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Award Address

Peptide Science: Exploring the Use of Chemical Principles and Interdisciplinary Collaboration for Understanding Life Processes[†]

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Introduction

It is a great honor to be the 2002 recipient of the American Chemical Society Ralph F. Hirschmann Award. Ralph F. Hirschmann is one of the great pioneers of peptide research¹ and has been a wonderful colleague and friend for many years. This Award truly recognizes the efforts and ideas of many students and collaborators whom I have had the privilege of working with during my 37 years in peptide and protein science. Their creativity, hard work, challenging ideas and criticisms, and friendship has been an inspiration and motivation. Perhaps most important were my early mentors who set me on a path I did not plan but for which I am eternally grateful: A. William Johnson at University of North Dakota with whom I received my M.S. degree, who motivated me to become a chemist; Alfred T. Blomquist at Cornell University with whom I received my Ph.D., who guided me to the rigors of chemistry and who allowed me to do something new; Vincent du Vigneaud of Cornell Medical College and Cornell University, who introduced me to the excitement of peptide and protein chemistry and biology and who set me on a path of collaborative interdisciplinary research that I have pursued with fun and excitement; and finally Carl S. Marvel, who nurtured and protected my young career when my colleagues were wondering what I was doing in biophysics, biology, and the medical sciences.

A major goal of our research from the beginning was to develop an understanding of the physical-chemical basis for information transduction in biological systems, with particular emphasis on peptide hormones and neurotransmitters and their receptors. To investigate this research area, we took the approach that this would require the development of necessary tools and ideas from chemistry, physics, and biology and hence would require extensive collaboration with other scientists, especially biological scientists who were at the forefront of their fields. We have been very fortunate to have worked with a number of such outstanding colleagues. Our overall goal was to use chemistry to solve biological problems that involved rigorous chemistry and to address the problems from the biologist's perspective, that is, to address their problems and goals as well as our own. This is only possible with true collaboration, where everyone has "ownership" of the problem. Furthermore, a highly multidisciplinary approach is needed involving state-of-the-art chemistry, biophysics, and biology. Thus, from the beginning, we have sought to incorporate into our research, in my research group and by collaboration, whatever tools and research methods that were needed to broadly address the chemical, physical, and biological aspects of biological activity. A summary of the major chemical, physical, and biological tools we have found essential to this research is given in Table 1. In my education and training, I was fortunate to have a strong background in physical chemistry, synthetic chemistry, and theoretical chemistry, and I was additionally fortunate that Professor de Vigneaud allowed me to learn biochemistry by teaching it to graduate students and medical students, to give lectures on the chemical and physical basics of pharmacological experiments, and to participate in bioassays. He did not believe that such

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Table 1. Chemical, Physical, and Biological Tools Essential for

 Peptide Science

I.	Synthesis						
	A. Total synthesis of peptides and peptide mimetics						
	1. SPPS						
	2. Solution synthesis						
	3. Macrocyclic synthesis						
	4. Asymmetric synthesis methodology						
	5. Complex orthogonal synthesis						
	6. Ligation methods						
	B. Combinatorial/parallel synthesis						
	C. Design and asymmetric synthesis of novel amino acids						
	and peptide mimetics						
II.	Robust analytical and biophysical methods						
	A. Separation science-HPLC, LPC, chiral, partition, etc.						
	B. High-resolution MS and MS/MS, CI, MALDI, etc.						
	C. Biophysical–NMR, IR, CD, UV, Raman, X-ray, PWR,						
	fluorescence, etc. spectroscopies						
III.	Conformational analysis						
	A. X-ray crystallography						
	B. NMR						
	C. CD, IR, Raman						
	D. Computational chemistry; molecular modeling						
IV.	Assays						
	1. Binding-kinetics and thermodynamics						
	2. Bioassays—in vitro; in vivo						
	3. Animal models—disease states vs normal states						

an education was "too broad" or "to general" (which unfortunately is still the attitude of many scientists) but encouraged me to appreciate the chemical aspects of all of these areas. I am eternally grateful to him and to Professors Blomquist and Johnson who encouraged me to explore the full breadth of a scientific problem, while at the same time focusing on solving the immediate scientific issues at hand. Reference to a few published studies at this time in the kind of scientific atmosphere allowed me to learn how to do science with hard work, an open mind, and when necessary, with close collaboration with others.²⁻⁷

Early Studies. Developing a Physical–Chemical Approach to the Chemical Biology of Peptides

In 1968, I began my independent career at the University of Arizona and set up a research laboratory that could do both synthetic peptide chemistry and organic chemistry, study the conformational properties of peptides, and examine their biological activities by collaboration with outstanding biologists. Though it was considered gauche at the time (everyone denies it today), I immediately set my lab up to do solid-phase peptide synthesis (SPPS), and with considerable help from Bruce Merrifield, we built our own automated SPPS instrument⁸ (the coauthors established Vega Biotechnologies a few years later). As soon as it became available, we set up high-pressure liquid chromatography (HPLC) instrumentation to purify our peptides. These tools became of critical importance for our conformational and other biophysical studies and for our biological studies as well. Soon we had developed our synthetic and purification methods to an extent that allowed us to obtain large quantities (a few hundred milligrams) of pure peptides much more quickly than before.

Our initial biophysical studies concentrated on oxytocin and vasopressin analogues and their cyclic and linear fragments. When it became clear that the 100 MHz instrument at the University of Arizona was not adequate, we were fortunate to obtain a collaboration with Frank Bovey and Ann Brewster at Bell Labs, which gave us access to one of the few 220 MHz instruments available at that time (1969), and a further collaboration with Professor Jay Glasel at the University of Connecticut, one of the top scientists on deuterium NMR, further expanded our research. The former collaboration allowed us to examine many of the conformations and dynamic properties of our bioactive peptides using deuterated analogues to make unambiguous assignments.^{9,10} The latter allowed us to be one of the first groups to directly investigate peptide hormone-macromolecular protein interactions (oxytocinneurophysin) at the molecular and dynamic levels.¹¹ As part of these investigations, we also established insights into structure-activity relationships and synthetic methodologies for preparing novel ²H- and ¹³C-labeled amino acids and peptides, semisynthesis methods for modifying larger peptide hormones (glucagon), and solid-phase synthesis methods for the preparation of larger bioactive peptides such as glucagon (29 amino acids) and α -MSH (13 amino acids). Space does not allow a discussion of these studies, but a few highlights that served to stimulate our subsequent research follow: (1) with Professor Mac Hadley, our determination that α -MSH release from the pituitary was not under the control of an oxytocin fragment¹² but biogenic amines;¹³ (2) the first demonstration of cis-trans isomerism about an χ -proline bond in a fragment of a bioactive peptide;¹⁴ (3) use of specifically ¹³C-labeled hormones, oxytocin and vasopressin, to investigate specific interactions of the hormones with their neurosecretory carrier proteins, the neurophysins,^{15,16} and the direct demonstration of the microdynamics of a tyrosine ring of oxytocin when bound to neurophysin using ¹³C NMR;¹⁷ (4) design and discovery of the first antagonist of a large peptide hormone, glucagon,^{18,19} and the demonstration with David Johnson, M.D., that such an antagonist could lower glucose levels in a diabetic animal;²⁰ (5) with Professor A. T. Tu, use of laser Raman in conjunction with CD spectra to determine chirality of disulfide bonds in oxytocin agonists and antagonists;²¹ and (6) demonstration, using NMR, that the oxytocin-antagonist analogue [l-penicillaninine]oxytocin had a conformation different from that of the agonist oxytocin because of specific conformational constraints. This led directly to the de novo design of other antagonists with similar properties.^{23,24}

Conformational Constraint, the Ramachandran Plot, and Design of Bioactive Peptides: Development of a Robust Strategy for Ligand-Based Peptide Design

During the 1970s, with the advent of high-field NMR and the lack of success of crystallizing most bioactive peptide hormones and neurotransmitters, it became clear that most of these compounds had considerable conformational flexibility in aqueous or DMSO solutions. In addition, it now had become clear that these compounds interacted with specific receptors on plasma membranes (established by development of methods for isolation of these plasma membranes and use of radioligand binding studies and second messenger assays), but no methods were available for isolating these receptors and crystallizing them. Thus, we recognized that development of a robust method of peptide hormone

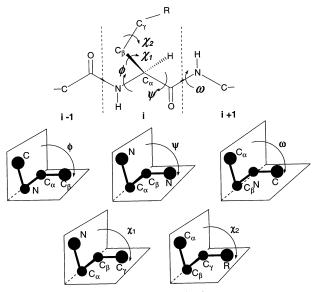


Figure 1. Definitions of ψ , φ , ω , χ^1 , χ^2 .

and neurotransmitter design would require the development of specific methods of conformational constraint. Our own laboratory studies of the conformational effects of β , β -dimethylcysteine (penicillaninine) in cyclic disulfide peptides and of the possibility of cis-trans isomerism about X-Pro bonds demonstrated the potential significance for use of conformational constraint in peptide ligand design of hormones and neurotransmitters. At the same time, it was becoming evident that the targets for all of these ligands were membrane proteins and even more interestingly that these ligands and their receptors (now commonly known to be Gprotein-coupled receptors (GPCRs)) controlled and/or modulated many crucial biological processes and animal (including human) behaviors such as feeding behavior, pain, pigmentation, fear-flight, addiction, sexual behavior, stress response, cardiovascular function, learning and other cognitive behaviors, etc. Indeed today more than 50% of current drugs display their bioactivity by interactions with integral membrane proteins.

Thus, we (and others) developed a robust strategy to develop bioactive peptide ligands into useful biological tools (agonists, antagonists, and inverse agonists) and drugs and at the same time to determine their bioactive conformations. Three reviews early in the 1980s^{24–26} focused attention on the potential of conformation constraint in bioactive peptide design.

Thus, in addition to our work on oxytocin and vasopressin design, we applied concepts of conformational constraint to all of the peptide hormone and neurotransmitter ligands we were investigating. Limitation of space will greatly limit our discussion, and thus, we will focus on aspects of our work that have provided critical impetus to subsequent studies. A major focus of our thinking about peptide conformation and design was the pioneering work of Ramachandran and coworkers, 27,28 which appeared as I entered the field and had a major impact. Ramachandran and co-workers investigated the conformational space accessible to the peptide backbone, which is defined by three torsional angles φ , ψ , and ω (see Figure 1 for definitions). Using simple computation methods, they demonstrated that only limited conformation space was available to most

 α -amino acids (except glycine) and that the accessible low-energy conformations were the α -helix, β -sheets, extended structures, and β -turns. Later, more sophisticated force field calculations and quantum mechanical calculations have been applied, but the basic conclusions of Ramachandran remain, and huge numbers of subsequent X-ray crystal structures have demonstrated the importance and significance of Ramachandran's insights. The lesson for us was very simple. We should try to design conformational constraints that would bias our peptides to one of these low-energy conformations and explore the significance of this conformation to the peptide's biological activity. Particularly noteworthy about peptide hormone and neurotransmitter ligands for GPCRs was the early realization that β -turn conformations might be particularly useful in many of the cases we were investigating. Table 2 provides an outline of the major approaches that were developed. Investigators who are interested in utilizing this approach in $\varphi - \psi$ space may wish to obtain information by examining reviews/overviews that have appeared in the literature.^{25,26,29–32} Investigations of constraints in χ space are somewhat more limited because inherently the torsional angles about the C_{α} - C_{β} , C_{β} - C_{γ} , etc. carbon atoms of the side chain groups (Figure 1) are more flexible than the φ , ψ , and ω torsional angles in peptides (see Figure 2 for a $\chi^1 - \chi^2$ plot for L-tyrosine). Constraining α -amino acids in χ space requires careful considerations of the interplay between γ space and $\varphi - \psi$ space as well as of the inherent steric and stereoelectronic effects of modifications of the side chain groups of α -amino acids used to constrain them.³²⁻³⁴ We have explored χ space by the careful use of steric and stereoelectronic effects. The use of covalent attachment of backbone nitrogen via a methylene bridge to an aromatic group in aromatic amino acids is one of the first kinds of constraints we explored. 1,2,3,4-Tetrahydroisoquinoline 3-carboxylic acids (Tic) are good examples of such a constraint because they can only exist with $\chi^1 = -60^\circ$ or $+60^\circ$ for an α -amino acid³⁵ (Figure 3). A bias to $\chi^1 = -60^\circ$ or $+60^\circ$ can be designed, 36,37 and by use of careful model studies, we were able to demonstrate in collaboration with Toniolo et al.³⁸ that these structures were completely compatible with being in either α -helix or β -turn structures. We found these compounds to be very useful and important in our de novo redesign of somatostatin from a compound that primarily interacts with somatostatin receptors to one that interacts primarily with μ opioid receptors as an antagonist.^{35,39,40} Two of the designed compounds D-Phec[Cys-Tyr-D-Trp-Orn,Thr-Pen]-Thr-NH2 (CTOP) and D-Phe-c[Cys-Tyr-D-Trp-Arg-Thr-Pen]-Thr-NH₂ (CTAP) are among the most potent and especially selective μ opioid receptor antagonists known and because of their complete stability against proteolytic degredation have been widely used in biological studies to help better understand the role of μ opioid receptors in a variety of biological systems^{41,42} and as a ligand for binding studies.43

Another approach we have taken for χ constraint is to use β -alkyl-substituted amino acids, and we have developed the asymmetric synthesis of a wide variety of β -methyl- and β -phenyl-substituted analogues of aromatic amino acids.^{44–58} Generally this requires the

Table 2. Some Major Approaches for Conformation Constraints of Pept	tides
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I.	Use of D-amino acids, prolines, and related amino acid residues —Stabilize turn structures, proline helices, and others
II.	Use of α-substituted amino acids —Stabilize helical structures, turn structures, extended structures, and others, depending upon substituents
III.	Use of side chain to side chain cyclizations for cyclic disulfides, lactams, lactones, sulfides, aromatic, etc. –Stabilize β -turns, α -helices, etc., depending on macrocyclic ring size
IV.	Use of side chain N- and C-terminal residues —Stabilize various secondary structures depending on ring size
V.	Backbone to backbone cyclization —Stabilize a variety of secondary structures
VI.	Metal complexes to peptide backbone or to side chain moieties
VII.	Ring-closing metathesis

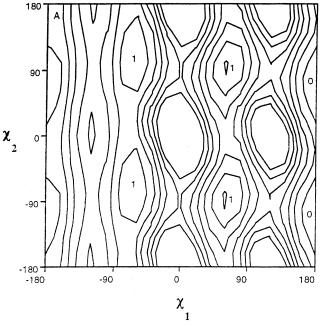


Figure 2. $\chi^1 - \chi^2$ space for L-tyrosine.

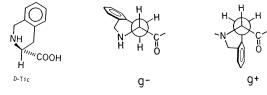


Figure 3. Conformations of D-Tic.

asymmetric synthesis of four isomers, and in most cases all four isomers were prepared. This allowed us to explore in detail the topographical requirements of the side chain groups as key pharmacophore moieties in a number of peptide hormones and neurotransmitters.^{34,59–65} Among the most interesting of the novel amino acids we have prepared are the four isomers (S,S; S, R; R, S; R, R) of β -methyl-2',6'-dimethyltyrosine (TMT) and β -methyl-2',6'-dimethylphenylalanine TMP (Figure 4). As pointed out before (Figure 2), the energy map for most common α -amino acids, such as L-tyrosine, in χ^{1} - χ^2 space is quite flat, with energy differences between gauche(-) [g(-)], gauche(+) [g(+)], and trans [t] (-60°) , +60°, and $\pm 180^{\circ}$, respectively, for an L-amino acids) generally less than 1 kcal/mol and with the energy barrier between them generally less than 5 kcal/mol. Hence, each conformation is readily accessible at physiological temperatures (40 °C). However, for a compound

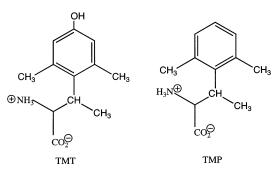


Figure 4. Structures of topographically constrained β -substituted α -amino acids β -methyl-2',6'-dimethyltyrosine (TMT) and β -methyl-2',6'-dimethylphenylalanine (TMP).

such as TMP (Figure 5) not only are the energy barriers between the different conformations much greater (often 5-15 kcal/mol or more)⁶⁶ but there are substantial energy differences between the gauche(–), gauche(+), and trans conformations.³⁴ The availability of these compounds as chirally pure derivatives allowed us to address an issue that had interested us for many years. Do biological systems (receptors, acceptors, enzymes, etc.) that utilize molecular recognition of a peptide ligand (hormone, neurotransmitter, substrate, etc.) for their biological activity utilize a *specific* χ conformation for their biological activity? How important is such a local (or specific) interaction for molecular recognition (binding) and for biological activity (agonist vs antagonist, etc.)?

Thus, we examined the effect of replacing the tyrosine-1 residue in our constrained bioactive cyclic enkephalin analogue H-Tyr-c[D-Pen-Gly-Phe-D-Pen]-OH (c[D-Pen²,D-Pen⁵]enkephalin, DPDPE),⁶⁷ which is a potent and selective ligand for the δ opioid receptor. DPDPE is an agonist with potent analgesic activities in vivo⁶⁸ and is completely stable to serum, brain homogenates, and pure enzymes to enzymatic breakdown.⁶⁹ Examination of its conformation properties in solution by NMR⁷⁰ and in the solid crystalline form by X-ray-crystallography⁷¹ showed that the conformation of the 14-membered disulfide ring is the same in solution and in the crystal but that the preferred side chain conformations of the key pharmacophore aromatic side chain groups of Tyr¹ and Phe⁴ were different in the different states. Studies with β -MePhe⁴-substituted DPDPE analogues indicated that the gauche(-) conformation for χ^1 was the most favorable for the bioactivity of DPDPE. To examine the exocyclic Tyr¹ residue, we turned to β -methyl-2',6'-dimethyltyrosine¹ (TMT¹)substituted DPDPE analogues (all four diastereoiso-

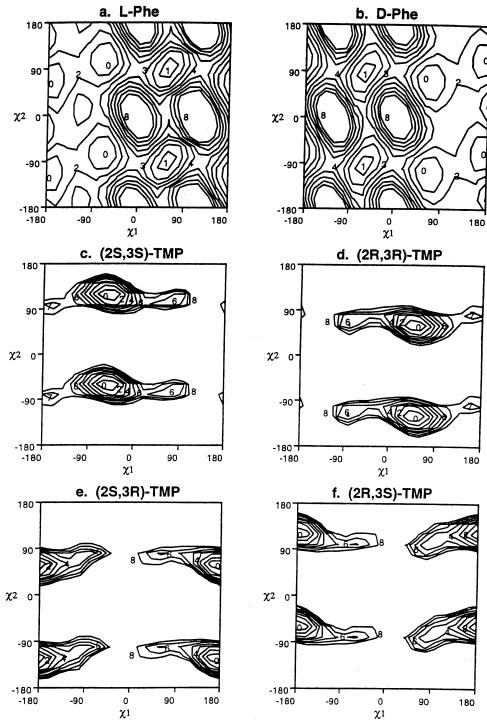


Figure 5. $\chi^1 - \chi^2$ energy map for β -methyl-2',6'-dimethylphenylalanine (TMP).

Table 3.	Binding Affinities	and Biological Activitie	es of TMT ¹ [DPDPE] Analogues ^a
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	binding data, IC_{50} (nM)		bioassay data, EC ₅₀ (nM)		
compd	μ^b	δ^c	GPI (μ)	MVD (δ)	
H-Tyr-c[D-Pen-Gly-Phe-D-Pen]-OH(DPDPE)	610	1.6	7300	4.1	
$[(2S,3S)-TMT^1]DPDPE$	720	210	290	170	
[(2S, 3R)-TMT ¹]DPDPE	4300	5.0	0% at 60 μ M, antagonist	1.8	
[(2R,3R)-TMT ¹]DPDPE	77000	3500	50000	2200	
[(2R, 3S)-TMT ¹]DPDPE	0% at 10 µM	9% at 10 μM	75% at 82 μM	28% at 10 $\mu { m M}$	

^a Data from ref 72. ^b Versus [³H]CTOP. ^c Versus [³H][p-ClPhe⁴]DPDPE.

mers). As shown in Table 3,⁷² using both binding affinity and in vitro bioassays (MVD, δ receptor; GPI, μ receptor), the (2*S*,3*R*) analogue in which χ^1 is trans was the most potent *and* selective DPDPE analogue, and the binding affinity differences for the different diastereoisomers are very consistent with the energy differences

for the various preferred side chain conformations of the four isomers of TMT. Indeed, extensive NMR studies⁷² showed that the only changes in conformation between DPDPE and the TMT¹-substituted DPDPE analogues were in the preferred side chain conformations of the TMT¹-substituted analogues. Interestingly, in functional assays (MVD and GPI), the (2S,3R) analogue $(\chi^1 =$ -60°) is a weak antagonist at the μ -opioid receptor, demonstrating that the preferred side chain conformation for agonist activity at δ and μ receptors for the Tyr¹ side chain group are very different. These results are completely consistent with the hypothesis that for peptide hormones and neurotransmitters that interact with G-protein-coupled receptors such as the opioid receptors, the topographical properties of side chain groups of key pharmacophores dominate the structureactivity relationships for these critically important modulators of bioactivity. The ancillary hypothesis is that the backbone of such peptide analogues thus serves primarily as a conformational template (privileged structure) for bioactivity. In this regard, backbone conformations of peptides and proteins (α -helix, β -sheets, β - and γ -turns, and extended conformations) serve as the most critical privileged structures in nature because they define the template structures of all peptide and proteins of biological importance.

Having a three-dimensional, topographical structure for DPDPE led us to utilize computational chemistry for the de novo design of a non-peptide mimetic of DPDPE that would be both as potent and as selective as DPDPE for the δ opioid receptors.^{73,74} Space does not allow a discussion of the approach we used, which can be found in the literature.⁷³ Suffice it to say that in structure-activity relationships, the peptide mimetic behaved like the peptide on which its design was based and not like non-peptide δ opioids, which are known to bind to δ opioid receptors and to show bioactivities different from the bioactivities of δ opioid peptides.⁷⁴ However, these de novo designed non-peptide mimetics show significant toxicity, much like other non-peptide opioids. Thus, we are continuing to develop synthetic strategies that will lead to nontoxic peptidomimetics in related structural classes.75,76

As discussed above, we have hypothesized that "simple" changes in topography of key pharmacophore elements in peptide hormones and neurotransmitters can profoundly affect their bioactivities without any significant changes in backbone conformation. To examine further this hypothesis, we designed a highly constrained bicyclic oxytocin antagonist analogue in χ space⁷⁷ based on our previously designed bicyclic oxytocin analogue

D-Pen-Tyr-Ile-Glu-Asn-Cys-Pro-Lys-Gly-NH2, which was

a potent, prolonged acting oxytocin antagonist at the uterine oxytocin receptor.^{78,79} Detailed conformational analysis of this bicyclic oxytocin analogues using NMR, computational studies, molecular modeling, and other biophysical studies had shown that oxytocin agonists and antagonists have a different structure–biological activity relationship and different receptor-binding conformations.^{80,81} Left unanswered, however, was the importance of the χ space topography of the tyrosine residue for molecular recognition at the oxytocin receptor. It previously was known that the chirality⁸² and

Table 4. Binding Affinities of Bicyclic Oxytocin Analogues Containing the Four Isomers of 4'-Methoxyl-β-2',6'-Trimethyltyrosine

peptide structure	binding affinities, IC ₅₀ (nM)
1 [D-Pen ¹ ,Glu ⁴ ,Lys ⁸]OT	130
2 [D-Pen ¹ , (2 <i>S</i> , 3 <i>S</i>)- <i>p</i> -MeOTMT ² , Glu ⁴ , Lys ⁸]OT	8.0
3 [D-Pen ¹ ,(2 <i>S</i> ,3 <i>R</i>)- <i>p</i> -MeOTMT ² ,Glu ⁴ ,Lys ⁸]OT	36000
4 [D-Pen ¹ ,(2 <i>R</i> ,3 <i>S</i>)- <i>p</i> -MeOTMT ² ,Glu ⁴ ,Lys ⁸]OT	19000
5 [D-Pen ¹ ,(2 <i>R</i> ,3 <i>R</i>)- <i>p</i> -MeOTMT ² ,Glu ⁴ ,Lys ⁸]OT	160

hydrophobicity⁸³ of the aromatic amino acid at position 2 were important for high-affinity antagonist activity. Hence, we utilized a designed novel amino acid, β -methyl-2',6'-dimethyl-4'-methoxytyrosine (p-OMe-TMT all four isomers: (2*S*,3*S*), (2*S*,3*R*), (2*R*,3*S*), and (2*R*,3*R*)), which incorporated the desired hydrophobicity and chiralities, and in addition placed χ^1 and χ^2 constraints, which favored specific topographical properties for each isomer,^{34,77} and incorporated each isomer into the 2-position of the bicyclic oxytocin analogue. The results of the binding studies are given in Table 4. It was very exciting to find that two of the diastereoisomer analogues were very potent binders, the (2S,3S)- and (2R,3R)-containing isomers (2 and 5, Table 4), whereas the other two diastereoisomers, 3 and 4 (Table 4), were virtually inactive. Indeed, compound 2 was 16 times more potent than the parent compound 1, and the other potent binder, 5, was nearly equipotent to 1. Examination of the low-energy conformations of all four isomers of the topographically constrained bicyclic oxytocins 2-5(Figure 6) clearly showed that a very particular topography of the tyrosine-2 side chain was critical for high affinity at the oxytocin receptor and for antagonist activity. Since the energy differences between the different χ -1 conformations (g(-), g(+), and trans) are 3–5 kcal/mol or more,³⁴ it is clear that a particular topography of the tyrosine side chain group is critical for high potency. Only the g(-) conformation for the (2S,3S)residue and the g(+) conformation for the (2R,3R)residue give potent antagonists (they both exist in the same topographical space (Figure 6)), and clearly the other two isomers, (2S,3R) and (2R,3S) structures 3 and 4, which have different topographies at the 2-position, do not recognize the oxytocin receptor probably because of unfavorable steric effects on interaction with the oxytocin receptor. Hence, topographical differences at only one key amino acid side chain in a critical pharmacophore residue are sufficient to affect molecular recognition at receptors by a 1000-fold or more, even though all other conformational and topographical properties of the pharmacophore needed for potent molecular recognition are present in favorable conformational space.

 α -Melanocyte Stimulating Hormone (α -MSH) and Melanocortin Receptors. A Remarkable Story of the Central Importance of Topographical Structure in Bioactivities Including Fundamental Human Behavioral Activities. α -MSH(Ac-Ser-Tyr-Ser-Met-Glu-His-Phe-Arg-Trp-Gly-Lys-Pro-Val-NH₂) is a potent peptide hormone and neurotransmitter that has several critical biological activities (pigmentation, feeding behavior, sexual behavior, pain, immune response,

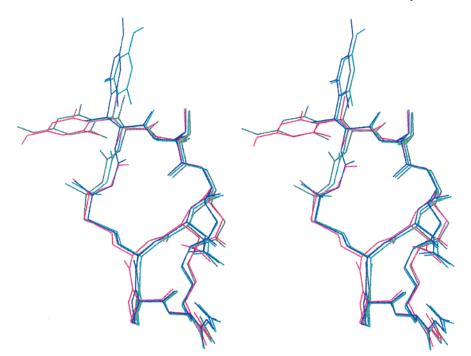


Figure 6. Stereoview of the low-energy conformations of the four [*p*-MeO-TMT²]BC-OT analogues: [(2*S*,3*S*)-*p*-MeO-TMT²]BC-OT (dark green); [(2*R*,3*R*)-*p*-MeO-TMT²]BC-OT (red); [(2*R*,3*S*)-*p*-MeO-TMT²]BC-OT (blue); [(2*S*,3*R*)-*p*-MeO-TMT²]BC-OT (green). From Liao, S.; et al. *J. Am. Chem. Soc.* **1998**, *120*, 7393–7394. Reprinted with permission from *Journal of the American Chemical Society* (page 7394, Figure 3). Copyright 1998 American Chemical Society.

etc.) that are central to survival.⁸⁴ This peptide is a processed product of the proopiomelanocortin (POMC) gene that produces several other peptide hormones and neurotransmitters (e.g., ACTH, β -endorphin, β -lipotropin, etc.) that are central to survival in most animals.⁸⁵ Initially the primary biological activity attributed to α -MSH was its affect on pigmentation of the skin and hair of virtually all animals including humans. Extensive structure-activity studies⁸⁶ in conjunction with extensive biological studies provided a comprehensive understanding of these primary properties of the hormone and its melanocortin receptor, now referred to as the melanocortin-1 receptor (MC1R). We initially entered the field in collaboration with Professor Mac Hadley, investigating the mechanism of release of α -MSH from the pituitary, and demonstrated that the ideas related to control of release were not correct^{12,13,87-89} and eventually showed that dopamine was the major neurotransmitter controlling α -MSH release.^{13,90} These studies led directly to examining the in vitro and in vivo biological activities of melanotropins. It soon became clear the α -MSH and the analogues known at that time⁹¹ were not adequate for developing good bioassay methods and especially for careful in vivo studies because of their rapid degredation by proteases. We therefore sought to develop more potent and stable analogues of α -MSH, and on the basis of previous studies of oxidation and racemization of α -MSH, we designed the ligand [Nle⁴,D-Phe⁷]- α -MSH⁹² (NDP- α -MSH, MT-I, Ac-Ser-Tyr-Ser-Nle-Glu-His-D-Phe-Arg-Trp-Gly-Lys-Pro-Val-NH₂). This compound not only was more potent than α -MSH but also showed highly prolonged (hours to weeks) biological activities both in vitro and in vivo93 in a calcium-dependent process and was quite stable against proteolytic breakdown by proteases and serum.^{94,95} These unique properties allowed the development of extensive biological studies of the role of α -MSH in pigmentation and melanoma cancer $^{96-100}$ and to the development of an adenylate cyclase assay to evaluate transduction processes in melanotropins.^{101,102} Eventually, in collaboration with our colleagues at the University of Arizona, we were able to do all the preclinical studies that allowed the clinical evaluation of NDP-a-MSH as a stimulator of skin darkening in humans and for use to protect against UV radiation damage to skin.^{103–106} It also provided an impetus for extensive modeling which led to the suggestion of the presence of a β -turn in the vicinity of the D-Phe⁷-Arg⁸ residues. This hypothesis was tested¹⁰⁷ by the use of conformational constraints of the linear peptide α -MSH to the cyclic peptide c[Cys⁴,Cys¹⁰]- α -MSH¹⁰⁷ in which the Met⁴ and Gly¹⁰ residues were replaced by cystine in a process we referred to as pseudoisosteric cyclization. On the basis of this design, a superpotent analogue of α -MSH was obtained in the classical frog skin (*R. pipiens*) bioassays,¹⁰⁷ though in vivo activity and biostability were not as good as NDP- α -MSH. However, we were able to demonstrate using this compound that α -MSH was involved as a neurotransmitter (done in collaboration with Tom O'Donohue et al.).108

Our finding that NDP-α-MSH and truncated analogues of NDP-α-MSH had prolonged biological activity led us into new directions: (1) Was the unique biological activity of NDP-α-MSH an effect of conformation? (2) What is the minimum pharmacophore for α-MSH? For the last question, we did a large number of careful experiments with many truncated analogues of α-MSH and numerous in vitro and in vivo biological activity studies with our biological collaborators.^{109–112} These extensive studies led to the conclusion that the minimum active sequence for full biological activity using only L-amino acids was -His-Phe-Arg-Trp-^{113,114} and that when a D-Phe⁷ was introduced, even tripeptides could

Table 5. Biological Activities of Cyclic Lactam Analogues of α -Melanotropins Using the Frog Skin (*R. pipiens*) and Lizard Skin (*A. carolinensis*) Assays^a

	biological activ	ities, b EC ₅₀ (nM)
compd	frog skin	lizard skin
α-MSH	0.50 (-)	1.0 (-)
Ac-Nle ⁴ -c[Glu ⁵ ,D-Phe ⁷ ,Lys ¹⁰ ,Gly ¹¹]α-MSH(4–13)-NH ₂	0.50 (+)	0.17 (+)
Ac-Nle ⁴ -c[Asp ⁵ ,D-Phe ⁷ ,Lys ¹⁰ ,Gly ¹¹]α-MSH(4-13)-NH ₂	0.50 (+)	0.010 (+)
Ac-Nle ⁴ -c[Glu ⁵ ,D-Phe ⁷ ,Lys ¹⁰] α -MSH(4–10)-NH ₂	1.0 (+)	0.11 (+)
Ac-Nle ⁴ -c[Asp ⁵ ,D-Phe ⁷ ,Lys ¹⁰]α-MSH(4-10)-NH ₂ (MT-II)	0.60 (+)	0.011 (+)
Ac-Nle ⁴ -c[Asp ⁵ ,D-Phe ⁷ ,Orn ¹⁰]α-MSH(4-10)-NH ₂	0.50 (-)	0.05 (-)
Ac-Nle ⁴ -c[Asp ⁵ ,D-Phe ⁷ ,Dab ¹⁰]α-MSH(4-10)-NH ₂	0.50 (-)	0.20 (-)
Ac-Nle ⁴ -c[Asp ⁵ ,D-Phe ⁷ ,Dpr ¹⁰]α-MSH(4-10)-NH ₂	50 (-)	0.20 (-)
Ac-Nle ⁴ -c[Asp ⁵ ,D-Phe ⁷ , ($\hat{2}S, \hat{3}S$)- β -MeTrp ⁹ ,Lys ¹⁰] α -MSH(4–10)-NH ₂	0.44(-)	1.0 (+)
Ac-Nle ⁴ -c[Asp ⁵ ,D-Phe ⁷ , (2 <i>S</i> ,3 <i>R</i>)- β -MeTrp ⁹ ,Lys ¹⁰] α -MSH(4–10)-NH ₂	29.(-)	6.7 (-)
Ac-Nle ⁴ -c[Asp ⁵ , D-Phe ⁷ , $(2R, 3S)$ - β -MeTrp ⁹ , Lys ¹⁰] α -MSH(4–10)-NH ₂	0.06(+)	1.43 (+)
Ac-Nle ⁴ -c[Asp ⁵ ,D-Phe ⁷ ,(2 <i>R</i> ,3 <i>R</i>)- β -MeTrp ⁹ ,Lys ¹⁰] α -MSH(4–10)-NH ₂	0.33(+)	1.0 (+)

^a Adapted from refs 117 and 119. ^b (-) means no prolonged biological activity; (+) means prolonged biological activity. See text.

have potent biological activity.¹¹⁵ Thus, melanotropin pharmacophore three-dimensional organization of biological function appears to be a function of a linear sequence of peptide information. This immediately raised the question about which conformations correlated to this linear structural information.

As mentioned above, our design of $c[Cys^4, Cys^{10}]-\alpha$ -MSH was based on a hypothesis that the potent bioactivity of NDP- α -MSH was due to a β -turn structure for the tetrapeptide sequence -His-D-Phe-Arg-Trp. Once appropriate force fields became available, we performed extensive conformational and dynamic calculations regarding the preferred conformation for selected melanotropins.¹¹⁶ These studies led to the design of cyclic lactam analogues of α-MSH such as Ac-Nle-c[Asp-His-D-Phe-Arg-Trp-Lys]-NH₂ (MT-II) in which the critical pharmacophore sequence -His-D-Phe-Arg-Trp- was conformationally constrained in a macrocyclic 23-membered lactam ring.¹¹⁶ Various sized lactam rings were investigated (Table 5),¹¹⁷ and it was found that though ring size (except for the 20-membered ring) did not greatly affect potency in the classical *R. pipiens* frog skin assay, in the lizard (A. carolinensis) assay, which we previously had shown gave structure-activity relationships similar to those of the mammalian MC1R (whereas the R. *pipiens* assay did not), the biological potency was very dependent on ring size. Also very interesting was the observation that prolonged biological activity of the cyclic lactam analogues was dependent on ring size (Table 5).

Prolonged Biological Activity. These and other studies led us to propose that prolonged biological activity was directly related to three-dimensional topographical properties of the peptide. As pointed out above, we had found that biological activities of peptide hormones and neurotransmitters are very dependent on the three-dimensional topographical properties of the peptide in χ space. This led Carrie Haskell-Luevano and Lakmal Boteju in my laboratory to design and synthesize four diastereoisomeric analogues of Ac-Nle⁴-c[Asp⁵,D-Phe7,Lys10]-a-MSH(4-10)-NH2 (MT-II)118-121 in which the Trp⁹ residue was replaced with all four isomers of the $\chi^1 - \chi^2$ constrained amino acid β -methyltryptophan [(2*S*,3*S*),(2*S*,3*R*),(3*R*,3*S*), and (2*S*,3*S*)].¹¹⁸ Examination of the biological activities of these compounds showed that they varied widely in potency (Table 5), and interestingly, they also varied widely in their prolonged biological activities (Figure 7). Comprehensive NMR

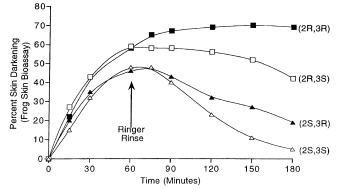


Figure 7. Prolonged biological activity of α-MSH in the frog skin (*R. pipiens*): $[(2S,3S)-\beta-MeTrp^9]MT-II (Δ); [(2R,3R)-\beta-MeTrp^9]MT-II (Δ); [(2R,3S)-β-MeTrp^9]MT-II (Δ)].$

strudies¹¹⁹ showed that the backbone conformations of the four diastereoisomeric analogues were essentially the same and that the only conformational difference was in the topographic arrangement of side chain pharmacophore groups in χ space.¹¹⁹ Additional careful studies of the dissociation rate constants for MT-II showed that the prolonged activity was due to the unusually slow dissociation rates from the MC1R.¹²¹ We later showed, using a fluorescently labeled multiligand construct of MT-II, that these prolonged acting analogues of α -MSH could bind to the cell-surface receptors, undergo association (patching), be transported into the cell to the nucleus, and then be recycled to the plasma membrane again as an intact ligand-receptor complex.^{122,123} These interesting constructs also could be used to examine a wide variety of cellular functions of melanotropins.^{124–126} These studies, and those discussed earlier, clearly demonstrate that the three-dimensional structure of biologically active peptides, for interactions with their cognate receptors, are dependent not only on the backbone conformation (φ , ψ , ω) but equally, or perhaps more importantly, on the topographic relationships in χ space (χ^1 , χ^2 , etc.) of key pharmacophore moieties. From the standpoint of de novo peptide design, and especially peptide mimetic design, it clearly is very important to carefully evaluate structure-activity relationships in γ space. In general, these considerations have not been widely incorporated into approaches to the design of peptides and peptide mimetics, but this will change.

Effects of Genomics and Proteomics on Ligand Design. New Melancortin Genes and New Melanotropin Ligands. Until the early 1990s, the major focus of research on the products of the POMC gene were α -MSH and ACTH, which respectively influence pigmentation (α -MSH) and response to stress (ACTH, adrenal function). In the early 1990s, as a result of extensive research in several laboratories, the mammalian melanocortin-1 (MC-1) and melanocortin-2 (MC-2) receptors were sequenced and cloned.^{84,127} This has proven to be very critical for subsequent studies of the biological functions of these two receptors. For example, very recently it was shown by Mogil et al.,¹²⁸ utilizing older¹²⁹ and recently discovered¹³⁰ melanocortin-1 receptor (MC1R) antagonists from our laboratory, that mammalian pathways, including human pathways, for the modulation of pain were different and distinct for males and females and that in females the MC1 receptor (MC1R) was involved in pain modulation.

From the standpoint of drug design, the most interesting findings from cloning were the discovery of three new melanocortin receptors, the MC3R, MC4R, and MC5R receptors, numbered in the order in which they were discovered.^{84,127} The MC3R and MC4R were found to be located primarily in the brain, though subsequent studies also have found them in the spinal column and in various peripheral tissues. The MC5R was found throughout various tissues in the body including the brain. Numerous previous studies had suggested that α -MSH might be important in a number of biological functions that involved the central nervous system, ^{127,131} in the neuroendocrine system, and in the immune system. To investigate the putative biological activities ascribed to these new receptors, there is a need to obtain potent and highly selective agonist and especially antagonist analogues for these new (and old) melanocortin receptors. Fortunately, as part of our earlier studies, we had available a large collection of ligands. By use of these ligands, e.g., NDP-α-MSH, MT-II, etc., it was determined that the new receptors were primarily the targets for α -MSH, that the central core sequence His-Phe-Arg-Trp still was of critical importance as the key pharmacophore for the MC3R, MC4R, and MC5R,^{132–135} and that γ -MSH had some selectivity for the MC3R. Within this context, our goal was to find selective agonists and especially antagonists for the new receptors.

Despite the efforts of ourselves and others, very few antagonist melanotropin ligands had been found. We earlier found weak antagonists for the MC1R, 129, 136 but efforts to follow up on these leads were largely unsuccessful because modifications of these leads led to agonist activity. Thus, we were unable to formulate any general hypothesis about structure – antagonist activity relationships at the melanocortin receptors. An important breakthrough in our laboratory came with the use of topographical constraints in our studies of melanotropin analogues. In this case, we investigated the substitution of D-Phe⁷ with naphthylalanine derivatives. There are two naphthylalanines (1' and the 2' isomers, Figure 8), and when they were substituted into MT-II to give the analogues Ac-Nle,⁴c[Asp⁵,D-Nal(2')⁷-Lys¹⁰]α-MSH-(4-10)-NH₂ (SHU-9119) and Ac-Nle⁴-c[Asp⁵,D- $Nal(1')^{7}$ -Lys¹⁰] α -MSH, two quite different biological

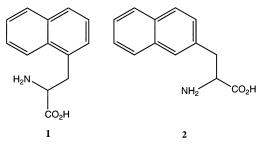


Figure 8. Structures of 1'-naphthylalanine (1) and 2'-naphthylalanine (2).

profiles were seen (Table 6).¹³³ In the case of the D-Nal-(2')-containing analogue, a compound with potent antagonist activity at the MC4R and MC3R receptors was obtained, which had some agonist activity at the MC5R and modest selectivity for the MC4R. On the other hand, the D-Nal $(1')^7$ -containing analogue was an agonist at all of the melanocortin receptors tested. Subsequent comprehensive studies in our laboratory have shown that in general (but not always) substitution of a D-Nal(2')in the 7-position of α -MSH analogues produces an analogue with antagonist activity at the MC4R and MC3R but not at the MC5R or mammalian MC1R.¹³⁷⁻¹⁴⁵ Interestingly, SHU-9119 is a potent antagonist in the classical frog skin bioassay,¹³³ and this small cyclic heptapeptide is 10 times more potent at the MC4R than the natural endogenous antagonist protein ligand for the MC4R, agouti.

The discovery of SHU-9119 as a potent mammalian MC4R and MC3R antagonist has been an important tool for the development of an understanding of the roles of α -MSH in a wide variety of animal behaviors. Space does not allow a comprehensive discussion of this emerging field in drug design and development and in the physiological significance of melanotropins in animal and human behavior. However, a few focused comments will be made related to our collaborations with biologists in this area. A very early application of the use of the potent MC4R agonist MT-II in conjunction with the potent MC4R receptor antagonist SHU-9119 was its use in demonstrating that melanotropin was a critical ligand for the control of feeding behavior.¹⁴⁶ In collaboration with Roger Cone and his colleagues, it was found that MT-II was a potent suppressor of feeding behavior and that the antagonist SHU 9119 could block the feeding behavioral effects of MT-II and of endogenous neurotransmitter (presumably α -MSH or a modified version). Subsequent studies in many laboratories have demonstrated that melanotropin peptides that bind to MC4 and MC3 receptors have profound effects on feeding behavior and energy homeostasis in animals, with agonists suppressing feeding behavior and antagonist stimulating feeding behavior. The use of agonists for treatment of obesity and of antagonists for treatment of anorexia and many related applications are under investigation in many drug and biotechnology companies, and the mechanisms of action are being studied in many laboratories as more selective agonist and antagonist ligands become available. The situation has been complicated by the lack of highly selective (>500fold selectivity) agonists and antagonists, for the melanocortin receptors. We are beginning to find success.

Table 6. Biological Activities of Macrocyclic Lactam Truncated Analogues of α-Melanotropin at Human Melanocortin Receptors^a

		EC ₅₀ (nM)	(M)	
compd	hMC1R	hMC3R	hMC4R	
α-MSH	0.091	0.67	0.21	
[Nle ⁴ ,D-Phe ⁷]α-MSH	0.023	0.13	0.017	
Ac-Nle ⁴ -c[Asp ⁵ ,D-Phe ⁷ ,Lys ¹⁰]α-MSH(4-10)-NH ₂ (MT-II)	—	0.27	0.057	
Ac-Nle ⁴ -c[Asp ⁵ ,D-Nal(2') ⁷ ,Lys ¹⁰]α-MSH(4–10)-NH ₂ (SHU-9119)	0.036	$pA_2, 8.3$	pA ₂ , 9.3	
Ac-Nle ⁴ -c[Asp ⁵ ,D-Phe(pI) ⁷ ,Lys ¹⁰] α -MSH(4–10)-NH ₂	0.055	$pA_2, 8.3$	pA ₂ , 9.7	

^a Adapted from ref 133.

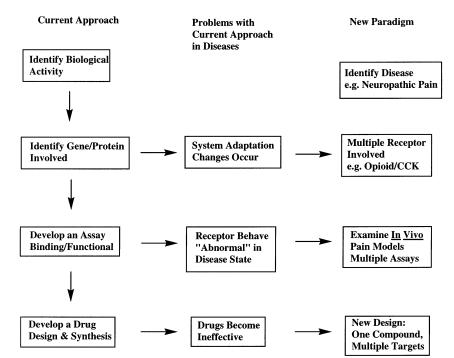


Figure 9. Drug design approaches.

An added complication in the development of drugs has been the broad spectrum of biological activities that involve melanotropin peptides, presumably via the various melanocortin receptors. Some examples from collaborations using our ligands MT-II and SHU-9119 and other more selective ligands will illustrate these exciting new areas of research. In the course of our investigations of the skin-darkening response of NDP- α -MSH¹⁴⁷⁻¹⁴⁹ (also see above) and MT-II, we discovered that MT-II could cause an erectile response.¹⁵⁰ Since we already had approval for human clinical investigations related to pigmentation, we sought approval to evaluate human volunteers with psychogenic erectile dysfunction. Studies were approved for peripheral administration, and in collaboration with Dr. Hunter Wessells, placebo controlled double blind experiments were accomplished in clinical trials with exceptionally promising results.^{150,151} Subsequent studies have shown that MT-II effects sexual desire and motivation in men^{152,153} and involves receptors in both the brain and the spinal column.¹⁵⁴ In other studies with biological collaborators using our specific melanotropin agonists and antagonist, it was shown that (1) cardiovascular control by α - and γ -MSH involves two distinct pathways,^{155,156} (2) that melanocortins have potent antipyretic effects, ^{157,158} (3) that melanocortin receptor antagonists such as SHU-9119 can prevent reflex natriuresis,¹⁵⁹ (4) that central melanocortins have a role in endotoxin-induced anorexia,¹⁶⁰ and (5) that melanocortins have differential

roles mediating leptin's central effects on feeding behavior and reproduction. In view of the central role of melanotropin peptides and melanocortin receptors in all of the above biological effects, and its additional effects on learning behavior, immune response, inflammation, and other critical behavioral and function bioactivities needed for life and survival, it is clear that there is still much to learn. The development of more selective ligands for the melanocortin receptors will lead to new insights into the importance of these receptors and ligands for the maintenance of good mental and physical health and in the treatment of a wide variety of diseases.

New Dimensions in Drug Design. The enormous progress being made in determining the complete genomes of many single cell and multiple cellular life, including man, provides new opportunities for the treatment of diseases and for designing drugs that actually address the changes inherent in the disease state rather than just the symptoms associated with a particular gene product (e.g., receptor) that may be involved. As shown in Figure 9, current drug design models often (generally) do not consider systems changes associated with disease and hence do not properly take into account that the receptors in disease states do not "behave" as in the normal healthy state (adaptation). Hence, a new paradigm briefly outlined in Figure 9 is required. We have initiated studies to face this new reality directly and to design molecules (ligands, poten-

Table 7.	Competitive I	Binding Assays	of Analogue De	sign with Binding	\mathbf{z} to δ and $\boldsymbol{\mu}$ Opi	oids and to CCK-A	and CCK-B Receptors

		opioid	opioid K _i (nM)		K _i (nM)
	compd	δ	μ	CCK-A	CCK-B
	H-Asp-Tyr-D-Phe-Gly-Trp-N-MeNle-Asp-Phe-NH ₂ (SNF-9002)	250	5200	3330	2.1
1	H-Tyr-D-Phe-Glu-Trp- <i>N</i> -MeNle-Asp-Phe-NH ₂	6.8	136	10000	2.1
2	H-Tyr-D-Nle-Gly-Trp-N-MeNle-Asp-Phe-NH2	1.6	25	3900	0.6
3	H-Tyr-Gly-Gly-Tip-N-MeNle-Asp-Phe-NH2	2000	610	870	1.3
4	H-Tyr-D-Phe-Gly-D-Trp-N-MeNle-Asp-Phe-NH2	0.5	5.7	1080	1.6
5	H-Tyr-D-Ala-Gly-D-Trp- <i>N</i> -MeNle-Asp-Phe-NH ₂	1.9	20	32	1.3

CCK Pharmacophore

H-Asp-Tyr-D-Phe-Gly-Trp-N-MeNle-Asp-Phe-NH₂

Opioid Pharmacophore

Figure 10. Design of ligands that act as agonists at opioid receptors and antagonists at CCK receptors based on SNF-9007.

tial drugs) that are designed specifically for the disease state. We have taken neuropathic pain, for which there are no currently effective drugs, as an example.^{161,162} Though we are in the early stages of development, we have made significant progress, enough to warrant a few paragraphs of discussion.

In various neuropathic pain states, it has been observed that enkephalins (opioids) and cholocystokinin (CCK) and their receptors are coexpressed in the brain and spinal column. Furthermore, it has been observed that CCK can act as an anti-opioid; that is, it can cause pain. From the standpoint of peptide drug design, a reasonable hypothesis would be to design a single ligand that could act as an agonist at μ and δ opioid receptors in the brain and spinal column and as an antagonist at CCKB and CCKA receptors in the spinal column. We therefore sought to design a single molecule with all of the above biological properties. From the standpoint of design, we considered our proposed conformational pharmacophores for opioid ligands^{70,71,73,163,164} and the CCK ligands.^{165,166} Interestingly, we had proposed^{166,167} that δ opioid and CCK bioactive conformations have similar conformational and topographical structural receptor requirements. Independently, in the course of developing highly potent and CCKB selective ligands, we had discovered a CCK-related compound H-Asp-Tyr-D-Phe-Gly-Trp-NMeNle-Asp-Phe-NH₂ (SNF-9007), which was a highly potent and selective CCKB ligand¹⁶⁸ but which also had weak δ opioid receptor binding affinity and in vitro and in vivo opioid biological activity. This led us to design molecules with overlapping opioid and CCK pharmacophore based on this lead structure (Figure 10). Our first goal was to convert the lead compound to a more potent opioid agonist with both δ and μ opioid receptor agonist activity. A few of the analogues we explored by removing the N-terminal Asp residue to give an N-terminal Tyr residue as is found in enkephalins, deltorphins, and other potent endogenous opioid ligands and by introducing Gly and other D-amino acids into what is now the 2-position of the des-Asp analogues are shown in Table 7. As can be seen, highly potent agonist analogues were obtained. It should be noted that to develop such analogues, at least eight in vitro bioassays are needed to evaluate the binding and biological activities of the analogues designed and synthesized (four binding assays, four second-messenger

assays). In this case, two additional classic functional in vitro assays, the GPI (μ) and MVD (δ) assays, also were used. We show only the binding assays here, but the other assays, though not shown, have been done and give results consistent with this discussion.

As can be seen in Table 7, a great improvement in the binding affinity and biological activity (not shown) is seen for the ligands (1, 2, and 3, Table 6) at the opioid receptor, though interestingly the Gly-2 analogue (3, Table 7) was quite inactive. Our next goal was to increase the CCK-A binding affinity (without losing the CCK-A affinity) and at the same time transform the CCK-A agonist activity to antagonist activity. This was done by substituting a D-Trp residue for the L-Trp residue (4 and 5, Table 7). Clearly compound 5 satisfies many of the criteria we set out in our initial design because 5 has good potency at all four receptors (Table 7) and has agonist activity at the δ and μ opioid receptors and antagonist activity at CCK receptors (data not shown). To stabilize the compound against biodegradation, we have designed and synthesized both cyclic disulfide and cyclic lactam analogues of the compounds in Table 7, and in preliminary studies, some of these compounds have potent and prolonged biological activity in neuropathic pain models.

We believe this approach is applicable to many other diseases associated with the central nervous system (CNS) and the peripheral endocrine system, as well as to cardiovascular diseases, diabetes, and cancer, and have research underway to further examine this hypothesis. Clearly there is a great need for new paradigms in drug discovery for disease states, and we expect that this approach to drug design will be of great importance in the future.

Future Perspectives

These are revolutionary times in the application of chemical principles to understanding life and living systems and to treating diseases in new ways. Though the human and other genome projects have generated and are continuing to generate huge amounts of data (information), it is clear that the scientific community has not yet developed an effective means for turning all of this information into general and useful knowledge so that a greater understanding of the physical and chemical principles that underlie all biological processes, including disease, can be obtained. In addition, current approaches in high-throughput screening and synthesis are providing tremendous amounts of data, but again, very modest new knowledge and understanding have been attained given the tremendous investment. It seems that there is a need for some contrary thinking ("outside the box") about our current paradigms.

(1) Though much is made of the apparent "complexities" in living systems, in fact, nature is enormously biased, and the real issue is the identification of the bias. From this perspective, it is not surprising that most "libraries" of non-peptide compounds being created by chemists give few, if any, good "hits" when confronted by a new biological protein or nucleic acid target. There is a critical need to develop a new view of "diversity" that is compatible with the enormous bias of living systems.

(2) Since nature has chosen peptides and proteins to do the bulk of the work, that is, work involving chemistry and structures needed for living systems, in conjunction with lipids, nucleic acids, sugars, and the rest of the periodic chart, it seems reasonable to ask why and how. We already know, as Ramachandran initially taught us, that the true "privileged" structures in nature are the α -helix, β -sheet, β -turn, and extended structures of proteins and peptides. These structures are convenient for interactions with nucleic acids, lipids, sugars, and other proteins and are wonderfully stable for supporting catalysis, information transduction, modulation of other structures, and convenient dynamic properties for scaffolding and other biological processes in time domains from nanoseconds to hours or days or years. A thorough understanding of the "simple" chemical and physical principles that make this possible and practical would be most helpful.

(3) The small differences in the genome and probably the proteome between human beings and our nearest evolutionary cousins such as apes and mice raise interesting questions about how new behavioral properties (e.g., cognition, language, music, culture, ethics, and other "human" qualities) arose. As demonstrated above, very minor changes in structure (a simple bond isomer, a torsion angle preference, etc.) for a key residue in a key ligand can lead to major changes in behavioral responses in an animal, including humans. The implications of this for drug design, especially as related to behavioral modifications, raise profound issues regarding our approach to such scientific studies, our responsibility to society, and the increasingly difficult task we will face in evaluating the potential adverse effects of our discoveries.

(4) As for new design principles and new chemistries related to peptide and peptidomimetic design and as for evaluation of their utility in biological systems, we are only at the beginning. Much more robust asymmetric synthetic methods are needed for the asymmetric synthesis of novel amino acids and amino acid mimetics that allow design in both conformational space and χ (topographical) space. Toward this end, in our most recent work using Ni(+2) chemistry, we have developed a simple scalable set of reactions that can lead to most of the possible chiral compounds that might be designed as derivatives or mimics of Glu, Gln, Asn, Asp, Pro, Cys, etc. with novel α , β , and γ substituents.^{169–177} In a similar manner, we are seeking also to develop mimics for the key secondary structures of peptides and proteins, i.e., α -helix, β -sheet, β -turn, and extended structures. Our most recent efforts are directed toward bicyclic heterocyclic systems that constrain putative β -turns both in $\varphi - \psi$ space and in χ space.^{177–182} The challenge of exploring all the available topographical space with 16, 32, or even more isomers is substantial, but certainly can be aided by combinatorial chemistry

such as the one-bead, one-compound method.¹⁸³. Equally challenging will be the design of non-peptide mimetics that can mimic the dynamic properties of proteins including interconversions from helix to turn structures, β -sheets to helical structures, etc.

This and many other challenges will make the coming years a continually exciting time to be a chemist, and I am looking forward with great joy to what we might learn in the coming years.

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Biography

Victor J. Hruby received his Ph.D. from Cornell University (A. T. Blomquist) and did a Postdoctoral with Vincent du Vigneaud. In 1968, he joined the Department of Chemistry, University of Arizona, where he is currently a Regents Professor of Chemistry. He was a recipient of Guggenheim and Senior Humboldt Fellowships, Pierce Award (now Merrifield Award), Javits Award, MERIT Award, and several other awards and honors. His major research interests include de novo design and synthesis of biologically active peptides and peptide mimetics, asymmetric synthesis, computation chemistry, combinatorial chemsity, conformation-biological activity relationships, design of ligands that affect pain, addictions, feeding behavior, sexual behavior, cancer, etc., the chemicalphysical basis for behavior, and structure-function of GPCRs. He is a strong proponent of interdisciplinary research and has collaborated extensively on the biological and medical implications of his research.

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