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## Protective Roles of Intestinal Microbiota derived Short Chain Fatty Acids in Alzheimer's Disease-type Beta-Amyloid Neuropathological Mechanisms

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### Abstract

**Background**—Dietary fibers are metabolized by gastrointestinal (GI) bacteria into short-chain fatty acids (SCFAs). We investigated the potential role of these SCFAs in  $\beta$ -amyloid (A $\beta$ ) mediated pathological processes that play key roles in Alzheimer's disease (AD) pathogenesis.

**Research design and methods**—Multiple complementary assays were used to investigate individual SCFAs for their dose-responsive effects in interfering with the assembly of A $\beta$ 1-40 and A $\beta$ 1-42 peptides into soluble neurotoxic A $\beta$  aggregates.

**Results**—We found that several select SCFAs are capable of potently inhibiting A $\beta$  aggregations, *in vitro*.

**Conclusion**—Our studies support the hypothesis that intestinal microbiota may help protect against AD, in part, by supporting the generation of select SCFAs, which interfere with the formation of toxic soluble A $\beta$  aggregates.

### Keywords

Alzheimer's disease; beta-amyloid (A $\beta$ ); fibrils; protein misfolding; microbial; microbiome; microbiota; neurodegeneration

## 1. INTRODUCTION

The term intestinal microbiota refers to the tens of trillions of commensal, symbiotic, and pathogenic microorganisms, including bacteria, fungi and archaea, which live in our

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### Declaration of interest

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intestine. There is a growing interest in the potential contributions of intestinal microbiota, particularly among the intestinal bacterial population, in human health and/or disease [1]. There is tremendous diversity among individuals' intestinal microbiota with respect to the composition of specific bacterial species and the density (number) of bacteria that are present for each of these bacterial species. Indeed, such interpersonal differences in intestinal bacteria composition have been associated with the presence or absence of an increasing number of health issues, including metabolic syndrome, obesity, immunological diseases, cardiovascular diseases, as well as neuro-degenerative disorders such as Alzheimer's disease (AD) and Parkinson's disease (PD) [1–4].

Gastrointestinal (GI) bacteria may affect host functions by interfering with potential pathogens, improving barrier function, immunomodulation, and/or production of neurotransmitters [5]. GI bacteria may also affect host functions through diet-based microbial influences, by metabolizing dietary compounds into readily absorbable, biologically available, bioactive forms that are responsible for modulation of select biological processes [6]. Accumulating evidence has demonstrated that such diet-based microbial influences may help promote resilience against diverse medical conditions, including neurological disorders such as AD, by modulation of metabolic and immunologic responses and/or other disease-specific pathological mechanisms [7–10]. An example of such diet-based microbial influence on neurodegenerative disorders is the critical role of gut microbiota in the bioactivity of dietary polyphenols. It has been estimated that about 90% of the dietary polyphenols are not absorbed by the small intestine and are accumulated in the colon where they are subjected to metabolism by GI microbial into phenolic acids, which are then readily absorbed [11,12]. Recent evidence revealed that some of these biologically available phenolic acids, such as caffeic acid and ferulic acid [13–16] are bioactive in inhibiting the generation of beta-amyloid (A $\beta$ ) peptides, a key pathogenic feature of AD [8], as well as in suppressing the elevated oxidative stress and inflammatory responses that are observed in AD as well as in other neurodegenerative disorders [9,10]. Moreover, our recent evidence revealed that other biologically available, GI microbiota-derived phenolic acids, such as 3-hydroxybenzoic acid and 3-(3'-hydroxyphenyl)propionic acid, are bioactive in interfering with the misfolding of A $\beta$  peptides into neurotoxic A $\beta$  aggregates that play key roles in AD pathogenesis [17]. Collectively, this evidence suggests that the GI microbiota may help attenuate the development and/or progression of AD through the generation of microbiota-derived phenolic compounds that mechanistically target diverse pathogenic mechanisms underlying AD.

Another example of diet-based microbial influence on AD is the involvement of GI microbials in the metabolism of dietary fibers. Dietary fibers are carbohydrate polymers, which cannot be hydrolyzed by the endogenous enzymes in the upper gut. Instead, dietary fibers are metabolized by the microbiota in the colon into short-chain fatty acids (SCFAs) with 5 carbons or less, including valeric acid and isovaleric acid (C5), isobutyric acid and butyric acid (C4), propionic acid (C3), acetic acid (C2), and formic acid (C1) [18,19]. It has been hypothesized that SCFAs generated by GI bacterial metabolism of dietary fibers may attenuate AD by serving as substrates for energy metabolism [7], and providing an alternative energy source to rectify brain hypo-metabolism that contributes to neuronal dysfunctions in AD and other neurodegenerative conditions [20]. Recent evidence suggests

that select SCFAs may also help modulate maturation and function of microglia in the brain [21], implicating the potential benefits of GI bacteria-derived SCFAs in modulating neuro-inflammatory processes that play important roles across diverse neurodegenerative disorders, including AD. More recently, it was shown that GI bacterial-mediated generation of butyric acid, an SCFA from dietary fibers, may provide therapeutic benefits for AD through epigenetic mechanisms of action by inhibiting histone deacetylase and normalizing aberrant histone acetylation in AD [22]. However, while neurotoxic A $\beta$  aggregates play a central role in AD onset and progression, it is currently unknown whether GI bacteria-derived SCFAs may modulate protein misfolding. Therefore, we hereby investigate whether GI bacteria-derived SCFAs may help modulate the self-assembly of A $\beta$  peptide, *in vitro*, using established assays. Outcomes from this study provide critical information for developing probiotics to help prevent and/or treat AD.

## 2. METHODS

### 2.1. Chemicals and Solvents

Chemicals were obtained from Sigma and, unless otherwise stated, were of the highest purity available. Solvents were HPLC grade and were obtained from Fisher. Water was double-distilled and deionized using a Milli-Q system (Millipore Corp., Bedford, MA).

### 2.2. Peptides and Proteins

Monomeric A $\beta$ 1-40 and A $\beta$ 1-42 peptides were synthesized, purified, and characterized as described previously [23]. Purified peptides were stored as lyophilizates at  $-20^{\circ}\text{C}$ . A stock solution of glutathione *S*-transferase (GST; Sigma-Aldrich) was prepared by dissolving the lyophilizate to a concentration of 250  $\mu\text{M}$  in 60 mM NaOH. Prior to use, aliquots were diluted 10-fold into 10 mM sodium phosphate, pH 7.4.

### 2.3. Preparation of A $\beta$ Solutions

Aggregate-free A $\beta$ 1-40 or A $\beta$ 1-42 solutions were prepared as described previously [24]. To prepare A $\beta$ , 200  $\mu\text{l}$  of a 2 mg/ml peptide solution in dimethyl sulfoxide was sonicated for 1 min using a bath sonicator (Branson Ultrasonics, Danbury, CT) and then centrifuged for 10 min at  $16,000 \times g$ . The resulting supernate was fractionated on a Superdex 75 HR column using 10 mM phosphate buffer, pH 7.4, at a flow rate of 0.5 ml/min. The middle of the LMW peak was collected around 25 minutes and used immediately. A 10- $\mu\text{l}$  aliquot was taken for amino acid analysis to determine quantitatively the peptide concentration in each preparation. Typically, the concentrations of A $\beta$ 1-40 and A $\beta$ 1-42 were 30–40 and 10–20  $\mu\text{M}$ , respectively.

### 2.4. Peptide Aggregation

Aggregation of A $\beta$ 1-40 (or A $\beta$ 1-42) peptide was conducted essentially as described previously [25]. In brief, A $\beta$  solutions (0.5-ml aliquots) were placed in 1-ml microcentrifuge tubes. Test compounds (SCFAs) were dissolved in ethanol to a final stock concentration of 2.5 mM. Peptide aggregation was conducted in 10 mM phosphate, pH 7.4, with 5  $\mu\text{M}$  A $\beta$ 1-40 (or A $\beta$ 1-42) peptide in the presence of either vehicle or individual SCFA a final 5

$\mu\text{M}$  or 20  $\mu\text{M}$  concentration, for a final SCFA:A $\beta$  molar ratio of 1:1 or 1:4. The tubes were incubated at 37 °C for 0–10 days without agitation.

## 2.5. Photoinduced cross-linking of unmodified proteins (PICUP)

A $\beta$  peptide oligomer frequency distributions were assessed using the photoinduced cross-linking of unmodified proteins protocol as described previously [25]. Briefly, 1  $\mu\text{l}$  of 1 mM tris(2,2'-bipyridyl)dichlororuthenium(II) (Ru(bpy)) and 1  $\mu\text{l}$  of 20 mM ammonium persulfate were added to 18  $\mu\text{l}$  of freshly prepared protein solution. We noted that addition of SCFA did not lead to observable change in the pH of reaction mixture. The mixture was irradiated for 1 s with visible light, and then the reaction was quenched with 10  $\mu\text{l}$  of Tricine sample buffer (Invitrogen) containing 5% (v/v)  $\beta$ -mercaptoethanol. An aliquot (20  $\mu\text{l}$ ) of each cross-linked sample was electrophoresed on a 10–20% gradient Tricine gel and visualized by silver staining (SilverXpress, Invitrogen). Non-cross-linked samples were used as controls in each experiment. To produce intensity profiles and calculate the relative amounts of each oligomer type, Densitometry was performed, and One-Dscan software (v. 2.2.2; BD Biosciences Bioimaging) was used to determine peak areas of baseline corrected data.

## 2.6. Thioflavin T (ThT) spectroscopic assay

The ThT assay was conducted essentially as described previously [25]. Ten  $\mu\text{l}$  of sample was added to 190  $\mu\text{l}$  of ThT dissolved in 10 mM phosphate buffer, pH 7.4, and then the mixture was vortexed briefly. ThT fluorescence was determined three times at intervals of 10 s using an Hitachi F-4500 fluorometer. Excitation and emission wavelengths were 450 and 482 nm, respectively. Sample fluorescence was determined by averaging the three readings and subtracting the fluorescence of a ThT blank.

## 2.7. Electron Microscopy (EM)

To study protofibril formation and the effects of SCFAs on it, A $\beta$  was incubated according to the aggregation protocol above. After incubation at 37 °C for 7 days in 10 mM sodium phosphate, pH 7.4, EM was used to determine the morphologies of A $\beta$ 1-40 or A $\beta$ 1-42 assemblies as described previously [25]. Briefly, a 10- $\mu\text{l}$  aliquot of each sample was spotted onto a glow-discharged, carbon-coated Formvar grid (Electron Microscopy Sciences, Hatfield, PA) and incubated for 20 min. The droplet then was displaced with an equal volume of 2.5% (v/v) glutaraldehyde in water and incubated for an additional 5 min. Finally, the peptide was stained with 8  $\mu\text{l}$  of 1% (v/v) filtered (0.2  $\mu\text{M}$ ) uranyl acetate in water (Electron Microscopy Sciences). This solution was wicked off, and then the grid was air-dried. Samples were examined using a JEOL CX100 transmission electron microscopy.

# 3. RESULTS

## 3.1. Effects of SCFAs on A $\beta$ protein-protein interactions

The self-assembly of A $\beta$  peptides into neurotoxic soluble A $\beta$  aggregates is one of the key neuropathological processes underlying AD. We used the PICUP assay to monitor the effect that individual SCFAs have in interfering with initial protein-protein interactions necessary for the assembly of A $\beta$ 1-40 or A $\beta$ 1-42 peptides into neurotoxic aggregates in the presence

or absence of individual SCFAs at a SCFA:A $\beta$  molar ratio of 1:1 or 1:4. Six SCFAs were tested using the PICUP assay: valeric acid, isovaleric acid, butyric acid, isobutyric acid, propionic acid and acetic acid. Monomeric A $\beta$ 1-40 or A $\beta$ 1-42 peptides and cross-linked multimeric A $\beta$  forms were resolved by SDS-PAGE and visualized by staining.

In the absence of cross-linking, only A $\beta$ 1-40 monomers were observed (Fig. 1A-B, lane 1). As we have previously reported [27], cross-linking of A $\beta$ 1-40 in the absence of SCFAs leads to the formation of A $\beta$ 1-40 dimer and trimer forms (Fig. 1A-B, lane 2, indicated by black arrow). We observed that valeric acid potently interferes with initial A $\beta$ 1-40 protein-protein interactions. In particular, the addition of valeric acid at a SCFA:A $\beta$  molar ratio of 1:1 (Fig. 1A-B, lane 13) completely inhibited the formation of the trimeric A $\beta$ 1-40 form and partially inhibited the formation of the dimer A $\beta$ 1-40 form (compare lane 13 vs. lane 2). The addition of an increasing molar ratio of valeric acid with a SCFA:A $\beta$  molar ratio of 4:1 (Fig. 1A-B, lane 14) completely blocked the formation of into dimeric or trimeric A $\beta$ 1-40 forms (compare lane 14 vs. lane 2). Both butyric acid and propionic acid also interfered with A $\beta$ 1-40 oligomerization but to a lesser extent in comparison to valeric acid. In particular, butyric acid, at a SCFA:A $\beta$  molar ratio of 1:1 (Fig. 1A-B, lane 11) or 4:1 SCFA:A $\beta$  (Fig. 1A-B, lane 12) almost completely inhibited the aggregation of A $\beta$ 1-40 monomers into A $\beta$ 1-40 trimers, but was not effective in modulating the formation of A $\beta$ 1-40 dimeric forms (compare lanes 11 and 12 vs. lane 2). Propionic acid, at a SCFA:A $\beta$  ratio of 4:1 (Fig. 1A-B, lane 10) almost completely inhibited the generation of A $\beta$ 1-40 trimers (compare lane 10 vs. lane 2). However, A $\beta$ 1-40 aggregation was not affected by the addition of a lower molar ratio of propionic acid, at a 1:1 SCFA:A $\beta$  molar ratio (Fig. 1A-B, lane 9) (compare lane 9 vs. lane 2). The remaining three SCFAs monitored (isobutyric acid, isovaleric acid and acetic acid) had no observable impact on the conversion of monomeric A $\beta$ 1-40 peptide (Fig. 1A-B, lanes 3-8) into higher-ordered multimeric A $\beta$ 1-40 forms in our PICUP assay (compare lanes 3-8 vs. lane 2).

In the absence of cross-linking, monomeric A $\beta$ 1-42 shows up in a trimeric form under SDS-PAGE (Fig. 1C-D, lane 1). The A $\beta$ 1-42 trimer band has been shown to be an SDS-induced artifact [26,27]. As we have previously reported [27], cross-linking of A $\beta$ 1-42 in the absence of SCFAs leads to the formation of A $\beta$ 1-42 oligomers of orders 2-6 (Fig. 1C-D, lane 2, indicated by black arrow). We observed that the addition of valeric acid, at a SCFA:A $\beta$  molar ratio of 4:1 (Fig. 1C-D, lane 14), completely inhibited the formation of all A $\beta$ 1-42 oligomers (compare lane 14 vs. lane 2). However, A $\beta$ 1-42 aggregation was not affected by the addition of a lower molar ratio of valeric acid, at a 1:1 SCFA:A $\beta$  molar ratio (Fig. 1C-D, compare lane 13 vs. 2). The conversion of A $\beta$ 1-42 monomers into higher-order multimeric forms was unaffected by the addition of butyric acid, propionic acid, isobutyric acid, isovaleric acid, and acetic acid at either a SCFA:A $\beta$  molar ratio of 1:1 or 4:1 (Fig. 1C-D, compare lanes 2-12 vs. lane 2).

In parallel, in the control PICUP study, which used glutathione S-transferase (GST) as a positive control for the cross-linking chemistry as we have used in the past [25], we observed that incubation of GST in the absence of SCFAs lead to the formation higher molecular weight GST aggregate forms (Fig. 1E-F, lane 2, indicated by a black arrow). We observed no alterations in GST cross-linking in the presence of SCFAs at a SCFA:GST

molar ratio of 1:1 (Fig. 1E-F, compare lanes 3, 5, 7, 8, 9, 11, 13 vs. lane 2) or 4:1 (Fig. 1E-F, compare lanes 4, 6, 8, 10, 12, 14 vs. lane 2). We therefore concluded that valeric acid, butyric acid and propionic acid inhibited A $\beta$ 1-40 and/or A $\beta$ 1-42 aggregation.

### 3.2. Effects of SCFAs on A $\beta$ fibril formation

Based on the evidence from our PICUP assay, we continued by assessing valeric acid and butyric acid for their potential effects on the assembly of monomeric A $\beta$  peptides into A $\beta$  fibrils by using the ThT spectroscopic assay to monitor for temporal changes in  $\beta$ -sheet contents of A $\beta$ 1-40 and A $\beta$ 1-42, which were incubated in the absence of SCFA (SCFA:A $\beta$  molar ratio of 0:1) or in the presence of individual SCFAs at a SCFA:A $\beta$  molar ratio of 1:1 or 4:1. We note that ThT fluorescence is not a direct measure of fibril content. However, since  $\beta$ -sheet formation correlates with fibril formation, ThT fluorescence is a useful surrogate marker [28].

We observed that both valeric acid and butyric acid attenuated the conversion of A $\beta$ 1-40 monomers to A $\beta$ 1-40 fibrils with a dose-response efficacy; the higher dose of valeric acid or butyric acid (SCFA:A $\beta$  molar ratio of 4:1) appeared more effective than the lower dose (SCFA:A $\beta$  molar ratio of 1:1) (Fig. 2A,B). We found that valeric acid also attenuated the conversion of A $\beta$ 1-42 monomers to A $\beta$ 1-42 fibrils with a dose-response efficacy; the higher dose of valeric acid (SCFA:A $\beta$  molar ratio of 4:1) appeared more effective than the lower dose (SCFA:A $\beta$  molar ratio of 1:1) (Fig. 2C). Lastly, we observed that butyric acid treatment also displayed a tendency to reduce the formation of A $\beta$ 1-42 fibrils, but there are no observable differences between the lower and higher dose (Fig. 2D).

Collectively, our evidence demonstrates that valeric acid (and to a lesser extent, butyric acid) is capable of interfering with the conversion of monomeric A $\beta$ 1-40 and A $\beta$ 1-42 into A $\beta$  fibrils.

### 3.3. Effects of valeric acid on the morphologies of the A $\beta$ assemblies

Our evidence from Figs. 1 and 2 demonstrating that, among the 6 SCFAs we tested, valeric acid most potently interferes with the aggregation of A $\beta$  peptides into higher-ordered assemblies. Based on this, we continued and used EM to monitor for effects of valeric acid on the morphologies of the A $\beta$ 1-40 and A $\beta$ 1-42 assemblies. Consistent with our prior observations [25], the incubation of A $\beta$ 1-40 (Fig. 3, panel I) or A $\beta$ 1-42 (Fig. 3, panel III) in the presence of vehicle leads to the generation of classical non-branched fibrils with helicity features. A $\beta$  incubation in the presence of valeric acid, at a SCFA:A $\beta$  molar ratio of 4:1, almost completely inhibited fibril formation from A $\beta$ 1-40 (Fig. 3, panel II) or A $\beta$ 1-42 (Fig. 3, panel IV).

## 4. DISCUSSION

The assembly of A $\beta$  peptides into low-n oligomers requires initial protein-protein interactions among A $\beta$  peptides. Our study is specifically designed to assess if a specific test compound is capable of interfering with such protein-protein interactions and therefore to disrupt the process A $\beta$  assembly into low n neurotoxic oligomers. We used independent in vitro assays to investigate 6 SCFAs that are derived from GI-microbiota metabolism of



amyloidogenic A $\beta$  isoforms, valeric acid, butyric acid, and propionic acid may also similarly interfere with the assembly of  $\alpha$ -synuclein and tau.

Accumulating published evidence suggests that GI bacteria may help promote resilience against AD through multiple mechanisms, the promotion of brain energy metabolism, modulation of neuro-inflammation, and modulation of epigenetic mechanisms (see Fig. 4). Our evidence revealed that GI bacteria may also improve AD by supporting the generation of select SCFAs that are capable of interfering with the assembly of A $\beta$ 1-40 and A $\beta$ 1-42 peptides into neurotoxic A $\beta$  aggregates (see Fig. 4). Future *in vivo* studies will be necessary to clarify whether certain SCFAs may attenuate AD  $\beta$ -amyloidosis through additional mechanisms.

## 5. CONCLUSION

Our observations provide the impetus for new investigations to identify and characterize select dietary fibers that support the generation of valeric acid, butyric acid, and propionic acid, as well as GI microbial that are capable of metabolizing dietary fibers to these SCFAs. Information gathered will lead to the development of next-generation probiotics that might help promote resilience to diverse neurodegenerative disorders.

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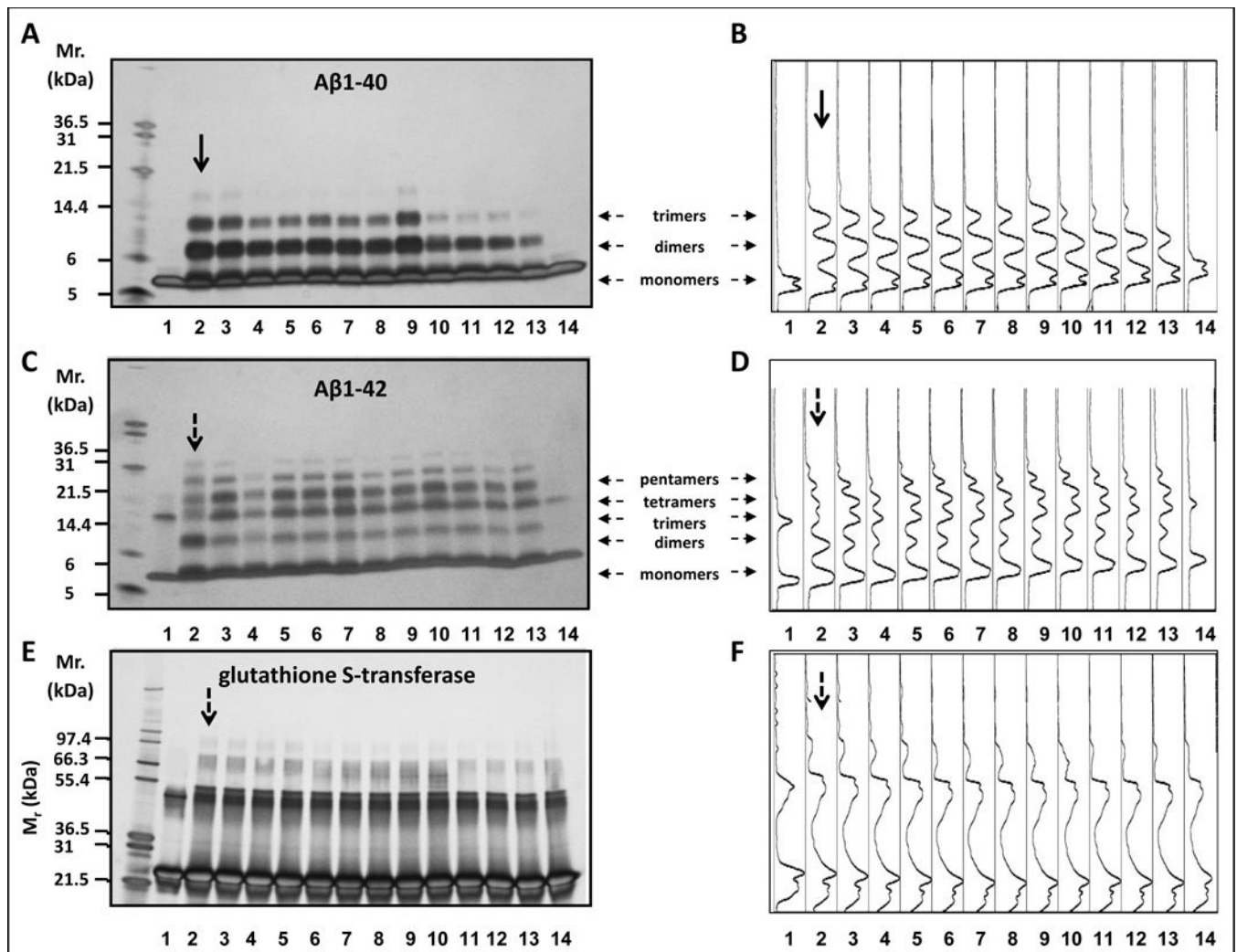


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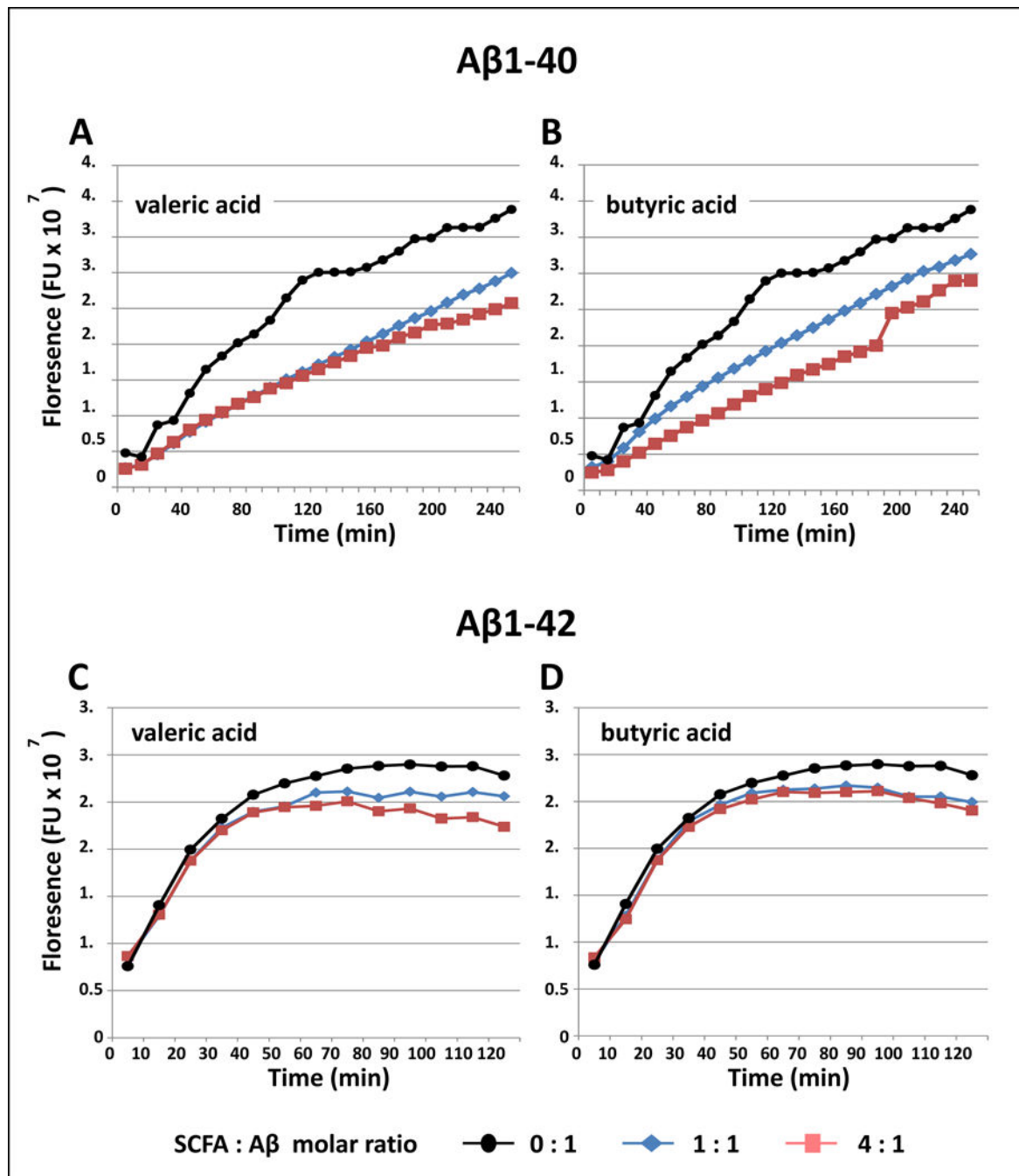
### KEY ISSUES

- The studies suggest that select bacterial species that support conversion of dietary fibers to short-chain fatty acids, which are relevant to neurodegenerative conditions.
- Our observation links gastrointestinal microbiota with mechanisms underlying AD-type A $\beta$  neuropathological mechanisms.
- Our observations suggest the feasibility of developing valeric acid for treating AD.
- Misfolding of diverse proteins in multiple neurological disorders, such as A $\beta$  in Alzheimer's disease, tau in tauopathies,  $\alpha$ -synuclein in Parkinson's disease and Huntington's disease, all share common mechanistic features. Our observation supports the potential development of valeric acid for treating these diverse neurological disorders.
- Our observations support further investigations to identify and characterize gastrointestinal bacterial specie(s) that support the generation of valeric acid.
- Our observations also support further investigations to characterize select dietary fiber preparations that supports the generation of valeric acids.
- Information from the study will lead to the development of next-generation probiotics that might help promote resilience to diverse neurodegenerative disorders.



**Figure 1.**

Select SCFAs potentially interfere with protein-protein interactions among  $A\beta$  peptides. (a, c, e) Monomeric, dimeric and higher-ordered cross-linked multimeric  $A\beta 1-40$  (a),  $A\beta 1-42$  (c) or GST (e) aggregates were visualized by silver staining of the gel. Shown are representative assays from three independent studies. (b, d, f) Densitometry intensity profiles for  $A\beta 1-40$  (b),  $A\beta 1-42$  (d) and GST (f). In (a-f, lane 1)  $A\beta 1-40$  (a,b),  $A\beta 1-42$  (c,d) or GST (e,f) alone without cross-linking. In (a-f, lanes 2–14)  $A\beta 1-40$  (a,b),  $A\beta 1-42$  (c,d) or GST (e,f) with cross-linking in the presence of vehicle (lane 2) or in the presence of individual SCFAs as follow: isobutyric acid at a SCFA: $A\beta$  (or GST) molar ratio of 1:1 (lane 3) or 4:1 (lane 4), isovaleric acid at a SCFA: $A\beta$  molar ratio of 1:1 (lane 5) or 4:1 (lane 6), acetic acid at a SCFA: $A\beta$  (or GST) molar ratio of 1:1 (lane 7) or 4:1 (lane 8), propionic acid at a SCFA: $A\beta$  (or GST) molar ratio of 1:1 (lane 9) or 4:1 (lane 10), butyric acid at a SCFA: $A\beta$  (or GST) molar ratio of 1:1 (lane 11) or 4:1 (lane 12), valeric acid at a SCFA: $A\beta$  (or GST) molar ratio of 1:1 (lane 13) or 4:1 (lane 14). In (a-d), horizontal arrows indicate monomers, dimers, trimers, tetramers and pentamers. In (a-f), vertical arrows indicate positive control studies in which  $A\beta 1-40$  (a-b),  $A\beta 1-42$  (c-d) or GST (e-f) were incubated in the absence of SCFA.



**Figure 2.**

Select SCFAs potentially interfere with Aβ fibril formation. Assembly of monomeric Aβ1-40 or Aβ 1-42 peptides into Aβ fibrils in the presence of valeric acid, butyric acid or vehicle were assessed using the ThT assay, which monitors ThT fluorescence as an indirect assessment of fibril contents. Periodically, aliquots were removed, and ThT binding levels were determined. Binding is expressed as mean fluorescence (in arbitrary fluorescence units (FU)). (a-d) Aβ1-40 (a-b) or Aβ1-42 (c-d) were incubated for up to 240 min at 37°C in 10 mM phosphate, pH 7.4, in the presence of vehicle (○), or in the presence of valeric acid (a,c)

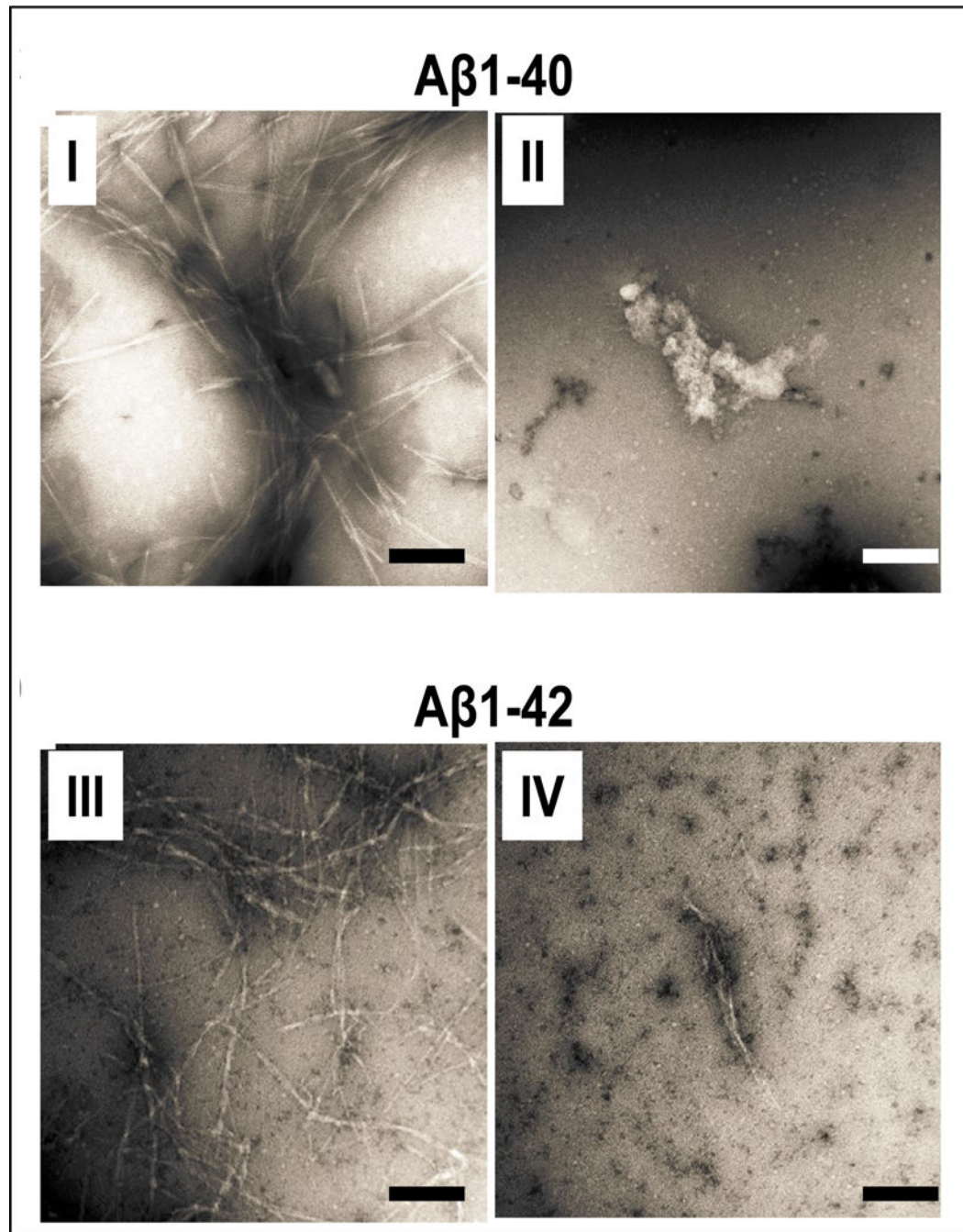
or butyric acid (b,d) at a SCFA:A $\beta$  molar ratio of 1:1 ( ) or 4:1 ( ). Shown are representative assays from three independent studies.

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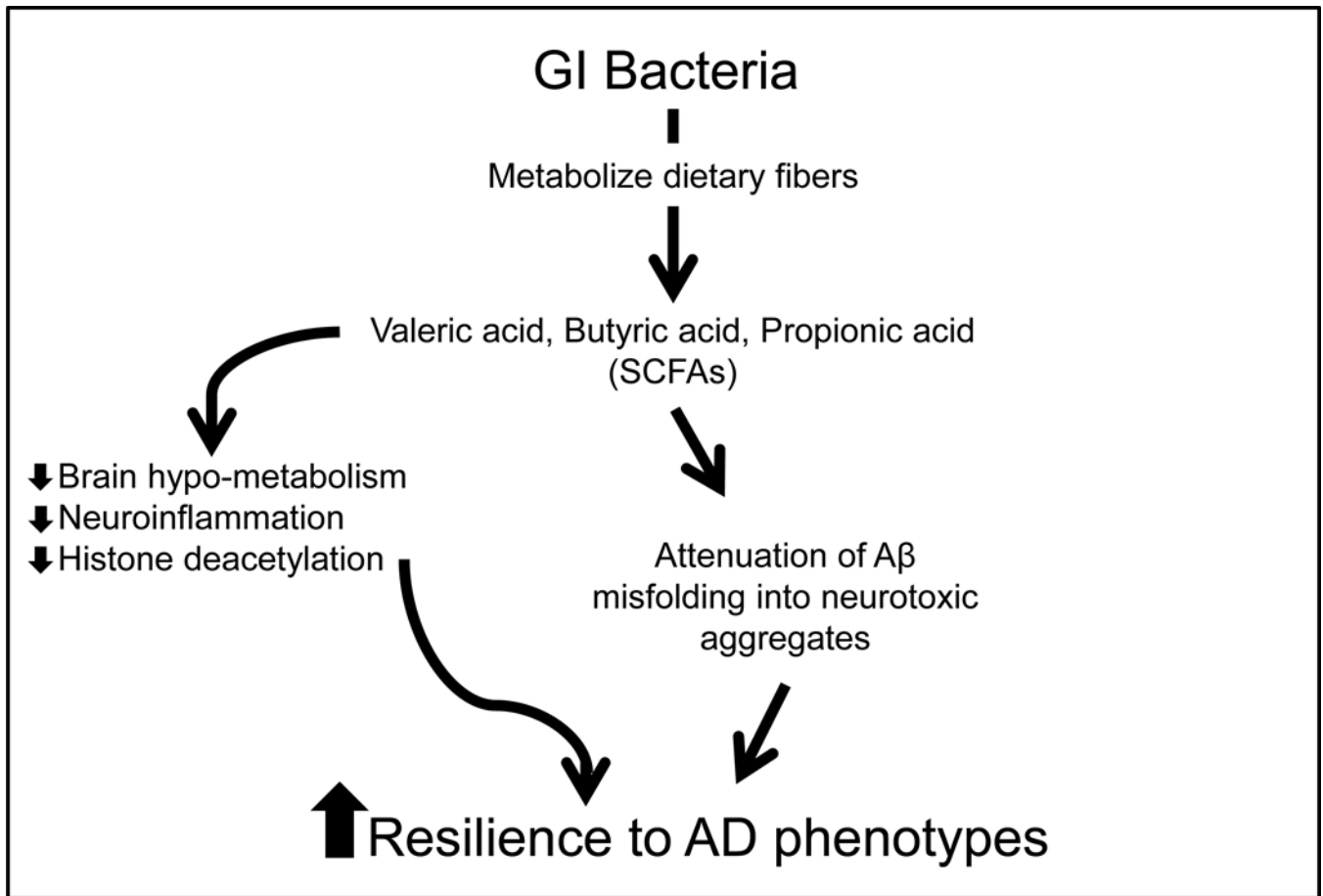
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**Figure 3.** Assessments of A $\beta$  protofibril morphology. (Panels I, II, III, IV) EM was used to determine the morphologies of protofibrils obtained by the incubation of A $\beta$ 1-40 (panels I and II) or A $\beta$ 42 (panels III and IV), in the presence of vehicle (panels I and III) or valeric acid at a valeric acid:A $\beta$  molar ratio of 4:1 (panels I and IV). Shown are representative assays from three independent studies. Scale bars indicate 100 nm.



**Figure 4.**

Schematics summarizing the mechanisms by which GI microbial-derived SCFAs may modulate AD. Intestinal bacteria help protect against AD by converting dietary fibers into biologically available SCFAs, which may promote resilience to AD through multiple cellular/molecular mechanisms. Previously published evidence suggests SCFAs may benefit AD by: (1) alleviating brain hypo-metabolism as SCFAs provide alternative substrates for brain energy metabolism [20], (2) attenuating neuro-inflammation by modulating the maturation and function of microglia in the brain [5], and (3) inhibiting histone deacetylases and normalize aberrant histone acetylation in the AD brain [7,14,34]. In addition, evidence from the present study suggests that certain SCFAs, particularly valeric acid, butyric acid, and propionic acid, may also benefit AD by attenuating A $\beta$ -mediated pathologic processes by interfering with the assembly of A $\beta$ 1-40 and A $\beta$ 1-42 peptides into neurotoxic A $\beta$  aggregates.