Role of intestinal brush border peptidases in the simulated digestion of milk proteins

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Scope: This study aimed to assess the impact of the “often neglected” intestinal brush border membranes (BBMs) hydrolases on dietary peptides, exploring the possibility that the disintegration of proteins progressed in the small intestine up to a “core” of intrinsically stable oligopeptides, persisting independently on the up-stream breakdown.

Methods and results: Samples of sodium caseinate, skim milk powder, and whey protein isolate were submitted to in vitro simulated gastropancreatic digestion using two different procedures: (i) a simplified model involving the main compartmental specific proteases; (ii) a static digestion method based on a frameset of parameters inferred from in vivo. The gastroduodenal digesta were further hydrolyzed with peptidases from porcine jejunal BBM. The peptidomes arising from the two digestion models, characterized by combined HPLC and MS techniques, differed to some extent. However, only specific protein domains survived digestion, among which are potential bioactive or immunogenic (food allergy) peptides. The degree of hydrolysis (DH) after BBM digestion (70–77%) practically did not differ between the digestion models and significantly increased the DH after duodenal steps.

Conclusion: Any in vitro digestion model should be supplemented with a jejunal phase to realistically determine the bioaccessibility and bioavailability of dietary peptides.

Keywords:
Brush border membrane hydrolases / Degree of hydrolysis / Gastrointestinal digestion / In vitro digestion models / Milk proteins

1 Introduction

The high stability of specific domains of dietary proteins to the harsh conditions present in the gastrointestinal (GI) tract suggests that some peptides are able to cross the gut mucosal barrier and could exert various beneficial effects (bioactive peptides) or, on the contrary, elicit an immune response (food allergy).

Under this standpoint, milk proteins, assumed as a model of dietary proteins, are by far the most extensively studied. According to a large body of literature, the peptides released during GI digestion cover a wide range of bioactive or immunogenic sequences. However, the evidences about the bioactive potential of milk-derived peptides have been almost entirely obtained in conditions sometimes divergent from those occurring along the human GI tract.

A simplified static and multiphasic in vitro model of the GI digestion, consisting of sequential simulated gastric, duodenal, and intestinal (peptidases from human intestinal brush border membrane (BBM) enzymes) phases, has been previously adapted and applied to identify both the casein-derived and whey protein derived peptides particularly resistant to the GI proteolysis [1, 2].

Composition of the digestion fluids, incubation times, and proteases-to-proteins ratio of such a simplified model differed in several aspects from those of the in vitro static model of the GI digestion that has been recently harmonized within the frame of the Infogest Cost Action [3]. According to this latter
procedure, ion composition and pH of the digestive juices as well as concentration of the hydrolytic enzymes have been defined on the basis of a set of parameters that has been deduced from in human determinations.

However, many milk-derived peptides that were found to endure proteolysis in simplified conditions corresponded to or in part overlapped those identified as resistant in vivo [4, 5], thus suggesting that specific domains of milk proteins have an intrinsic stability to digestion and could be good candidates to exhibit biological activity. On the other hand, the number and amount of milk-derived peptides that survive the simplified simulated digestion were greatly reduced if compared to other models of the gastroduodenal digestion, mainly because the process also included a final step of degradation with the endo-/exopeptidases from intestinal BBMs. To date, several studies have demonstrated that some milk-derived peptides surviving the gastropancreatic digestion are degraded by the BBM-associated peptidases [2, 6].

The entire intestinal tract is lined by a continuous layer of epithelial enterocytes characterized by apical structures that compose thousands of microvilli (BBM vesicles), which generate a strikingly large membrane surface area. The microvilli protrusions are particularly accentuated in the jejunum that in an adult individual is ~2.5–3.0 m long. Intestinal BBM vesicles contain at least 12 evolutionarily highly conserved peptidases, within a more than double number of general hydrolases (e.g. glicosidasas) [7]. Interestingly, the inventory of the intestinal hydrolases has been significantly extended, even up to an order of magnitude higher, by recent proteomic investigations [8]. Such a body of information highlights the key physiological role played in vivo by the intestinal BBM peptidases for subserving the terminal peptide digestion into short oligopeptides and free amino acids.

Although food-derived oligopeptides could exert biological actions locally, at level of the intestinal lumen, the resistance to intestinal epithelial hydrolases is a prerequisite for the intestinal absorption of peptides and access to the subepithelial lymphocytes as well as for systemic distribution. In this sense, in vitro digestion models that include a step of intestinal digestion with BBM peptidases have an already validated physiological consistency, as they supported, for instance, the discovery of wheat prolamin derived peptides that elicit celiac disease in vivo [9–11].

In spite of its importance to assess the bioaccessibility and bioavailability of potential bioactive or immunogenic peptides, the intestinal phase of digestion with BBM peptidases has been omitted in the majority of the in vitro digestion models developed so far, probably also because, differently from the other digestion compartments, a consensus about the parameters relevant to the simulated jejunal digestion remains far from being established.

In this work, we analyzed comparatively the digesta of three milk protein samples, namely sodium caseinate (CN) skim milk powder (SMP), and whey protein isolate (WPI), arising from two digestion procedures: (i) the original “simplified” model [1, 2], which was adapted to fit the conditions by Shan et al. [9]; (ii) a model integrated with parameters inferred from in vivo determinations, thereafter referred to as “integrated” model, which used conditions very similar to those of the recently harmonized static model [3]. Both the procedures were completed with an additional step of simulated intestinal degradation with BBM enzymes. In the perspective of the definition of physiologically relevant parameters to set up comprehensive in vitro models of the GI digestion, this study investigated the impact of the intestinal BBM hydrolases on the production and evolution of dietary proteins and peptides.

2 Materials and methods

2.1 Powdered milk proteins and chemicals

Samples of CN, SMP, and WPI powders were provided by the Fonterra Dairy Co. via the Riddett Institute (New Zealand). Porcine pancreatic enzymes (pepsin > 2500 U/mg, trypsin > 10 000 BAEE U/mg (where BAEE is N-α-benzoyl-l-arginine ethyl ester), chymotrypsin > 40 U/mg, and elastase > 4 U/mg), solvents, and chemicals, including phosphatidylcholine, bile salts/ acids (taurocholate/glicodeoxycholic acid), and MALDI matrices, were purchased from Sigma (St. Louis, MO, USA). Carboxypeptidase A was from Roche (Mannheim, Germany).

2.2 Simplified in vitro gastroduodenal digestion

Gastroduodenal digestion of CN, SMP, and WPI was substantially performed as previously described [1, 2]. Briefly, CN, SMP, and WPI were dissolved in 5% formic acid at the concentration of 2 mg/mL and incubated at 37°C with pepsin (1:100 enzyme/protein ratio, w/w) for 60 min, under low magnetic stirring. Before pancreatic digestion, the samples were evaporated and reconstituted twice with deionized water. Peptic digests were redissolved in 0.1 M sodium phosphate buffer (pH 7.0) supplemented with trypsin (1:100, w/w), chymotrypsin (1:100, w/w), elastase (1:500, w/w), and carboxypeptidase A (1:100, w/w) and incubated 1 h at 37°C. The reaction was stopped by heating for 5 min in a boiling water bath. The aliquots for the subsequent intestinal reactions were directly supplemented with BBM, omitting the 5-min boiling. As checked by RP-HPLC, heating induced no significant alteration of the peptide patterns.

2.3 Integrated gastroduodenal static digestion model

The “integrated” procedure was developed during a “pre-harmonization” stage of the static in vitro digestion model recently standardized in the framework of the Infogest project [3]. CN, SMP, and WPI were digested under conditions very close to those of the harmonized model [3], in line
with the procedure described by Sanchez-Rivera et al. [12].

The oral phase of digestion was omitted, due to the absence of starchy matrices in the milk protein samples. Briefly, CN, SMP, and WPI were dissolved (13 mg/mL of protein) in simulated gastric fluid (35 mM NaCl) acidified with HCl at pH 2 and preheated at 37°C. Gastric digestion was carried out with porcine pepsin at an enzyme/substrate ratio of 1:20 w/w (182 U/mg) at 37°C for 1 h, in the presence of phosphatidylcholine vesicles and 2.5 mM CaCl₂. Peptic digestion was stopped by adjusting the pH of the reaction mixture to 7.0 with NaOH. The in vitro duodenal digestion was carried out on the products from stomach digestion supplemented with 1 M CaCl₂, 0.25 M Bis-Tris pH 6.5, and 0.125 M equimolar mixture of sodium taurocholate and glycineoxycholic acid. The final concentrations within the mixture were 3.9 mg/mL of protein, 7.4 mM of bile salts, 7.6 mM of cholic acid. The final concentrations in each sample, 0.25 mL of 0.01% 2,4,6-trinitrobenzene sulfonic acid (Sigma) was added and incubated at 37°C for 2 h. The sampling volumes were calculated taking into account the opportunity to add additional milk or milk protein samples. The absorbance values were averaged. DH = h/h₀ × 100 was measured as the percentage of cleaved (h) with respect to the total number of peptide bonds (h₀), this latter being separately determined after acid hydrolysis of the milk protein substrates.

2.5 Simulated intestinal digestion with porcine BBM

The peptide digests arising from gastroduodenal digestion were twofold diluted with 0.1 M sodium phosphate buffer pH 7.2, supplemented with 100 µL BBM/100µg peptides, and incubated at 37°C up to 6 h. The peptidase activity-to-substrate ratio was selected according to previous literature studies [14]. The amount of the peptide substrate was estimated according to the original protein material, hence containing at this stage free amino acids too. Aliquots were picked up and analyzed at intermediate incubation times. The entire digestion procedures were performed in triplicate.

2.6 Determination of the degree of hydrolysis

The degree of hydrolysis (DH) was determined with the 2,4,6-trinitrobenzene sulfonic acid method [15], according to Hermanson (1996) [16]. Briefly, 5.0 µg of the sample proteins (CN, SMP and WPI) and the corresponding digests were diluted in 0.5 mL of 0.1 M sodium bicarbonate, pH 8.5. To each sample, 0.25 mL of 0.01% 2,4,6-trinitrobenzene sulfonic acid (Sigma) was added and incubated at 37°C for 2 h. The sampling volumes were calculated taking into account the opportunity to add additional milk or milk protein samples. The absorbance values were averaged. DH = h/h₀ × 100 was measured as the percentage of cleaved (h) with respect to the total number of peptide bonds (h₀), this latter being separately determined after acid hydrolysis of the milk protein substrates.

2.7 RP-HPLC analysis

The course of simulated gastroduodenal-(intestinal) hydrolysis was monitored by RP-HPLC using an HP1100 modular system (Agilent, Palo Alto, CA, USA) equipped with a Jupiter® C18 RP column, 2.0 mm id × 250 mm, 4 µm particle diameter (Phenomenex, Torrance, CA, USA). Peptide separation (25 µg for each sample) was carried out with a 5–60% gradient of solvent B over 60 min at a flow rate of 0.2 mL/min, after 5 min of isocratic elution at 5% B. Solvent A was 0.1% TFA v/v in water; solvent B was 0.1% TFA v/v in ACN. The column was equilibrated at 5% B. The column effluent was monitored by UV detection (220 and 280 nm) using DAD.

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The identification of free Phe, Tyr, and Trp was confirmed by separate injections of the standard amino acids (Sigma). RP-HPLC analyses were also performed to assess the reproducibility of the digestion procedures.

2.8 RP-HPLC-MS/MS analysis

RP-HPLC-MS/MS analyses of peptide digesta were carried out using an Agilent 1100 HPLC System (Agilent Technologies) coupled to an Esquire 3000 quadrupole IT (Bruker Daltonik GmbH, Bremen, Germany) equipped with an ESI source. Peptide separations were performed with a Mediterranean Sea18 150 mm × 2.1 mm column (Teknokroma, Barcelona, Spain), applying a linear gradient from 0 to 45% of solvent B (TFA 0.027% in ACN) in 120 min, after 5 min of isocratic elution at 0%. Solvent A was 0.037% TFA in water. The injection volume was 50 μL and the flow rate 0.2 mL/min. The ESI capillary voltage was 4 kV. Spectra were recorded over the 250–1500 m/z range. In these analyses, the target mass was set at 750 m/z. Data were processed using the Data Analysis™ software (Ver. 4.0; Bruker Daltonik GmbH). Peptides were identified from the MS(n) spectra with the aid of the BioTools (Ver. 3.2) software (Bruker Daltonik GmbH), searching an homemade database with bovine caseins, most abundant whey proteins and main genetic variants thereof. No cleavage specificity was indicated. Identifications were considered successful when the measured molecular weight (MW) corresponded to the expected value and a sequence of at least three (two for low sized peptides, MW < 600) consecutive b- or y-fragment ions occurred in the spectrum. Entries occurring in both of two replicate analyses, with a score higher than the threshold value corresponding to the identity (p < 0.05), were included into the data set. Peptide identification was validated by manual inspection of the MS/MS spectra.

2.9 MALDI-TOF and TOF/TOF MS

Prior to MALDI analysis peptide mixtures were desalted using C_{18} ZipTip micro-columns (Millipore, Watford, UK). MALDI-TOF MS and LIFT™ (where LIFT is laser-induced forward transfer) MS/MS spectra were acquired using an Autoflex speed™ Instrument (Bruker Daltonik GmbH) operated in the positive reflector ion mode. In MS mode, the 600–4500 m/z range was explored. Precursor ions for LIFT MS/MS fragmentation were automatically selected when they overcame a threshold of 4 × 10³ ion counts at a laser power in the range 30–55%. α-Cyano-4-hydroxycinnamic acid (saturated solution in 30% ACN/0.1% TFA, v/v) and 2,5-dihydroxybenzoic acid (10 mg/mL in 50% ACN/0.1% TFA) were used as the matrices. Matrix (0.5 μL) and peptide solutions (0.5 μL) were mixed directly onto the Anchor Chip™ MALDI target (Bruker Daltonik GmbH) and air-dried. Spectra were externally calibrated using a mixture of standard low molecular mass peptides (Bruker Daltonik GmbH).

3 Results and discussion

3.1 Monitoring of digestion kinetics of milk proteins by RP-HPLC

The digestion kinetics of milk proteins was monitored by RP-HPLC. In line with a wealth of literature evidences, casein degradation started early as compared to the whey proteins. As expected [1, 17], CN was promptly degraded by pepsin whereas whey proteins, mostly β-lactoglobulin (β-Lg), were still in detectable amounts in SMP and WPI after 1-h incubation with pepsin in a simulated gastric environment. The outcomes of the peptic digestion were substantially similar regardless of the model between the two tested models (data not shown).

After simulated duodenal hydrolysis, intact milk proteins were no longer detectable, while the HPLC chromatograms exhibited complex patterns of small- and medium-sized peptides (Fig. 1, blue lines).

The hydrolytic enzymes of pancreatin in the integrated model were employed at a higher proteases-to-milk proteins ratio and included bile salts for stabilizing emulsions. Thus, the duodenal phase of the integrated model was expected to hydrolyze milk proteins more extensively, compared to the simplified one. Even so, free tryptophan (HPLC peak at 24 min, identified by DAD) was much more abundant in the digesta arising from the simplified model, which included elastase and carboxypeptidase A in the proteolytic system, in addition to trypsin and chymotrypsin. The peptide patterns of the duodenal digesta appeared rather different between the two models, reflecting the substantial difference of the digestion conditions (Fig. 1).

So far, no specific indications are available about a physiological like use of BBM jejunal enzymes. For this reason, we adopted conditions and levels of enzyme activities in line with those procedures that have already demonstrated a certain in vitro–in vivo consistency [10, 14].

The peptides arising from all the milk protein substrates incubated at final step with BBM were intensely degraded, independently on the up-stream model of gastroduodenal digestion. Indeed, at the end of both the simulated intestinal digestion procedures, only a low amount of peptides was detected by HPLC (Fig. 1, red lines) while the intense peak of free aromatic amino acids, especially tryptophan, dominated all the chromatographic profiles. The level of free tryptophan can be exploited as an indicative parameter of the hydrolysis degree of food proteins [18]. Free tryptophan after digestion with BBM, deduced from area under the peaks, had comparable values for the same protein substrates digested according the two different methods, thereby indicating a similar DH achieved by BBM peptidases. The digestion procedures produced reproducible peptide patterns, as
3.2 Degree of protein hydrolysis

DH values obtained at the several stages of digestion are reported in both the table and graphical layout in Fig. 2.

In spite of the lower pepsin-to-protein ratio (1:100 versus 1:20), the gastric digestion with the simplified model split milk proteins into medium- and large-sized (poly)peptides more efficiently, due to the protective effect of phospholipid vesicles used in the integrated model [19–21]. The hydrolysis progression was largely reverted after duodenal digestion. Due to the higher relative amount of hydrolytic enzymes present in the pancreatin preparation (used at an approximate ratio 1:10 w:w) as well as to the emulsifying properties of bile salts that remarkably promote proteolysis [22], DH was 55.3–59.3% for the integrated model, clearly higher than 34.5–41.1% for the simplified model (values are means of three replicate determinations). These figures contrast to some extent with the higher amounts of free aromatic amino acids detected by HPLC in the digesta obtained with the simplified model. However, this apparent discrepancy has to be considered as the result of different proteolytic systems and dissimilar cleavage specificity at the level of the aromatic amino acids, which is testified by a prominent pepsin–chymotrypsin and carboxypeptidase A sequential action in the simplified model. The occurrence of longer peptides in the duodenal pools obtained with the integrated model is most likely due to a less effective primary proteolysis that occurred in the gastric phase (Fig. 2). The DH values measured after gastroduodenal digestion with the integrated model are in good agreement with those previously determined on similar protein substrates, using the o-phthalaldehyde method [23].

At the end of the intestinal phase, DH values were ultimately equalized, i.e. 70.7–77.4 versus 70.6–77.5%. In particular, DH of CN was practically identical between the two digestion procedures. Only minor differences between DH values were measured for the whey protein containing samples (SMP and WPI). In other terms, the final peptide
degradation with BBM enzymes had a “leveling” effect regardless of the digestion model. Roughly three-fourths of all the peptide bonds of milk proteins were cleaved, contributing to intrigue the still unaddressed issue about the actual survival of medium- and large-sized peptides at concentrations that could be physiologically relevant.

The outstandingly high DH values determined for the three protein substrates are consistent with the HPLC analysis, which showed the progressive appearance of intense peaks of free aromatic amino acids (i.e. tryptophan, tyrosine, and phenylalanine) and the survival of very low amounts of longer peptides at the end of digestion. These figures of DH did not conflict with the relatively high MS-based coverage of β-casein and β-Lg (see below), since DH and protein coverage are not correlated. Indeed, a given peptide can derive from a very low percentage of the total parent protein.

### 3.3 Comprehensive characterization of digesta by MS-based techniques

To identify the most resistant domains of the milk proteins, as well as to infer information about the impact of relevant operative parameters on proteolysis, the digesta derived from the complete gastroduodenal–intestinal BBM degradation were characterized by complementary MS-based techniques. More in details, peptides resulting from the digestion of CN, SMP, and WPI with both the models were analyzed by RP-HPLC-ESI-IT-MS/MS and MALDI-TOF-MS also followed by LIFT-TOF/TOF-MS/MS. Confirming previous outcomes [1], free aromatic amino acids (primarily tryptophan) were largely dominant in all the digesta. The intense peaks of Tyr, Phe, and Trp were assigned by DAD monitoring of the RP-HPLC-MS analysis as they missed in the TIC chromatograms (detection in the m/z range 250–1500). Consistently, the full scan TIC-MS chromatograms showed only relatively low intensity ions, confirming the occurrence of very low peptide amounts in the digesta (not shown). The chromatograms of SMP digesta did not significantly differ from those obtained for CN and, for some minor traits, from WPI samples (see also below).

TIC profiles of CN digested according the two models appeared quite different while the patterns of WPI digesta were more similar to each other. Whey proteins are characterized by a defined folding sustained by disulfide bridges and by fat binding properties (especially β-Lg) while caseins are substantially rheomorphic proteins with extremely open and flexible conformation. Thus, this somehow unexpected finding suggests that digestion conditions affected casein degradation at larger extent than whey proteins.

The task of peptide identification was not straightforward due to the presence of a multitude of low-abundant peptides generated by random or not predictable cleavage along the backbone of proteins. Partial exopeptidase hydrolysis produced a series of progressively shortened peptides differing from each other by a single amino acid residue. The milk-derived peptides survived at a low amounts and the resolution of the HPLC separation decreased when higher amounts of digesta were injected, due to the presence of interfering compounds. Approximately from 50 to 75 peptides were identified in the digesta by software-assisted MS data mining and manual inspection of the ESI-IT MS and MS(n) spectra, also aided by previous results [1, 24]. The information deriving from the MALDI-based MS spectra was as much valuable, especially for the identification of relatively large peptides.

The TIC chromatograms of the digesta arising from the integrated model contained out-of-scale peaks at high retention times not detected by UV (not shown), due to co-eluting phospholipids and bile salts, omitted in the simplified procedure. Gross comparison of the relative peptides-to-lipids peak ratio confirmed that only low amounts of peptides survived digestion. The largest part of peptides in the CN digestes was derived from β-casein and αs1-casein (70 and 30%, respectively). The vast majority of peptides of WPI digesta arose from β-Lg. Many of the identified peptides arising from the simplified digestion model corresponded to those already described [1], as the hydrolysis conditions were practically the same, except for the origin of intestinal BBM vesicles that were porcine in the current study instead of human.

The Fig. 3 depicts the comparison between β- and αs1-casein peptides in the CN digesta obtained from the two digestion models after BBM hydrolysis. The peptides were identified by complementary ESI and MALDI MS based techniques. The two digesta share only a few common β-casein peptides. This observation confirmed that the hydrolysis conditions have a key impact on the nature of the produced protein fragments. Nevertheless, a great percentage of peptides in both digesta arose from only three β-casein regions, namely 74–92, 130–138, and 184–209, subsequently shortened by the action of duodenal carboxypeptidase A and BBM exopeptidases. Thus, it partly holds the hypothesis that only a few specific casein domains are intrinsically stable to proteolysis.

Our analysis also revealed that the pattern of the β-casein peptides from the integrated model was similar to that observed in vivo, by analysis of the intestinal aspirates [5]. On the other hand, peptides in the in vivo digesta were much more numerous and abundant, arguably because at least part of them had not reached intestinal apical membranes yet. Interestingly, the stable regions of β-casein are precursors of sequences described as bioactive peptides: the region 74–92 harbors IPP and VPP described as digestion-resistant antihypertensive triptides [25], which are also able to translocate cell models of the intestinal epithelium [26]; similarly, β-casein f193-209 contained in the 184–209 domain appears to partly survive digestion and to pass across Caco-2 cell monolayers [27]; β-casein f130-138 encryps the angiotensin-converting enzyme I inhibitor pentapeptide HPLLP that is resistant to digestive enzymes and, once absorbed, is processed by blood proteases, releasing still active fragments [28]. Peptides belonging to the strategic zone of the β-casomorphins (region 60–70) were detected at trace amounts especially with the integrated model.
It remains to establish if the actual bioaccessibility of the potential bioactive peptides, strongly reduced by BBM peptides, is high enough to induce relevant bioactive effects in vivo.

The comparison between αs1-casein-derived peptides (Fig. 3, right panel) supports the conclusion that only a few intrinsically stable peptide regions survive the proteolytic breakdown of the whole process, as there is a common domain in both CN digests where the majority of the identified peptides belonged, i.e. the 180–193 region. Interestingly, several processed forms of the phosphorylated αs1-casein f104-119 were identified in the CN digested according with the simplified model. Only one peptide from κ-casein f152-156 and one from αs2-casein (phosphorylated f138-146) were identified in the digesta following the simplified model.

Comparison of the peptides released from β-Lg in the WPI digesta is summarized in Fig. 4. As already emphasized for the UV-based detection, peptide digesta of whey proteins are similar to each other if compared to casein-containing samples. Indeed, in both cases, most of the β-Lg peptides derived from three protein regions, variously trimmed at the N- and C-terminus, i.e. the 40–60, 125–138, and 149–162 (protein C-terminal) regions, the latter containing Cys 60, linked through a disulfide bridge to Cys 66 of the 61–70 domain. The intact disulfide cross-linked peptides were identified by MALDI-TOF MS (not shown). Importantly, all of the three most represented domains have been described as the potential IgE-binding immunoreactive epitopes of β-Lg [29]. Thus, although this result should not be considered a general trait, the (partial) resistance to digestion in this case appears a prerequisite for the immunogenic activity. It has to be also underlined that in general, the MS detectability of the peptides is not correlated to their actual quantity in the digesta. However, information about the peptide abundances can be inferred by the relative peak intensities along the UV chromatograms (after expansion along the Y-axis). The UV detection also confirmed that β-Lg peptides arising from the 125–138 and 40–60 regions were the most abundant.

Only five and three short peptides from α-lactalbumin (α-La) were identified, in the digesta of the simplified and integrated models, respectively, one of which, α-La f114-117, shared by the two digesta. Three α-La peptides identified in the digesta from the simplified model were highly acidic (region 80–90, sequence FLDDDNLDDM), indicating that, as observed for β-Lg (several peptides from the 125–138 region), very acidic sequences are relatively resistant to digestion and
could be candidates to be immunogenic in vivo, also because they are spatially located on the external surface of the native IgE binding globular whey proteins. Notably, the α-La fβ0-90 is practically the unique region of α-La found at significant amount in human intestinal aspirates during milk digestion [5]. Minor amounts of high MW peptides (m/z 3500–3800), previously assigned to multiply S-S cross-linked α-La peptides [1], were also detected by MALDI-TOF MS. SMP contains both caseins and whey proteins, in the ordinary ratio of bovine milk. Thus, HPLC and HPLC-MS(n) patterns of peptides occurring in the SMP digesta roughly reflected the ratio of casein to whey proteins, of bovine milk (nearly 80% casein and 20% whey proteins). SMP, in fact, contained most of the casein-derived peptides identified in CN and minor amounts of the β-Lg peptides identified in WPI (not shown). This result indicates that the digestion of caseins and whey proteins in mixture was not appreciably affected by possible mutual interactions.

4 Concluding remarks

The harmonization of the in vitro digestion models and the definition of experimental protocols that rely on in vivo inferred parameters represent significant advances toward our knowledge about the fate of dietary proteins in the GI tract and their potential impact on human physiology. Relying on a series of parameters determined in human, the integrated model—and even more the standardized one [3]—is expected to provide more strict physiological consistency than the simplified model. Clearly, the in vitro–in vivo correspondence of the outcomes is the criterion that should drive the choice of a simulated digestion model. On the other hand, while the physiological consistency of any in vitro digestion model remains to be convincingly validated, the simplified model has some technical advantages because it is easy to be performed and in the duodenal step it makes use of lower amounts of pooled purified enzymes at high specific activity if compared to pancreatin. The digesta from the simplified model do not contain the bulk of interfering species (e.g. pancreatic enzymes, phospholipids, bile salts) that complicate the identification of peptides and proteins arising from more elaborated protocols [23]. Thus, depending on the research purposes and on the food matrix, selected parameters of the simplified protocol can be included in procedures of simulated digestion in order to balance simplicity and consistency [3].

As a major result, the outcomes of this study point out the need to include a phase of peptide degradation with BBM enzymes within any in vitro digestion model, to mimic the final digestion occurring in vivo in the jejunum. Intestinal peptidases contribute to heavily hydrolyze internally and “gnaw” the peptides released by the gastroduodenal breakdown up to a “core” of (oligo)peptides, these last resistant to a further hydrolytic cleavage. The striking increase in the DH induced by BBM enzymes up to a value that is ultimately independent on the up-stream production cannot be neglected when the in vitro determination of bioaccessibility and, subsequently, bioavailability of dietary peptides is required. Obviously, dedicated investigations are still needed to define the appropriate operative parameters with true physiological significance, for mimicking the intestinal digestion. In this sense, it is expected that the intestinal mucus also plays a key role as a physicochemical barrier able to delay (or impede) peptides and peptidases to come across.

The potential capability of nutrients to transduce nutritional information to the rest of the body by stimulating intestinal receptors—an issue someway related to the possible incomplete BBM-mediated hydrolysis and, hence, to the actual bioaccessibility of dietary peptides—launches a further research challenge that is emerging as the “gut chemosensing” field [30].

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5 References


