Designing Phenylalanine-based Hybrid Biological Materials: Controlling Morphology via Molecular Composition

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Phenylalanine-based Hybrid Biological Materials: Controlling Morphology via Molecular Composition

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ABSTRACT

Harnessing the self-assembly of peptide sequences has demonstrated great promise in the domain of creating high precision shape-tunable biomaterials. The unique properties of peptides allow for a building blocks approach to materials design. In this study, self-assembly of mixed systems encompassing two peptide sequences with identical hydrophobic regions and distinct polar segments is investigated. The two peptide sequences are diphenylalanine and phenylalanine-asparagine-phenylalanine. The study examines the impact of molecular composition (namely, the total peptide concentration and the relative tripeptide concentration) on the morphology of the self-assembled hybrid biological material. We report a rich polymorphism in the assemblies of these peptides and explain the relationship between peptide sequence, concentration and the morphology of the supramolecular assembly.

Keywords: Diphenylalanine, Phenylalanine-asparagine-phenylalanine, Self-assembly, Peptide mixtures, Martini, Molecular Dynamics

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INTRODUCTION

Recent advances in novel biological materials via peptide self-assembly has been driven by their potential use in a wide range of applications, such as neurodegenerative disease treatment [1-6], therapeutics[6-11], peptide-based electronics[12-15] and nanobiomaterials[16-24]. Earlier studies have reported peptides to assemble into nanofibers[25-29], nanotubes[30-37], vesicles[38-42] and nanosheets[41, 43]. Peptides are composed of a combination of any number of the 20 amino acids. This allows for a unique building blocks approach to biological materials design, providing a high degree of control over the morphology of supramolecular peptide assemblies.

Among the various peptide sequences employed for creating biological materials, diphenylalanine has been extensively studied using experimental approaches[30, 32, 37, 44-49] and computational techniques[48, 50, 51] . It is a small and stable peptide that has been reported to form supramolecular assemblies including vesicles and nanotubes[50-53] . More recently, diphenylalanine derivatives such as triphenylalanine (FFF) and diphenylalanine-fluorenylmethyloxycarbonyl chloride (FF-Fmoc) have been explored for their potential to self-assemble into nanostructures. These efforts have found a large diversity of assemblies including nanowires, ribbons and nanofibers[54]. The primary focus of these studies has been in developing nanostructures self-assembled from a single peptide sequence.

The creation of nanostructures with specific control on their material characteristics can be fulfilled by using a variety of peptide sequences. The contribution of each sequence and the synergistic interplay between their molecular characteristics can generate materials with specific sequence-property relations. An earlier computational study reported mixtures of

diphenylalanine and triphenylalanine to generate toroidal structures[54], which were verified experimentally. Yet, there is a dearth in the understanding of sequence-property relations of biological materials encompassing distinct peptide sequences. In addition, very little is known about the mechanics of the assembly of distinct peptide sequences to form a hybrid biological material with a target property.

In this study, we examine the impact of molecular composition on the properties (specifically, morphology) of self-assembled hybrid biological materials. For simplicity, we focus on diphenylalanine (FF) and its derivative phenylalanine-asparagine-phenylalanine (FNF). The derivative changes the sequence of diphenylalanine by the addition of asparagine between the two phenylalanine groups. In addition, these two sequences allow us to examine the impact of differences in the polar groups of the peptide species on the self-assembled hybrid material morphology. We vary the molecular composition through the total concentration of the peptides and the relative concentration of the tripeptide (FNF). We address the large molecular composition parameter space by adopting a computational approach (namely, the Molecular Dynamics simulation technique), which is used in conjunction with a coarse-grained force field. We find that the total concentration of the peptides along with the relative concentration of the tripeptides can control the morphology of the hybrid assemblies. The results from this study provide insight into (1) assembly mechanics of specific peptide sequences, and (2) shape control of supramolecular nanostructures.

COMPUTATIONAL METHODS

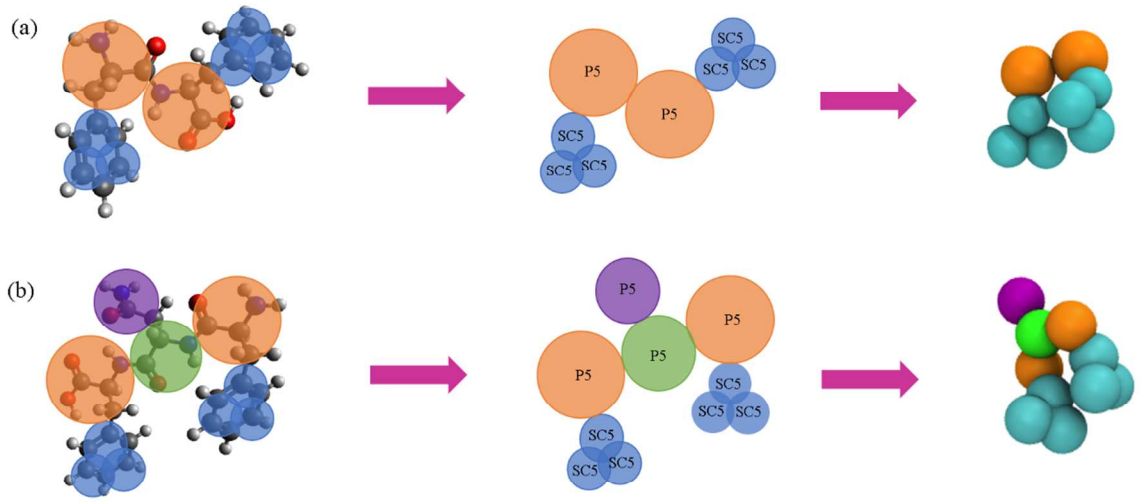

Figure 1: Coarse-grained mapping details for (a) diphenylalanine (FF) and (b) phenylalanine-asparagine-phenylalanine (FNF). Coarse-grained representations of the peptides in the Molecular Dynamics simulations shown on the right side.

The assembly of diphenylalanine (FF) and phenylalanine-asparagine-phenylalanine (FNF) was promoted by the hydrophobic effect. We used the Molecular Dynamics (MD) simulation technique to capture the dynamics of the aggregation process along with the structure and morphology of the hybrid peptide materials. This required simulating the aggregation of several hundreds of molecules that were dispersed in an aqueous environment. An all-atom representation of the molecules would have been too demanding in terms of computational resources in resolving the temporal scales associated with the assembly process along with capturing the multiscale structural characteristics of the self-assembled material. To circumvent this difficulty, we employed coarse-grained representations of the peptides.

For this study, we used the Martini v2.2 coarse-grained (CG) force field[55] for biomolecules[56, 57], an established, generalizable force field that has been demonstrated to capture

the behavior of a wide range of biomolecules.. Atoms of the peptides were mapped using the Martini CG model[57] (see figure 1). Particle type P5 was used for the backbone of each residue, as well as for the for the sidechain of asparagine. Three SC5 particles were used to represent the aromatic sidechain of phenylalanine. Since the peptides are assumed to be in a zwitterionic state, charges of +1e and -1e were assigned to the N and C termini respectively. The CG mapping details are presented in Supplementary information (SI) Tables 1 and 2 and represented graphically in Figure 1. van der Waals forces were represented by a 12-6 Lennard-Jones approximation, while electrostatics were calculated using a shifted Coulomb potential. All cutoffs were maintained at 1.2nm in accordance with the Martini CG model.

Simulations were performed using the GROMACS package (v5.2.1)[58-62] . The simulations were set up by using the inbuilt GROMACS functions to insert the FF and FNF molecules into the simulation box and solvate them. Since the system is charge neutral, no counterions are required. To prevent physically unrealistic freezing of the Martini water[55], a 0.1 mole fraction of antifreeze particles was maintained. The system was then energy minimized by the steepest descent integrator to remove any overlaps between particles. This was followed with a 500 ps (effective time) equilibration followed by a production simulation for 4 μs (effective time). The duration of the production simulation was selected so as to generate a single, stable self-assembled nanostructure.

All simulations were carried out in the isothermal-isobaric ensemble. The temperature was maintained at 310K[50, 54] using velocity rescaling with a stochastic term to ensure correct sampling[63, 64]. Pressure was maintained at 1 bar using the Parrinello-Rahman barostat[65-67]. The timestep was maintained at 25 fs and all simulations were run for an effective time of 4 μs. The neighbor lists were updated every 0.25 ps with a 1.2 nm cutoff. The particle trajectories were

sampled every 0.25 ns for analysis and visualization. The LINCS algorithm was employed to constrain bond lengths in the aromatic phenylalanine sidechains.

All the simulations were carried out using systems encompassing a total of 500 peptide molecules. The peptide molecules were assumed to exist in a zwitterionic state. The total peptide concentration was controlled via pre-selecting the box size and appropriately populating the box with solvent beads. The relative tripeptide concentrations were implemented by varying the ratio of dipeptides (FF) to tripeptides (FNF), while still maintaining the total number of peptide molecules to 500.

We examined 5 total peptide concentrations (0.1, 0.15, 0.2, 0.25 and 0.3 peptides/nm^3) and 11 relative tripeptide concentrations (ranging from 0% to 100%). The results for each system was based upon 10 independent particle trajectories. Hence, the study is based upon a total of 550 simulations. Further details of the simulation box are provided in the supplementary information (SI) Table3.

While interpreting timescales in simulations that use the Martini coarse-graining scheme, a four-fold speedup is assumed in the diffusion dynamics as compared to real systems, since the Martini force field's reduced frictional component from the removal of atomistic degrees of freedom leads to a smoother energy landscape[55]. Therefore, unless explicitly stated, we use an "effective" time instead of the simulation time for the remainder of this paper.

RESULTS AND DISCUSSION

All molecular compositions explored in this study are observed to spontaneously assemble into nanostructures encompassing bilayers. The assembly is driven by the hydrophobic effect, wherein the hydrophobic aromatic rings of the phenylalanine side chains minimize their

interface with the solvent by preferentially interacting with other aromatic sidechains. In addition, the hydrophilic backbones and asparagine side chains preferentially interact with the solvent particles. These simultaneous processes drive peptide aggregation, which continues until a single, stable aggregate forms for the duration of the simulation[50, 54, 68-72].

The morphology of the hybrid nanostructures can be classified into three categories by their relationship in the three spatial dimensions. We classify a structure as "open" in a given spatial direction if one of the following criteria are met: (i) it extends infinitely (through periodic walls) along that direction, or (ii) if it does not extend infinitely in a given direction, two edges of the bilayer perpendicular to that direction are exposed to the solvent. Therefore, if the bilayer of the nanostructure is open in two dimensions, it is classified as a lamella, it may extend infinitely along two axes, or along one axis but have edges exposed to the solvent. If the bilayer of the nanostructure is closed in all three spatial dimensions (i.e. does not extend infinitely through periodic walls), it is classified as a vesicle. In the event that the bilayer of the nanostructure is closed in two dimensions but extends infinitely in the third dimension, it is classified as a nanotube.

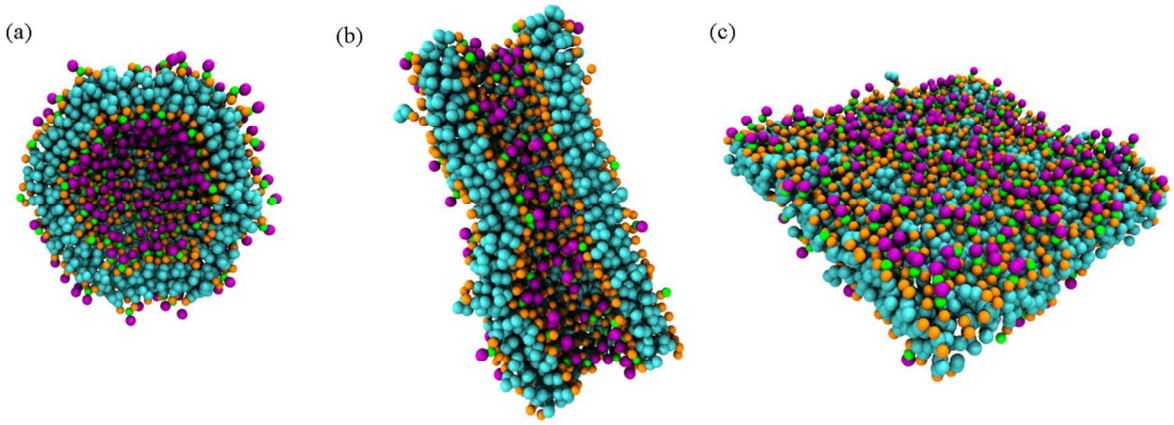

Figure 2: Self-assembled hybrid nanostructures: (a) diametrical cross-sectional view of a vesicle, (b) cylindrical axis cross-sectional view of a nanotube, and (c) lamellar bilayer.

Representatives of these assemblies are shown in Figure 2a-c. The cross-sectional views of the vesicle (see Figure 2a) and the nanotube (see Figure 2b) indicate the presence of an internal cavity in the nanostructures. The internal cavity is stabilized by the interface between the solvent and the hydrophilic backbones and asparagine side chains.

There is a fourth category of self-assembled nanostructures, which is not representative of an organized morphology. These nanostructures are classified as "disordered" assemblies. Whereas the peptide species in these nanostructures are organized into bilayers at a local scale, their morphology cannot be classified as either vesicles, nanotubes or lamellae. The morphologies of the nanostructures for different molecular compositions are summarized in Table 1.

Total Peptide Conc. (peptides/nm^3)	0% Tripeptide				10% Tripeptide				20% Tripeptide				30% Tripeptide				40% Tripeptide				50% Tripeptide				60% Tripeptide				70% Tripeptide				80% Tripeptide				90% Tripeptide				100% Tripeptide			
	U	EV	NT	BL	U	EV	NT	BL	U	EV	NT	BL	U	EV	NT	BL	U	EV	NT	BL	U	EV	NT	BL	U	EV	NT	BL	U	EV	NT	BL	U	EV	NT	BL	U	EV	NT	BL	U	EV	NT	BL
0.3			7	3		1	4	5			6	4		1	4	5			4	6	1		2	7				10			1	9	1		1	8	3			7	3			7
0.25		3	4	3		3	3	4		4	3	3		1	5	4			3	7		1	2	7	1	2		7		1	3	6			10			1	9	3			7
0.2		8	2			5		5		6	3	1		9	1			7	1	2		3	1	6	1	4		5		1	1	8		3	1	6		2		8	1	2	1	6
0.15		10				10				9	1			10				8	1	1		8	1	1		9		1		8		2		5		5	1	5		4		6	1	3
0.1		10				10				10				10				10				10				9		1		10				10				10			3	7		

Table 1: Summary of the morphologies for the hybrid nanostructures for different values of the total and relative concentration of the peptide molecules. Note: EV: elongated vesicle, NT: nanotube, BL: bilayer (lamellar) and U: unstructured/disordered. Color scheme is as follows: pink (vesicles/lamellae), purple (nanotubes/lamellae/vesicles), orange (nanotubes/lamellae) , green (lamellar bilayers), cyan (vesicles).

The phase space of the morphology of the nanostructures as a function of the total concentration of the peptides and the relative concentration of the tripeptides in Table 1 is further decomposed into four histograms, shown in Figures 3, 4, 5 and SI Figure 1. Each histogram summarizes the statistics for a given morphology of the hybrid nanostructure. Figure 3 shows the frequency of occurrence of vesicles in the ten independent trajectories for every molecular composition examined in this study. The molecular composition constitutes the total concentration of peptides and the relative concentration of the tripeptides. Vesicles are consistently observed for the lower total concentrations of the peptides (0.1-0.15 peptides/nm^3).

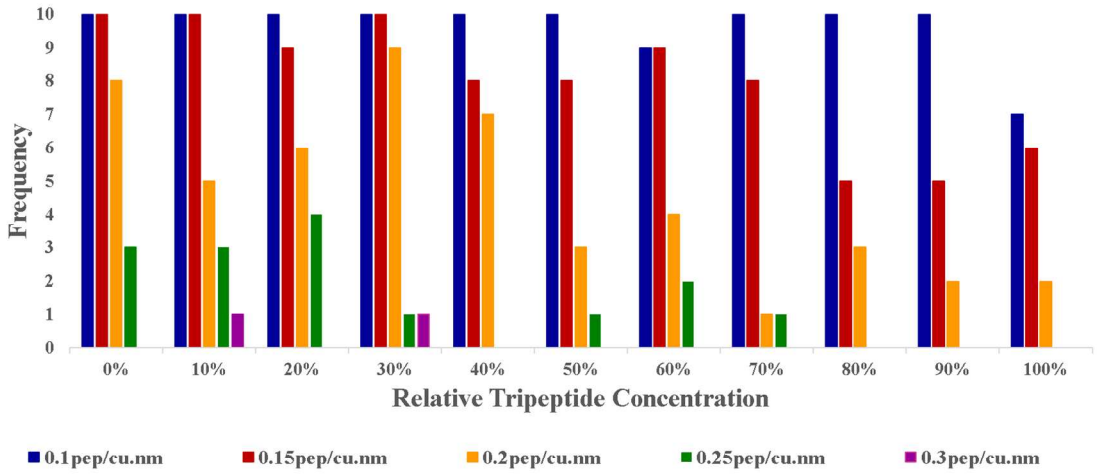

Figure 3: Histogram of the occurrence of vesicles in mixtures of FF and FNF for different molecular composition (that is, the values of the total peptide concentration and relative tripeptide concentration). These measurements used 10 independent particle trajectories for each molecular composition.

As the total concentration of the peptides increase, the propensity of the peptides to form vesicles decreases. This trend is consistent across all relative tripeptide concentrations, ranging from 0% (a pure FF system) to 100% (a pure FNF system). Increasing the total concentration of peptides, however, increases the propensity of the peptides to form lamellar bilayers. This effect is particularly pronounced at 0.25 and 0.3 peptides/nm^3, as shown in Figure 4. Lamellae are also observed at medium values of the total concentration of the peptides (0.2 peptides/nm^3) but only for high relative tripeptide concentrations (70% - 100%).

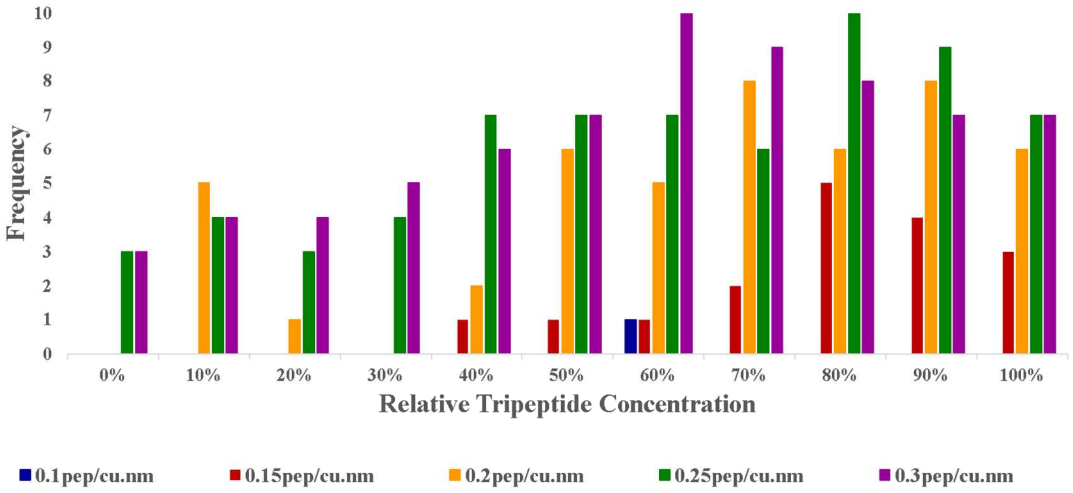

Figure 4: Histogram of the occurrence of lamellar bilayers in mixtures of FF and FNF for different molecular composition (that is, the values of the total peptide concentration and relative tripeptide concentration). These measurements used 10 independent particle trajectories for each molecular composition.

Nanotubes are a relatively infrequent occurrence, but can be observed for higher values of the total concentration of peptides (0.2-0.3 peptides/nm^3) and low-to-medium relative tripeptide concentrations (20%-50%), as demonstrated in Figure 5. Nanotubes are also observed when the net peptide concentrations are low and the relative tripeptide concentrations are high. For example, at 100% tripeptide with total concentrations of 0.1, 0.2, 0.25 and 0.3 peptides/nm^3. However, these are relatively rare occurrences.

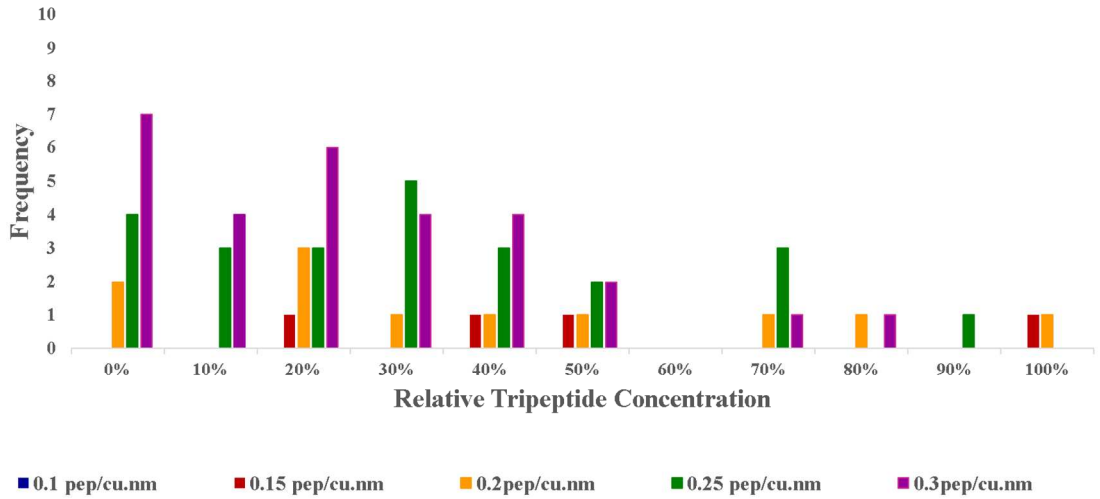

Figure 5: Histogram of the occurrence of nanotubes in mixtures of FF and FNF for different molecular composition (that is, the values of the total peptide concentration and relative tripeptide concentration). These measurements used 10 independent particle trajectories for each molecular composition.

The assembly pathways are observed to depend upon the relative concentration of tripeptides in the system. For FF alone, it has been shown experimentally and with exhaustive Monte Carlo simulations on discrete lattices that the peptide forms nanostructures in a concentration dependent fashion, from vesicles to nanotubes to lamella[73]. We observe the same transitions in Molecular Dynamics at similar dipeptide concentrations, supporting the assumption that these calculations are approaching equilibrium. Similarly, Guo et al[50] reported assembly pathways that included the fusion of smaller sized vesicles for pure FF systems with low concentration of peptides and the folding of bilayers into nanotubes for high concentration of peptides. This is thought to occur through a mechanism where, at low values of the total concentration of peptides (0.1-0.15 peptides/nm^3) (see Figure 6), small vesicles are observed to diffuse in solution until they encounter other small vesicles and coalesce to form larger sized vesicles. At higher values of the relative tripeptide concentrations however, the peptides tend to

assemble into a bilayer that then either stabilizes itself via periodic boundary interactions, or bends and closes its free edges to form a vesicle or a nanotube.

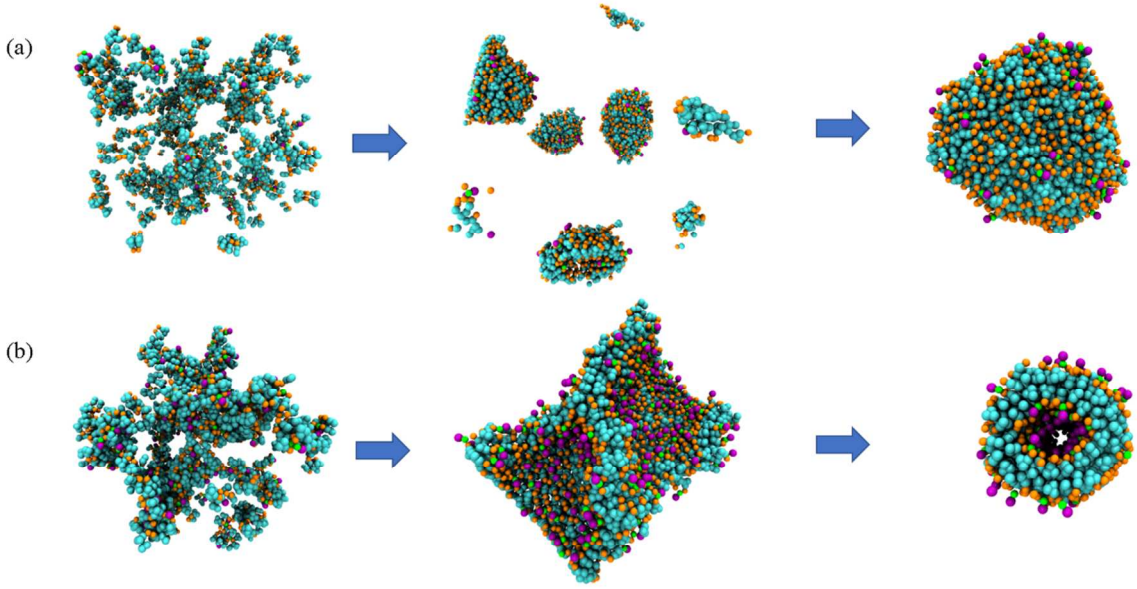

Figure 6: Assembly Pathways: (a) At low concentrations of both the total peptide as well as the relative tripeptide, smaller vesicles first form and then fuse into a larger vesicle. (b) At higher concentrations, bilayer like structures first form and then fuse their free edges into nanotubes or vesicles (nanotube shown here).

Morphology also depends on the relative concentrations of di- and tri-peptides. For all peptide ratios, we found a preference for vesicles at the lowest total peptide concentration, and lamellar bilayers at the highest total concentrations. In addition, we have identified an additional degree of freedom, i.e. the relative tripeptide concentration. From the statistics gathered from our simulations, we have constructed a molecular-composition phase-space diagram (presented in Figure 7) that shows distinct molecular composition parameters promoting the formation of vesicles, lamellar bilayers and nanotubes. At the bottom of the phase space (representing low total peptide concentrations), we find that the system is in the vesicle regime. We attribute this

result to the fact that low total peptide concentrations do not form structures large enough to interact through periodic boundaries. Therefore, the most favorable configuration is a fully closed vesicle, as this morphology would minimize any interactions of the hydrophobic aromatic side chains with the water particles.

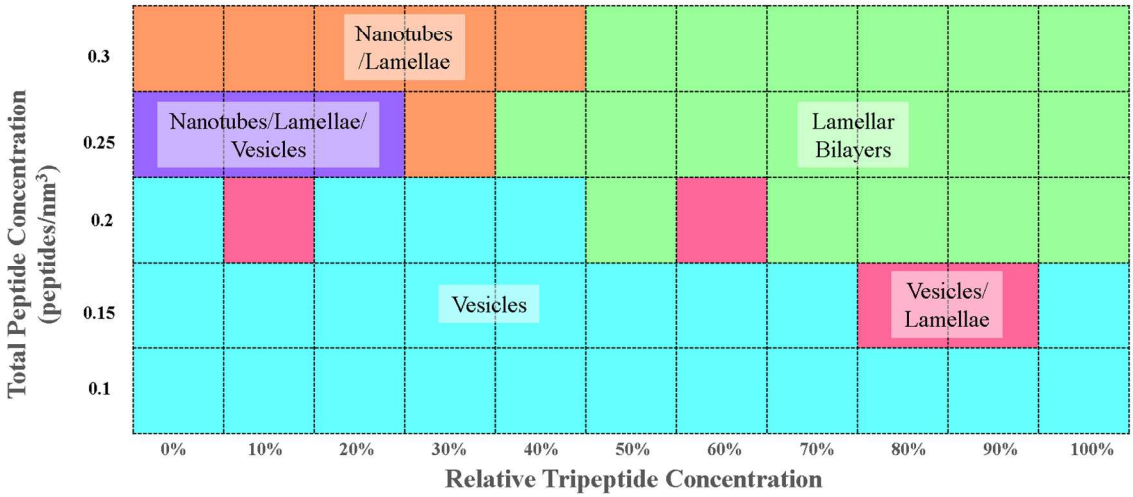

Figure 7: Phase space map showing regimes of Vesicles, Nanotubes, and Lamellar Bilayers. Of the ten trajectories, the most representative structure is presented here. In the case where there are two or more structures listed, that is because there were close to equal representations of both morphologies.

At higher total concentrations of peptides, as the size of the aggregates increase, the nanostructures in the systems have a higher tendency to interact through periodic walls and thereby, stabilizing themselves. The morphology of such nanostructures can be categorized by the number of period walls they interact through. Vesicles do not extend infinitely through periodic walls, nanotubes do so through two opposite periodic walls, and lamellar bilayers, through four periodic walls. To the upper left portion of the molecular composition phase space (shown in Figure 7), there is an overlap between the nanotube and bilayer regimes. This regime overlap is attributed to two competing effects: the tendency of the peptides to form bilayers at

high concentrations, and the curvature-inducing effect of the tripeptides in low-to-medium relative tripeptide concentrations.

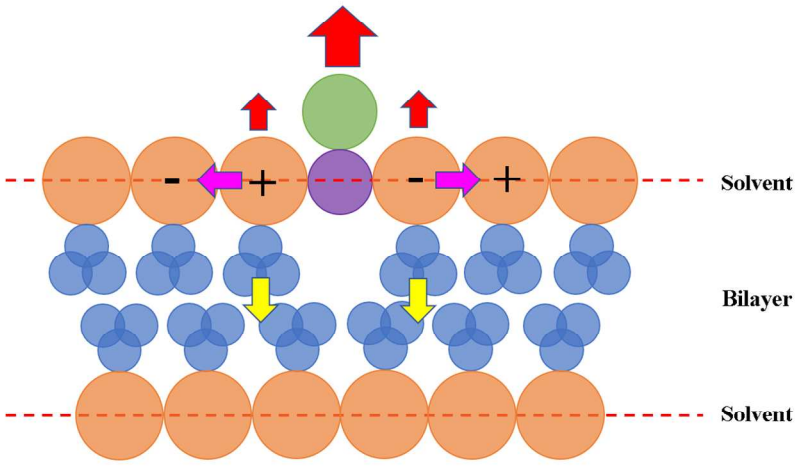

Figure 8: Tripeptide in a bilayer: yellow arrows represent hydrophobic attraction between aromatic side chains. Red arrows represent hydrophilic interactions between amino acid backbones and the asparagine side chains and water particles. Purple arrows indicate electrostatic attraction between the C and N termini. The resultant force differential tends to induce curvature in a FF-FNF bilayer.

Figure 8 shows the competing forces acting on a FNF tripeptide molecule that is embedded in a bilayer. The competing forces include the electrostatic attraction between adjacent C and N termini of the peptides, favorable hydrophilic interactions between the backbones and the asparagine side chain and the solvent particles, and favorable hydrophobic interactions between the aromatic phenylalanine side chains. These various forces create a force differential, which coupled to the hinge-like structure of the tripeptide, due to the presence of asparagine in the middle, makes this force differential manifest as a "pinching" effect that induces curvature. To quantify this effect, the average angle made by the FNF backbone was measured (see Figure 9).

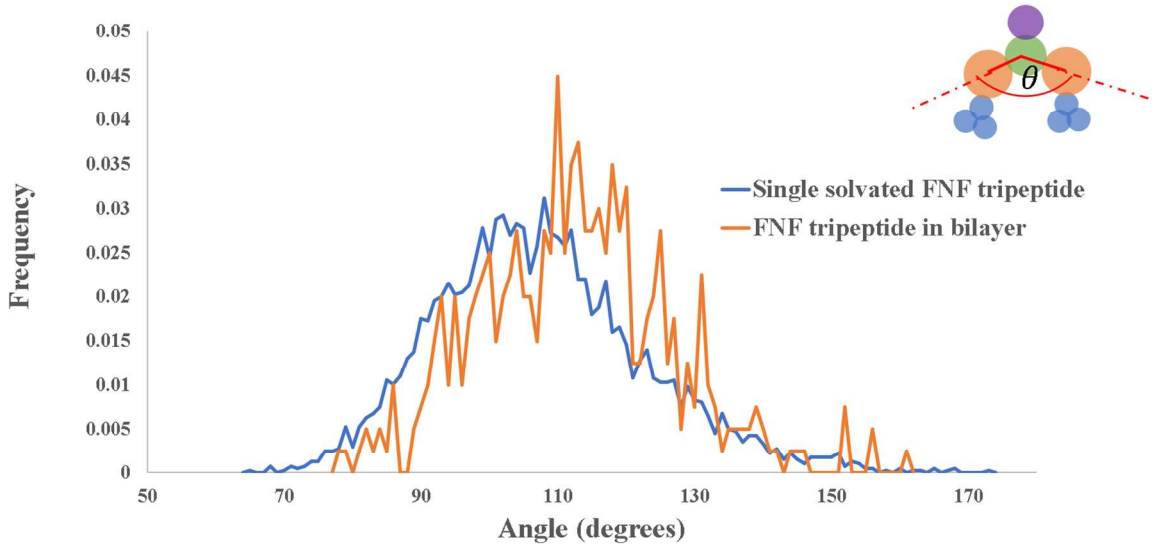

Figure 9: Distribution of the angle (theta) of the tripeptide (FNF). The average angle is 112.9˚, compared to the equilibrium angle of a single solvated FNF peptide pf 107.4˚.

The angle between the backbone beads (~113˚) is significantly distorted as compared to the equilibrium angle (107˚). This indicates that the tripeptide stretches laterally while the asparagine side chain experiences an attractive force, pulling it into the solvent and keeping the hinge correctly aligned, thereby inducing a local curvature in the bilayer.

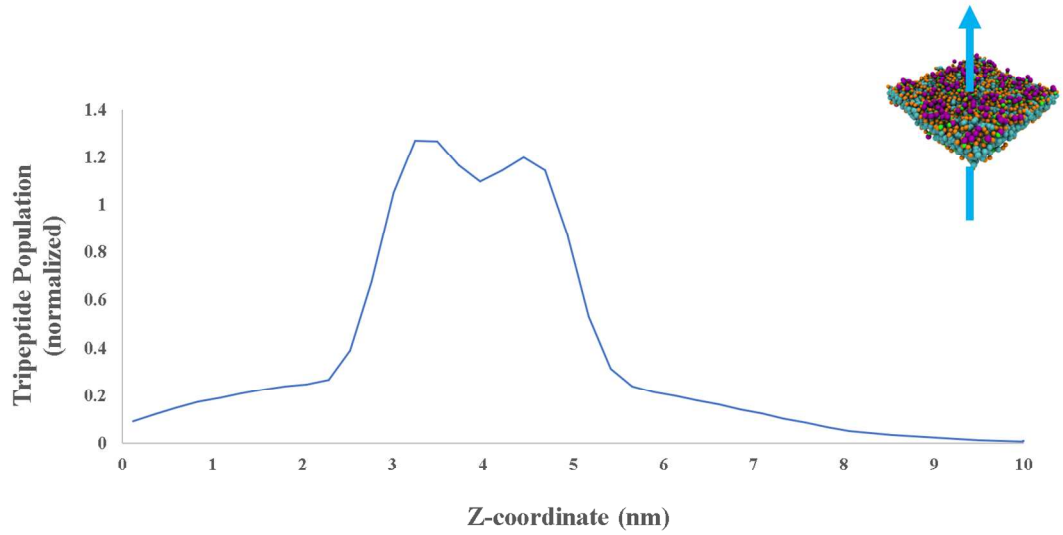

Figure 10: Population density of FNF tripeptides plotted against the Z axis coordinate for Total Peptide Concentration = 0.3 peptides/nm^3 and relative tripeptide concentration of 50%. Two closely spaced peaks show that the tripeptide distributes itself relatively evenly on both sides of the bilayer, leading to the lamella lacking a preference to fold in any specific direction.

To the upper right of the phase map (see Figure 7), the lamellar bilayers are observed to dominate the molecular composition phase space. We attribute this result to the fact that in addition to the high overall peptide concentration, the high tripeptide concentration makes it far more likely that the tripeptides distributed uniformly on either side of the bilayer. This uniform distribution negates any preference to induce local curvature in a specific direction. A representative example of the bilayer tripeptide spatial distribution is measured and shown in Figure 10. At lower tripeptide concentrations, a difference can be observed in the distribution of peptides on either side of the bilayer for different morphologies. This is demonstrated in Table 2.

	Nanotube	Vesicle	Lamella
Inside	13	19	24 (top)
Outside	37	31	26 (bottom)

Table 2: Distribution of tripeptides on either side of the bilayer for different morphologies. Total peptide concentration is 0.25 peptides/nm^3 at 10% tripeptide concentration. A representative system for each morphology was chosen and the number of peptides on either side of the bilayer were counted.

At high relative tripeptide concentrations (90%-100%), a small number of irregular or disordered nanostructures are observed (see Figure 11). This suggests that an overabundance of tripeptide "hinges" in the bilayer decreases its ability to attain a stable morphology. Additionally, overlaps are observed in the domains of the three main morphologies (that is, vesicles, nanotubes and lamellae). This indicates a transition between morphologies for specific values of the total concentration of peptides and relative concentrations of the tripeptides. It is important to note that nanotubes do not have an exclusive molecular composition parameter space like lamellae or vesicles.

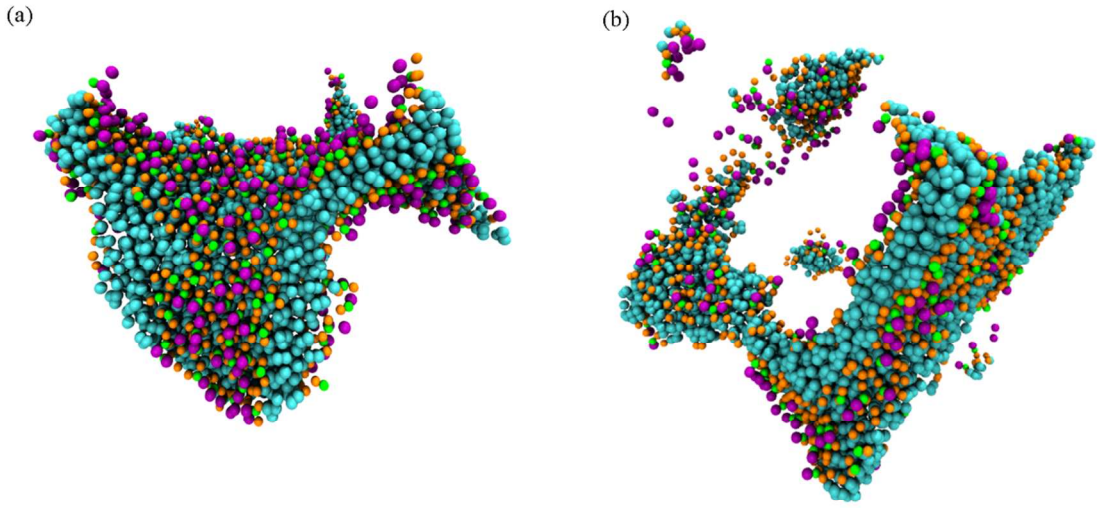

Figure 11: Disordered assembly occurring at 0.3 peptides/nm^3 and (a) 90% tripeptide, (b) 50% tripeptide.

CONCLUSIONS

We explored the impact of molecular composition on the morphology of phenylalanine-based hybrid biological materials. We focused our investigation on peptide species with different polar groups but identical hydrophobic groups, that is FF and FNF. We examined the morphology of the self-assembled hybrid, peptide nanostructures by varying the molecular composition. The molecular composition constituted five total concentrations of the peptides and eleven relative concentrations of the tripeptides (FNF). We used MD simulation in conjunction with CG models to study the large molecular composition parameter space.

Our results demonstrate a rich polymorphism in the assembly of these peptide mixtures. Distinct molecular composition regimes promoting the formation of vesicles, nanotubes and lamellar bilayers have been identified. The morphology of self-assembled nanostructures is observed to depend upon both the total concentration of peptides as well as the relative tripeptide concentration. Low concentrations (~20-30%) of FNF tripeptides, when mixed with FF dipeptides, while maintaining a very high total peptide concentration (~0.3 peptides/nm^3), display the greatest diversity of assembled structures. This region of the molecular composition parameter space yields vesicles, nanotubes and lamellar bilayers. We propose that this finding arises due to competing effects of the high total concentration of peptides biasing the system towards lamellar bilayers and the presence of the tripeptides inducing local curvature in the self-assembled hybrid nanostructures. This unique behavior is attributed to the molecular structure of the FNF tripeptide.

The results from this investigation demonstrate that the morphology of the phenylalanine-based hybrid biological materials is controlled via the molecular composition. Our findings can be used to potentially guide the selection of peptides for the design of novel hybrid biological

materials with target morphologies: specifically, sequences of peptides with carefully placed hydrophobic and hydrophilic regions and charges can be selected to design novel peptide sequences that assemble into nanostructures with target morphologies and other characteristics.

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