

ADVANCES IN POLYMER SCIENCE

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Conformation- Dependent Design of Sequences in Copolymers I

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Conformation-Dependent Design of Sequences in Copolymers I

Volume Editor: Alexei R. Khokhlov

With contributions by

P. G. Khalatur · A. R. Khokhlov · E. E. Makhaeva

I. M. Okhapkin · C. Wu · G. Zhang



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Preface

For a long time, chemical industry was focused on polymers mainly from the viewpoint of obtaining advanced construction materials, such as plastics, rubbers, fibers, polymer composites. These materials provided a number of important benefits, including improved strength and long-term durability, light weight, environmental resistance, and design flexibility. Starting from about the early 1980s, the main focus of interest shifted to functional polymers. Among these are superabsorbents, nanoporous rate-controlling membranes, reversible adhesives, electro-conductive polymers and nanowires. In the 1990s, the scientific and industrial polymer community started to discuss “smart” or “intellectual” polymer systems (e.g., soft manipulators, polymer systems for controlled drug release, field-responsive polymers, shape memory networks, and self-healing coatings); the meaning behind these terms is that simply the functions performed by polymers become more sophisticated and diverse. The line of research concentrating on polymer systems with more and more complex functions will certainly be in the mainstream of polymer science in the 21st century.

One of the ways to obtain new polymers for sophisticated functions is connected to the synthesis of novel building blocks – monomer species – where the required function is linked to the chemical structure of these blocks. However, the potential of this approach is rather limited because complicated and diverse functions of polymeric materials would then require a very complex structure of monomers, which normally means that the organic synthesis is more expensive and less robust. An alternative approach is to use known building blocks and to try to design a copolymer with a given sequence of these units. At the present time, there are many synthetic and theoretical strategies directed towards varying the chemical sequences of copolymers: from the variation of their composition and blocky structure to more sophisticated features like “tapered” and gradient structures. In a broad sense, most conventional chemical syntheses, especially polymer syntheses, can be regarded as *bottom-up nanotechnology* leading to the assembly of building blocks into the final macromolecules. Unfortunately, in most conventional polymerization processes, the physical control of assembly during the reactions is practically impossible.

With these difficulties in mind, it is instructive to look at main biological macromolecules – proteins, DNA, and RNA – that have precise and specific structures. These polymers in living systems are responsible for functions, which are incomparably more complex and diverse than the functions that we

normally discuss for synthetic copolymers. The molecular basis for this ability to perform sophisticated functions is associated with the primary sequences of biopolymers. In particular, the unique functions of proteins reflect their molecular structure, so that the sequence of amino acids in a protein defines its secondary and tertiary structure (fibrous versus globular, for example) as well as its function. Therefore, the study of biopolymers at the molecular level may point to new directions in materials design and construction – not just actually using biomolecules themselves to construct novel materials, but mimicking the specific primary sequences of biological polymers. Indeed, by taking this biomimetic route, significant and path-breaking achievements may be made by materials scientists and engineers. Thus, a promising path related to the design of new synthetic copolymers is to learn the rules of biologically driven controlled synthesis and directed assembly *in vivo* and eventually to apply these rules to the creation of engineered synthetic polymer systems from cheap and commonly available building blocks.

Original ideas connected with the biomimetic design of sequences in synthetic functional copolymers were formulated by us in 1998. They were based on the simple and well-known fact that the function of all globular proteins depends on two main factors: (1) they are globular and (2) they are soluble in aqueous medium. The combination of these two factors is nontrivial, e.g., for homopolymers and random copolymers the transition to globular conformation is usually accompanied by the precipitation of globules from the solution. Protein globules are soluble in water because of the special primary sequence: in the native conformation most of hydrophobic monomer units are in the core of the globule while hydrophilic monomer units form the envelope of this core. Keeping the biomimetic approach described above in mind, one can formulate the following problem: is it possible to design such a sequence of synthetic HP copolymer (copolymer consisting of monomer units of two types, H and P) that, in the most dense globular conformation, all hydrophobic H-units are in the core of this globule while the hydrophilic (polar) P-units form the envelope of this core? The corresponding bio-inspired two-letter HP copolymers generated on a computer were called *protein-like* copolymers. Of course, the degree of function complexity that we hope to achieve for designed copolymers, is much less than current biopolymers, but the behavior of copolymers with designed sequences can exhibit many useful features distinguishing them from the “scratch” (e.g., statistically random) sequences.

The approach formulated in 1998 is based on the assumption that a copolymer obtained under some preparation conditions is able to “remember” features of its original conformation from which it was built and to store the corresponding information in the resulting sequence. Therefore, this approach may be called *conformation-dependent sequence design*.

Most of the contributions collected in volumes 195 and 196 are dedicated to the review of the results obtained recently in this direction, i.e., dealing with the conformation-dependent sequence design of copolymers and the study of

their properties. The contributions collected present the up-to-date research results on most of the topics related to this approach. Surface and interfacial phenomena are also major topics of these volumes. The individual chapters are diverse in purpose and in style. Some of them paint the field in broad, conceptual strokes, others in fine methodical detail. Some present information, others arguments or interpretation. Some summarize past activities, others point to future potential.

Volume 195 begins with a chapter by Khalatur and Khokhlov that gives a survey of the simulation methods as applied to the design of nontrivial sequences in synthetic copolymers aimed to achieve desired functional properties. Several new synthetic strategies allowing for the synthesis of copolymers with a broad variation of their sequence distributions are reported. Synthetic copolymers exhibiting long-range statistical correlations, large-scale compositional heterogeneities, and physical complexity are the focal point of this review. Roughly speaking, the physical complexity of a sequence is understood as the amount of information that is stored in that sequence about a particular environment.

Zhang and Wu review the experimental results on the folding of different hydrophilically or hydrophobically modified copolymers in extremely dilute solutions. The focus is on the formation of stable and soluble mesoglobules made of several amphiphilic copolymers and on the folding of single copolymers – both linear and grafted – into core-shell nanostructures that have various applications. All these features are directly related to the unique chemical sequence of the copolymer chains under discussion. The authors discuss the insights that can be obtained by the analysis of the data of laser light scattering and the use of this method as a potential probe of fine molecular structures, including the so-called “molten” globule state. Emphasis is put on the most recent achievements, although important historical contributions are also mentioned.

A concept of amphiphilicity, as applied to single monomer units of designed water-soluble polymers, is presented in the third chapter by Okhapkin, Makhaeva, and Khokhlov. The concept is relevant to biomolecular structures and assemblies in aqueous solution. The authors consider the substantial body of information obtained experimentally and theoretically on surface molecular chemical structures, including those that are prospective for surface catalysis. Unusual conformational behaviors of single amphiphilic polymers recently observed in simulations are also discussed in detail.

The problems related to the colloidal stability of amphiphilic polymers in water are reviewed by Aseyev, Tenhu, and Winnik in the first chapter of volume 196. The focus is on the derivatives of thermally responsive smart macromolecules – both on copolymers and homopolymers – which are present in a solution as stable micelles potentially having various applications.

One of the promising synthetic strategies of conformation-dependent sequence design is based on direct copolymerization under unusual conditions.

This strategy was first realized by Lozinsky et al., who studied the redox-initiated free-radical copolymerization of thermosensitive N-vinylcaprolactam with hydrophilic N-vinylimidazole at different temperatures, as well as by Chi Wu and coworkers. Lozinsky presents an extensive review of the experimental approaches, both already described in the literature and potential new ones, to chemical synthesis of protein-like copolymers capable of forming core-shell nanostructures in a solution.

Continuing along the chemical theme, Kuchanov and Khokhlov review comprehensively the diffusion-controlled polymer-analogous reactions and free-radical copolymerization. The field of polymer chemistry today is distinguished by its depth of mathematical and quantitative rigor in the pursuit of a wide array of challenging new subjects. These ingredients are present in full in this chapter, where the quantitative theory of solution and interphase free-radical copolymerization is discussed from the viewpoint of statistical chemistry and statistical physics of polymers. It is shown that the interaction of these two disciplines has significant impact on the development of new synthetic strategies and technologies in polymer chemistry, including those related to the conformation-dependent design of nontrivial copolymer sequences.

The final short historical review by Grosberg and Khokhlov is devoted exclusively to the discussion of fundamental ideas initially formulated in polymer physics by the outstanding Russian scientist I.M. Lifshitz and especially to today's development of his ideas. Major attention is focused on the statistical theory of heteropolymers covering such areas as protein folding and the sequence design both of protein macromolecules and of synthetic copolymers mimicking some protein properties. In particular, the ideas of sequence design in functional copolymers were originated within the school of Lifshitz; thus, in volume 196, it seems natural to give a review of the achievements along the lines of all major ideas initially formulated by Lifshitz in the field of polymer science.

All of the selected contributions that are present in these special volumes are good representatives for manifesting the importance of the concepts based on conformation-dependent sequence design. It has been our intention to provide the scientific and industrial polymer community with a comprehensive view of the current state of knowledge on designed polymers. Both volumes attempt to review what is currently known about these polymers in terms of their synthesis, chemical and physical properties, and applications. We will feel the volumes have been successful if some of the chapters presented here stimulate readers to become interested in and solve specific problems in this rapidly developing field of research.

Moscow, November 2005

Alexei R. Khokhlov

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Computer-Aided Conformation-Dependent Design of Copolymer Sequences

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Abstract A survey is given of the simulation methods as applied to the design of nontrivial sequences in synthetic copolymers aimed at achieving desired functional properties. We consider a recently developed approach, called conformation-dependent sequence design (CDSD), which is based on the assumption that a copolymer obtained under certain preparation conditions is able to “remember” features of the original conformation in which it was built and to store the corresponding information in the resulting sequence. The emphasis is on copolymer sequences exhibiting large-scale compositional heterogeneities and long-range statistical correlations between monomer units. Several new synthetic strategies and polymerization processes that allow synthesis of copolymers with a broad variation of their sequence distributions are reported. We demonstrate that the CDSD polymer-analogous transformation is a versatile approach allowing various functional copolymers to be obtained. Another synthetic strategy is the CDSD step growth copolymerization which is carried out under special conditions. It includes the intrinsic possibilities of exploiting the heterogeneities of the reaction system to control the chemical microstructure of the synthesized copolymers, making possible new paradigms for synthesis and production of polymeric materials. In both cases, we try to show how the preparation conditions dictate copolymer sequences. Also, we discuss advances that have recently been achieved in the computer simulation and theoretical understanding of designed copolymers in solution and in bulk. The focus is on amphiphilic protein-like copolymers and on hydrophobic polyelectrolytes. Here, we demonstrate how copolymer sequence dictates structure and properties.

Keywords Charged heteropolymers · Copolymers · Phase behavior · Polyamphiphiles · Sequence design · Simulation · Solution properties

Abbreviations

A	amphiphilic group (monomer, monomeric unit)
α^2	chain expansion factor
$[A_M]$	mole fraction of intermolecular aggregates of size M
ATC	adsorption-tuned copolymer
ATRP	atom transfer radical polymerization
b	bond length
C	symmetric matrix of direct correlation functions
χ	Flory-Huggins interaction parameter
$\tilde{\chi}$	effective interaction parameter
C_α^0	bulk concentration of monomer species α
$C_\alpha(\mathbf{r})$	instant local concentration of monomer species α
$C_\alpha(z)$	equilibrium concentration profile of monomer species α
$c(r)$	direct site-site pair correlation function

CRP	controlled radical polymerization
DCTT	degenerative chain transfer technique
CDSD	conformation-dependent sequence design
DF	density functional
DFA	detrended fluctuation analysis
ΔG	change in association free energy
D_L	block length dispersion
D_λ	dispersion within a sliding window of length λ
$\Delta\mu_s$	solvation free energy
$\Delta(q)$	determinant of matrix integral equation
ΔT^*	change in transition temperature
ε	energy parameter
\mathbf{E}	unit diagonal matrix
ε^*	critical adsorption energy
ε_{PP}	attraction energy between hydrophilic (polar) segments
f	fraction of charged monomers
Φ	volume fraction of macromolecules
φ_α	average fraction of monomer species α in copolymer chain
ϕ_α	volume fraction of monomer species α
$\varphi_\alpha^{(i)}$	intrachain composition profile of monomer species α
$\phi_\alpha(\mathbf{r})$	volume fraction field of monomer species α
$F_D(\lambda)$	detrended local fluctuations within a window of length λ
$f(\lambda)$	block length distribution function
F_s	sequence free energy
γ	solvation parameter
h	Shannon's entropy
H	hydrophobic monomer (monomeric unit)
\mathbf{H}	symmetric matrix of total site-site correlation functions
HA model	hydrophobic-amphiphilic (side-chain) model
HPE	hydrophobic polyelectrolyte
HP model	hydrophobic-hydrophilic(polar) model
$h(r)$	total site-site pair correlation function
JS	Jensen-Shannon divergence measure
K	association equilibrium constant
k_B	Boltzmann constant
ℓ	block length
L	average block length
λ	length of sliding window along copolymer sequence
L_H	average length of hydrophobic blocks
L_P	average length of hydrophilic (polar) blocks
LRC	long-range correlation
m	average number of copolymer chains per aggregate
MAST	macrophase separation transition
MFPT	mean first passage time
MIST	microphase separation transition
N	total chain length, number of repeat units
N_α	number of repeat units of type α ($\alpha = A, B$) in the chain
NIPA	poly(<i>N</i> -isopropylacrylamide)
n_j	number of crosslinks
N_τ	current chain length