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Quasiracemic Crystallization as a Tool To Assess the Accommodation of Noncanonical Residues in Nativelike Protein Conformations

David E. Mortenson,[†] Kenneth A. Satyshur,[‡] Ilia A. Guzei,[†] Katrina T. Forest,*[,‡] and Samuel H. Gellman*[,†]

[†]Department of Chemistry and [‡]Department of Bacteriology, University of Wisconsin, Madison, Wisconsin 53706, United States

Supporting Information

ABSTRACT: Quasiracemic crystallization has been used to obtain high-resolution structures of two variants of the villin headpiece subdomain (VHP) that contain a pentafluorophenylalanine (F_5Phe) residue in the hydrophobic core. In each case, the crystal contained the variant constructed from L-amino acids and the native sequence constructed from D-amino acids. We were motivated to undertake these studies by reports that racemic proteins crystallize more readily than homochiral forms and the prospect that quasiracemic crystallization would enable us to determine whether a polypeptide containing a noncanonical residue can closely mimic the tertiary structure of the native sequence. The results suggest that quasiracemic crystallization may prove to be generally useful for assessing mimicry of naturally evolved protein folding patterns by polypeptides that contain unnatural side-chain or backbone subunits.

Artificial proteins that retain desirable activities of natural prototypes while displaying improved properties, such as greater conformational or metabolic stability, are subjects of considerable interest. Unnatural subunits featuring noncanonical side chains and/or backbones are potentially valuable tools for generating functional mimics of natural proteins.[1−3] Rational polypeptide engineering with noncanonical subunits, however, requires that one understand the structural consequences of a given substitution. Functions such as recognition and catalysis often depend sensitively on protein conformation, and replacing canonical with noncanonical residues could lead to structural perturbations. The extent of possible perturbations is difficult to predict: thousands of protein structures containing exclusively natural subunits have been determined via X-ray crystallography, but only a handful of high-resolution data sets showing how unnatural subunits are accommodated within protein tertiary structures are available. Here we illustrate the use of quasiracemic crystallization as a tool for identifying polypeptides that contain unnatural α-amino acid residues yet conformationally mimic a target protein comprising only canonical residues. We have applied this tool to polypeptides containing fluorinated side chains, which have attracted interest because of their unique physical properties and may serve as useful building blocks for rational protein design.[2]

Racemic pairs of small molecules appear to crystallize more readily than individual enantiomers, although the origin of this trend has been a subject of debate.[4] Initial studies of racemic protein crystallization were inspired by the advantages of centrosymmetric molecular arrangements (impossible for single enantiomers) for structure solution,[5] but this motivation has become less urgent with the advent of multiwavelength anomalous dispersion methods for structure determination. Such efforts have been motivated also by the prospect that racemic proteins would crystallize more readily than pure enantiomers,[5b,e,6] as predicted by Wukovitz and Yeates.[7] However, several examples have shown that racemic proteins need not adopt arrangements obeying rigorous crystallographic symmetry operations in order to cocrystallize.[6c,8] In the context of these observations, it is intriguing that Kent and co-workers have described one example in which *quasiracemic* protein crystallization was used for heavy-atom incorporation into a crystal.[6a] In a quasiracemic pair of molecules, one partner is very similar to the enantiomer of the other. Pasteur first noted that such pairs could cocrystallize [e.g., (+)-bitartrate and (−)-bimalate salts],[9] and the phenomenon has subsequently been documented extensively among small molecules.[9b,10] We were intrigued by the prospect that quasiracemic protein crystallization could provide a sensitive test for the ability of a polypeptide bearing at least one noncanonical subunit to mimic the three-dimensional shape of a prototype containing only canonical residues.

As an initial test of our hypothesis, we examined variants of the 35-residue villin headpiece subdomain (VHP) that contain pentafluorophenylalanine (F_5Phe). The hydrophobic core of native VHP contains three closely packed Phe side chains (from residues 6, 10 and 17; Figure 1). We previously used this system to evaluate the effect on conformational stability of Phe → F_5Phe substitutions at these core sites.[11] Phe10 → F_5Phe was found to be moderately stabilizing. NMR analysis of this variant indicated that the spatial arrangement of the three aromatic rings from residues 6, 10, and 17 does not change substantially upon incorporation of the unnatural side chain.[12] This result suggests that the Phe10 → F_5Phe variant constructed from L residues and VHP itself constructed from D residues (D-VHP) might form a crystalline quasiracemate, and that attempts to cocrystallize D-VHP with each of the six other L-Phe → F_5Phe variants involving positions 6, 10, and 17 would indicate whether any among these polypeptides is a close structural mimic of VHP.

Our crystallization efforts were based on the chicken VHP sequence with a single residue change (Asn27 → His; Figure

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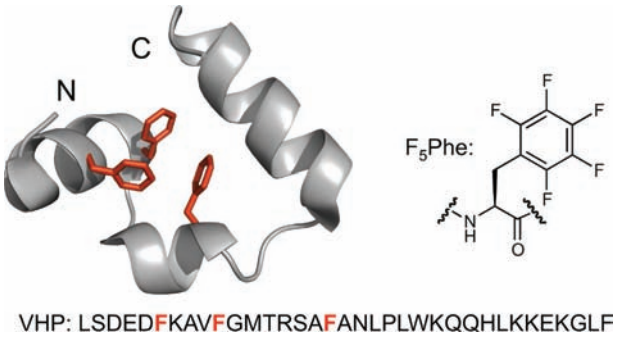

Figure 1. Previously reported structure of a VHP variant (PDB entry 1YRF) and sequence of VHP. Phe → F_5Phe substitutions were made for core phenylalanine residues (shown in red).

1), as this variant has provided the highest-resolution VHP crystal structure reported to date (PDB entry 1YRF).[13] In preliminary efforts, two crystalline forms of racemic VHP were obtained, and both structures were solved.[14] One racemate structure proved to be centrosymmetric (space group $P\bar{1}$), whereas the other is not centrosymmetric, but contains a fourfold rotoinversion axis and a glide mirror plane, both of which invert the handedness of the chiral centers (space group $I\bar{4}c2$). Crystallization in space group $P\bar{1}$ was expected on the basis of theoretical arguments[7] as well as the high frequency with which this space group has been observed among previously reported racemic protein structures.[6a,c,d,8a,b] This structure was refined at 2.1 Å resolution to R_{work}/R_{free} = 0.291/0.352; these values correspond to R_{work}/R_{free} = 0.197/0.241 for a noncentrosymmetric model having similar coordinate error.[15] The structure of the VHP racemate in space group $I\bar{4}c2$ was refined at 2.3 Å resolution. Space group $I\bar{4}c2$ has not been previously observed in any protein structure deposited in the Protein Data Bank but is theoretically possible for cocrystals of enantiomeric molecules.

Among the seven variants of L-VHP generated by replacing one, two, or three among Phe6, Phe10 and Phe17 with F_5Phe, two yielded crystals as quasiracemates with D-VHP (Figures 2

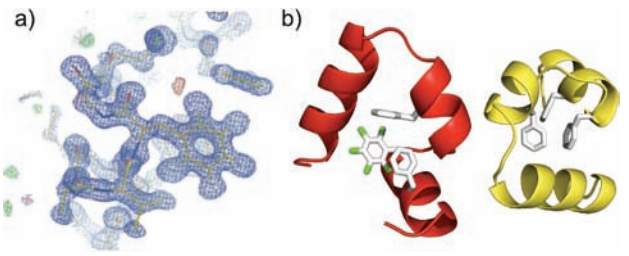

Figure 2. (a) $2F_o - F_c$ and $F_o - F_c$ maps of density surrounding F_5Phe10, contoured at 1.5σ and ±3.5σ, respectively. (b) Structure of the L-(Phe10 → F_5Phe)VHP + D-VHP quasiracemate.

and 3). One crystalline quasiracemate involved L-Phe10 → F_5Phe, as anticipated from NMR results,[12] and the other involved L-Phe17 → F_5Phe. In both cases, microcrystals were obtained from ~20% of the precipitant conditions examined in sparse-matrix screening, while the other five quasiracemic mixtures did not produce crystals under any of the 242 conditions examined. Although it is perilous to try to interpret crystallization failures, one is tempted to speculate that the five quasiracemic mixtures that did not produce crystals contained Phe → F_5Phe substitution patterns that resulted in conformational instability or a different folding pattern relative to VHP itself.

For the L-(Phe17 → F_5Phe)VHP + D-VHP mixture, the asymmetric unit (i.e., the full unit cell) contains one molecule of each polypeptide, and these quasienantiomers are related by a pseudoinversion center. This structure, solved by direct methods and refined at 1.00 Å resolution,[14] is essentially pseudo-$P\bar{1}$; however, for the purpose of making comparisons between quasienantiomers, which must be chemically distinct, we refined this structure in the space group $P1$. Although the arrangement of quasienantiomeric molecules in this structure is pseudocentrosymmetric, the crystal packing is not related in any significant way to the structure of the VHP racemate in space group $P\bar{1}$. The L-(Phe10 → F_5Phe)VHP + D-VHP structure contains a pseudo-fourfold rotoinversion, i.e., this structure can be seen as pseudo-$I\bar{4}c2$, but space group $F222$ was found to give better data processing and refinement statistics than the higher-symmetry space group $I\bar{4}c2$, presumably because $F222$ accommodates the intrinsic differences between quasienantiomers. This structure was refined at 1.46 Å resolution. The asymmetric unit contains one copy each of L-(Phe10 → F_5Phe)VHP and D-VHP (Figure 2). The packing of L and D proteins in this structure is virtually identical to that in the $I\bar{4}c2$ racemate structure, contains crystallographic improper symmetry operations. The root-mean-square deviation (rmsd) calculated between *all heavy atoms* in the Phe10 → F_5Phe quasiracemate asymmetric unit [i.e., L-(Phe10 → F_5Phe) + D-VHP] and the corresponding pair of polypeptides in the $I\bar{4}c2$ racemate structure (one being generated via space-group symmetry) is 0.87 Å; this finding indicates that the packing of the quasiracemic pair mimics the packing in the $I\bar{4}c2$ racemate structure.

The four new structures we solved provide seven versions of VHP that can be compared with one another and the previously reported structure 1YRF: two independent molecules in the $P\bar{1}$ racemate unit cell, one molecule from the $I\bar{4}c2$ structure of racemic VHP, and two each from the quasiracemate structures (the mirror image was used for the D-VHP molecules in these cases). The rmsd values between all pairs of new structures and pairings with 1YRF were calculated using various combinations of backbone atoms or only the side-chain carbons of the three Phe/F_5Phe residues at positions 6, 10, and 17.[14] The conclusions discussed here are based on the side chain comparisons (Table 1), but the same conclusions can be drawn from the backbone comparisons. Some comparisons between polypeptides from different crystals yielded rmsd values that are less than or comparable to the experimental uncertainty, but in many cases, the rmsd values are significant. For both L-(Phe10 → F_5Phe)VHP and L-(Phe17 → F_5Phe)-VHP, comparison of the variant with the quasienantiomer in the same crystal provides a measure of the perturbation caused by the noncanonical side chain in very similar packing environments. In both cases, the rmsd values are ~0.2 Å, which is larger than estimated coordinate errors but small relative to values calculated between models determined from *different* crystals (Table 1; Table S1 in the Supporting Information). This result indicates that the F_5Phe side chain may effectively mimic the Phe side chain it replaced. Similar conclusions may be drawn from the relatively small rmsd values (<0.5 Å) observed for most other comparisons in Table 1.

Somewhat larger differences (rmsd = 1.3−1.5 Å) were observed for phenylalanine clusters between either molecule in the Phe17 → F_5Phe quasiracemate crystal and all of the other

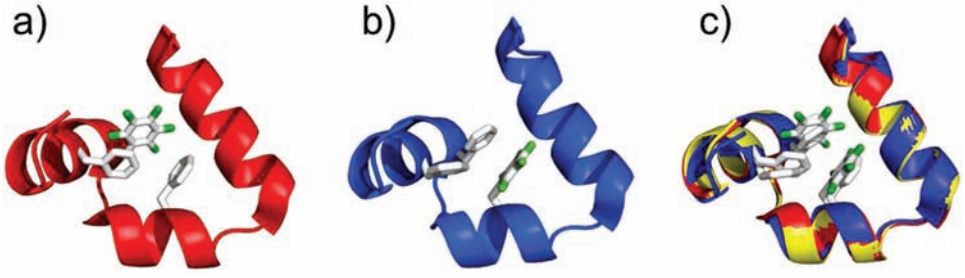

Figure 3. (a) Structure of (L-Phe10 → F_5Phe)VHP obtained via quasiracemic crystallization. (b) Structure of (L-Phe17 → F_5Phe)VHP obtained via quasiracemic crystallization. (c) Overlay of the two F_5Phe-containing forms of VHP with L-VHP from the racemate structure obtained in space group $I\bar{4}c2$. Side-chain C atoms are shown in white, and F atoms in F_5Phe residues are shown in green.

Table 1. Rmsd Values (Å) between All Pairs of Structures under Study and PDB Entry 1YRF Calculated Using Core Phe and F_5Phe Side-Chain Atoms[a]

		$P\bar{1}$ racemate		$I\bar{4}c2$ racemate	Phe10 → F_5Phe		Phe17 → F_5Phe	
structure	molecule	L_1	L_2	D	L	D	L	D
$P\bar{1}$ racemate	L_1	–						
	L_2	*0.15*	–					
$I\bar{4}c2$ racemate	D	*0.29*	0.28	–				
Phe10 → F_5Phe	L	0.32	0.35	*0.22*	–			
	D	0.26	0.28	*0.11*	0.20	–		
Phe17 → F_5Phe	L	1.34	1.32	1.48	1.46	1.46	–	
	D	1.26	1.24	1.39	1.38	1.38	0.18	–
1YRF	L	0.29	0.26	0.43	0.45	0.46	1.37	1.28

[a]The rmsd values calculated between polypeptides within a crystal are small (0.15–0.20 Å), while those calculated between polypeptides in different crystals vary considerably. Values were calculated using the positions of all 21 side-chain C atoms (Cβ, Cγ, Cδ_{1+2}, Cε_{1+2}, Cζ); F atoms were not included in these calculations. Values in italics are smaller than the estimated uncertainties in the atomic positions obtained from the refined models.

VHP structures, including 1YRF. The contrast between the similarity of the L-(Phe17 → F_5Phe)VHP variant to the mirror image of D-VHP in the same crystal and the more pronounced difference between either member of this pair and the other VHP structures presumably reflects the fact that these polypeptides retain some conformational flexibility in their folded states, enabling structural adaptation between members of a quasiracemic pair upon crystallization. Thus, D-VHP can adopt tertiary structures in which the aromatic side-chain cluster rmsd values differ by as much as 1.5 Å in order to adapt to the L-(Phe10 → F_5Phe)VHP variant versus the L-(Phe17 → F_5Phe)VHP variant.

Both structures of F_5Phe-containing VHP quasiracemates involve pseudoinversion operations; this result was expected for peptides that are very nearly enantiomeric on the basis of the predictions of Wukovitz and Yeates.[7] The structure solved in the space group $F222$ (Phe10 → F_5Phe quasiracemate) does not contain improper symmetry elements; however, the packing arrangement of L and D peptides in this structure is virtually identical to that in the $I\bar{4}c2$ racemate structure, which contains a crystallographic fourfold rotoinversion operation (Figure 4). Further details of the relationship between these two structures are provided on page S16 in the SI.

We have found that quasiracemic crystals are obtained preferentially over crystals containing only one enantiomer, even though quasienantiomeric peptides cannot crystallize in centrosymmetric arrangements. These observations support the notion that there could be considerable leeway in the selection of peptides that behave as quasienantiomers. Our results provide support for the hypothesis that quasiracemic protein crystallization can be used to identify polypeptides that contain noncanonical residues but nevertheless mimic the tertiary

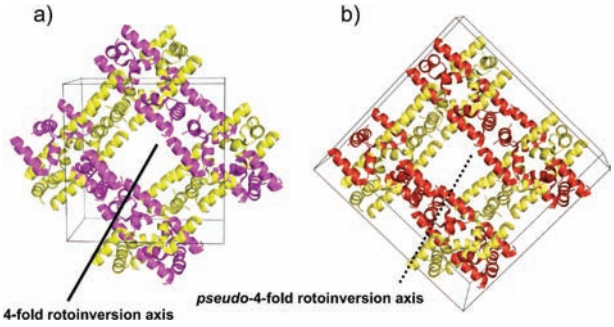

Figure 4. (a) Crystallographic unit cell of the VHP racemate structure in space group $I\bar{4}c2$, with polypeptides from adjacent cells shown for comparison with the quasiracemic structure in (b). The unit cell itself contains eight copies each of L-VHP (magenta) and D-VHP (yellow). (b) Crystallographic unit cell of the (Phe10 → F_5Phe) quasiracemate structure in space group $F222$. The unit cell contains 16 copies each of L-(Phe10 → F_5Phe)VHP (red) and D-VHP (yellow).

structure of a prototype derived exclusively from natural residues. We have explored this hypothesis in the context of amino acid residues bearing fluorinated side chains, an increasingly popular class of noncanonical building blocks for protein design,[2] and our efforts have provided the first high-resolution structures in which F_5Phe is accommodated by a folded protein core. It will now be important to determine whether the quasiracemate crystallization strategy can be applied to a broader range of unnatural subunits, including those that differ in the backbone[3] rather than in the side chain relative to canonical α-amino acid residues.[16]

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■ ASSOCIATED CONTENT

Supporting Information

Experimental details, including polypeptide characterization, X-ray diffraction data collection and processing, structural solution and refinement, and calculated rmsd values. This material is available free of charge via the Internet at http://pubs.acs.org. Model coordinates and structure factors have been deposited in the Protein Data Bank as entries 3TRW ($P\bar{1}$ racemate), 3TRY ($I\bar{4}c2$ racemate), 3TJW (Phe10 → F_5Phe quasiracemate), and 3TRV (Phe17 → F_5Phe quasiracemate).

■ AUTHOR INFORMATION

Corresponding Author

forest@bact.wisc.edu; gellman@chem.wisc.edu

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