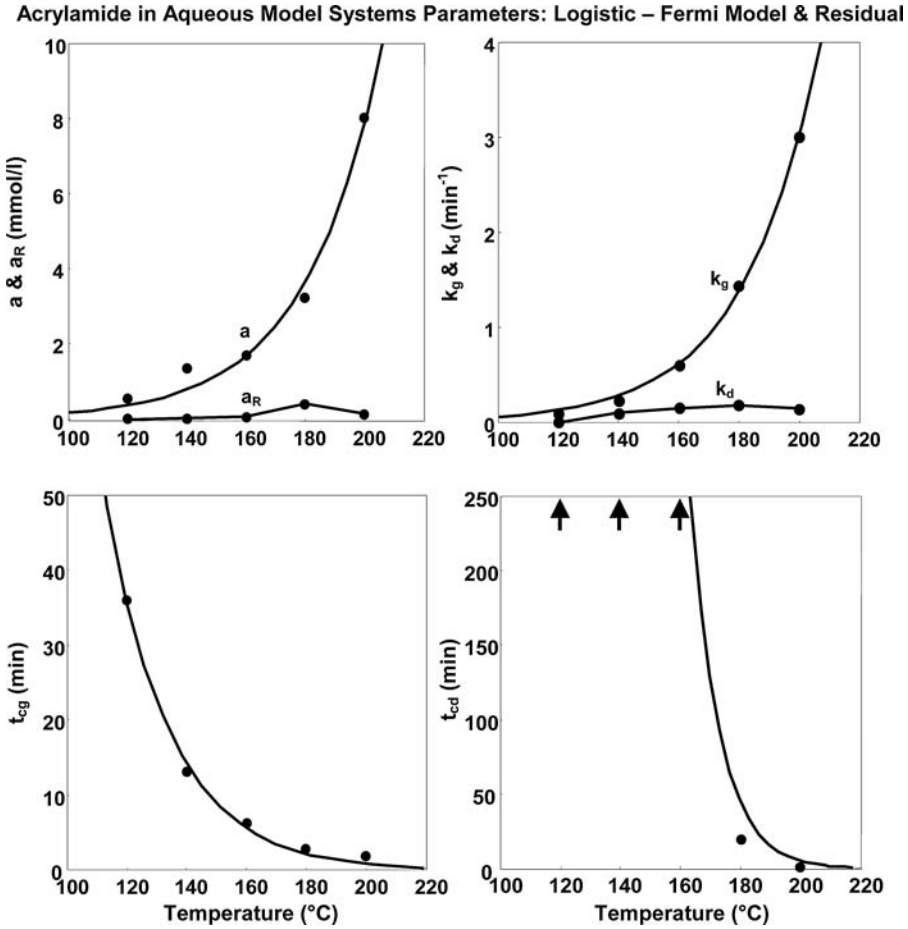

Figure 22 The temperature dependence of the Logistic-Fermi and a Residual model's parameters when applied to acrylamide formation in an asparagine-glucose model system. The fit of the model itself is shown in Fig. 20. The original data are from Knol et al. (2005).

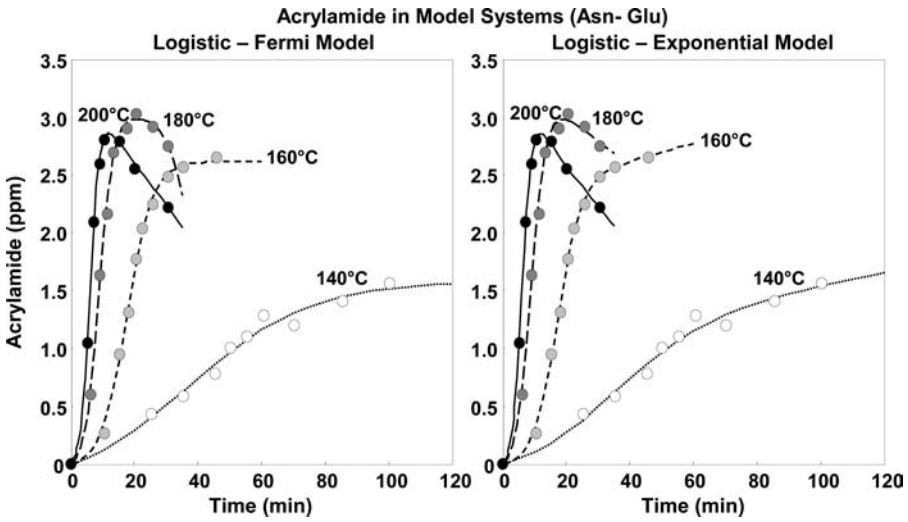

Figure 23 Isothermal acrylamide concentration vs. time relationships of asparagine-glucose model system, fitted with the Logistic-Fermi and Logistic-Exponetial models. The original data are from Claeys et al (2005b).

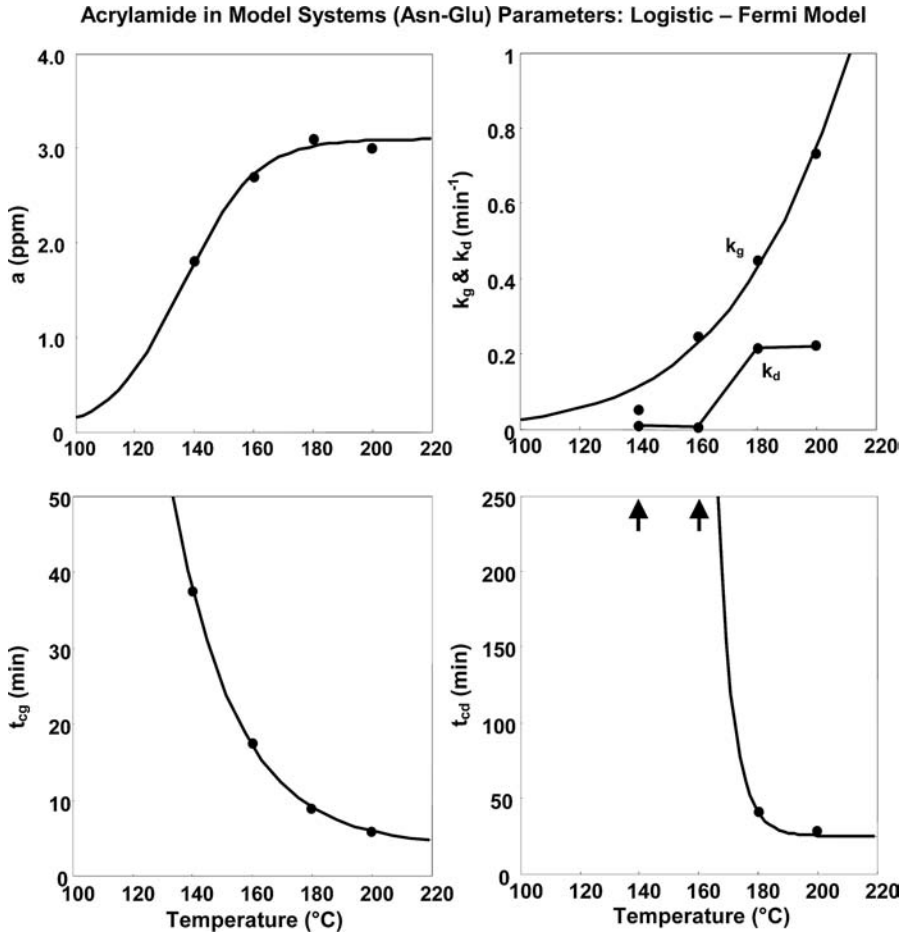

Figure 24 The temperature dependence of the Logistic-Fermi model's parameters when applied to acrylamide formation in asparagine-glucose model system. The fit of the model is shown in Fig.23. The original data are from Claeys et al. (2005b).

degradation products (D), respectively, and k_F and k_E are the formation and extinction rate constants respectively. Thus the whole isothermal process is characterized by two rate parameters only. The magnitude of these rates at the four temperatures (140, 160, 180, and 200°C) is listed in the two first columns of the table. Clearly, both rates increased monotonically with temperature, in a manner following the Arrhenius equation according to the authors. The ratio k_E/k_F at the four temperatures was 255, 244, 246, and 243, respectively, i.e., about the same, as would be expected from the notion that the two rates' temperature dependences were governed by almost exactly the same energy of activation. (The entries in the table are all rounded.) Since k_F relates to the reactants concentration, which was large relative to that of the formed acrylamide, the actual rates of synthesis and extinction are not obvious from the magnitudes of k_F and k_E. Moreover, since the two increased with temperature in unison, and since their ratio had remained basically fixed at the range of temperatures examined, the temperature where the shift from a sigmoid concentration curve to one that has a clear peak is not evident from these parameters' list alone. The logistic-Fermi model, see Table 1, has five adjustable parameters and therefore is more sensitive to artifacts. However, while both k_g and k_d increased with temperature, the complimentary parameters, t_{cg} and t_{cd} dramatically *decreased*, accounting for the transformation in the curves shapes. The ratios between k_g and k_d of the Logistic-Fermi models, has no clear meaning since the former is of an entity with a range from zero to a, while the latter from zero to one or from a_R to one, as already mentioned. But what is clear from the comparison of the table and Figs. 20 and 23 is that when t_{cd} dropped to below about a hundred minutes–the time scale of the test duration–the acrylamide concentration curves had a visibly discernable peak.

The model proposed by Knol et al. (2005) had six rate parameters (Fig.1-bottom) and only four of them are shown in Table 1. Because these authors' model system was not identical to that studied by Claeys et al. (2005b), comparison between the rate constants of the respective models would be only meaningful if focused on their general temperature dependence. Here again, all four parameters, increased with temperature in unison. But since the energy of activation associated with k_4, the rate of the acrylamide synthesis, and the

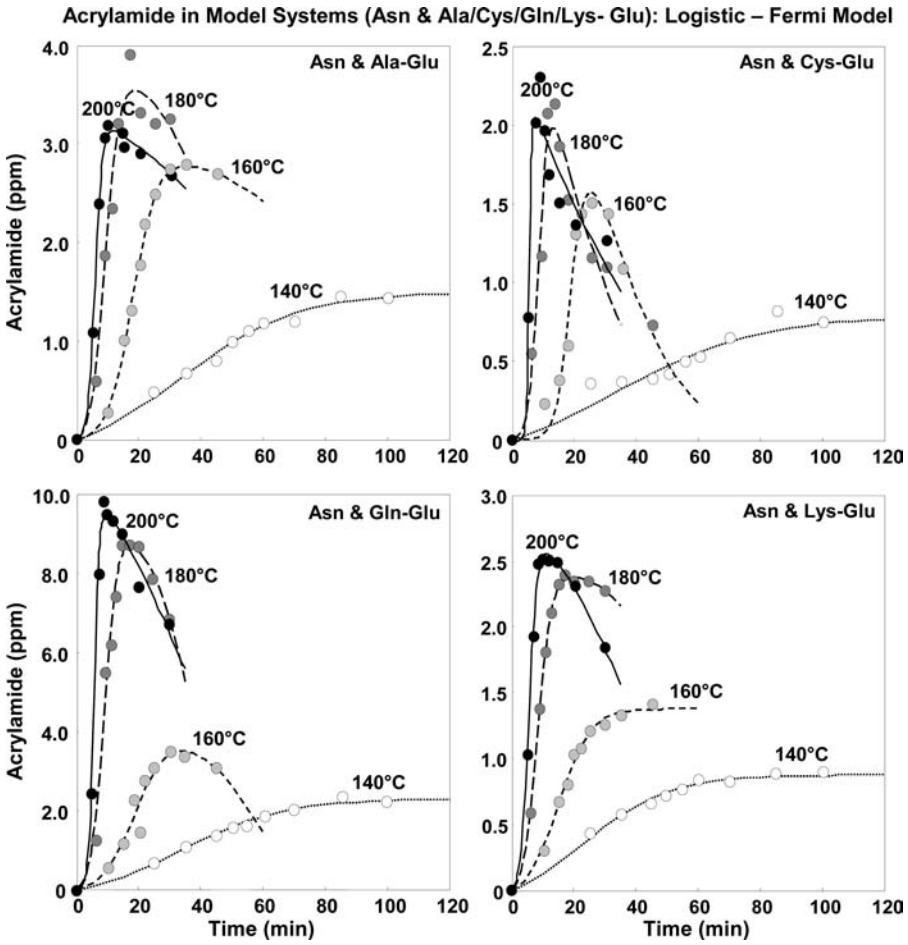

Figure 25 Isothermal concentration vs. time relationships of asparagine-glucose model systems, to which alanine, cysteine, glutamine, and lysine had been added, fitted with the Logistic-Fermi model. The original data are from Claeys et al. (2005b).

energies of activation associated with the other rates were not the same, the magnitude of their ratios did vary with temperature. Hence, and because each relates to a different chemical reaction, their interpretation requires a more thorough analysis than can be offered here. The corresponding parameters of the Logistic-Fermi model also changed monotonically with temperature albeit not always in the same direction. While, as expected, a(T), k_g(T) and k_d(T) increased with temperature, both t_{cg}(T) and t_{cd}(T) dramatically decreased. And again, when the calculated t_{cd}(T) dropped to a time close to or within the heat treatment duration, it marked the appearance of a peak acrylamide concentration—as in the system studied by Claeys et al. (2005b).

Comparison of models having a different number of adjustable parameters should always be viewed with caution. In the case of Knol et al.'s report (2005), the model's constants had been derived by monitoring the concentration of both the initial *and* the intermediate reactants. Therefore they are based on additional information which could not be derived from the shapes of the concentration curves alone. Thus from a mechanistic viewpoint, the model offered by the Knol et al. (2005) is "stronger" and more enlightening than either the model of Claeys et al. (2005b) and the Logistic-Fermi model and its modified versions. The main advantage of Claeys et al.'s model is its very small number of parameters. The only potential usefulness of the Logistic-Fermi model is the intuitive meaning of its parameters which comes at a cost of having five of them.

The Effect of Added Amino Acids as Viewed Through the Models of Claeys et al. (2005b) and the Logistic-Fermi Model Combination

The entries in Table 2 show that regardless of the system's composition, the rate constants of the Claeys et al.'s model, k_F and k_E, increased with temperature in unison. By and large, the "energies of activation" associated with the acrylamide synthesis (k_F) were about the same, i.e., 170–180 kJ · mol $^{-1}$. The exception was the cysteine containing system, in which case it was about 200 kJ · mol^{-1}. The energies of activation of the degradation process, represented by k_E, were on the order of

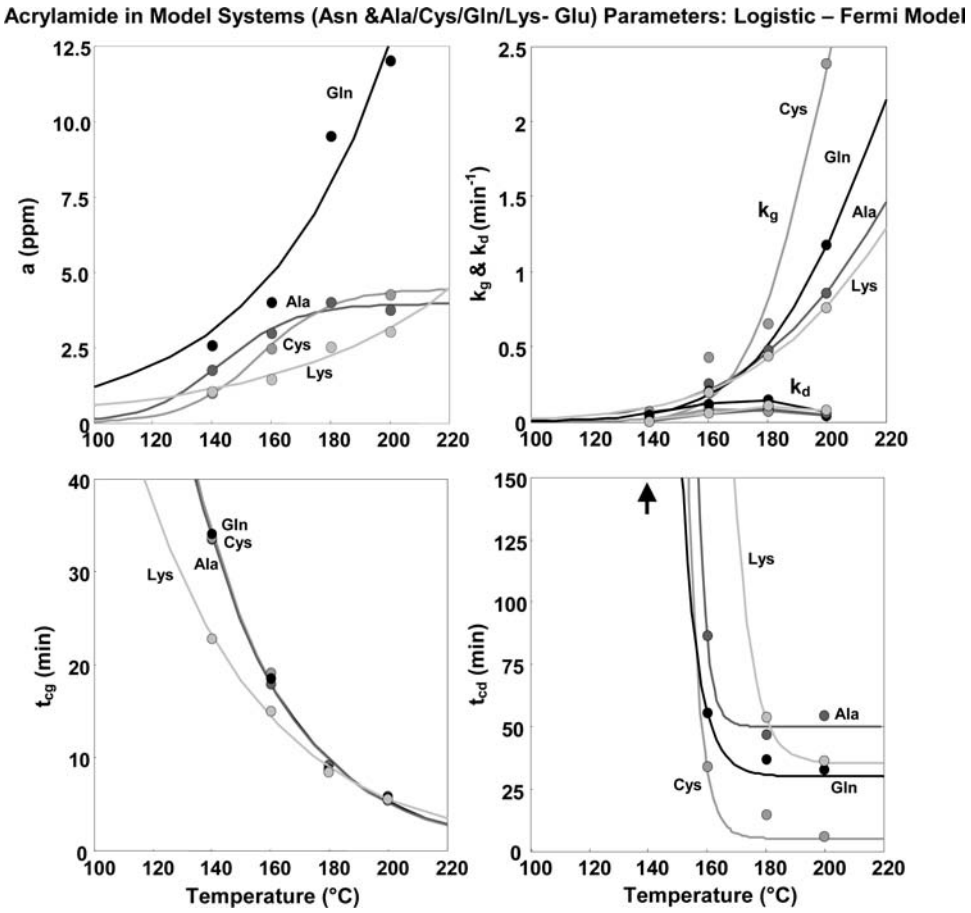

Figure 26 The temperature dependence of the parameters of the Logistic-Fermi model, with which the data shown in Fig. 25 have been fitted.

$140-180\,\mathrm{kJ}\cdot\mathrm{mol}^{-1}$ except for the glutamine containing system where it was only about $100\,\mathrm{kJ}\cdot\mathrm{mol}^{-1}$. Normally, this would indicate that the presence of cysteine renders the acrylamide synthesis rate less temperature dependent and that the presence of glutamine makes its degradation rate more temperature sensitive. However, establishing whether this is an observation of a universal phenomenon will require additional tests and the examination of asparagine-cysteine and asparagine-glutamine mixtures of different ratios. Again, because k_F relates to the initial reactants' concentration while k_E to that of the already formed acrylamide, it is difficult to discern the added amino acids effect from the k_F's and k_E's alone. Their role in the process could only be revealed by examination of the concentration curves themselves, which was indeed done and reported by Claeys et al. (2005b). A simultaneous increase in the k_F and a decrease in k_E will certainly indicate a synergetic effect on the acrylamide formation and vice versa. But neither combination alone can tell whether there is a acrylamide concentration peak and how fast the acrylamide will disappear after reaching a maximum level. The logistic-Fermi model, see Table 2, is slightly more revealing here. A consistent higher a(T) value indicates a higher level of acrylamide production. And, in addition, a short gap between t_{cd} and t_{cg} indicates the appearance of an acrylamide concentration peak within the experiment's duration. The actual gap between these two-time scale markers might serve as a rough estimate of the peak's width. According to the Logistic-Fermi model, only glutamine had a significant synergetic effect on the acrylamide formation at all four temperatures. Lysine was an antagonist at 140, 160, and 180 °C, cysteine had a mixed effect depending on temperature, and alanine was a promoter of acrylamide synthesis but only at 180 and 200 °C. Again, establishing the generality of these observations will require a more expanded database that will include the presence of the above amino acids at various concentration ratios.

NON-ISOTHERMAL FORMATION AND DEGRADATION OF ACRYLAMIDE

Prediction of the outcome of non isothermal complex chemical processes, with very few exceptions, requires the derivation of a model in the form of a *rate equation*. The coefficients of such models are usually algebraic expressions that contain the temperature history, or "profile," T(t), as a term. Models of this kind are based on the notion that the generation or elimination *rate* of the compound of interest, and that of any of the reactants'

Table 2 Effect of added amino acids on the kinetic parameters of acrylamide formation and degradation ("extinction") obtained by two different models.

		Claeys et al. (2005)[1)] (See Fig. 1- top)				Logistic – Fermi combination (Eq. 4- see Fig. 24)				
Amino acid added	Temp. (°C)	k_F (10^{-3} min^{-1})	k_E (10^{-3} min^{-1})	E_{aF} (kj mol^{-1})	E_{aE} (kj mol^{-1})	a (ppm)	k_g (min^{-1})	t_{cg} (min)	k_d (min^{-1})	t_{cd} (min)
None	140	0.047	12	170	170	1.8	0.05	37.6	0.008	5000
(control)	**160**	0.45	110			2.7	0.25	17.5	0.006	750
	180	3.5	860			3.1	0.45	8.9	0.215	40.9
	200	23	5600			3.0	0.73	5.9	0.221	28.4
Glutamine	140	0.17	68	170	100	2.6	0.06	34.1	0.05	1000
	160	1.64	270			4.0	0.20	18.5	0.12	55.8
	180	13	980			9.5	0.48	8.8	0.144	36.8
	200	83	3150			12.0	1.18	5.7	0.06	32.6
Cysteine	140	0.031	24	210	180	1.00	0.04	33.6	0.0011	3000
	160	0.5	270			2.50	0.43	19.2	0.09	33.7
	180	6.3	2400			4.00	0.65	8.7	0.07	14.5
	200	64	18400			4.25	2.39	5.5	0.044	6.1
Lysine	140	0.053	43	180	140	1.05	0.07	22.8	0.016	1500
	160	0.59	280			1.45	0.20	15.1	0.06	500
	180	5.3	1600			2.53	0.44	8.4	0.1	53.8
	200	40	7500			3.02	0.76	5.6	0.076	36.2
Alanine	140	0.045	11	170	170	1.75	0.05	33.5	0.004	1000
	160	0.47	100			3.00	0.26	18.0	0.056	86.6
	180	3.9	830			4.00	0.44	9.2	0.086	46.6
	200	27	5600			3.75	0.86	5.8	0.04	54.2

[1] Rounded entries. The rate constants at 140, 180 and 200°C where calculated with the reported "energies of activation" and 160°C (433°K) as the reference temperature using the Arrhenius equation as a model.

and intermediate products, is determined by *both* the changing momentary temperature and the momentary state of the system, which is a function of time too. [Whenever the kinetics of a reaction is of any order other than zero, even the isothermal momentary rate is a function of time. In the case of first order kinetics, it is the exponential or logarithmic rate that remains unchanged, i.e., dlogC(t)/dt = const., and not the rate itself.]

Non Isothermal Synthesis of Acrylamide between 100 and 160°C

Up to about 160°C, the isothermal formation of acrylamide can be described by Eq.1 as a model. As already mentioned, Eq.1 is not a unique model and any particular sets of experimental concentration vs. time data can probably be described by alternative three or four-parameter models with the same or perhaps even better degree of fit. One of the mathematical characteristics of Eq.1 (and certain other three-parameter models) is that it has an *analytical inverse*. Or in other words, the term y = f(t) can be converted algebraically into t = f^{-1}(y). This allows the formulation of a rate model in the following way (Peleg et al., 2005):

Recall that the momentary isothermal formation rate in a region obeying Eq.1 is:

$$\left.\frac{dC(t)}{dt}\right|_{T=const} = \frac{dY_1(t)}{dt} \tag{10}$$

i.e.,

$$\frac{dC(t)}{dt} = \frac{a(T)k_g(T)\exp\left\{k_g(T)\left[t + t_{cg}(T)\right]\right\}}{\left\{\exp\left[k_g(T)\,t\right] + \exp\left[k_g(T)\,t_{cg}(T)\right]\right\}^2}. \tag{11}$$

The time, t*, that corresponds to any given momentary concentration C(t), see Fig. 4-left, is the inverse of Eq.1, i.e.,

$$t^* = t_{cg}(T) - \frac{1}{k_g(T)} \cdot Log_e\left\{\frac{a(T)}{\frac{a(T)}{1+\exp[k_g(T)t_{cg}(T)]} + Y_1(t)} - 1\right\} \tag{12}$$

Combining Eqs.11 and Eq.12 yields the rate equation:

$$\frac{dC(t)}{dt} = \frac{k_g(T)\left\{\frac{a(T)}{1+\exp\left[k_g(T)t_{cg}(T)\right]} + Y_1(t)\right\}^2 \cdot \left\{\frac{a(T)}{\frac{a(T)}{1+\exp\left[k_g(T)t_{cg}(T)\right]} + Y_1(t)} - 1\right\}}{a(T)} \tag{13}$$

Although very cumbersome in appearance, Eq. 13 is an ordinary differential equation (ODE) that can be easily solved numerically by modern software like Mathematica®, (Wolfram Research, Inc., Champaign, IL-the software used in this work).

It can also be converted into a *difference equation*, in which case it can be solved numerically with general purpose software like MS Excel® (Corradini et al., 2006). All that is required is to express the temperature profile, T(t), and the temperature dependence of the models coefficient, namely a(T), k_g(T) and t_{cg}(T), algebraically. These terms can then be converted into time dependent terms, i.e., a[T(t)], k_g[T(t)] and t_{cg}[T(t)] by replacing the temperature, T, by the temperature profile expression, T(t), and inserting it into the rate equation (Eq. 13). Notice though that this model will work if and only if the temperature during the simulated or predicted process never exceeds about 160 °C, the approximate upper limit of Eq. 1's applicability as the acrylamide formation's model.

Non Isothermal Formation of Acrylamide at Varying Temperatures between 100 and 200 °C

The concentration curves of acrylamide at temperatures above about 160 °C have a clear peak. Hence, the curves' slope changes direction and the same observed concentration can have two corresponding times, before and after the peak (see Fig. 4-right). Moreover, the isothermal concentration's model equation (Eq. 4) has no analytical inverse, unlike Eq.1 and most other two or three-parameter isothermal model equations. This means that t*, the time that corresponds to any momentary concentration C(t), cannot be expressed algebraically. The problem has already been encountered in microbial inactivation and growth models (Peleg, 2003; 2004; Corradini and Peleg, 2006b). It can be circumvented by expressing t* not as an algebraic term but as the *numerical solution of the isothermal model's equation at any concentration C(t)* in the appropriate syntax. When the software used is Mathematica®, one can write:

$$tstar[t\_] := t/.x \rightarrow First[NSolve[C[x] == C(t), x]] \tag{14}$$

or

$$tstar[t\_] := t/.x \rightarrow First\,[Find\,Root[C[x] == C(t), \{x,\ 0\}]] \tag{15}$$

What these two equations say is that the momentary value of t*, tstar[t] at any time t, is the first term rendered by the program's numerical solution of C(x) = C(t) with respect to x, where C(t) is the momentary concentration at that particular time, t. [The user can solve the equation by either the NSolve or FindRoot commands.] This expression of t*, tstar[t] in the language of Mathematica®, can be inserted into the rate equation and it would be treated by the program as if it were an algebraic term. If Eq. 4 is used to describe the isothermal production and elimination of the acrylamide, then the momentary isothermal rate is:

$$\left.\frac{dC(t)}{dt}\right|_{T=const} = \frac{d}{dt}\left[\left\{\frac{a(T)}{1+\exp\{k_g(T)[t_{cg}(T)-t]\}} - \frac{a(T)}{1+\exp[k_g(T)t_{cg}(T)]}\right\}\cdot\frac{1}{1+\exp[k_d(T)[t-t_{cd}(T)]]}\right] \tag{16}$$

which will yield a grossly cumbersome expression if written explicitly. In fact all we have to do is to define a new function that we may call diffC(t), say, defined in Mathematica® as:

$$\text{diffC[t]} := \text{D[C[t], t]} \tag{17}$$

In Mathematica®, *D*[*function*[*t*], *t*] means the first derivative of the function of t with respect to t. Once the derivative is obtained, each t in the expression is replaced by t* as defined by Eq.14 or 15. As before, the rate equation's, coefficients, which remain constant under isothermal conditions, are now functions of time determined by the temperature profile T(t), i.e., a(t)=a[T(t)], k_g(t) =k_g[T(t)], etc.

The resulting differential equation can then be solved by the command:

$$\text{result} = \text{NDSolve[\{C[t] == diffC[t], C[0] == } C_0\text{\}],}\ \text{C[t], \{t, 0, tProcess\}]} \tag{18}$$

In the language of Mathematica®, NDSolve[ ] is the command to solve a differential equation numerically. Here, it is the command to find the function C(t), whose time derivative, C'(t), dC(t)/dt, is diffC[t]. The boundary condition is that at t = 0, C[0] = C_0. The last term at the right of Eq.18 signifies that the sought solution is for the time between zero to tProcess.

Although the procedure must appear very complicated to the uninitiated, it is rather straightforward to those who are working with Mathematica® routinely. However, application of the described method to calculate the non isothermal concentration curve using Eq. 4 as a model has yielded mixed results. Because of the rate equation's complexity and that the same momentary concentration can have two corresponding times, pre and post peak – see Fig. 4, the solutions rendered by Mathematica® were very slow to come and in certain cases they were totally unrealistic (e.g., they could imply the existence of negative concentration after a long time in certain cases). But even when the procedure did work, the results themselves were suspect, as the warning comments generated by the program indicated.

To avoid this problem, we have replaced the five-parameter isothermal model, expressed by Eq. 4 by a simpler

four-parameter totally empirical model in the form:

$$C(t) = \frac{a^m t^n}{b^m + t^m} \tag{19}$$

where a, b, m and n are constants. According to this model when n=m, C(t) has a sigmoid shape, i.e., when $t \to \infty$, the concentration approach as an asymptotic level, a^m. If m>n, C(t) will have a true peak, whose location and height can only be calculated numerically. [Eq. 19 is equivalent to $C(t) = at'^n/(b'+t^m)$ where $a^m = a'$ and $b^m = b'$. By writing the model in the more elaborate form of Eq. 19, the magnitude of the parameter b does not become excessively large. According to Eq. 19, n > m corresponds to a monotonic increase in the acrylamide concentration beyond the inflection point. But, since such patterns have not been observed in acrylamide formation, this combination of the model's parameters will not concern us here. Either way, when $m \neq n$, Eq. 9 has no analytical inverse. Consequently the time that corresponds to a given concentration, t^* has to be expressed as the numerical solution of $C(t)$ with respect to t, i.e., in the language similar to that of Mathematica®:

$$tstar[t\_] := t/.x \to First \left[NSolve \left[\frac{a^m x^n}{b^m + x^m} == C(t), x \right] \right] \tag{20}$$

or $tstar[t\_] := t/.x \to First$

$$\left[FindRoot \left[\frac{a^m x^n}{b^m + x^m} == C(t), \{x,\ 0\} \right] \right] \tag{21}$$

What it says is that tstar[t], t^*, becomes the time that assumes the value of x, which is the numerical solution of the equation when the concentration is C(t). The momentary *isothermal rate* at a temperature T, at any given time t is the derivative of Eq. 19, i.e.,

$$\left.\frac{dC(t)}{dt}\right|_{T=const} = \frac{a(T)^{m(T)} n(T) t^{n(T)-1}}{b(T)^{m(T)} + t^{m(T)}} - \frac{a(T)^{m(T)} m(T) t^{m(T)+n(T)-1}}{[b(T)^{m(T)} + t^{m(T)}]^2} \tag{22}$$

Under non isothermal conditions, we assume that the momentary rate is the isothermal rate at the momentary temperature at a time, t^*, that corresponds to the momentary concentration. If so, and if the temperature history is expressed algebraically by T(t), then at any time t, the equation's parameters become, a[T(t)], b[T(t)], m[T(t)] and n[T(t)]. Incorporating all the above in Eq. 22 produces the model's rate equation:

$$\frac{dC(t)}{dt} = \frac{a[T(t)]^{n[T(t)]} n[T(t)]\ t^{*n[T(t)]-1}}{b[T(t)]^{m[T(t)]} + t^{*m[T(t)]}} - \frac{a[T(t)]^{m[T(t)]} m^{[T(t)]}\ t^{*m[T(t)]+n[T(t)]-1}}{\left\{b[T(t)]^{m[T(t)]} + t^{*m[T(t)]}\right\}^2} \tag{23}$$

where t^* is defined by the algorithm expressed by Eq. 20 or 21, except that at each iteration during the rate equation's numerical solution, a(t) = a[T(t)], b(t) = b[T(t)], m(t) = m[T(t)] and n(t) = n[T(t)]. Eq. 23 is quite a cumbersome rate model but it is solved by Mathematica® fairly rapidly in contrast with the Logistic-Fermi model and without ambiguities. Consequently, we have used Eq. 23 as the model to simulate hypothetical non isothermal synthesis and degradation of acrylamide. Its parameters (see below) were derived from the published experimental results of the rye dough whose isothermal concentration curves and their coefficients temperature dependence are shown in Figs. 5 and 6.

Simulated Non Isothermal Formation in Heated Doughs

The acrylamide's concentration curves of wheat and rye doughs at three constant temperatures, fitted with Eq. 19 as a model are shown in Fig. 27. Although the model had only four adjusted parameters its fit was very close to that of the more elaborate Logistic-Fermi and Logistic-Exponential models – (compare with Figs. 5 and 9). This is one more demonstration that the same data can be fitted with more than one model and that these can have a totally different mathematical structure. The temperature dependence of Eq. 19's parameters is shown in Fig. 28. These data were used for the simulation, assuming that the parameters' temperature dependence could be expressed by the ad hoc empirical terms:

$$a(T) = \frac{1.9}{1 + \exp[0.13\,(155.8 - T)]} \tag{24}$$

$$b(T) = 49.6 - 0.18\ T \tag{25}$$

$$m(T) = 5.65 + 0.000012 \cdot \exp[0.064 \cdot T] \tag{26}$$

$$n(T) = 5.7 + Log\,\{1 + \exp[0.22\,(T - 188.7)]\} \tag{27}$$

The temperature profiles, used to convert the above terms into functions of times, i.e., a(t)=a[T(t)], b(t)=b[T(t)], n(t)=n[T(t)] and m(t)=m[T(t)], were of three kinds intended to examine three different scenarios; fast vs. slow heating, Fig. 29, "high temperature, short time" (HTST) vs. "low temperature, long time" (LTLT), Fig. 30 and the potential effect of the temperature level reversal; "high" followed by "low", or vice versa, Fig. 31. The corresponding T(t) expressions that were used to generate the temperature histories shown in the figures are listed in Table 3. Combining Eqs. 24–27 and the temperature profiles listed in the table determined the coefficients of the acrylamide formation's rate model, i.e., Eq. 23. Once these had been specified, the equation was solved numerically by Mathematica® to

Table 3 Temperature histories, T(t)'s, used to generate the simulated heating regimes shown in Figs. 29–31.

Heating regime	Temperature history (T in °C, t in min)	Fig.
"Fast heating"	$T(t) = 50 + \dfrac{t}{0.017 + 0.007\,t}$	29
"Slow heating"	$T(t) = 50 + \dfrac{t}{0.053 + 0.006\,t}$	29
"High temp, short time" (HTST)	$T(t) = 50 + \dfrac{152\,t}{0.2 + t} \cdot \dfrac{1}{1 + \exp[1.25\,(t - 12.5)]}$	30
"Low temp, long time" (LTLT)	$T(t) = 50 + \dfrac{130\,t}{1.5 + t} \cdot \dfrac{1}{1 + \exp[0.25\,(t - 52.5)]}$	30
"High" first, "low" second	$T(t) = \dfrac{155}{1 + \exp[0.25\,(25 - t)]} + \dfrac{30 + \left(\dfrac{195\,t}{2 + t}\right)}{1 + \exp[0.25\,(t - 25)]}$	31
"Low" first, "high" second	$T(t) = 30 + \dfrac{142.5\,t}{2 + t} + \dfrac{30}{1 + \exp[0.5\,(35 - t)]}$	31

generate the corresponding concentration-time curves, C(t) vs. t, that are shown in the three figures.

Effect of the Heating Rate

If the concept which the model expressed by Eq. 23 is correct, then the heating rate plays a significant role in the acrylamide formation. As shown in Fig. 29, the peak amount could vary considerably and so is the onset of the acrylamide synthesis. In the two hypothetical processes described in the figure, the early onset of the degradation stage eliminated the formed acrylamide so that the residual level after an hour was very low in both cases. This is, of course, all hypothetical. But the model can be tested by actually monitoring the acrylamide's concentrations under similar non-isothermal conditions and comparing the results with those predicted by the model.

HTST vs. *LTLT*

The simulations shown in Fig. 30, again generated with Eq. 23 as a rate model predict a dramatic effect of the time-temperature combination on the amount of acrylamide synthesized and retained. If the model is correct, then exposure to a (relatively) very high temperature for a short time rather than to a lower temperature for a longer time can be an option to reduce the residual level of the acrylamide in the food of concern. Again, if the model is valid, which is yet to be found experimentally-see below, then simulations of the kind shown in the figure can help to find a heating profile that will produce a desirable flavor, color, and texture, but only a minimal amount of acrylamide. According to the model used, and the underlying concept discussed in the previous sections, the elevated temperature has a stronger effect on the acrylamide's degradation than on the synthesis rate. This is manifested in shortening the onset time of the degradation

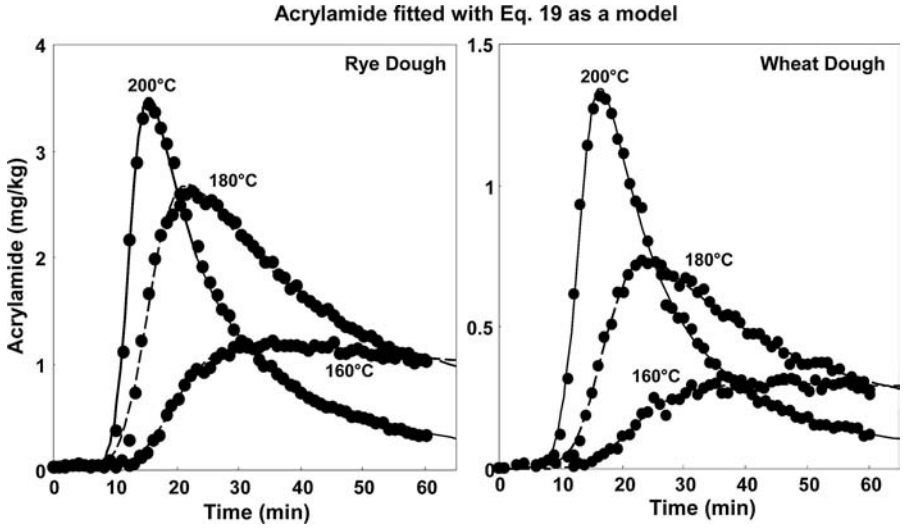

Figure 27 Isothermal acrylamide concentration vs. time relationships of wheat and rye doughs fitted with the four parameter empirical model $C(t) = a^m t^n / (b^m + t^m)$, Eq. 19. Notice the comparable fit to the five and six parameter models shown in Figs. 5 and 9.

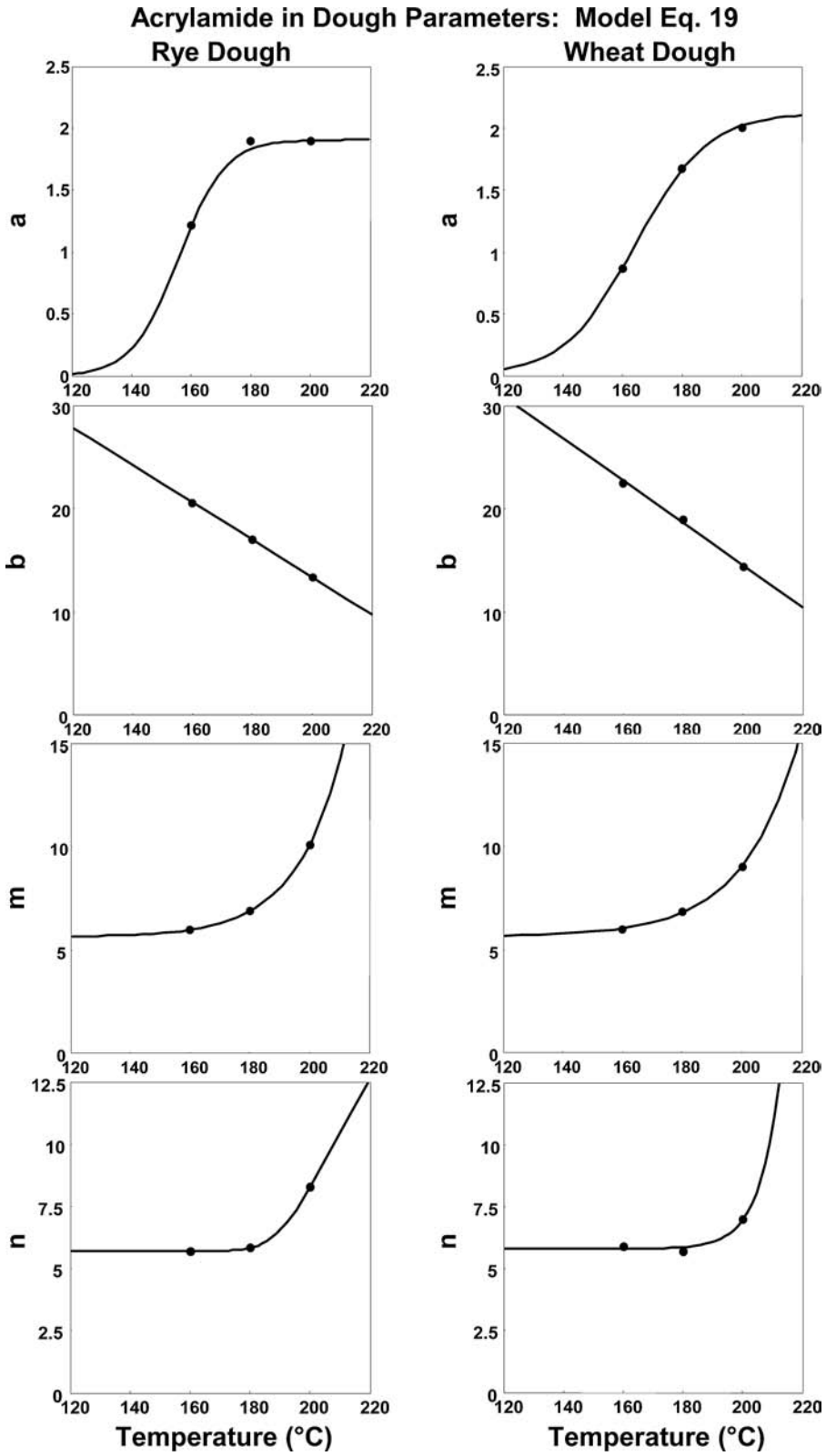

Figure 28 The temperature dependence of the four-parameter empirical model (Eq. 19), when applied to the rye and wheat dough data shown in Fig. 27.

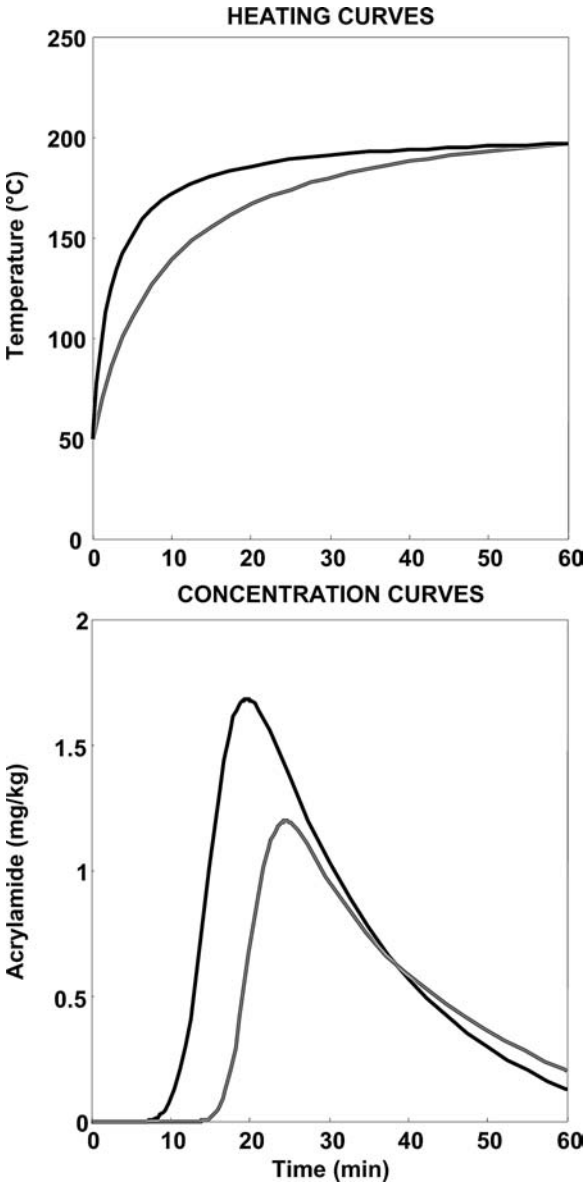

Figure 29 Two simulated heating curves and the corresponding acrylamide formation patterns generated with Eq. 23 as the rate model. The generation parameters are listed in the text and Table 3.

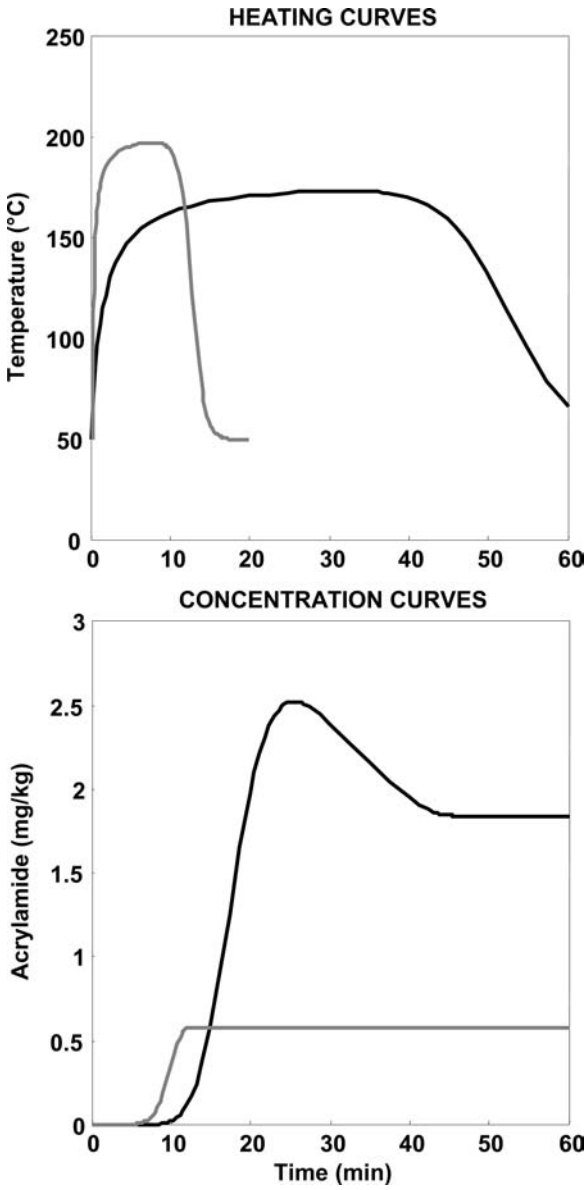

Figure 30 Simulation of acrylamide formation in a "high temperature, short time" (HTST) and "low temperature, long time" (LTLT) processes using Eq. 23 as the rate model. Notice that, theoretically, the temperature history can have a dramatic effect on the residual acrylamide found. The generation parameters are listed in the text and Table 3.

processes and in that what remains of the compound is only a small fraction of the amount that could have been produced. The same in fact was already observed in the published isothermal data, where the acrylamide's residual amount after 60 min at 200°C could be significantly *lower* than that formed at 160°C and 180°C.

High-low vs. *low-high*

Suppose one wants to program a heating process that will result in a product having certain qualities. [Since the main theme of the discussion is kinetics, and since the validity of the rate model used here (Eq. 23) has not yet been confirmed experimentally, we will not address the technological aspects of the hypothetical scenarios that will be examined below.] A question that may arise is what the acrylamide implications will be if a "hot stage"' will precede a "colder stage," or vice versa. This question can be answered by simulating the acrylamide formation (and perhaps that of other compounds) in the two scenarios and compare the resulting concentration curves. The simulations depicted in Fig. 31 indicate that, at least theoretically, the effect of the temperature history can again be dramatic. Although the two contemplated heating regimes produce about the same time-temperature exposure, the shapes of the two corresponding acrylamide concentration vs. time curves are very different. When the high temperature preceded the low, there was a high peak concentration and, after 60 min, a considerable

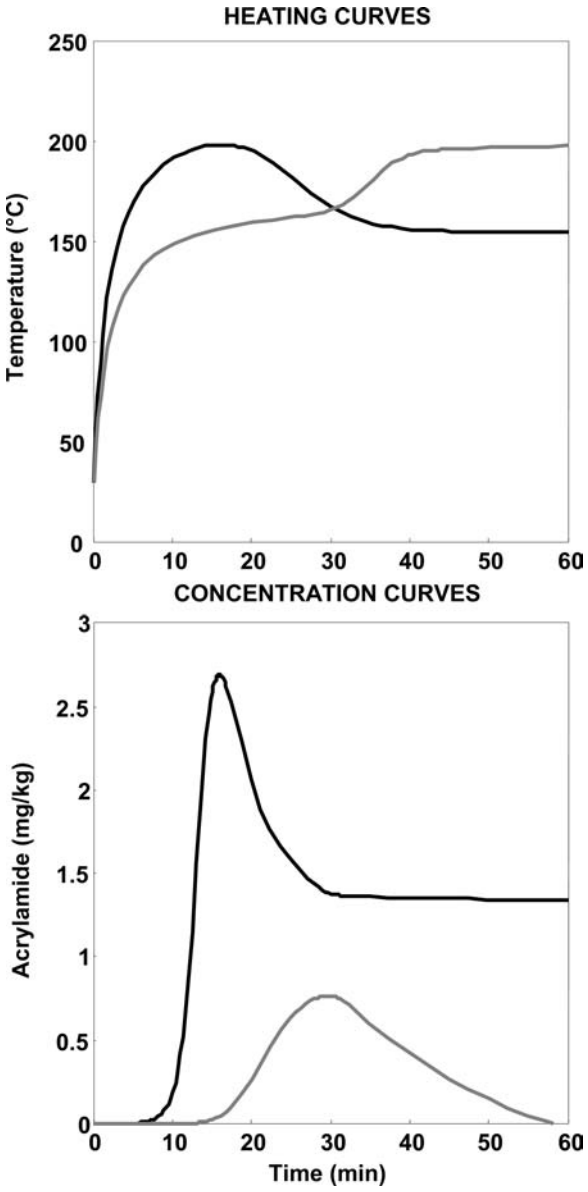

Figure 31 Two simulated heating curves and corresponding acrylamide formation patterns generated with Eq. 23 as a rate model. Notice that, theoretically, reversing the sequence of the high and low temperature regimes can have a dramatic effect on the acrylamide formation. The generation parameters are listed in the text and Table 3.

residual. When the lower temperature preceded the higher, the much smaller peak not only came much later, but also all the synthesized acrylamide had practically vanished before the 60 min mark was reached.

Again, until the model could be confirmed experimentally, all the above would remain a theoretical speculation. However, examining the two scenarios would be an excellent way to test the model and confirm or refute the assumptions on which it is based. Concentration curves of the kind shown in Fig. 31 are so distinct that it is unlikely that any experimental scatter will be able to blur the conclusion. If indeed the model is confirmed, then simulations of the kind shown in Fig. 31, as well as in Figs. 29 and 30, would help the model's user to evaluate the acrylamide implications of existing as well as new heat processes.

CONCLUDING REMARKS

Published data on foods and asparagine-glucose model systems, coming from different sources, all indicate that isothermal acrylamide formation follows two basic patterns:

At temperatures up to about 160°C, the concentration vs. the time curve has a sigmoid shape and at temperatures above 160°C a true peak concentration. The differences between the systems examined were quantitative rather than qualitative, i.e., the curves' shapes were basically the same, except for the concentration scale which varied considerably. The curves themselves could be described, with almost the same degree of fit, by mathematical models that had been derived from very different considerations. For some, the starting point has been the kinetics of the chemical reactions that produce and eliminate the formed acrylamide (Claeys et al., 2005b; Knol et al., 2005). The reactions themselves have been treated at different levels of scrutiny. But it has been assumed by the authors that all the reactions follow a first order kinetics and that the temperature dependence of all their rate constants follows the Arrhenius model. Whether these two assumptions can be appropriate not only for modeling acrylamide formation in model systems but also in real foods where the reactions state continuously changes is unclear at this time. The Fermi-Logistic type of models proposed here for the first time, for acrylamide formation, stem from the "global view" that all the processes that result in the acrylamide synthesis can be accounted for by a single logistic term and all those that are responsible for the acrylamide elimination by a single Fermian term. According to this concept the shape of the acrylamide's concentration curve, including whether it will show a peak concentration, is primarily but not exclusively determined by the characteristic *time scales* of the synthesis and degradation processes. This is a different *kind* of assumption, which does not require detailed knowledge of any of the molecular mechanisms involved. The same published experimental concentration curves can also be described by purely empirical mathematical models (like Eq. 19), in which case no mechanistic assumption of any kind is required. For the construction of such models is limited to interpretation and mathematical convenience and adequate fit are the only considerations. The utility of this type of model is limited to simulations since they reveal nothing at all about the underlying processes kinetics and their relative roles. Yet, because of their mathematical simplicity and the total independence of their structure of the changing kinetics, they can be conveniently used for predicting the acrylamides changing concentration during non isothermal heat treatments, at least in principle.

In contrast with the studies aimed at elucidating the reactions kinetics in model systems, the published reports on acrylamide formation in real foods have either two few data points, too few temperatures (three or less), or both. Thus, the development

of a reliable quantitative model of the temperature role from what's now available in the literature is extremely difficult. This is regardless of the approach, be it kinetic, descriptive, or purely empirical. But more disturbing from the modeler point of view is that isothermal and non isothermal data on the same foods are extremely difficult to find—perhaps they do not even exist. Such data, needless to repeat, are essential for validating *any* proposed kinetic model, by demonstrating its ability to predict the results of the non isothermal experiments from data obtained under isothermal conditions. At this point, one must conclude, the traditional, the Logistic-Fermi, and the purely empirical rate model are all on the same footing. They all can *describe* the process but their predictive ability is yet to be demonstrated experimentally. Hopefully, future research will produce the missing data so that the different approaches to the modeling of acrylamide formation in foods could be better compared.

It has been demonstrated, that *in principle*, one can predict the results of a non isothermal heating experiment using a rate model that has been derived from an empirical description of the isothermal data (Eq. 23 in our case). It is worth mentioning, that if the underlying concept is proven valid, then *any* empirical model that fits the isothermal data well could be used for the purpose. This is provided that the predictions are restricted to the time and temperature ranges of the isothermal data. The same can be said about interpolation. Any model of a comparable fit can be used to generate the concentration curve at intermediate temperatures but none can be used for extrapolation to a temperature well above the highest actually examined. Since at temperature below 100°C let's say, acrylamide formation is negligible. This is less of a problem than at the other end.

A remaining open question is what assumptions are allowed when one wants to develop a model for a complex reaction governed by competing mechanisms and taking place in a complex environment. Is the first order kinetics really necessary? Can one legitimately assume that the rate of every intermediate process is only temperature dependent (and not of time) and that it must obey the Arrhenius equation? In light of the other types of models that incorporate none of these assumptions and can also describe the same experimental data, is there any criterion according to which one can decide which is "more appropriate"? It is doubtful that these questions have a definite answer, but future research might settle the issues by showing which kind of model performs better under specific circumstances.

The shortcoming of all three approaches discussed in this article is that they have produced what can be called a "point model." Or in other words, they can currently describe and, hopefully, will be able to predict, the formation of acrylamide in a very small volume of food, where the temperature can be assumed to be uniform. During the roasting, baking, or frying of foods, the temperature is not only a function of time but also of *location*. Thus it will be a challenge to future researchers to predict how much acrylamide is produced in a given food volume that might have different shapes. This will require marrying the kinetic models with heat transfer models and in some cases, where the diffusion of the reactants might be a factor, with mass transfer models as well. The mathematical tools to handle such problems already exist. Nevertheless, they might need adaptation and modification in order to be useful for solving problems involving *changing environments*, as is the case of frying, where the food's physical and thermal properties at different regions vary at different rates.

And a final word. The application of the concept that the momentary rate of a complex process under non isothermal conditions is the isothermal rate at the momentary temperature at a time that corresponds to the system's momentary state has been demonstrated in vitamins degradation and in microbial inactivation and growth. In fact, it has been the starting point of several well-known models of bacterial growth for years. But in almost all previous implementations of this concept, the resulting models have been almost exclusively applied to monotonic growth or decay. In this and two previous articles, we have demonstrated that, mathematically at least, the concept can be extended to processes where growth (accumulation) and decay (degradation) occur simultaneously. Or in other words, the mathematical tools to develop rate models equations for combined synthesis-degradation reactions and for their solution already exist. Thus, if the underlying assumptions could be verified experimentally for acrylamide, the same methodology could also be employed for modeling and the prediction of the kinetics of other reactions, in which competing molecular mechanisms operate at the same time, but at different pace at different temperatures.

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