MODELING OF HYALURONIC ACID CONTAINING CURCUMIN-LOADED POLYLACTIC-CO-GLYCOLIC ACID BIOCONJUGATES FOR TARGETED DELIVERY TO CANCER CELLS

by

Abeedin Adulphakdee

Dissertation submitted in partial fulfillment of the requirement for the Bachelor of Engineering (Hons) (Chemical Engineering)

SEPTEMBER 2011

Universiti Teknologi PETRONAS Bandar Seri Iskandar 31750 Tronoh Perak Darul Ridzuan

CERTIFICATION OF APPROVAL

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(CHEMICAL ENGINEERING)

(Assoc. Prof. Dr. Mohd Azmuddin Abdullah)

UNIVERSITI TEKNOLOGI PETRONAS

TRONOH, PERAK

SEPTEMBER 2011

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CERTIFICATION OF ORIGINALITY

This is to certify that I am responsible for the work submitted in this project, that the original work is my own except as specified in the references and acknowledgements, and that the original work contained herein have not been undertaken or done by unspecified sources or persons.

อาปลิน อฏลภักส์

ABEEDIN ADULPHAKDEE

ABSTRACT

This project investigates the 3D molecular modeling of hyaluronic acid (HA), curcumin, polylactic-co-glycolic acid (PLGA) and polyethylene glycol bis amine (PEG-bis amine) and all the possible conjugated forms between the compounds as bioconjugates for targeted delivery to cancer cells. Modeling work had been done using Discovery Studios 2.5 from Accelrys Inc. USA. The study focuses on targeted delivery of curcumin to colorectal cancer cells. The generated model will be used in the studies of drug delivery to cancer cells.

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ABBREVIATION AND NOMENCLATURE

3D	Three Dimensional
DCC/DMAP	Dicyclohexylcarbodiimide/(dimethyl)aminopyridine
DNA	Deoxyribonucleic Acid
DS	Discovery Studio 2.5
ECM	Extracellular Matrix
EDAC	1-ethyl-3-dimethylamino-propyl carbodiimide
FAO	Food and Agriculture Organization
FDA	Food and Drug Administration
GRAS	Generally Recognized As Safe
HA	Hyaluronic Acid/Hyaluronan
KDa	Kilo Dalton
NHS	N-hydroxyl succinamide
PEG	Poly(ethylene glycol)
PEO	Polyethylene oxide
PLGA	Polylactic-co-glycolic Acid
USA	United States of America
WHO	World Health Organization

CHAPTER 1

INTRODUCTION

1.1 BACKGROUND OF STUDY

Cancer is one of the major diseases that cause 13% of all human deaths in 2007 (Gul-e-Saba et al., 2010). Cancer is a result of rapid growth of normal cells, which can harm human body (Pal & Nayak, 2010). Drugs such as cisplatin, doxorubicin have been developed for chemotherapy but most have side effects towards particular tissues or cells which are not the cancer cells or tumors. Curcumin, a natural polyphenolic compound, has shown promising chemopreventive and chemotherapeutic activities in cancer (Yallapu, et al., 2010) but couldn't achieve its optimum therapeutic outcome in the past clinical trials, largely due to its low solubility and poor bioavailability (Basnet & Basnet, 2011). Targeted drug delivery to cancer cells is of utmost important to selectively target diseased tissue while leaving healthy tissue untouched (Sutton et al., 2007). Hyaluronan (HA) is a major component of extracellular matrix (ECM) and main ligand of CD44 receptor cells (Gul-e-Saba, et al., 2010). HA-CD44 binding will play major role in development of targeted control drug delivery to cancer cells. One of the advanced tools that could help drug developers is the computational modeling for designing, testing and simulating the molecular structure of the drugs. The need for drug modeling assists better understanding of the interactions of the drug with microenvironment in the body at the disease sites. In this study, hyaluronic acid containing curcumin-loaded polylactic-co-glycolic acid bioconjugates as a potential anticancer drug will be modeled and discussed for targeted delivery.

1.2 PROBLEM STATEMENT

When any new type of drugs is to be used in human body, the process of design and development of drug will involve many trial and error experiments based on previous research. This method is time consuming, costly and fraught with uncertainties. Computational modeling to design the molecular structure to see the behavior of a drug reacting once injected or consumed in human cells, is a rational approach in drug design and modification which is economical and saves time with limited risk of failures as far as screening for lead compounds is concerned and it is also reduce the limitations of potent anticancer agents.

1.3 OBJECTIVES

- 1.3.1 To model the molecular structure of Hyaluronic Acid (HA) containing curcumin-loaded PLGA bioconjugates by using Discovery Studio 2.5.
- 1.3.2 To demonstrate the application of controlled, targeted drug delivery system based on 3D molecular model developed.

1.4 SCOPE OF STUDY

In this project, the 3D molecular structure of Hyaluronic Acid (HA) containing curcumin-loaded PLGA bioconjugates as potential anticancer drug for controlled, targeted delivery to cancer cell will be modeled using Discovery Studio 2.5 (Accelrys Inc., USA).

1.5 FEASIBILITY STUDY

Discovery Studio 2.5 (Accelrys Inc., USA) is available in UTP computer lab for students to use at all time and together with the project itself involves the compounds that have been known its molecular structure, therefore computational modeling of them is possible to generate and complete within project timeframe. Drug design using computational modeling is one of the advanced tools yet that could help drug developers and could play a key role in the pharmaceutical industry (Kumar et al., 2006).

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CHAPTER 2

LITERATURE REVIEW

2.1 COLORECTAL CANCER

Colorectal cancer is one of the most common tumors and a major cause of cancer death worldwide (Fiore et al., 2007). It is a disease in which malignant (cancer) cells form in the inner lining of the colon or rectum (Rex & Liangpunsakul, 2007). Fig. 2.1 shows developmental phases of colorectal cancer. The risk is increased with low fiber intake, high fat diet, and low calcium/micronutrient intake (Johnson & Mukhtar, 2007). Epidemiologic studies have revealed a number of risk factors for colorectal cancer including age, family history of colon cancer or inflammatory bowel disease, smoking, alcohol consumption, obesity, and diet (Byrne, 2008). Regular colorectal cancer screening which is the process of looking for cancer or symptoms or pre-cancer in people who show no symptoms is one of the ways for preventing colorectal cancer.

2.2 CURCUMIN AS ANTI-CANCER COMPOUND

Curcumin [(1E,6E)-1,7-bis(4-hydroxy-3-methoxyphenyl)-1,6-heptadiene-3,5-dione] is a natural extract from Curcuma longa herb or normally known as turmeric (Fig. 2.2) commonly used in India and Eastern Asia. It is an orange-yellow, crystalline powder with melting point of 183°C, molecular formula of C₂₁H₂₀O₆ and molecular weight of 368.37 g/mol (Lin & Lin, 2008). There are three major curcuminoids in namely curcumin (diferuloylmethane), demethoxycurcumin, and turmeric. bisdemethoxycurcumin (Fig. 2.3) (Basnet & Basnet, 2011). Curcumin has shown anti-inflammatory and anti-cancer properties (Sharma et al., 2005), highly hydrophobic agent (Anand et al., 2007), prevent the transformation, proliferation, and invasion of tumor cells (Shishodia et al., 2007). Turmeric is Generally Recognized As Safe (GRAS) by the US FDA, and curcumin has been granted an acceptable daily intake level of 0.1-3 mg/kg-BW by the Joint FAO/WHO Expert Committee o Food Additives, 1996 (Institute, 1996). Based on the safety and toxicity profile in several clinical studies shows that the targeted doses for curcumin can be recommended in between 4,000-8,000 mg to obtain the maximum therapeutic effects (Basnet & Basnet, 2011). The only factor that limits the use of free curcumin for cancer therapy is its poor solubility in water, which in turn limits its systemic bioavailability when administered orally (Dinarvand, et al., 2011). Utilization of nanotechnology has proven to be very effective in solving this problem (Bharali, et al., 2011). Some studies demonstrated that curcumin encapsulation in PLGA nanoparticles produced a very stable nanoformulation and also enhanced cellular drug uptake and retention, as well as sustained release of curcumin (Dinarvand, et al., 2011).

Anti-cancer agent refers to a compound capable of negatively affecting cancer in a subject, for example, by killing, inducing apoptosis, reducing the growth rate of one or more cancer cells, reducing the incidence or number of metastases, reducing a tumor's size, inhibiting a tumor's growth, reducing the blood supply to a tumor or one or more cancer cells, promoting an immune response against one or more cancer cells or a tumor, preventing or inhibiting the progression of a cancer, or increasing the lifespan of a subject with a cancer (Klostergaard, et al., 2010).

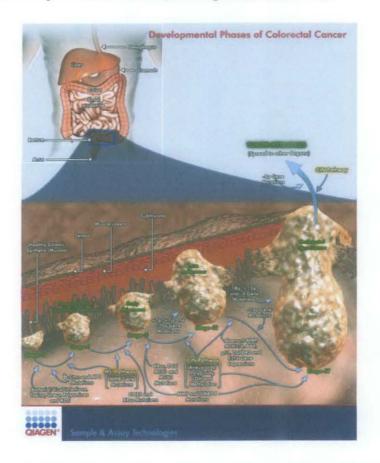


Figure 2.1 Developmental phases of colorectal cancer (QIAGEN, 2011).



Figure 2.2 Curcuma longa (Duvoix et al., 2005).

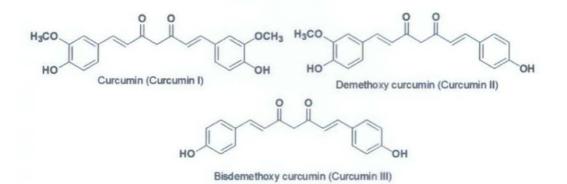


Figure 2.3 Fractions of turmeric known as curcuminoids (curcumin, demethoxycurcumin, and bisdemethoxycurcumin) (Basnet & Basnet, 2011).

2.3 PLGA AS A DRUG-DELIVERY AGENT

Drug-delivery agent or drug-carrier nanoparticles are defined as submicroscopic colloidal systems that may act as drug vehicles, either as nanospheres (matrix system in which the drug is dispersed) or nanocapsules (reservoirs in which the drug is confined in a hydrophobic or hydrophilic core surrounded by a single polymeric membrane) (Jeanneret, 2008). Figure 2.4 shows two major loading models— Liposome and Micelle—for effectively loading water soluble and water insoluble natural chemopreventive agents, respectively (Muqbil, et al., 2011). Figure 2.6 shows how nanoparticles do interact with immune system; a) The effect of nanoparticle size, charge, hydrophobicity and targeting or immunotoxicity and b) Some nanoparticles (shown schematically) can trigger certain immune responses as listed there, a characterization scheme for nanoparticles intended for biomedical applications must include testing for these responses, such tests may exclude a potentially harmful drug candidate from the development pipeline and inform future studies relevant to the immunomodulatory properties of nanoparticles (Dobrovolskaia & McNeil, 2007).

Polylactic-co-glycolic acid (PLGA) has been developed to be one of the carrier molecules for targeted delivery of the anticancer drug (Yadav et al., 2010). It is one of the most studied diblock copolymer biomaterials for drug encapsulation and is present in several commercially available pharmaceutical products (Mansour et al., 2010). Schematic representation of PLGA molecular structure is shown in Fig. 2.5. In a study to test for the quality of the curcumin-loaded PLGA nanospheres as potential anticancer drug, PLGA grade of Poly(D,L-lactide-co-glycolide) 50:50 has been used, having inherent viscosity 1.13 dl/g and MW 50000 (Mukerjee & Vishwanatha, 2009). A unified atomic mass unit of PLGA of 40-75KDa has been reported (Yadav et al., 2010). Studies have shown the possibility of having PLGA nano-formulation of curcumin as anticancer agent (Basnet & Basnet, 2011).

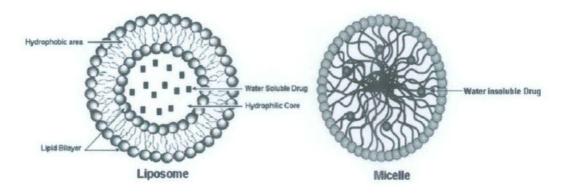


Figure 2.4 Two major loading models - Liposome and Micelle (Muqbil, et al., 2011).

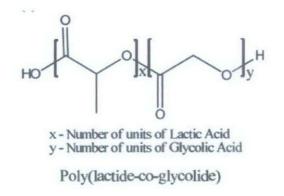


Figure 2.5 Structure of PLGA (Mansour et al., 2010).

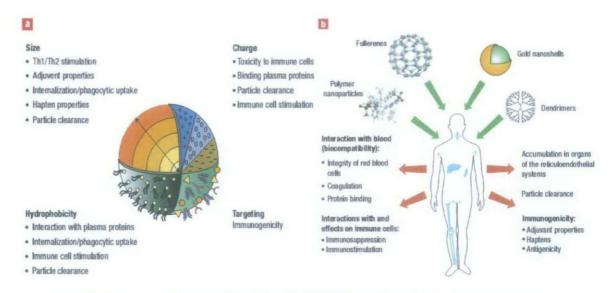


Figure 2.6 Nanoparticle properties determine their interaction with the immune system (Dobrovolskaia & McNeil, 2007).

2.4 HYALURONIC ACID CONTAINING BIOCONJUGATES

Hyaluronic acid (HA) is a repeating disaccharide units composed of D-glucuronic acid and N-acetyl-D-glucosamine and can be considered as the main component of the extracellular matrix of the cell membrane. It plays an important role in the mechanical support of the cell of many tissues, such as skin, tendons, muscles and cartilage (Mohapatra et al., 2008). HA can interact with CD44, its receptor at the cell surface which can lead to the site-specific delivery or targeted delivery of drug (Yadav et al., 2010), which later on degraded inside the cells (Luo et al., 2009). Nanoparticles composed of HA, can be encapsulated and formulated with various peptide, DNA and drugs (curcumin) for cell specific drug delivery. The nanoparticles are natural polymers, biocompatibles and biodegradables such as PLGA, PLGA allows controlled release of the active molecules such as anti-cancer drug and their orientation towards the target tissues (Mohapatra et al., 2008). Targeting anti-cancer agents to tumor cells and tumor metastases can be accomplished by receptor-mediated uptake of bioconjugates such as anti-cancer agents conjugated to HA, followed by the release of free drugs through the degradation of HA in cell compartments (Luo et al., 2009). Fig. 2.7 shows the structure of HA-curcumin conjugates and Fig. 2.8 shows CD-44 receptor on cell membrane.

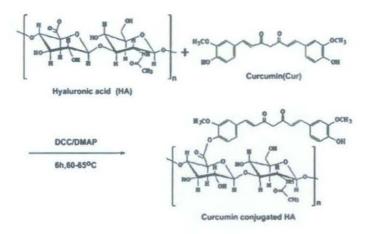


Figure 2.7 Structure of hyaluronic acid (HA)-curcumin conjugate.

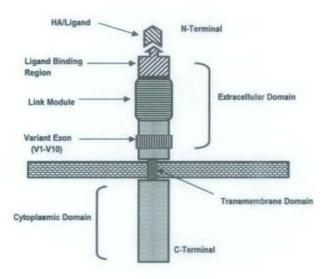


Figure 2.8 Schematic representation of CD44 molecule (Gul-e-Saba et al., 2010).

2.5 POLYETHYLENE GLYCOL BIS AMINE AS CROSSLINKING AGENT

Poly(ethylene glycol) (PEG), also known as polyethylene oxide (PEO), is a largely exploited polymer for advanced physical and chemical stability of drugs and its "stealth" properties (Mansour, et al., 2010). When PEG is properly linked to a polypeptide, it modifies many of its features while the main biological functions, such as enzymatic activity or receptor recognition maybe maintained (Veronese, 2001). Addition of PEG or PEG-containing copolymers to the nanoparticle surface results in an increase of half-life in the blood circulation by several orders of magnitude (Dinarvand, et al., 2011).

Polyethylene glycol-bis amine (PEG-bis amine) is used as an intermediate in the synthesis of crosslinking agents for polymerization and surface modification of hemoglobin or other proteins for pharmacological use (Hai, et al., 2003). A two step mechanism for the preparation of PEG-bis amine comprising a first step of reacting the terminal hydroxyl groups of PEG with a halogen substituted aromatic sulfonyl halide in a solvent to form a disubstituted sulfonyl activated polyethylene glycol intermediate and in a second step the intermediate is directly aminated with ammonia to give PEG-bis amine (Fig. 2.9) (Hai, et al., 2003).

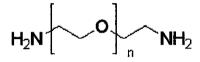


Figure 2.9 Structure of polyethylene glycol bis amine (Sigma-Aldrich, 2011).

CHAPTER 3

METHODOLOGY

3.1 RESEARCH METHODOLOGY

The study has been divided into 2 stages for molecular modeling as follows:

3.1.1 Uni-molecular Modeling

All of the following main molecules will be modeled separately using Discovery Studios 2.5 (Accelrys Inc., USA):

3.1.1.1 An anticancer agent (curcumin)
3.1.1.2 A carrier molecule (PLGA)
3.1.1.3 Hyaluronic acid (HA)
3.1.1.4 Spacer Arm (PEG-bis amine)

3.1.2 Multi-molecular Modeling

The following conjugates will be modeled using Discovery Studios 2.5 (Accelrys Inc., USA):

3.1.2.1 PLGA-HA3.1.2.2 Curcumin-HA3.1.2.3 PLGA-PEG-HA3.1.2.4 Curcumin-PLGA-PEG-HA

3.2 PROJECT ACTIVITIES

The following shows the instruction of molecular modeling for each of the molecules according to previous session which will be described in details using Discovery Studios 2.5 (Accelrys Inc., USA).

The molecular modeling has been divided into 2 stages:

3.2.1 Uni-molecular Modeling

All of the following main molecules had been modeled separately using Discovery Studios 2.5 (Accelrys Inc., USA) together with their instruction step-by-step for each of the modeled molecule:

3.2.1.1 An anticancer agent (curcumin)

The study chose curcumin I to be modeled (refer to Fig.2.3) and the following shows its modeling instruction:

- Discovery Studios 2.5 was opened by using its software icon on the desktop.
- Molecule window was opened from menu File | New | Molecule Window.
- 3) The Ring Tool was selected from Sketching Toolbar.
- 4) The 2 rings with 6 carbon atoms each was created by clicking in molecular window for 2 times on left and right of the screen.
- 5) The Draw Tool was selected from Sketching Toolbar.
- 6) For the 1st ring on the left of the screen, the lower left atom was clicked then the mouse was dragged to lower left and single click was pressed after that to make a new atom and by clicking on the new atom, it released the cursor. Then, the upper left atom of the ring was clicked and the mouse was dragged to upper left side with single clicking to make 1 atom and one more clicking to the left to add another 1 atom. The cursor was released by clicking on the new atom just added. Since both of the 1st atoms added and attached to the ring is oxygen atom so that changing of the atom was needed. This was successfully done by choosing Select Tool from View Toolbar then right mouse button was clicked to show the pull-down menu then option Element > O was selected for both of the atoms.

Note: Releasing the cursor can be done also by dragging the mouse out of document window.

7) For the 2nd ring on the right of the screen, the lower right atom was clicked then the mouse was dragged to lower right and single click was

pressed after that to make a new atom and by clicking on the new atom, it released the cursor. Then, the upper right atom of the ring was clicked and the mouse was dragged to upper right side with single clicking to make 1 atom and one more clicking to the right to add another 1 atom. The cursor was released by clicking on the new atom just added. Since both of the 1st atoms added and attached to the ring is oxygen atom so that changing of the atom was needed. This was successfully done by the same method as previous step 6).

- 8) The Chain Tool was selected from Sketching Toolbar.
- 9) The upper right atom of the 1st ring was clicked and the new atom appeared then it was clicked while holding the left mouse button down. The mouse was dragged across to make the side chain of totally 9 atoms; it was the number appearing to show the number of atom in the chain while dragging the mouse.
- 10) The whole 2nd ring was selected using the Select Tool then the mouse was clicked and dragged to draw a region covering the whole 2nd ring and once it had been done, the selected ring will be highlighted with yellow color. Next, the whole 2nd ring was moved and placed nearby another side of the chain drew in previous step and by selecting Draw Tool, the atom of the chain at the end was clicked and then the link between this atom and the upper left corner atom of the 2nd ring was released with the same method as previously mentioned.
- 11) The single atom was added on the side chain at atom number 3 and 5 using Draw Tool. These atoms were changed into oxygen atoms by the same method as mentioned before in step 6).
- 12) The Select Tool was chose and all the single bonds that need to be converted to double bond had been selected. Then by pressing number 2 on the keyboard or by clicking on Double Bond in Chemistry Toolbar, it automatically changed into double bond.
- 13) The Show Hydrogen was selected from Chemistry Toolbar. This made the hydrogen appeared on each of the atoms that available on the modeled structure.

- 14) Optimizing the geometry of the structure was needed since the drawing model was not yet precise and accurate in terms of standard bond length, bond angles and Van der Waals radii for close contact. The Clean Geometry was chose from Chemistry Toolbar; this can be clicked repeatedly until there's no longer changing in the model.
- 15) Annotation to the model was needed by choosing Annotation Tool in Sketching Toolbar and left clicking on the place where to put the annotation then the word 'Curcumin' was typed in the dialog box and finally the 'OK' button was pressed. The completed model of curcumin has illustrated in the next chapter (Fig. 4.1).

3.2.1.2 A carrier molecule (PLGA)

The current study choose to model only some portion of PLGA molecular structure as shown in previous chapter (refer to Fig. 2.5). PLGA modeling instruction has been illustrated as follow:

- The Chain Tool was chosen from Sketching Toolbar to draw the chain total of 7 atoms.
- 2) The single atom was added on the side chain at atom number 2, 3 and 5 using Draw Tool. The atom added at number 2 and 5 were changed into oxygen atom together with atoms on the chain number 1, 4 and 7 by the same method used in previous curcumin model.
- 3) The Select Tool was chose and all the single bonds that need to be converted to double bond had been selected. Then by pressing number 2 on the keyboard or by clicking on Double Bond in Chemistry Toolbar, it automatically changed into double bond.
- 4) The Show Hydrogen was selected from Chemistry Toolbar. This made the hydrogen appeared on each of the atoms that available on the modeled structure.
- Optimizing the geometry of the structure was needed using the same method mentioned in previous model.
- 6) The annotation of PLGA was added using the same method explained in curcumin model. The complete model structure of PLGA has been illustrated in the next chapter (Fig. 4.2).

3.2.1.3 Hyaluronic acid (HA)

The modeling of HA refers to the structure in Fig. 2.7 and the following is its modeling instruction:

- The Ring Tool was selected from Sketching Toolbar in order to draw the two rings with the size of 6 atoms each.
- 2) The Draw Tool was selected to add all the chain to both 2 rings.
- Some of the atoms have changed into oxygen atom and nitrogen atom by the same method used for curcumin.
- All the double bond had been located using Double Bond button in Chemistry Toolbar.
- 5) The 2 rings had been connected using Draw Tool to draw the bond between these two structures at the atom according to Fig. 2.7.
- 6) The Show Hydrogen was selected from Chemistry Toolbar. This made the hydrogen appeared on each of the atoms that available on the modeled structure.
- The modeling of HA had been optimized by clicking on Clean Geometry button in Chemistry Toolbar until there's no changing in the model.
- 8) The annotation of HA was added using the same method explained in curcumin model. The complete model structure of HA has been illustrated in the next chapter (Fig. 4.3).

3.2.1.4 Spacer arm (PEG-bis amine)

The modeling of PEG-bis amine refers to the structure in Fig. 2.9 and the following is its modeling instruction:

- The Chain Tool was chosen from Sketching Toolbar to draw the chain total of 7 atoms.
- 2) The Select Tool was chosen from View Toolbar then right mouse button was clicked on atom number 1 to show the pull-down menu then option Element > N was selected for nitrogen. The same procedure was done for atom number 7 as well but it was difference for atom number 4 which has been changed into oxygen atom.

- The Show Hydrogen was selected from Chemistry Toolbar. This made the hydrogen appeared on each of the atoms that available on the modeled structure.
- 4) The modeling of PEG had been optimized by clicking on Clean Geometry button in Chemistry Toolbar until there's no changing in the model.
- 5) The annotation of PEG was added using the same method explained in curcumin model. The complete model structure of PEG has been illustrated in the next chapter (Fig. 4.4).

3.2.2 Multi-molecular Modeling

The following conjugates have been modeled using Discovery Studios 2.5 (Accelrys Inc., USA):

3.2.2.1 PLGA-HA

The structure of these conjugated molecules has shown in Fig. 3.1.

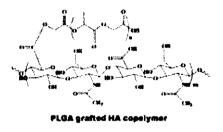


Figure 3.1 PLGA grafted HA copolymer (Lee, Ahn, & Park, 2009).

The modeling structure of these conjugated molecule had been completed for only one HA molecule which is smaller than structure shown in Fig 3.1 which contains two HA molecules. The modeling instructions of these conjugated structure is simply take the uni-molecule that we have in previous modeling and make a link bond between these two molecules as illustrated in Fig. 3.1. The completed modeling of this conjugated structure will be shown in the next chapter (Fig. 4.5).

3.2.2.2 Curcumin-HA

This modeling structure refers to Fig. 2.7. The modeling instruction of curcumin conjugated HA had been done by taking those two uni-structures and then make a

link bond between them as illustrated in Fig. 2.7. Clean Geometry tool had used to optimize the conjugated molecule and the completed modeling structure will be shown in the next chapter (Fig. 4.6).

3.2.2.3 PLGA-PEG-HA

The structure of these conjugated molecules has shown in Fig. 3.2.

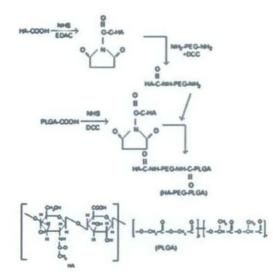
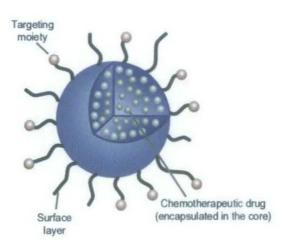


Figure 3.2 Schematic representation of synthesis of HA-PEG-PLGA polymer (Yadav, et al., 2010).

The modeling instruction of HA-PEG-PLGA polymer had been done by taking those three uni-structures and then makes a link bond between them as illustrated in Fig. 3.2. Clean Geometry tool had used to optimize the conjugated molecule and the completed modeling structure will be shown in the next chapter (Fig. 4.7).

3.2.2.4 Curcumin-PLGA-PEG-HA





This modeling structure refers to Fig. 2.4 and Fig. 3.3. The modeling instruction of curcumin-PLGA-PEG-HA had been done by taking one molecule of curcumin and those PLGA-PEG-HA polymers in previous result and then makes a spherical shape over curcumin by selecting the curcumin molecule and the option under Tools Tab which is 'Define and Edit Binding Site' category followed by selecting 'Create Sphere'. The spherical shape appeared covering curcumin inside. Then covering the sphere by selecting PLGA-PEG-HA polymer and copying it and pasting it at the surface of sphere but need to make sure that only PLGA molecule would touch the sphere as inner with the outer of HA molecule. The completed modeling structure will be shown in the next chapter (Fig. 4.8).

3.3 TOOLS REQUIREMENT

Tools requirement as for development of the molecular modeling are shown below.

- 3.3.1 Hardware
 - Computer
- 3.3.2 Software
 - Discovery Studios 2.5 (Accelrys Inc., USA)

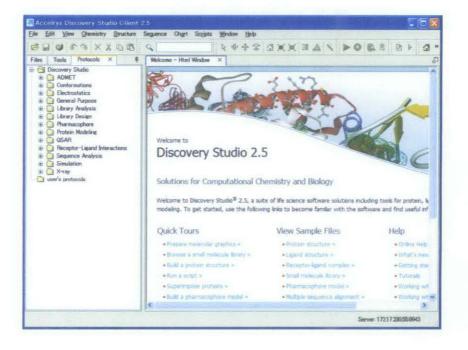


Figure 3.4 User interface of Discovery Studios 2.5 (Accelrys Inc., USA).

3.4 PROJECT TIMELINE

	W1	W2	W3	W4	W5	W6	W7	W8	W9	W 10	W 11	W 12	W 13	W 14	W 15	W 16	W 17
Activities in FYP I	15/5	22/5	29/5	5/6	12/6	19/6	26/6	3/7	17/7	24/7	31/7	7/8	14/8	21/8	28/8	4/9	11/9
Selection of project topic																	
Preliminary research work																	
a) Literature review: Modeling of HA containing curcumin-loaded PLGA nanosphere bioconjugates for targeted delivery to cancer cells																Week	Week
Submission of extended proposal															eek	tion W	tion W
Proposal defense]					Study week	Examination	Examination
Project work continues															St	d Ex	I Ex
b) Execute the uni-molecular modeling																Final	Final
c) Execute the multi-molecular modeling																	
Submission of Interim Draft Report																	
Submission of Interim Report																	

Table 3.1: Final Year Project I (May 2011) proposed activities timeline.

Activities in FYP II	WI	W2	W3	W4	W5	W6	W7	W8	W9	W10	W11	W12	W13	W14	W15	W16	W17
Activities in FYF II	26/9	3/10	10/10	17/10	24/10	31/10	7/11	14/11	21/11	28/11	5/12	12/12	19/12	26/12	31/12	9/1	16/1
Project work continues																	
I) Execute the simulation studies		ar ar	12-11-	1.5.2%	Sec.	1.67	and a	21-00-									
Submission progress report									1 Acres								
Project work continues																	
) Report writing: discussion, conclusion and recommendations																eek	ook
Pre- EDX															eek	tion W	Hon W
Submission of Draft Report															Study week	aminat	Ruima
Submission of Dissertation (soft bound)															St	Final Examination Week	Final Evamination Week
Submission of Technical Paper	-]		I	-
Dral Presentation																	

Table 3.2: Final Year Project II (September 2011) proposed activities timeline.

CHAPTER 4

RESULTS AND DISCUSSION

4.1 MOLECULAR MODELING

The following content illustrate the molecular modeling developed by using Discovery Studios 2.5 (Accelrys Inc., USA).

4.1.1 Uni-molecular Modeling

4.1.1.1 An anticancer agent (curcumin)

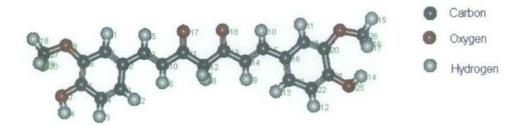


Figure 4.1 Molecular modeling of curcumin (with atom number).

The modeling of curcumin has been shown in Fig. 4.1. The red atom indicates oxygen atom, the dark grey atom indicates carbon atom and the light grey atom indicates hydrogen atom. The bond length between each atom has also been calculated using function in the software together with its basic properties as shown in Table 4.1 and 4.2, respectively.

No.	Name	Parent	Order	Туре	Length (Å)
1	C1 - C2	Curcumin	2	Double	1.32923
2	C2 - C3	Curcumin	1	Single	1.46169
3	C3 - C4	Curcumin	2	Double	1.32782
4	C4 - C5	Curcumin	1	Single	1.4662
5	C5 - C6	Curcumin	2	Double	1.35625
6	C6 - C1	Curcumin	1	Single	1.47053
7	C5 - 07	Curcumin	1	Single	1.39542
8	C6 - O8	Curcumin	1	Single	1.45342

Table 4.1 Bond and bond length of curcumin.

No.	Name	Parent	Order	Туре	Length (Å)
9	C9 - C10	Curcumin	2	Double	1.33412
10	C10 - C11	Curcumin	1	Single	1.45658
11	C11 - C12	Curcumin	- 1	Single	1.50271
12	C12 - C13	Curcumin	1	Single	1.5026
13	C13 - C14	Curcumin	1	Single	1.45672
14	C14 - C15	Curcumin	2	Double	1.33515
15	C15 - C16	Curcumin	1	Single	1.48623
16	C2 - C9	Curcumin	1	Single	1.47967
17	C11 - O17	Curcumin	2	Double	1.23582
18	C13 - O18	Curcumin	2	Double	1.23587
19	C19 - C20	Curcumin	2	Double	1.33295
20	C20 - C21	Curcumin	1	Single	1.55536
21	C21 - C22	Curcumin	2	Double	1.33191
22	C22 - C23	Curcumin	1	Single	1.45423
23	C16 - C19	Curcumin	1	Single	1.45691
24	C16 - C23	Curcumin	2	Double	1.33304
25	C20 - O24	Curcumin	1	Single	1.45352
26	C21 - O25	Curcumin	1	Single	1.42368
27	O24 - C26	Curcumin	1	Single	1.41594
28	O8 - C27	Curcumin	1	Single	1.43531
29	C1 - H1	Curcumin	1	Single	1.06021
30	C3 - H2	Curcumin	1	Single	1.05826
31	C4 - H3	Curcumin	1	Single	1.06032
32	O7 - H4	Curcumin	1	Single	0.988694
33	C9 - H5	Curcumin	1	Single	1.06027
34	C10 - H6	Curcumin	1	Single	1.05684
35	C12 - H7	Curcumin	1	Single	1.09892
36	C12 - H8	Curcumin	1	Single	1.0992
37	C14 - H9	Curcumin	1	Single	1.05716
38	C15 - H10	Curcumin	1	Single	1.06027
39	C19 - H11	Curcumin	1	Single	1.0602
40	C22 - H12	Curcumin	1	Single	1.0603
41	C23 - H13	Curcumin	1	Single	1.05659
42	O25 - H14	Curcumin	1	Single	0.941025
43	C26 - H15	Curcumin	1	Single	1.0993
44	C26 - H16	Curcumin	1	Single	1.09957
45	C26 - H17	Curcumin	1	Single	1.09965
46	C27 - H18	Curcumin	1	Single	1.09929
47	C27 - H19	Curcumin	1	Single	1.09989
48	C27 - H20	Curcumin	1	Single	1.09983

The curcumin structure shows the total measurement of 48 bond length with average bond length of 1.266556 Å.

Properties	Curcumin	
Number of Atoms	47	
Molecular Formula	C21 H20 O6	
Molecular Composition	C: 0.685, H: 0.055, O: 0.261	
Molecular Weight	368.391	
Exact Molecular Weight	368.126	
Net Formal Charge	0	

Table 4.2 Basic properties of curcumin.

According to Table 4.2, the exact molecular weight of curcumin is slightly lower than its molecular weight because exact molecular weight is the mass of a molecule calculated with only the most abundant isotopes present which are usually the lightest isotopes (University of Colorado, 2011). Since curcumin is the neutral molecule therefore the net formal charge is equal to zero.

4.1.1.2 A carrier molecule (PLGA)



Figure 4.2 Molecular modeling of PLGA (with atom number).

The molecular modeling of PLGA has been demonstrated in Fig. 4.2. The color of atoms indicates the same element as in previous modeling. The bond length of PLGA and its basic properties has also been evaluated as appeared in Table 4.3 and 4.4, respectively.

No.	Name	Parent	Order	Туре	Length (Å)
1	O1 - C2	PLGA	1	Single	1.42944
2	C2 - C3	PLGA	1	Single	1.50007
3	C3 - O4	PLGA	1	Single	1.40999
4	O4 - C5	PLGA	1	Single	1.44509
5	C5 - C6	PLGA	1	Single	1.5004
6	C3 - O7	PLGA	2	Double	1.23722
7	C5 - C8	PLGA	1	Single	1.55092
8	C6 - O9	PLGA	2	Double	1.23615

Table 4.3 Bond and bond length of PLGA.

No.	Name	Parent	Order	Туре	Length (Å)
9	01 - H1	PLGA	1	Single	1.05003
10	C2 - H2	PLGA	1	Single	1.09
11	C2 - H3	PLGA	1	Single	1.09
12	C5 - H4	PLGA	1	Single	1.09
13	C6 - H5	PLGA	1	Single	1.09
14	C8 - H6	PLGA	1	Single	1.08996
15	C8 - H7	PLGA	1	Single	1.09003
16	C8 - H8	PLGA	1	Single	1.09003

The PLGA structure shows the total measurement of 16 bond length with average bond length of 1.249333 Å.

Properties	PLGA
Number of Atoms	18
Molecular Formula	C5 H8 O5
Molecular Composition	C: 0.405, H: 0.054, O: 0.540
Molecular Weight	148.119
Exact Molecular Weight	148.037
Net Formal Charge	0

Table 4.4	Basic	properties	of PLGA.
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4.1.1.3 Hyaluronic acid (HA)



Figure 4.3 Molecular modeling of HA (with atom number).

The molecular structure of HA contains nitrogen atom which indicates in blue color of modeling in Fig. 4.3. Detail bond length between atoms of HA and its basic properties are shown in Table 4.5 and 4.6, respectively.

No.	Name	Parent	Order	Туре	Length (Å)
1	C1 - C2	Hyaluronic Acid	1	Single	1.59635
2	C2 - C3	Hyaluronic Acid	1	Single	1.4931
3	C3 - C4	Hyaluronic Acid	1	Single	1.59474
4	C4 - O5	Hyaluronic Acid	1	Single	1.48098
5	O5 - C6	Hyaluronic Acid	1	Single	1.38242
6	C6 - C1	Hyaluronic Acid	1	Single	1.55595
7	C6 - C7	Hyaluronic Acid	1	Single	1.50029
8	C7 - O8	Hyaluronic Acid	2	Double	1.23601
9	C7 - O9	Hyaluronic Acid	1	Single	1.39077
10	C1 - O10	Hyaluronic Acid	1	Single	1.4566
11	010 - C11	Hyaluronic Acid	1	Single	1.43783
12	C2 - O12	Hyaluronic Acid	1	Single	1.42998
13	C3 - O13	Hyaluronic Acid	1	Single	1.42868
13	C4 - 014	Hyaluronic Acid	1	Single	1.45673
15	014 - C15	Hyaluronic Acid	1	Single	1.45659
16	C15 - C16	Hyaluronic Acid	1	Single	1.49247
17	C15 - C10 C16 - C17	Hyaluronic Acid	1	Single	1.60289
17	C10-C17	Hyaluronic Acid	1	Single	1.4804
10	018 - C19	Hyaluronic Acid	1	Single	1.37854
20	C19 - C20	Hyaluronic Acid	1	Single	1.56016
20	C19 - C20 C20 - C15	Hyaluronic Acid	1	Single	1.57294
21	C20 - C13	Hyaluronic Acid	1		1.42935
22	C19 - C22		1	Single	1.53752
	C19 - C22 C22 - O23	Hyaluronic Acid	1	Single	1.42903
24		Hyaluronic Acid	1	Single	
25	C17 - O24	Hyaluronic Acid	1	Single	<u>1.43032</u> 1.43136
26	024 - C25	Hyaluronic Acid	1	Single	
27	C16 - N26	Hyaluronic Acid	1	Single	1.45817
28	N26 - C27	Hyaluronic Acid	1	Single	1.34361
29	C27 - C28	Hyaluronic Acid	1	Single	1.49999
30	C27 - O29	Hyaluronic Acid	2	Double	1.23771
31	<u>C1 - H1</u>	Hyaluronic Acid	1	Single	1.09
32	C2 - H2	Hyaluronic Acid	1	Single	1.09
33	$\frac{\text{C3} - \text{H3}}{\text{C4} + \text{H4}}$	Hyaluronic Acid	1	Single	1.09
34	C4 - H4	Hyaluronic Acid	1	Single	1.09
35	C6 - H5	Hyaluronic Acid		Single	1.09
36	<u>09 - H6</u>	Hyaluronic Acid	1	Single	1.05003
37	C11 - H7	Hyaluronic Acid	1	Single	1.08996
38	C11 - H8	Hyaluronic Acid	1	Single	1.09003
39	C11 - H9	Hyaluronic Acid	1	Single	1.09003
40	012 - H10	Hyaluronic Acid	1	Single	1.05003
41	013 - H11	Hyaluronic Acid	1	Single	1.05003
42	C15 - H12	Hyaluronic Acid	1	Single	1.09
43	C16 - H13	Hyaluronic Acid	1	Single	1.09
44	C17 - H14	Hyaluronic Acid	1	Single	1.09
45	C19 - H15	Hyaluronic Acid	1	Single	1.09

 Table 4.5 Bond and bond length of HA.

No.	Name	Parent	Order	Туре	Length (Å)
46	C20 - H16	Hyaluronic Acid	1	Single	1.09
47	O21 - H17	Hyaluronic Acid	1	Single	1.05003
48	C22 - H18	Hyaluronic Acid	1	Single	1.09
49	C22 - H19	Hyaluronic Acid	1	Single	1.09
50	O23 - H20	Hyaluronic Acid	1	Single	1.05003
51	C25 - H21	Hyaluronic Acid	1	Single	1.08996
52	C25 - H22	Hyaluronic Acid	1	Single	1.09003
53	C25 - H23	Hyaluronic Acid	1	Single	1.09003
54	N26 - H24	Hyaluronic Acid	1	Single	1.07
55	C28 - H25	Hyaluronic Acid	1	Single	1.08996
56	C28 - H26	Hyaluronic Acid	1	Single	1.09003
57	C28 - H27	Hyaluronic Acid	1	Single	1.09003

The HA structure shows the total measurement of 57 bond length with average bond length of 1.280556 Å.

Table 4.6 Basic properties of HA.

Properties	HA		
Number of Atoms	56		
Molecular Formula	C16 H27 O12 N1		
Molecular Composition	C: 0.452, H: 0.064, O: 0.451, N: 0.033		
Molecular Weight	425.399		
Exact Molecular Weight	425.153		
Net Formal Charge	0		

Since some specific HA receptors (CD44) are overexpressed in various malignant cell types, linking an antitumor drug to HA might improve targeting to cancerous cells and overcome the problem of low drug hydrosolubility (Leonelli et al., 2008).

4.1.1.4 PEG-bis amine



Figure 4.4 Molecular modeling of PEG-bis amine (with atom number).

The molecular structure of PEG-bis amine contains carbon, hydrogen, oxygen and nitrogen atom which indicates in dark grey, light grey, red and blue color respectively of modeling in Fig. 4.4. Detail bond length between atoms of PEG-bis amine and its basic properties are shown in Table 4.7 and 4.8, respectively.

No.	Name	Parent	Order	Туре	Length
1	N1 - C2	Poly(ethylene glycol) bis(amine)	1	Single	1.46616
2	C2 - C3	Poly(ethylene glycol) bis(amine)	1	Single	1.53352
3	C3 - O4	Poly(ethylene glycol) bis(amine)	1	Single	1.42302
4	O4 - C5	Poly(ethylene glycol) bis(amine)	1	Single	1.42302
5	C5 - C6	Poly(ethylene glycol) bis(amine)	1	Single	1.53352
6	C6 - N7	Poly(ethylene glycol) bis(amine)	1	Single	1.46616
7	N1 - H1	Poly(ethylene glycol) bis(amine)	1	Single	1.02949
8	N1 - H2	Poly(ethylene glycol) bis(amine)	1	Single	1.02949
9	C2 - H3	Poly(ethylene glycol) bis(amine)	1	Single	1.09939
10	C2 - H4	Poly(ethylene glycol) bis(amine)	1	Single	1.09939
11	C3 - H5	Poly(ethylene glycol) bis(amine)	1	Single	1.09913
12	C3 - H6	Poly(ethylene glycol) bis(amine)	1	Single	1.09913
13	C5 - H7	Poly(ethylene glycol) bis(amine)	1	Single	1.09913
14	C5 - H8	Poly(ethylene glycol) bis(amine)	1	Single	1.09913
15	C6 - H9	Poly(ethylene glycol) bis(amine)	1	Single	1.09939
16	C6 - H10	Poly(ethylene glycol) bis(amine)	1	Single	1.09939
17	N7 - H11	Poly(ethylene glycol) bis(amine)	1	Single	1.02949
18	N7 - H12	Poly(ethylene glycol) bis(amine)	1	Single	1.02949

Table 4.7 Bond and bond length of PEG-bis amine.

The PEG-bis amine structure shows the total measurement of 18 bond length with average bond length of 1.208747 Å.

Properties	PEG-bis amine		
Number of Atoms	19		
Molecular Formula	C4 H12 O1 N2		
Molecular Composition	C: 0.461, H: 0.116, O: 0.154, N: 0.269		
Molecular Weight	104.154		
Exact Molecular Weight	104.095		
Net Formal Charge	0		

Table 4.8 Basic	properties	of PEG-bis	amine.
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4.1.2 Multi-molecular Modeling

4.1.2.1 PLGA-HA

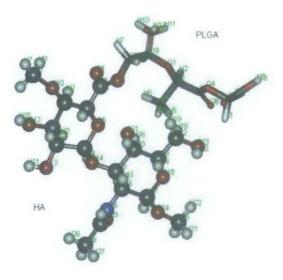


Figure 4.5 Molecular modeling of PLGA-HA conjugate (with atom number).

The PLGA-HA conjugate contains only one of each molecule as illustrated in Fig. 4.5 whereas PLGA is in stick representation. PLGA acts as a drug carrier while HA is the tumor-specific targeting vehicle to interact with CD44 receptor at tumor cell. Table 4.9 shows PLGA-HA bond length while Table 4.10 shows its basic properties.

No.	Name	Parent	Order	Туре	Length (Å)
1	O1 - C2	PLGA	1	Single	1.45449
2	C2 - C3	PLGA	1	Single	1.4912
3	C3 - O4	PLGA	1	Single	1.38889
4	O4 - C5	PLGA	1	Single	1.42627
5	C5 - C6	PLGA	1	Single	1.49706
6	C2 - C7	PLGA	1	Single	1.55577
7	C3 - O8	PLGA	2	Double	1.23613
8	C6 - O9	PLGA	2	Double	1.23605
9	C6-010	PLGA	1	Single	1.38972
10	C2 - H2	PLGA	1	Single	1.09863
11	C5 - H3	PLGA	1	Single	1.10014
12	C5 - H4	PLGA	1	Single	1.09925
13	C7 - H5	PLGA	1	Single	1.09859
14	C7 - H6	PLGA	1	Single	1.09911
15	C7 - H7	PLGA	1	Single	1.09946
16	O10 - H8	PLGA	1	Single	0.989376
17	O1 - C19	HA	1	Single	1.40638

Table 4.9 Bond and bond length of PLGA-HA conjugate.

No.	Name	Parent	Order	Туре	Length (Å)
18	C19 - C22	HA	1	Single	1.5023
19	C22 - H6	HA	1	Single	1.09869
20	C22 - H7	HA	1	Single	1.09861
21	C19 - O25	HA	2	Double	1.23636
22	C19 - H9	HA	1	Single	1.05814
23	O25 - H10	HA	1	Single	0.956449
24	O25 - H11	HA	1	Single	0.955898
25	O25 - H12	HA	1	Single	0.957543
26	C1 - C2	HA	1	Single	1.65527
27	C2 - C3	HA	1	Single	1.43775
28	C3 - C4	HA	1	Single	1.64816
29	C4 - O5	HA	1	Single	1.5115
30	O5 - C6	HA	1	Single	1.31797
31	C6 - C1	HA	1	Single	1.58321
32	C6 - C7	HA	1	Single	1.48369
33	C7 - O8	HA	2	Double	1.23591
34	C7 - O9	HA	1	Single	1.3794
35	C1 - O10	HA	1	Single	1.45766
36	O10 - C11	HA	1	Single	1.44215
37	C2 - 012	HA	1	Single	1.4279
38	C3 - O13	HA	1	Single	1.42559
39	C4 - 014	HA	1	Single	1.455
40	014 - C15	HA	1	Single	1.462
41	C15 - C16	HA	1	Single	1.45104
42	C16 - C17	HA	1	Single	1.66827
43	C17 - O18	HA	1	Single	1.52245
44	O18 - C19	HA	1	Single	1.31818
45	C19 - C20	HA	1	Single	1.57756
46	C1) - C20 C20 - C15	HA	1	Single	1.6257
47	C20 - C13	HA	1	Single	1.4359
48	C19 - C22	HA	1	Single	1.52833
49	C10 - C22 C22 - O23	HA	1	Single	1.42626
50	C17 - O24	HA	1	Single	1.42995
51	024 - C25	HA	1	Single	1.42998
52	C16 - N26	HA	1	Single	1.42988
53	N26 - C27	HA	1	Single	1.34458
54	C27 - C28	HA	1	Single	1.4954
55	C27 - C28	HA	2	Double	1.23692
56	C1 - H1	HA		Single	1.09839
57	C2 - H2	HA	1	Single	1.09906
58	C2 - H2 C3 - H3	HA	1	Single	1.10303
<u>50</u>	C3 - H3 C4 - H4	HA	1	Single	1.09817
<u> </u>	C4 - H4 C6 - H5	HA	1	Single	1.10296
61	C11 - H7	HA	1		1.10290
61 62	C11 - H7	HA HA	1	Single	1.0989
02			1	Single Single	1.08047
63	C11 - H9	HA		N 100 m 10	

No.	Name	Parent	Order	Туре	Length (Å)
65	013 - H11	HA	1	Single	0.988772
66	C15 - H12	HA	1	Single	1.09629
67	C16 - H13	HA	1	Single	1.10109
68	C17 - H14	HA	1	Single	1.09631
69	C19 - H15	HA	1	Single	1.10263
70	C20 - H16	HA	1	Single	1.09749
71	O21 - H17	HA	1	Single	0.986586
72	C22 - H18	HA	1	Single	1.09779
73	C22 - H19	HA	1	Single	1.09873
74	O23 - H20	HA	1	Single	0.988731
75	C25 - H21	HA	1	Single	1.09904
76	C25 - H22	HA	1	Single	1.09957
77	C25 - H23	HA	1	Single	1.09928
78	N26 - H24	HA	1	Single	0.993172
79	C28 - H25	HA	1	Single	1.09945
80	C28 - H26	HA	1	Single	1.09947
81	C28 - H27	HA	1	Single	1.09947
82	O9 - C22	HA	1	Single	1.41757

The PLGA-HA conjugate shows the total measurement of 82 bond length with average bond length of 1.266312 Å.

Properties	PLGA-HA conjugate		
Number of Atoms	81		
Molecular Formula	C23 H39 O18 N1		
Molecular Composition	C: 0.447, H: 0.064, O: 0.466, N: 0.023		
Molecular Weight	617.572		
Exact Molecular Weight	617.217		
Net Formal Charge	0		

 Table 4.10 Basic properties of PLGA-HA conjugate.

4.1.2.2 Curcumin-HA

One molecule of HA conjugated with one molecule of curcumin appearing in stick representation as illustrated in Fig. 4.5. Table 4.11 shows the bond length of this conjugate structure and Table 4.12 shows its basic properties.

In a study shows another important aspect of HA-Curcumin conjugate micelles is the protection of curcumin from degradation at physiological pH. Almost 90% of curcumin degradation occur within 30 min, but the conjugation has resulted in minimal change in the adsorption maximum even after 8 hr of incubation at 37°C (Manju & Sreenivasan, 2011).

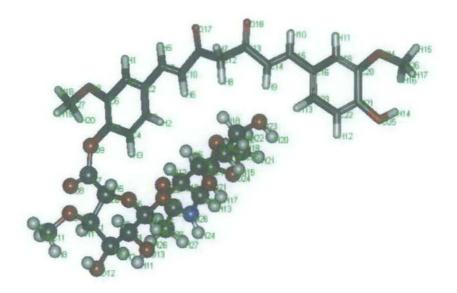


Figure 4.6 Molecular modeling of Curcumin-HA conjugate (with atom number).

No.	Name	Parent	Order	Туре	Length (Å)
1	C1 - C2	Curcumin	2	Double	1.32394
2	C2 - C3	Curcumin	1	Single	1.43878
3	C3 - C4	Curcumin	2	Double	1.32559
4	C4 - C5	Curcumin	1	Single	1.48737
5	C5 - C6	Curcumin	2	Double	1.36542
6	C6 - C1	Curcumin	1	Single	1.47133
7	C6-08	Curcumin	1	Single	1.46237
8	C9 - C10	Curcumin	2	Double	1.33506
9	C10 - C11	Curcumin	1	Single	1.45425
10	C11 - C12	Curcumin	1	Single	1.49463
11	C12 - C13	Curcumin	1	Single	1.49428
12	C13 - C14	Curcumin	1	Single	1.4547
13	C14 - C15	Curcumin	2	Double	1.33452
14	C15 - C16	Curcumin	1	Single	1.48586
15	C2 - C9	Curcumin	1	Single	1.48015
16	C11 - O17	Curcumin	2	Double	1.23584
17	C13 - O18	Curcumin	2	Double	1.23586
18	C19 - C20	Curcumin	2	Double	1.33284
19	C20 - C21	Curcumin	1	Single	1.55537
20	C21 - C22	Curcumin	2	Double	1.33199
21	C22 - C23	Curcumin	1	Single	1.45335
22	C16 - C19	Curcumin	1	Single	1.4565
23	C16 - C23	Curcumin	2	Double	1.33299
24	C20 - O24	Curcumin	1	Single	1.45357
25	C21 - O25	Curcumin	1	Single	1.42359
26	O24 - C26	Curcumin	1	Single	1.41593
27	O8 - C27	Curcumin	1	Single	1.43541

 Table 4.11 Bond and bond length of Curcumin-HA conjugate.

No.	Name	Parent	Order	Туре	Length (Å)
28	C1 - H1	Curcumin	1	Single	1.06019
29	C3 - H2	Curcumin	1	Single	1.05252
30	C4 - H3	Curcumin	1	Single	1.02923
31	C9 - H5	Curcumin	1	Single	1.06019
32	С10-Н6	Curcumin	1	Single	1.05784
33	C12 - H7	Curcumin	1	Single	1.09886
34	C12 - H8	Curcumin	1	Single	1.10038
35	C14 - H9	Curcumin	1	Single	1.0563
36	C15 - H10	Curcumin	1	Single	1.0602
37	C19 - H11	Curcumin	1	Single	1.06021
38	C22 - H12	Curcumin	1	Single	1.06026
39	C23 - H13	Curcumin	1	Single	1.05705
40	O25 - H14	Curcumin	1	Single	0.941093
41	C26 - H15	Curcumin	1	Single	1.09934
42	C26 - H16	Curcumin	1	Single	1.09958
43	C26 - H17	Curcumin	1	Single	1.09959
44	C27 - H18	Curcumin	1	Single	1.09924
45	C27 - H19	Curcumin	1	Single	1.09991
46	C27 - H20	Curcumin	1	Single	1.09995
47	C1 - C2	HA	1	Single	1.64311
48	C2 - C3	HA	1	Single	1.43863
49	C3 - C4	HA	1	Single	1.63816
50	C4 - O5	HA	1	Single	1.52075
51	O5 - C6	HA	1	Single	1.33557
52	C6 - C1	HA	1	Single	1.58622
53	<u>C6 - C7</u>	HA	1	Single	1.52527
54	C7 - O8	HA	2	Double	1.23583
55	C7 - O9	HA	1	Single	1.46687
56	C1 - O10	HA	1	Single	1.45904
57	010 - C11	HA	1	Single	1.44321
58	C2 - O12	HA	1	Single	1.42779
59	C3 - O13	HA	1	Single	1.42528
60	C4 - 014	HA	1	Single	1.43113
61	O14 - C15	HA	1	Single	1.46174
62	C15 - C16	HA	1	Single	1.47818
63	C16 - C17	HA	1	Single	1.67568
64	C17 - O18	HA	1	Single	1.52053
65	O18 - C19	HA	1	Single	1.31474
66	C19 - C20	HA	1	Single	1.57355
67	C20 - C15	HA	1	Single	1.61159
68	C20 - O21	HA	1	Single	1.43504
69	C19 - C22	HA	1	Single	1.52861
70	C22 - O23	HA	1	Single	1.42564
71	C17 - O24	HA	1	Single	1.43039
72	O24 - C25	HA	1	Single	1.43002
73	C16 - N26	HA	1	Single	1.47832
74	N26 - C27	HA	1	Single	1.34839

No.	Name	Parent	Order	Туре	Length (Å)
75	C27 - C28	HA	1	Single	1.49404
76	C27 - O29	HA	2	Double	1.23677
77	C1 - H1	HA	1	Single	1.09839
78	C2 - H2	HA	1	Single	1.09929
79	C3 - H3	HA	1	Single	1.10267
80	C4 - H4	HA	1	Single	1.09536
81	C6 - H5	HA	1	Single	1.09457
82	C11 - H7	HA	1	Single	1.09889
83	C11 - H8	HA	1	Single	1.08652
84	C11 - H9	HA	1	Single	1.09909
85	O12 - H10	HA	1	Single	0.979841
86	O13 - H11	HA	1	Single	0.988798
87	C15 - H12	HA	1	Single	1.09834
88	C16 - H13	HA	1	Single	1.10064
89	C17 - H14	HA	1	Single	1.09307
90	C19 - H15	HA	1	Single	1.10252
91	C20 - H16	HA	1	Single	1.09109
92	O21 - H17	HA	1	Single	0.987153
93	C22 - H18	HA	1	Single	1.10075
94	C22 - H19	HA	1	Single	1.09852
95	O23 - H20	HA	1	Single	0.988783
96	C25 - H21	HA	1	Single	1.09902
97	C25 - H22	HA	1	Single	1.09959
98	C25 - H23	HA	1	Single	1.09926
99	N26 - H24	HA	1	Single	0.992856
100	C28 - H25	HA	1	Single	1.09925
101	C28 - H26	HA	1	Single	1.10017
102	C28 - H27	HA	1	Single	1.09939
103	O9 - C5	HA	1	Single	1.46764

The Curcumin-HA conjugate shows the total measurement of 103 bond length with average bond length of 1.280048 Å. HA-Curcumin conjugates is amphipilic in nature containing both hydrophobic core by curcumin and the hydrophilic HA protruding outwardly and form shell layer (Gul-e-Saba, et al., 2011).

Properties	Curcumin-HA conjugate		
Number of Atoms	100		
Molecular Formula	C37 H45 O17 N1		
Molecular Composition	C: 0.573, H: 0.058, O: 0.351, N: 0.018		
Molecular Weight	775.774		
Exact Molecular Weight	775.269		
Net Formal Charge	0		

4.1.2.3 PLGA-PEG-HA

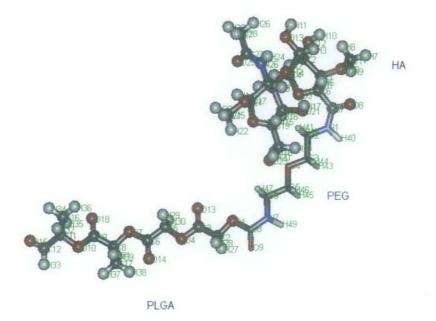


Figure 4.7 Molecular modeling of PLGA-PEG-HA conjugate (with atom number).

One molecule of HA conjugated with one molecule of PEG-bis amine as a spacer appearing in stick representation and one molecule of PLGA as illustrated in Fig. 4.7. This conjugated structure has been modeled from skeletal structure in Fig.3.2. Table 4.13 shows the bond length of this conjugate structure and Table 4.14 shows its basic properties.

No.	Name	Parent	Order	Туре	Length (Å)
1	C1 - C2	HA	1	Single	1.65421
2	C2 - C3	HA	1	Single	1.43798
3	C3 - C4	HA	1	Single	1.64219
4	C4 - O5	HA	1	Single	1.51794
5	O5 - C6	HA	1	Single	1.32966
6	C6 - C1	HA	1	Single	1.58803
7	C6 - C7	HA	1	Single	1.54045
8	C7 - O8	HA	2	Double	1.23577
9	C1 - O10	HA	1	Single	1.45877
10	O10 - C11	HA	1	Single	1.44341
11	C2 - 012	HA	1	Single	1.4279
12	C3 - 013	HA	1	Single	1.42562
13	C4-014	HA	1	Single	1.45506
14	O14 - C15	HA	1	Single	1.46159
15	C15 - C16	HA	1	Single	1.45083

Table 4.13 Bond and bond length of PLGA-PEG-HA conjugate.

No.	Name	Parent	Order	Туре	Length (Å)
16	C16 - C17	HA	1	Single	1.66793
17	C17 - O18	HA	1	Single	1.52218
18	O18 - C19	HA	1	Single	1.31802
19	C19 - C20	HA	1	Single	1.57516
20	C20 - C15	HA	1	Single	1.61966
21	C20 - O21	HA	1	Single	1.43594
22	C19 - C22	HA	1	Single	1.53067
23	C22 - O23	HA	1	Single	1.42623
24	C17 - O24	HA	1	Single	1.42983
25	O24 - C25	HA	1	Single	1.42979
26	C16 - N26	HA	1	Single	1.46651
27	N26 - C27	HA	1	Single	1.34448
28	C27 - C28	HA	1	Single	1.49547
29	C27 - O29	HA	2	Double	1.2369
30	C1 - H1	HA	1	Single	1.0983
31	C2 - H2	HA	1	Single	1.09903
32	C3 - H3	HA	1	Single	1.10268
33	C4 - H4	HA	1	Single	1.09819
34	C6 - H5	HA	1	Single	1.10187
35	C11 - H7	HA	1	Single	1.09891
36	C11 - H8	HA	1	Single	1.08611
37	C11 - H9	HA	1	Single	1.099
38	O12 - H10	HA	1	Single	0.979109
39	O13 - H11	HA	1	Single	0.988776
40	C15 - H12	HA	1	Single	1.09638
41	C16 - H13	HA	1	Single	1.10112
42	C17 - H14	HA	1	Single	1.09635
43	C19 - H15	HA	1	Single	1.10271
44	C20 - H16	HA	1	Single	1.09509
45	O21 - H17	HA	1	Single	0.986539
46	C22 - H18	HA	1	Single	1.10032
47	C22 - H19	HA	1	Single	1.09901
48	O23 - H20	HA	1	Single	0.989312
49	C25 - H21	HA	1	Single	1.09903
50	C25 - H22	HA	1	Single	1.09954
51	C25 - H23	HA	1	Single	1.0993
52	N26 - H24	HA	1	Single	0.993187
53	C28 - H25	HA	1	Single	1.09942
54	C28 - H26	HA	1	Single	1.09951
55	C28 - H27	HA	1	Single	1.09947
56	N1 - C7	PEG-HA	1	Single	1.34936
57	N1 - C2	PEG-bis amine	1	Single	1.43977
58	C2 - C3	PEG-bis amine	1	Single	1.53534
59	C3 - O4	PEG-bis amine	1	Single	1.42819
60	O4 - C5	PEG-bis amine	1	Single	1.42779
61	C5 - C6	PEG-bis amine	1	Single	1.53802
62	<u>C6 - N7</u>	PEG-bis amine	1	Single	1.43419

No.	Name	Parent	Order	Туре	Length (Å)
63	N7 - C8	PEG-bis amine	1	Single	1.39519
64	C8 - O9	PEG-bis amine	2	Double	1.23641
65	N1 - H40	PEG-bis amine	1	Single	1.07
66	C2 - H41	PEG-bis amine	1	Single	1.09
67	C2 - H42	PEG-bis amine	1	Single	1.09
68	C3 - H43	PEG-bis amine	1	Single	1.09
69	C3 - H44	PEG-bis amine	1	Single	1.09
70	C5 - H45	PEG-bis amine	1	Single	1.09
71	C5 - H46	PEG-bis amine	1	Single	1.09
72	C6 - H47	PEG-bis amine	1	Single	1.09
73	C6 - H48	PEG-bis amine	1	Single	1.09
74	N7 - H49	PEG-bis amine	1	Single	1.07
75	C8 - O1	PLGA-PEG	1	Single	1.39224
76	O1 - C2	PLGA	1	Single	1.43024
77	C2 - C3	PLGA	1	Single	1.49798
78	C3 - O4	PLGA	1	Single	1.39185
79	O4 - C5	PLGA	1	Single	1.42868
80	C5 - C6	PLGA	1	Single	1.49864
81	C6 - O7	PLGA	1	Single	1.4095
82	07 - C8	PLGA	1	Single	1.44536
83	C8 - C9	PLGA	1	Single	1.49838
84	C9 - O10	PLGA	1	Single	1.40994
85	O10 - C11	PLGA	1	Single	1.44508
86	C11 - C12	PLGA	1	Single	1.50032
87	C3 - O13	PLGA	2	Double	1.23636
88	C6 - O14	PLGA	2	Double	1.23702
89	C12 - O15	PLGA	2	Double	1.23615
90	C11 - C16	PLGA	1	Single	1.55065
91	C8 - C17	PLGA	1	Single	1.55089
92	C9 - O18	PLGA	2	Double	1.23706
93	C2 - H27	PLGA	1	Single	1.09
94	C2 - H28	PLGA	1	Single	1.09
95	C5 - H29	PLGA	1	Single	1.09
96	C5 - H30	PLGA	1	Single	1.09
97	C8 - H31	PLGA	1	Single	1.09
98	C11 - H32	PLGA	1	Single	1.09
99	C12 - H33	PLGA	1	Single	1.09
100	C16 - H34	PLGA	1	Single	1.08996
101	C16 - H35	PLGA	1	Single	1.09003
102	C16 - H36	PLGA	1	Single	1.09003
103	C17 - H37	PLGA	1	Single	1.08995
104	C17 - H38	PLGA	1	Single	1.09003
105	C17 - H39	PLGA	1	Single	1.09003

The PLGA-PEG-HA conjugate shows the total measurement of 105 bond length with average bond length of 1.274163 Å. Considering the bond no. 56 it indicates the bond between N7-C7 atoms where the conjugation between PEG and HA occurred and also at the bond no.75 indicates where the conjugation between PEG and PLGA occurred with C8-O1 atoms.

Properties	PLGA-PEG-HA conjugate		
Number of Atoms	104		
Molecular Formula	C31 H49 O21 N3		
Molecular Composition	C: 0.466, H: 0.062, O: 0.420, N: 0.053		
Molecular Weight	799.754		
Exact Molecular Weight	799.286		
Net Formal Charge	0		

Table 4.14 Basic properties of PLGA-PEG-HA conjugate.

The PLGA-PEG-HA conjugates can successfully prepared via reaction of one of the amino groups of PEG-bis amine with carboxylic group of HA and reacting second free amino group with PLGA (Fig. 3.2) (Yadav, et al., 2010). This conjugate molecule will be used for preparation of nanoparticles as a drug carrier.

4.1.2.4 Curcumin-PLGA-PEG-HA

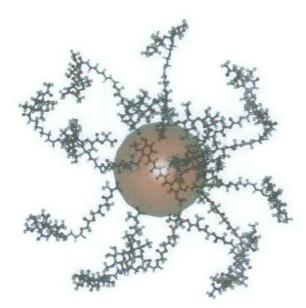


Figure 4.8 Molecular modeling of Curcumin-PLGA-PEG-HA nanoparticle.

Fig 4.8 shows the PLGA-PEG-HA nanoparticle with one molecule of curcumin as anticancer agent inside the hydrophobic core of spherical shape whereas at the surface of nanoparticle contains hydrophilic micelles of 15 PLGA-PEG-HA molecules. The basic process of synthesizing this nanoparticles is, first is to synthesize the empty nano-conjugates of PLGA-PEG-HA. Secondly, the curcumin is put into it by preparing the curcumin solution formed in water miscible organic solvents and during the synthesis of curcumin containing in nanoparticles, the streams of polymer (PLGA-PEG-HA) will collide with other stream of curcumin. Third, the hydrophobic curcumin and conjugate polymers will precipitate out of solution in an attempt to avoid the water molecules and finally the polymers immediately self-assemble onto the curcumin to form a coating with the hydrophobic portion attached to the nanoparticle core containing curcumin and the hydrophilic portion containing HA stretching out into the water solution.

Since the major roadblocks in curcumin development as a therapeutic for cancer is its poor water solubility and limited bioavailability therefore by using biodegradable nanoparticle like PLGA-PEG would exhibit enhanced cellular uptake and increase its bioavailability (Anand, et al., 2009). It is also been reported that grafting of PEG to the surface of nanoparticle containing PLGA will reduce the interaction between the nanoparticles and digestive enzymes, increases uptake of the encapsulated drug in the bloodstream and lymphatic tissue and also increase its half-life in the blood circulation (Dinarvand, et al., 2011). Conjugation to HA not only further increases the drug solubility but more importantly it enhances the chances to reach the cancer site. CD44 is overexpressed in human cancer cells and it is cell membrane-localized receptors or HA binding proteins therefore HA can bind to the cell surface via interactions with CD44 (Luo, et al., 2009). HA-PEG-PGLA uptake by CD44 receptor via endocytosis. The main advantage of the conjugation of drug to biodegradable polyester like PLGA-PEG is, first to prevent the initial burst and control the sustained release of molecules from nanoparticles (Oh, et al., 2007) and secondly is drug-polymer conjugates are easily formulated into nanoparticles by nano-precipitation method with very high encapsulation efficiency (almost 100%) (Anand, et al., 2009). In the study of Yadav, et al. (2010) has concluded that PLGA-PEG-HA nanoparticles can serve as efficient tools to ferry large doses of anti-cancer drug to tumor sites, with reduced access to non-tumor tissues.

CHAPTER 5

CONCLUSION

5.1 CONCLUSION

The three dimensional molecular modeling of the following molecule had been successfully developed using Discovery Studio 2.5: Curcumin, PLGA, HA, PEG-bis amine, PLGA conjugated HA, Curcumin conjugated HA, PLGA-PEG-HA conjugates and Curcumin-PLGA-PEG-HA nanoparticles. HA conjugates with nanoparticles molecules have high potential as targeted delivery vehicle to transport the anticancer agent to cancer cells and it also improves the stability, bioavailability of anticancer hydrophobic drug as compared to free curcumin. These molecular modeling might be further used as one of the references regarding the drug development method or molecular modeling study. Furthermore the nanoparticle model can also be modeled for CD44 target and this could possibly pave the way for rational design of target-specific drug delivery.

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