Title: NUCLEATION AND CRYSTALLIZATION OF POLYMERS

Abstract: Molecular modeling of specific nucleation and crystallization mechanisms of polymers to allow the prediction of whether a specific additive molecule will act as a nucleating agent for a specific polymer, and to allow the prediction of the specific polymer that will be formed by a given nucleation and crystallization mechanism.
NUCLEATION AND CRYSTALLIZATION OF POLYMERS

BACKGROUND OF THE INVENTION

1. Technical Field.

This invention relates generally to the field of nucleation and crystallization mechanisms of polymers and more specifically to the field of molecular modeling of specific nucleation and crystallization mechanisms of polymers to allow for the design and development of molecules that will act as effective nucleators or clarifiers in polymers.

2. Prior Art.

A crystal is a three dimensional arrangement of atoms or molecules with an orientation and positional order. In ionic crystals and molecular crystals, atoms and molecules are arranged in three-dimensional order. In polymer crystals, the polymer chains, which have one-dimensional order in a specific conformation, are arranged in a two-dimensional pattern. Due to statistical mechanical requirements, a whole polymer chain cannot form a single straight stem. The straight stems are limited to a certain length depending on the crystallization temperature. Therefore, these stems fold and reenter into a lattice. This reentry can be adjacent to the previous stem called adjacent reentry or at a random lattice point called random reentry.

The perfectly ordered portion of the polymer is crystalline and the folded surface is amorphous in nature and hence polymers are always semi-crystalline. The crystalline portion may occur either in isolation or as an aggregate with other similar crystals leading to the formation of mats or bundles or spherulites. The first step in the formation of spherulites in which a straight stem of a polymer chain called a nucleus forms from the random coil is called nucleation. The rest of the process that includes lamellae growth and spherulite formation is cumulatively called crystal growth. In general, polymer single crystals take the form of thin lamellae, which are large in two dimensions but are bounded in the third dimension by the folds that constitute the basal plane. Typically all the lamellae within one spherulite originate from a single point. As the spherulite grows, the lamellae get
farther and farther apart. When the distance between two lamellae reaches a critical value, they branch nor-crystallographically. Since the growth process is isotropic, the spherulites have a circular shape in 2D and spherical shape in 3D for solidification in a uniform thermal field.

Depending on the processing condition, three major types of nucleation can occur: homogeneous nucleation (spontaneous nucleation), self-nucleation (seeded nucleation), and heterogeneous nucleation. The most important type of nucleation in polymers is heterogeneous nucleation. Heterogeneous nucleation occurs when a foreign substance present in the melt aids the polymer nucleation process, resulting in nucleation occurring at a higher supercooling than seen in homogeneous nucleation. These substances are called as nucleating agents. The polymer nucleus is formed on the surface of heterogeneous object and then the crystal grows concurrently in different directions radiating from the central heterogeneous object. This process occurs simultaneously in numerous sites resulting in spherulites of uniform shape. Simultaneous nucleation and growth is called athermal nucleation.

Athermal nucleation is where all the crystals grow at the same time. In thermal nucleation new crystals start growing throughout the process of crystallization. Heterogeneous nucleation may be either athermal or thermal. Since the number of heterogeneous nuclei is limited, thermal nucleation of heterogeneous origin must level off after all nuclei are exhausted. In modeling crystallization kinetics, thermal and athermal nucleation are dealt with differently.

There are several types of nucleating agents used in polymer crystallization that evolved over decades. The nucleating agents are expected to have certain physical and chemical properties. Nucleating agents are broadly classified into two types: dispersion type, where the nucleating agent is dispersed in the molten polymer and remains in the solid state; and dissolution type, where the nucleating agent is dissolved in the polymer at the melting temperature.

Dibenzylidene sorbitol (DBS), an important nucleator, was initially used as a gelling agent for organic liquids. DBS based compounds are dissolution type
nucleators that must be melted and uniformly dissolved in the resin at a temperature higher than the melting point. DBS can be used to improve transparency in polyolefin plastics. Two modifications of DBS improve its performance and the properties of the resultant polymer. The first modification is to change the structure of DBS itself, while the second is to couple DBS with some other additive.

Most of the structural changes for DBS are made on the benzylidene group of the DBS molecule by substituting various chemical groups and ions at one or more positions in the benzene ring. For example, adding an alkyl group improves bleeding resistance, adding a methyl or ethyl substitution on the para or ortho position improves resistance to shrinkage, adding a chlorine and bromine atom improves transparency as well as physical and chemical properties, adding fluorine 3,3'-difluoro or 3,4,3',4'-tetra fluorodibenzylidene sorbitol improves resistance to shrinkage and heat deterioration without loss of mechanical strength, adding sulfur improves resistance to oxidative degradation, and adding di- substituted aryclidene or hetero aryclidene improves the transparency and crystallization response of polyolefins.

Secondary additives also modify the performance of DBS. For example, adding hindered amine improves radiation resistance, adding cyclodextrin improves odor non-emitting property, adding tri-allyl trimellitate improves radiation resistance, adding hindered amine, alkyl phosphite hindered phenolic antioxidant improves resistance to discoloration, adding higher fatty acid and its saponification product in water improves bleeding prevention, adding peroxide agent and linear low density polyethylene improves multi dimensional physical properties, and adding diphenylene diphosphite improves melting point depression.

Crystallization of polymers using nucleators provides a number of advantages including reduced cycle time of injection molding, increased elasticity modulus, and haze reduction. Techniques for studying crystallization kinetics are still developing. Two parallel themes describing the aspects of crystallization of polymers have been developed. One uses a thermodynamic approach and provides a statistical description of morphology that is related to polymer
crystallization. The other considers a kinetic description of the development of lamellar structures that are basic to nucleation, growth and stability in the solid state. The modeling of the solidification process and the prediction of the microstructure are difficult because of the different length scales present.

Molecular movement caused by the intermolecular interactions is the starting point of transition. The detailed mechanisms of polymer crystallization and the significance of chain connectivity or entanglement are very difficult to be elucidating by experiment only. Particularly when the changes occur in molecular level, there are no experimental techniques to directly identify the changes. Hence there is complete reliance on simulations of molecular motions based on classical mechanical of the theory. Computer modeling enables the visualization of the shape and motion of polymer molecules individually, thus allowing evaluation of much more detailed information on the static and dynamic properties of the system than any experimental measurements. Increasing computer power has led the computer simulations, especially Molecular Dynamics (MD) simulation and Monte Carlo (MC) techniques, to be recognized as powerful and promising tools for investigation in this field to complement theoretical and experimental approaches.

Thus, it can be seen that a novel approach for determining how the nucleation mechanism operates in the crystallization of polymers such that the nucleation mechanism can be modeled and the crystallization for a specific reaction can be simulated is desirable. Once the nucleation mechanism is modeled and the crystallization reaction simulated, one will be able to evaluate the use of specific molecules as nucleators and/or design molecules with specific properties necessary to control nucleation in polymers. It is to this need that the present invention is directed.

**BRIEF SUMMARY OF THE INVENTION**

Many of the properties of polymers are dependent on the nucleation and crystallization mechanisms that form the polymers. For example, the transparency of certain polymers is dependent on the size of the spherulites formed during
nucleation. Polymer transparency is a property of interest in the medical and food storage industries as transparent polymers provide a level of protection for items contained in the polymer while still allowing one to view the item through the transparent polymer.

The present invention is a molecular modeling method for predicting and determining the nucleating mechanisms of polymers, for determining whether a specific molecule will act as an effective nucleator, and for screening and designing molecules to be nucleating additives. Isotactic polypropylene (iPP) was used as the base example polymer because nucleators have been developed and are well known for iPP, and there is a body of data to which the present invention can be compared. A number of nucleating agents were used as the base example nucleating agents, including conventional benzoates and sorbitol based nucleators, which are known to work in iPP and allow for a comparison with the present invention.

To perform the molecular modeling of the present invention, first, one selects a polymer molecule on which the modeling will take place. The polymer molecule is built on the computer using conventional molecule modeling techniques. One generates the coordinates of the individual atoms of the selected polymer molecule preferably to minimize the energy needed to relax the structure from the typical twisted structure to a more linear structure.

Second, one selects and builds on the computer, again using conventional molecule modeling techniques, an additive molecule for investigation as to whether and how the additive molecule will function as an effective nucleating agent for the selected polymer. The selected polymer and the selected additive molecule can be cloned, generally on the computer, to generate the required or desired number of polymer chains and additive molecules necessary or desired for the simulation.

The first two steps can be reversed if one desires to investigate a particular additive molecule with a series of different polymers.
Third, one builds an appropriately sized three-dimensional (3-D) periodic cell or box in which the molecular modeling will occur. In general, the larger the cell, the better the simulation. However, larger cells require more time to conduct the simulation, so a balance between cell size and simulation time must be made. Cell size can be changed by changing either the length or the number of the polymer chains.

Fourth, one conducts the simulation and analyzes the resulting polymer. It is not necessary or practical to conduct the simulation to equilibrium, but only to a point where the nature of the resulting polymer can be determined. By analyzing the geometry of the resulting polymer, one can determine whether the selected additive molecule is an effective nucleating agent and/or what the resulting polymer will be when using a selected additive molecule with a selected polymer.

It is an object of the present invention to provide a molecular modeling method for determining whether a selected additive molecule will be an effective nucleating agent for a selected polymer.

It is another object of the present invention to provide a molecular modeling method for designing an additive molecule that will be an effective nucleating agent for a selected polymer.

It is another object of the present invention to provide a molecular modeling method for screening additive molecules to determine which if any of the additive molecules will be an effective nucleating agent for a selected polymer.

It is another object of the present invention to provide a molecular modeling method for determining the extent to which an additive molecule will act as a nucleating agent for a selected polymer.

It is another object of the present invention to provide a molecular modeling method for determining for which polymers a selected additive molecule will act as a nucleating agent.

It is another object of the present invention to provide a molecular modeling method for determining whether a selected additive molecule will act as a nucleating agent for polymers.
It is another object of the present invention to provide a molecular modeling method for determining what polymers will result from the use of a selected additive molecule as a nucleating agent.

These objects, and other objects, features and advantages of the present invention, will become more apparent to those of ordinary skill in the relevant art when the following detailed description of the preferred embodiments is read in conjunction with the attached figures.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1 illustrates the crystal structure of isotactic polypropylene.

FIG. 2 illustrates a single strand of isotactic polypropylene removed from the crystal structure.

FIG. 3 illustrates isotactic polypropylene in the all trans conformation.

FIG. 4 illustrates isotactic polypropylene as seen in the alpha crystal.

FIG. 5 illustrates the left-handed helix conformation of an isotactic polypropylene crystal.

FIG. 6 illustrates the right-handed helix conformation of an isotactic polypropylene crystal.

FIG. 7 illustrates the two-dimensional energy map of an isotactic polypropylene segment.

FIG. 8 illustrates the three-dimension energy map of an isotactic polypropylene segment.

FIG. 9 shows the energy profile resulting from a typical simulation of the present invention.

FIG. 10 shows the temperature profile resulting from a typical simulation of the present invention.

FIG. 11 shows the volume profile resulting from a typical simulation of the present invention.

FIG. 12 shows the pressure profile resulting from a typical simulation of the present invention.
FIG. 13 shows the effect of chain length on the orientation of the backbone crystal over time resulting from a typical simulation of the present invention.

FIG. 14 shows the normalized results shown in FIG. 13.

FIG. 15 illustrates the radial distribution function of crystals, with FIG. 15(a) illustrating a face-centered crystal and FIG. 15(b) illustrating a simple cubic lattice.

FIG. 16 illustrates the radial distribution function for liquids and gases.

FIG. 17 illustrates the radial distribution function of isotactic polypropylene as a function of time from a typical simulation of the present invention.

FIG. 18 illustrates the radial distribution function of isotactic polypropylene as a function of time for various additives from a typical simulation of the present invention.

FIG. 19 illustrates the amorphous box structure of isotactic polypropylene before the simulation of the present invention.

FIG. 20 illustrates the amorphous box structure of isotactic polypropylene after 100 picoseconds of simulation of the present invention.

FIG. 21 is a graph of the time versus number of oriented backbone carbon atoms for various additives used in orienting the backbone using the simulation of the present invention.

FIG. 22 is a graph of the time versus number of oriented backbone carbon atoms showing the chain length dependence of the polymer using the simulation of the present invention.

**DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS**

In spite of tremendous growth and continuous innovation, prior experimental techniques are not capable of investigating molecular level interactions in polymers. The detailed mechanisms of polymer crystallization and the significance of chain connectivity or entanglement are difficult to elucidate by experiment only. One procedure that can aid in understanding these complete mechanisms is molecular modeling simulations. Such simulations, which now typically are carried out using computer simulation, provides a direct route from the microscopic details of a
system (the masses of the atoms, the interactions between them, molecular geometry etc.) to macroscopic properties of experimental interest (the equation of state, transport coefficients, structural order parameters, and so on). In the atomic approach the chemical bonds are simply treated as inter atomic potential energy terms.

A. Theoretical Background.

Molecular simulations are classified into three main categories: Molecular mechanics, Molecular Dynamics and Monte Carlo simulations.

Molecular mechanics (MM) (also called force field calculations) normally are used to determine the molecular structures, conformational energies, and other molecular properties using concepts from classical mechanics. Electrons are not explicitly included in the MM method. MM alternatively can be thought of as a ball and spring model of molecules with classical forces between the atoms. These forces are described by potential energy functions of structural features such as bond lengths, bond angles, and torsional angles. The potential energy functions contain a number of parameters, which are determined by fitting computed properties to experimental ones or, in some methods, to properties calculated by *ab initio* quantum chemical methods. A force field is one, which consists of a set potential energy functions and a set of parameters for these functions. The total energy of the molecule $E_{\text{tot}}$ in a given geometry is assumed to be the sum of different energy contributions as shown in the following equation

$$E_{\text{tot}} = E_s + E_b + E_{\text{tor}} + E_{\text{vdw}} + E_{\text{elec}} + E_{\text{other}}$$

where $E_s$ is the energy contributions due to bond stretching/compression, $E_b$ is the energy contributions due to angle bending, $E_{\text{tor}}$ is the energy contribution due to torsional interactions, and $E_{\text{vdw}}$ is the energy term due to van der Waals interactions.

For molecules with polar functional groups, an energy contribution due to electrostatic interactions, $E_{\text{elec}}$, should be included. Hydrogen bonds and cross terms are included in $E_{\text{other}}$ energy term. Description of these energy terms varies with the force fields selected. $E_{\text{tot}}$ is the difference in energy between the actual
conformation of the molecule and a hypothetical structure in which all the structural features (bond lengths, bond angles, etc.) have ideal values equal to their reference values. $E_{\text{tot}}$ generally is arrived at by comparing the differences between the calculated $E_{\text{tot}}$ of different conformations of the same molecule or different stereochemical arrangements. Such energy differences correspond closely to conformational enthalpies.

Energy minimization (geometry optimization) is an integral part of any molecular mechanics method. This minimization procedure mathematically repositions the atoms and calculates the energy until a minimum energy is reached.

Minimization of a molecule is done in two steps. First, an equation describing the energy of the system as a function of its coordinates is defined and evaluated for a given conformation. Next, the conformation is adjusted to lower the value of the function value. A minimum value may be found after several adjustments depending on the nature of the algorithm and the size of the molecule. Minimization algorithms include steepest descents, conjugate gradient and Newton-Raphson method.

When two molecules are present in the vicinity of each other the effect of inter-molecular forces (attractive and repulsive) are pronounced. Hence MM also can be used to study the interaction between isolated molecules. Isolation means that the pressure and temperature effects are ignored in the calculation. The intermolecular and intra-molecular interactions are calculated and the minimum interaction energy is determined by systematically repositioning one or all of the atoms of the molecules under investigation. That is, to determine the interaction energy between molecule A and polymer B, the position of the atoms in the backbone of B is fixed such that the backbone torsions are not varied. Molecule A is moved along the length of the polymer and rotated around the polymer axis to determine the minimum energy, radial and longitudinal positions. The new position of A is either predetermined or is a result of minimization procedure and has no implication on the force between A and B.
The one to one interactions and the structural requirements for nucleators can be studied by using molecular mechanics. While using molecular dynamics, it is more difficult to visualize the molecular nature of a specific additive and its surroundings because the presence of numerous atoms and their periodic 3-D images complicate the calculations. In molecular mechanics the polymer and additives can be isolated and the interactions separately studied.

Molecular dynamics (MD) simulation computes the motion of individual molecules in models of solids, liquids and gases. In contrast to MM where atomic positions are predetermined, the positions of every atom in molecular dynamics are determined by solving the classical equation of motion, which relates the relative displacement of the atoms to the forces acting on the atom. Unlike quantum mechanics which is probabilistic, classical mechanics is completely deterministic. Given the exact positions and velocities of all particles at a given time, along with the force function $\vec{F}_i$, one can use Newton's Equation of motion to calculate the future positions and velocities of all particles at any other time.

$$F_i = m \vec{r}_i$$

where $m$ is the mass of the molecule, and $\vec{r}_i$ is the vector location of the molecule with respect to a laboratory-fixed set of coordinate axes.

The relationship of the force function to potential energy is given as below:

$$\vec{F}_i = -\nabla_i V(\vec{r}_i)$$

where $V(\vec{r})$ represents the potential energy of the system as a function of the positions of all $N$ particles. In three dimensions, $\vec{r}_i$ is the vector specifying the position of $i^{th}$ atom. The coordinates and velocities for a complete dynamics run are called the trajectory. Because trajectories are sensitive to initial conditions, the same simulation run with a different simulation engine or on a different computer may not produce identical trajectories.

A standard method of solving an ordinary differential equation numerically is the finite-difference method. Given the initial coordinates and velocities and other
dynamic information at time $t$, the positions and velocities at time $t + \Delta t$ are calculated. The time step $\Delta t$ depends on the integration method as well as the system itself. The main limitation imposed by the system is the highest frequency motion that must be considered. A period of vibration must be split into at least 8-10 segments for molecular systems to satisfy the Verlet assumption that the velocity and accelerations are constant over the time step used. The highest vibrational frequency is that of C-H bond stretching, whose period is on the order of $10^{-14}$ seconds (10 fs). The integration time step should therefore be about 0.5-1 fs. There are different kinds of integrators available, including Verlet leapfrog integrator, Verlet velocity integrator, Adams-Bashforth-Moulton fourth order (predictor corrector method) integrator, and Runge-Kutta-4 integrator. The default Verlet leapfrog integrator was used in this embodiment.

The simulation of this invention is an initial value problem, where the initial positions and velocities are to be assigned to each of the atomic units. The initial atomic positions are generated by one of the molecular modeling software builders. The initial velocities are generated so as to produce a Maxwell-Boltzmann distribution at the desired temperature, and the distribution does not remain constant as the simulation continues.

The major applications of molecular dynamics are to perform conformational searches, to generate statistical ensembles and to study the motions of molecules. They are often used to relax structures, relieve local strain, and refine models of macro molecular structure. Dynamics simulations are useful in studies of the time evolution of a variety of systems at nonzero temperatures, for example, biological molecules, polymers, or catalytic materials, in a variety of states, for example, crystals, aqueous solutions, or in the gas phase. In this embodiment, the motions of molecules at constant temperature and pressure were studied.

Many statistical ensembles are available such as constant temperature constant volume (NVT), constant temperature constant pressure (NPT), constant energy constant volume (NVE) and constant pressure constant enthalpy (NPH). To
study the transition in this embodiment, the temperature and pressure of simulation must remain constant and NPT simulation is used.

In Monte Carlo (MC) simulations, ensembles of configurations of a system are generated using a Metropolis importance sampling scheme. Each configuration is sampled with the Boltzmann probability for the desired temperature of the system. From this set of configurations, or ensemble, average properties can be evaluated that depend on the coordinates only. In the limit of infinitely long ensembles, the ensemble average is equal to the expectation value for the property,

\[ \xi(\Psi) = \lim_{N_{MC} \to \infty} \frac{1}{N_{MC}} \sum_{i=1}^{N_{MC}} \Psi_i \]

where \( N_{MC} \) is the number of Monte Carlo steps. The size of an ensemble is necessarily finite in practical calculations, and the expectation value \( \xi(\Psi) \) of some property \( \Psi(q^N) \) is approximated by the calculated ensemble average \( \langle \Psi(q^N) \rangle \).

Because configuration space is non-deterministically sampled in Monte Carlo simulations, dynamic properties are not directly available from these simulations.

The force field contains the necessary building blocks for the energy and force calculations. A list of atoms, atomic charges and atom typing rules, functional forms of the components of energy expression and parameters of the function terms comprises the basic set. Certain force fields also include rules to generate parameters and the functional forms that have not been explicitly defined. The goal of a force field is to describe entire class of molecules with reasonable accuracy.

The force field interpolates and extrapolates from the empirical data of the small set of molecules used to parameterize the force field to a large set of related molecules and structures. The results of any mechanics or dynamics calculation depend on the force field. The quality of the description of both the system and the particular properties being analyzed is of greatest importance. Several force fields have been developed and are broadly classified into four categories: second generation force fields capable of predicting many properties; force fields applicable to a broad range of the periodic table; classical, first generation force fields mainly applicable to
biochemistry; and special-purpose force fields that are narrowly applicable to particular applications or type of molecules, such as force fields for glass, zeolites and polyvinylidene fluoride. Dreiding is among the best available force fields for the calculations of the present invention. CFF and PCFF force fields also are acceptable and could give better results.

There are several commercial software packages available to performing molecular modeling for different platforms ranging from desktop computers to Super computers. Cerius² is a comprehensive molecular modeling software consisting of several simple modules coupled with a user-friendly graphical interface and was used in this embodiment. Cerius² is developed by MSI (Molecular Simulation Inc.) for SGI and IBM platforms.

In the view of usage and power, MD and MM vary in several aspects. MM determines intermolecular and intra molecular interactions and helps in identifying the structural requirements of a nucleator, uses isolated calculations and hence easy to understand the results, calculates energies, analyzes results based on energy of interaction, and has a faster computation speed. MD determines changes with respect to time, simulates the crystallization process in the presence of additives, includes environmental conditions like pressure and temperature with 3-D periodic boundary conditions, provides results that are quite complicate to understand, calculates forces and velocity and position of the atoms in molecules, analyzes results based on geometric measurements such as distances and torsion angles, and is time consuming.

B. General Techniques For The Invention.

The preferred embodiment of this invention is to provide a simulation for the mechanism by which polymers are nucleated. A representative but not exclusive mechanism for developing the simulation is the mechanism by which DBS nucleates PP. Experimental evidence shows that in spite of the close resemblance of sorbitol to DBS, sorbitol does not nucleate PP at all, where as DBS nucleates PP very well. The PP-DBS and PP-Sorbitol systems were studied in an attempt to identify the structural differences between DBS and sorbitol that helps PP to nucleate.
Demonstrating the ability of MD simulation to reproduce the experimental results and identifying the molecular aspect of DBS crucial in nucleating DBS were the two important objectives. The additives taken into consideration for the MD studies include dibenzylidene sorbitol (MW 358.392), d-sorbitol (MW 182.174), dinaphthalidene sorbitol (MW 458.412), s-trinaphthalidene sorbitol (MW 596.681), r-trinaphthalidene sorbitol (MW 596.681), dimethyldibenzylidene sorbitol (MW 414.498), dinitro dibenzylidene sorbitol (MW 448.384), and n-alkyldibenzylidene sorbitol (MW 727.036). These additives are similar to DBS but produce varying effects on PP nucleation.

Molecular mechanics studies can be employed to understand the intermolecular and intra-molecular interaction energies. The important molecular event during crystallization is the formation of proper conformation. At high temperature the total energy of the system will be high such that the gradient of energies of different conformation will be negligible. This condition enables the polymer to form any conformation at a specific instance, which keeps changing. However, at low temperature the total energy is substantially lowered and the gradient between the low energy and the high energy conformation is prominent. MM calculations often are carried out ignoring the temperature. That is, temperature is not a factor in these calculations. Thus the molecular mechanical calculation results are assumed to be the results at 0K or the frozen state of the polymer. However the interaction energy calculations calculated through MM reveals the preferred orientation/conformation of the molecules of interest.

FIG. 1 shows the ball and stick representation of iPP crystal structure and FIG. 2 shows an iPP strand stripped out of the crystal. FIG. 3 shows a segment of iPP chain in all trans conformation. If viewed with head in the bottom and tail in the top, all the methyl groups lie on the right side of the backbone. The same chain with the conformation as seen in alpha crystal is shown in FIG. 4. The two torsional angles defined as $\chi_1$ (C-C$_\alpha$-C-C$_\alpha$) and $\chi_2$ (C$_\alpha$-C-C$_\alpha$-C) are $\pm 180$ and $-60$ respectively. This structure is same as the one seen in FIG. 3 only the backbone conformation is changed and generates a right-handed helix. When the same chain
is viewed from the other end, all the methyl groups will lie on the left side of the backbone and will generate a left handed helix. As seen in FIG. 1, the crystal structure of iPP has both right-handed and left-handed helices. Knowledge of this would be a key to analyze the results of dynamic simulation. The torsion angle $\chi_1$ when measured from either side will give same value of $\pm 180$. $\chi_2$ when measured from head to tail gives $-60$, and when measured from tail to head gives $60$. Thus, for a particular chain in the crystal, the torsion angles measured will be equal to $-60$ or $60$ depending on the numbering scheme. FIG. 5 shows the end projection of the left-handed helix, and FIG. 6 shows the end projection of the right-handed helix.

As the torsional angles $\chi_1$ and $\chi_2$ are important in the formation of specific conformation for crystal structure, the energy map of iPP as a function of $\chi_1$ and $\chi_2$ is generated. For the ease of calculation, a chain with only five backbone carbon atoms similar to pentane (2 propylene units) is chosen, instead of a lengthy polymer. The instant calculation was done using the conformer search module of Cerius$^2$ molecular modeling software with Grid Search algorithm, and can be done with the equivalent module of other molecular modeling software packages. To get a smooth contour the grid size was chosen to be 5 degrees and the energy was calculated between $-180$ and $180$. The energy was minimized at every stage, keeping the torsional angles rigid. FIG. 7 shows the calculated energy distribution in a 2-D pattern. As seen from the energy map, the lowest energy and most probable conformations occur with the values of $\chi_1$ and $\chi_2$ to be $180$ and $-60$ respectively. FIG. 8 represents the same energy map in a 3-D pattern. The gradients of energy can be easily visualized in FIG. 8. The value of energy is arbitrary and generally varies with the force fields used in the calculation. However, the energy difference between the highest and lowest points, which is around 40 Kcal/mol, tends to be consistent with different force fields. From this energy map, it is clear that the crystal structure is composed of the lowest energy conformation, which is also the most probable conformation.

C. MD Methodology For The Invention.
Many of the properties of polymers are dependent on the nucleation and crystallization mechanisms that form the polymers. For example, the transparency of certain polymers is dependent on the size of the spherulites formed during nucleation. Polymer transparency is a property of interest in the medical and food storage industries as transparent polymers provide a level of protection for items contained in the polymer while still allowing one to view the item through the transparent polymer.

The present invention is a molecular modeling method for predicting and determining the nucleating mechanisms of polymers, for determining whether a specific molecule will act as an effective nucleator, and for screening and designing molecules to be nucleating additives. Isotactic polypropylene (iPP) was used as the base example polymer because nucleators have been developed and are well known for iPP, and there is a body of data to which the present invention can be compared. A number of nucleating agents were used as the base example nucleating agents, including conventional benzoates and sorbitol based nucleators, which are known to work in iPP and allow for a comparison with the present invention.

MD simulation involves several steps that generally fall in the categories of setting up the model for simulation, generating a method to perform simulation, and analyzing the results. Setting up the model for simulation includes generation of the polymer molecule, adding the additive molecule, creating an amorphous box with the constituents, and then relaxing the structure for hot spots. Hot spots are locations where atoms overlap or present in close vicinity. These steps now will be disclosed in more detail.

To perform the molecular modeling of the present invention, first, one selects a polymer molecule on which the modeling will take place. The polymer molecule is built using molecule modeling techniques. One generates the coordinates of the individual atoms of the selected polymer molecule preferably to minimize the energy needed to relax the structure from the typical twisted structure
to a more linear structure. Atoms are also numbered in a sequential order, which is very important for automated analysis of the results.

Second, one selects and builds, again with molecule modeling techniques, an additive molecule for investigation as to whether and how the additive molecule will function as an effective nucleating agent for the selected polymer. The energy needed to relax the additive molecule structure also preferably is minimized. The molecular structure can be obtained from known crystallographic databases. The selected polymer and the selected additive molecule can be cloned, typically on the computer, to generate the required or desired number of polymer chains and additive molecules necessary or desired for the simulation.

The first two steps can be reversed if one desires to investigate the nucleating effects a particular additive molecule may have on a series of different polymers.

Third, one builds an appropriately sized three-dimensional (3-D) periodic cell or box in which the molecular modeling will occur. In general, the larger the cell, the better the simulation. However, larger cells require more time to conduct the simulation, so a balance between cell size and simulation time must be made. The cell size can be changed by changing either the length or the number of the polymer chains.

Fourth, one conducts the simulation and analyzes the resulting polymer. It is not necessary or practical to conduct the simulation to equilibrium, but only to a point where the nature of the resulting polymer can be determined. By analyzing the geometry of the resulting polymer, one can determine whether the selected additive molecule is an effective nucleating agent and/or what the resulting polymer will be when using a selected additive molecule with a selected polymer. Relaxing the structure of the resulting polymer after addition of appropriated charges should ease analysis.

The environmental parameters involved in the MD simulation are temperature and pressure. As with other simulations, these parameters, including other physical properties, and are not appropriately associated with any units, and
their values are used only to graduate their magnitude and should not be taken as absolute values. Implementing a proper set of values to these parameters is essential in obtaining the best results. The other variables in the simulation are size of the simulation box and length of the chain.

The integration time step is in femto seconds ($10^{-16}$ s). However, the transitions taking place in polymers are in the order of milliseconds to seconds. The real time taken per time step depends on the size of the model system and the speed of the molecular modeling technique. In the present example, computer modeling was used and, therefore, another factor affecting the speed of the simulation is the speed of the computer. For the current example, the speed of the simulation was about 5 sec/step for a model with four PP chains of 90 backbone carbon atoms in each (a week for 100ps). At this rate, it is impractical with current technology to simulate the whole process of transition as it would take about $10^{12}$ steps for one set of data (about 1.5 million years). However, the simulation at the initial stages of crystallization reveals the alignment of the backbone carbon atoms to the form suitable for the lattice and thus the simulation can be terminated when the density of the system is equilibrated. FIGS. 9 - 12 show the profiles of energies, temperature, volume and pressure of a typical simulation. It can be observed from FIGS. 9 and 10 that the energies and temperature drops over time. This means that the system is tending towards the equilibrium and has not attained equilibrium.

However, FIGS. 11 and 12 show that the volume and pressure attained equilibrium within a short period. The reason is that the system starts at a high temperature where the polymers have great mobility to orient and organize themselves. As the simulation proceeds, the cell shrinks considerably, thereby arresting the mobility of the atoms. As mentioned earlier, the value of any of these parameters should not be taken as is, but should be used to only compare the magnitude.

3-D periodic boundary condition was used to simulate the amorphous liquid state. 3-D boundary condition is a requirement to avoid wall effects. This condition creates a 3-D period image of each unit in the cell and when one unit leaves the cell from one wall its image enters from the opposite wall of the cell. Selecting a larger
cell can circumvent the influence of 3-D periodicity on the long-range order. Because the larger the cell size, the more the time taken for computation, a reasonable cell size must be selected as a compromise. A molecular box of four PP chains with 90 carbon atoms in the backbone was selected as the model as this cell is easy to simulate and produces good results.

Cell size can be changed by either keeping the number of polymer chains constant and increasing the length of each chain or keeping the chain length constant and increasing the number of chains in the cell. The length of the polymer used for simulation is 3-4 orders of magnitude smaller than the real length. Hence, by increasing the chain length, the effect of chain length and the effect on size can be studied simultaneously. FIGS. 13 and 14 show the effect of chain length on the orientation of backbone carbon atoms. The concentration of additive (DBS) was held constant. The chain lengths were 90, 180, 270 and 360 for each chain and 4 PP chains and 4 nucleator molecules were present in each simulation. It can be observed from FIG. 13 that if the chain length increases the data becomes more oscillatory. The reason for increase and decrease in the orientation is the nucleation and melting. As chain length increases, the probability of orientation and disorientation increases. FIG. 14 shows the normalized oriented backbone carbons. The values of 90, 180, 270, 360 chains are divided by 1, 2, 3, and 4 respectively. It can be observed that all of the results merge together showing that the influence on chain-length and cell-size are negligible.

Temperature is a thermodynamic quantity, and is meaningful only at equilibrium. It is related to the average kinetic energy of the system through the equipartition principle, which states that every degree of freedom (either in momenta or in coordinates) that appears as a squared term in the Hamiltonian has an average energy of kT/2 associated with it. Temperature and pressure forms a parameter of simulation. If high temperature or zero pressure is used, the oriented molecules disorient often such that the orientation cannot be observed. If very low temperature or high pressure is used, the mobility of the atoms is arrested and no orientation can be observed. The preferred values for temperature and pressure
were determined to be 400 K and 1 Gpa respectively, which gave reasonable results.

D. Model For The Simulation Of The Invention.

The model for simulation consists of four isotactic polypropylene chains of 90 backbone carbons each. Generally, every simulation had four additive molecules such that the resultant mixture has approximately 15% additive by weight for DBS. The weight fraction varied depending on the molecular weight of the additive used. Simulation was also carried out with varying concentrations of DBS.

Setting up the MD simulation involves first setting up the environment for MD simulation like temperature and pressure. Evald summation of charges should be used for periodic systems. After setup, the MD simulation is run. At this stage the data from the simulations are stored in a trajectory file, which consists of atomic coordinates and velocities together with elemental details and system properties such as temperature, pressure, and volume, and potential, kinetic and total energies. The simulation is terminated after a fixed amount of time.

The amount of data generated by MD simulation is huge. Although the system properties such as pressure, temperature, volume and energies such as shown in FIGS. 9 to 12 relate to the attainment of system equilibrium, analysis of atomic trajectory is the only way to identify the geometrical modification underwent by the polymer during simulation. Conventionally, a radial distribution function (RDF) is used to determine how atoms organize themselves around one another. The RDF depends on density and temperature, and therefore, in MD simulations, this serves as a helpful indicator of the nature of the phase assumed by the simulated system. The behavior of RDF of solid, liquid and gases are different. For solids the atoms are frozen into sites of regular crystal lattice structures – such as face centered cubic lattice, body centered cubic lattice, and hexagonal closed packed lattice. RDF takes the form of a sequence of delta symbols. This is illustrated in FIG. 15. The behavior of RDF in low density gases is far different as given by the following equation.
\[
\lim_{\rho \to 0} g(r) = \exp\left[-\frac{u(r)}{kT}\right]
\]

where \(u(r)\) is the pair potential energy function. A plot of this low-density limit is shown in FIG. 16. For liquids and amorphous solids the behavior of RDF is intermediate between crystal and gas. Liquids exhibit short-range order similar to that in crystal but long-range disorder like that in gases, as shown in FIG. 16. For polymers the short-range order is predominant.

FIGS. 17 and 18 show the RDF function obtained from the simulations. The RDF in FIG. 17 is obtained at different time intervals during the simulation. It can be observed that there is short range order as expected for polymers and a slow development of long range order. In FIG. 18 the RDF of PP with and without additives are compared. From these two figures it is clear that the differences are nominal and RDF cannot be used to determine the nucleating behavior of additives. The orderliness developed within the time frame of simulation is negligible compared to the one expected for crystalline PP.

When the simulation time is very short compared to the time required for the real process to occur, the traditional ways of analyzing the trajectory data are found to be inadequate because they only reflect the end results of the geometric modifications and do not derive information out of geometric modifications. For example, if a perfect TG\(_\perp\) sequence is obtained in the PP backbone then the distance between the neighboring pendant carbon atoms are 4.3 Å. If several perfect TG\(_\perp\) sequence are present, then the number of atoms present at a distance 4.3 Å will be considerably high and show a spike in the RDF graph. But during the simulation the attainment of perfect TG\(_\perp\) sequence is remote and hence one would not be able to see the spike at 4.3 Å at all. On the other hand it can be observed that there are several near TG\(_\perp\) sequence present in the system that occurs and disappears. As the simulation proceeds the occurrence surpasses the disappearance and hence the orientation is physically observed. By near TG\(_\perp\) sequence we mean that the Trans conformation is close to 180±10 and gauche±
conformation is close to 60±10. To exploit this fact to understand the orientation a
new method of analysis has been established.

E. Analyzing MD Results According To The Preferred Embodiment
Of The Invention.

The ability to track the molecular motion of the polymer and its constituting
atoms provides an advantage in determining whether the proper or desired
conformation is achieved during such motion. FIG. 1 shows the crystal structure of
isotactic polypropylene (alpha form) and FIG. 2 shows a strand of PP stripped out
from the crystal. From the structure it can be observed that the 3:1 helix is formed
by alternative trans and gauche±(TG±) states of the backbone. This is the proper
conformation required for PP to nucleate.

An MD simulation as disclosed previously is run on the polymer. FIG. 19
shows an amorphous box of iPP built using 4 molecules of iPP each having 90
carbons on its backbone. In a specific instance, the amorphous iPP has a few or no
alternating (TG±) sequence. But as the inventive simulation proceeds, after
quenching to 400K, more and more backbone carbon orients itself to the alternating
TG± sequence. FIG. 20 shows a typical amorphous box after 100 picoseconds of
simulation where several backbone carbons are oriented to the TG± sequence.
Considering that the helix formed by TG± sequence is the key for nucleation, the
total number of such helixes formed is the estimate of the extent of nucleation in the
amorphous box.

The post MD analysis that provides the basis for the invention comprises the
following steps:

a. March from the head to tail of the polymer to determine the
individual backbone torsion of the polymer. This a laborious task that can be
overcome using TCL scripts or other computerized techniques;

b. From the available backbone torsions, find the number of TG±
sequence within a given tolerance limit. The tolerance limit selected for this
model was 10 degrees;

c. Integrate the TG± sequence over the entire simulation box; and
d. Repeat steps 1 through 3 for every time frame the results are stored.

Several simulation runs should be carried out to validate the procedure. The validation involves checking the data physically one by one to verify whether the procedure is working properly. The trajectory can also be displayed on screen using the visualizer interface of Cerius² or other molecular modeling software packages and played to see the occurrence of orientation during simulation. The validated procedure can be used to analyze several data of different simulations with various nucleators. The molar concentration was held constant in each case.

FIG. 21 shows the effectiveness of various additives in orienting the backbone. Additives like DBS, DNS and R-TNS produce enormous orientation in the backbone compared to sorbitol. S-TNS produces nuclei at certain instances that dissolved after a period of time. FIG. 22 shows the formation of nucleus over the chain length at different time frames. As time proceeds, small segments of oriented atoms merge together to form a large segment. However, at some instances it can be observed that some of the orientation is destroyed, which reiterates the fact that the simulation box is a liquid.

The inventive simulation establishes a methodology for determining the effectiveness of different additives in nucleating PP. Of the known additives, DBS and sorbitol form excellent specimens due to their contrasting behavior, in spite of their structural similarity. The examples for this methodology concentrate on the DBS-PP system and sorbitol-PP system, as their effectiveness are also established experimentally. However, the invention is not limited to these systems. Several other additives also are suitable. For example, R-TNS and S-TNS also behave contradictory to each other. These additives can be used to validate the simulation parameters and analysis techniques.

First, the results obtained from simulating pure PP and PP with DBS are compared. From FIGS. 19 and 20, it can be observed that the orientation caused in PP-DBS system is considerably higher (about 2.5 times) than the one formed in system without any additive. Then comparing PP-Sorbitol system with PP-DBS
system, it can be observed that the PP-Sorbitol system produces same effect as PP system without any additive. Of the two PP-TNS systems, the one with R-TNS produced more orientation and the melting of the orientation is much less, such that the orientation is retained for longer times. The system with S-TNS produces orientation but dissolution is also high such that the effective orientation is much low than the one seen with DBS or R-TNS. DNS also produces results similar to DBS. The efficiency of different methyl, alkyl or nitro- substituted DBS could not be distinguished well from the available results.

One main observation comparing the molecules is that the backbones of the sorbitol chain in DBS and DNS are stiffened by the cyclic groups on them. Sorbitol without any stiffener is left loose and hence can form into any conformation in the bulk PP system.

Using the above disclosed and below claimed method, results were obtained that correlate well with the known data. Thus, a novel method for simulating the mechanism by which polymers are nucleated has been developed that is accurate and more economical, both in time and effort, than the previous methods. The above detailed description of the preferred embodiments, including the example methods, and the appended figures are for illustrative purposes only and are not intended to limit the scope and spirit of the invention, and its equivalents, as defined by the appended claims. One skilled in the art will recognize that many variations can be made to the invention disclosed in this specification without departing from the scope and spirit of the invention.
What is Claimed is:

1. A method for simulating the nucleation of polymers by additive molecules comprising the steps of:
   a. selecting a polymer molecule;
   b. selecting an additive molecule for use as a nucleating agent for the selected polymer;
   c. selecting an appropriately sized three dimensional periodic cell; and
   d. conducting the simulation and analyzing the resulting polymer.

2. The method as characterized in Claim 1, wherein the selected polymer is built using molecule modeling techniques.

3. The method as characterized in Claim 2, wherein the coordinates of the individual atoms of the selected polymer molecule are generated to minimize the energy needed to relax the structure from the typical twisted structure to a more linear structure.

4. The method as characterized in Claim 1, wherein the selected additive molecule is built using molecule modeling techniques.

5. The method as characterized in Claim 1, further comprising the step of cloning the selected polymer and the selected additive molecule to generate a desired number of polymer chains and additive molecules desired for the simulation.

6. The method as claimed in Claim 1, wherein step b is carried out prior to carrying out step a.

7. The method as characterized in Claim 1, wherein the resulting polymer is analyzed to determine whether the selected additive molecule acts as an effective nucleating agent for the selected polymer.

8. The method as characterized in Claim 7, wherein the resulting polymer is analyzed to determine the extent to which the selected additive molecule acts as a nucleating agent for the selected polymer.
9. The method as characterized in Claim 1, wherein the resulting polymer is analyzed to determine whether the selected additive molecule acts as an effective clarifying agent for the selected polymer.

10. The method as characterized in Claim 9, wherein the resulting polymer is analyzed to determine the extent to which the selected additive molecule acts as a clarifying agent for the selected polymer.

11. The method as characterized in Claim 1, wherein the resulting polymer is analyzed to determine what the structure of the resulting polymer is for the selected additive molecule.

12. The method as characterized in Claim 1, wherein the simulation is brought to equilibrium.

13. The method as characterized in Claim 1, wherein the simulation is not brought to equilibrium, but only to a point where the nature of the resulting polymer can be determined.

14. The method as characterized in Claim 1, wherein the selected polymer, the selected additive molecule, and the three-dimensional periodic cell are all built using molecular modeling techniques.

15. The method as characterized in Claim 14, wherein the simulation is conducted using molecular modeling techniques.

16. The method as characterized in Claim 15, wherein the resulting polymer is analyzed by:
   i. marching from the head to tail of the polymer to determine the individual backbone torsion of the resulting polymer;
   ii. finding the number of TG± sequences within a preselected tolerance limit from the available backbone torsions; and
   iii. integrating the TG± sequence over the entire three-dimensional periodic cell.

17. The method as characterized in Claim 16, wherein the individual backbone torsion of the resulting polymer is carried out using computerized techniques.
18. The method as characterized in Claim 16, wherein the preselected tolerance limit is 10 degrees.

19. The method as characterized in Claim 16, wherein steps i through iii are repeated for every time frame the results are stored.

20. A molecular modeling method for simulating the nucleation of polymers by additive molecules comprising the steps of:

   a. selecting polymer molecule on which the molecular modeling will take place and building the selected polymer using molecular modeling techniques;

   b. selecting an additive molecule for investigation as to whether and how the additive molecule will function as an effective nucleating agent for the selected polymer and building the additive molecule using molecular modeling techniques;

   c. selecting an appropriately sized three-dimensional periodic cell in which the molecular modeling will occur and building the three-dimensional periodic cell using molecular modeling techniques;

   d. conducting the simulation using molecular modeling techniques; and

   e. analyzing the resulting polymer by:

      i. marching from the head to tail of the polymer to determine the individual backbone torsion of the resulting polymer;

      ii. finding the number of TG± sequences within a preselected tolerance limit from the available backbone torsions; and

      iii. integrating the TG± sequence over the entire three-dimensional periodic cell.
FIG. 15

FIG. 16

SUBSTITUTE SHEET (RULE 26)
### INTERNATIONAL SEARCH REPORT

**INTERNATIONAL APPLICATION No.**

**PCT/US01/05279**

---

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(7) : G01N 33/48  
US CL : 702/19  

According to International Patent Classification (IPC) or to both national classification and IPC.

---

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

- U.S. : 395/500.23; 435/6,7.1; 530/333; 53625.3; 702/19,22

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched.

---

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
Please See Extra Sheet.

---

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

<table>
<thead>
<tr>
<th>Category*</th>
<th>Citation of document, with indication, where appropriate, of the relevant passages</th>
<th>Relevant to claim No.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Y</td>
<td>US 5,553,004 A (GRONBECH-JENSEN et al.) 03 September 1996, see especially the abstract, Figure 5, and related discussion.</td>
<td>1-20</td>
</tr>
<tr>
<td>Y</td>
<td>US 5,597,457 A (CRAIG et al.) 28 January 1997, see especially the abstract and the Detailed Description of the Invention section in columns 4-11.</td>
<td>1-20</td>
</tr>
</tbody>
</table>

---

**X** Further documents are listed in the continuation of Box C.  

---

See patent family annex.

---

* Special categories of cited documents:
  - **A** document defining the general state of the art which is not considered to be of particular relevance.
  - **E** earlier document published on or after the international filing date.
  - **L** document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified).
  - **G** document referring to an oral disclosure, use, exhibition or other means.
  - **P** document published prior to the international filing date but later than the priority date claimed.

---

Date of the actual completion of the international search: 29 MAY 2001  

Date of mailing of the international search report: 14 JUN 2001

---

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231  

---

Authorized officer: ARDEL MARSCHEL  
Telephone No. (703) 308-0196  

---

Form PCT/ISA/210 (second sheet) (July 1998)*
<table>
<thead>
<tr>
<th>Category</th>
<th>Citation of document, with indication, where appropriate, of the relevant passages</th>
<th>Relevant to claim No.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Y</td>
<td>CRAIG et al. HO and DNase I Probing of Eo70 RNA Polymerase -λPr Promoter Open Complexes: Mg2+ Binding and Its Structural Consequences at the Transcription Start Site. Biochemistry. 1995, Volume 34, Number 48, pages 15624-15632, see especially the abstract, Figure 5 on page 15630, and related discussion.</td>
<td>1-20</td>
</tr>
<tr>
<td>Y</td>
<td>ANDINO et al. Poliovirus RNA synthesis utilizes an RNP complex formed around the 5'-end of viral RNA. The EMBO Journal. 1993, Volume 12, Number 9, pages 3587-3598, see especially Figure 6 on page 3593 and related discussion.</td>
<td>1-20</td>
</tr>
</tbody>
</table>
B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

CAS, MEDLINE, EMBASE, WEST, BIOTECH ABS, WPI covering search terms: model, simulate, polymer, nucleate, 3-dimension, additive, agent, TG, gauche, trans, cell, and periodic