

CHAPTER IX

HOLLOW TORUS BASED ON INCLUSION OF BIOACTIVE MOLECULE INVESTIGATED BY SURFACE TENSION, CONDUCTANCE AND NMR

9.1. Introduction

In modern day cyclodextrin (CD) are used for the controlled release of various compounds and drugs [1]. Due to the exceptional truncated conical shape it has the capability to form inclusion complex with a variety of guest molecules including drug, vitamins, ionic liquids, neurotransmitters etc [2]. Cyclodextrin is a cyclic oligosaccharides having glucopyranose units six (α -CD), seven (β -CD) and eight (γ -CD) linked by α -(1-4) bonds [3] (scheme 2). The conical structure of CD have hydrophobic interior and hydrophilic rim with primary and secondary -OH groups. These hydroxyl groups are responsible of forming hydrogen bonding with guest molecules [4]. CD is considered safe for human body. In order to be biologically active a molecule should retain its integrity and should be able to cross the lipophilic membrane. CD has the ability to encapsulate the guest without any chemical modification of it. Sometimes it also increases the solubility of guest. The controlled release of CD is also used in food cosmetic, paint industry and removal of different toxic materials, pollutants, waste products without any chemical change [5]

L-Cysteine is an amino acid which is building block of protein (Scheme 1). It is a powerful anti oxidant. It is also used to metabolize of lipid, boosting the immune system. L-cysteine increase male fertility, reduce inflammation and combats decrease osteoporosis. In the body, cysteine is also used to produce the amino acid taurine as well as coenzyme A, biotin and heparin. Cysteine is component in beta keratin and it is proved that it preserve skin elasticity. It also protects the lining of digestive system [6-7].

In the present study we investigate the nature of formation and stoichiometry of inclusion complex of α and β -CD with natural amino acid L-cysteine in aqueous media .Aim of this work is the formation, carrying and controlled release of L-

cysteine by forming inclusion complex with host cyclodextrin molecules without chemical and biological modification of the guests.

9.2. Experimental Section

2. 1. Source and Purity of Samples

The amino acid L-cysteine and CDs of puriss grade were purchased from Sigma-Aldrich, Germany. The mass fraction purity of L-cysteine, α -CD and β -CD were 0.97, 0.98, and 0.98 respectively.

2. 2. Apparatus and Procedure

Conductance measurement was carried out in Mettler Toledo seven multi conductivity meter having uncertainty $1.0 \mu\text{Sm}^{-1}$. The conductivity of solution was studied in a thermo stated water bath at 298.15K with accuracy $\pm 0.001\text{K}$. HPLC grade water was used with specific conductance $10\mu\text{Sm}^{-1}$. The 0.01M aqueous KCl solution using for calibrated of the conductivity cell.

Surface tension of the solution was studied by platinum ring detachment technique using a tensiometer (K9, Krüss; Germany) at 298.15K with uncertainty $\pm 0.1\text{mN.m}^{-1}$. The temperature of the system was maintained by circulating thermo stated water through a double- wall glass vessel holding the solution.

NMR spectra were recorded using D_2O as a solvent. ^1H NMR spectra were recorded at 298.15K in 400 MHz and 500 MHz respectively using Bruker Avance 400MHz and 500MHz instrument. Residual protonated solvent Signals are quoted as δ values in ppm using internal standard (D_2O : δ 4.79ppm). Data are reported as chemical shifts.

3. Result and Discussion

3.1 ^1H NMR study establishes inclusion

^1H -NMR study confirms the inclusion phenomenon between the host CDs and the above mentioned amino acid cysteine [8-9] In the present work the molecular interactions of L-cysteine with α and β -cyclodextrins have been studied using the ^1H NMR spectra by taking a 1: 1 molar ratio of the amino acid and CDs in D_2O at 298.15 K. Insertion of L- cysteine in the hydrophobic cavity of CDs results chemical shifts of both the acid and CDs due to interaction between them. From scheme 3 it can be observed that the H3 and H5 protons of CD are located inside the cavity,

Table 1. Data for surface tension study of aqueous L-cysteine with α -CD and β -CD system at 298.15K^a

Volm. of CD (mL)	Total volm. (mL)	Conc. of L-cysteine (mM)	Conc. of CD (mM)	Surface tension in α -CD (mN m ⁻¹)	Surface tension in β -CD (mN m ⁻¹)
0	10	10.000	0.000	64.2	64.2
1	11	9.091	0.909	65.3	65.3
2	12	8.333	1.667	66.2	66.2
3	13	7.692	2.308	67.0	66.9
4	14	7.143	2.857	67.7	67.6
5	15	6.667	3.333	68.3	68.2
6	16	6.250	3.750	68.8	68.7
7	17	5.882	4.118	69.3	69.1
8	18	5.556	4.444	69.7	69.5
9	19	5.263	4.737	70.1	69.9
10	20	5.000	5.000	70.6	70.1
11	21	4.762	5.238	70.8	70.2
12	22	4.545	5.455	70.9	70.3
13	23	4.348	5.652	71.0	70.4
14	24	4.167	5.833	71.2	70.5
15	25	4.000	6.000	71.3	70.6
16	26	3.846	6.154	71.4	70.7
17	27	3.704	6.296	71.5	70.8
18	28	3.571	6.429	71.7	70.9
19	29	3.448	6.552	71.8	71.0
20	30	3.333	6.667	71.9	71.1

^aStandard uncertainties in temperature u are: $u(T) = \pm 0.01$ K.

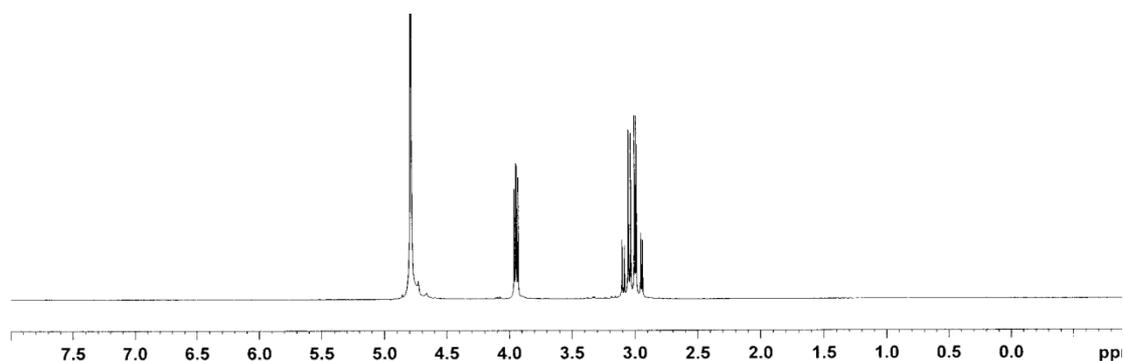
Table 2. Data for conductivity study of aqueous L-cysteine with α and β -CD system at 298.15K^a

Volm. of CD (mL)	Total volm. (mL)	Conc. of L-Leucine (mM)	Conc. of -CD (mM)	Conductivity in α -CD (mN m ⁻¹)	Conductivity in β -CD (mN m ⁻¹)
0	10	10.000	0.000	130	130
1	11	9.091	0.909	127	128
2	12	8.333	1.667	124	125
3	13	7.692	2.308	122	123
4	14	7.143	2.857	120	122
5	15	6.667	3.333	118	120
6	16	6.250	3.750	116	119
7	17	5.882	4.118	115	118
8	18	5.556	4.444	114	117
9	19	5.263	4.737	113	116
10	20	5.000	5.000	112	115
11	21	4.762	5.238	112	115
12	22	4.545	5.455	112	114
13	23	4.348	5.652	111	114
14	24	4.167	5.833	111	114
15	25	4.000	6.000	111	114
16	26	3.846	6.154	111	114
17	27	3.704	6.296	111	114
18	28	3.571	6.429	110	114
19	29	3.448	6.552	110	114
20	30	3.333	6.667	110	114

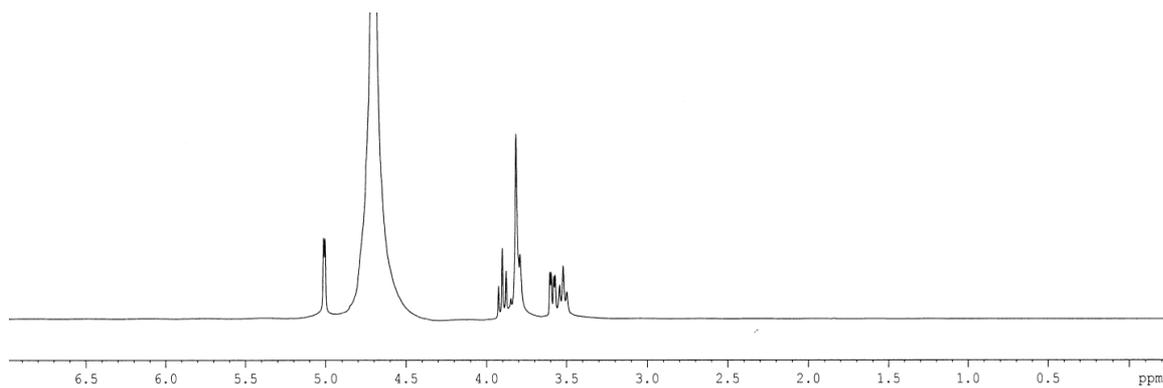
^aStandard uncertainties in temperature u are: $u(T) = \pm 0.01$ K.

Table 3: Values of surface tension (γ) at the break point with corresponding concentrations of cyclodextrins and amino acids and values of conductivity (μSm^{-1}) at the break point with corresponding concentrations of cyclodextrins and amino acids at 298.15 K

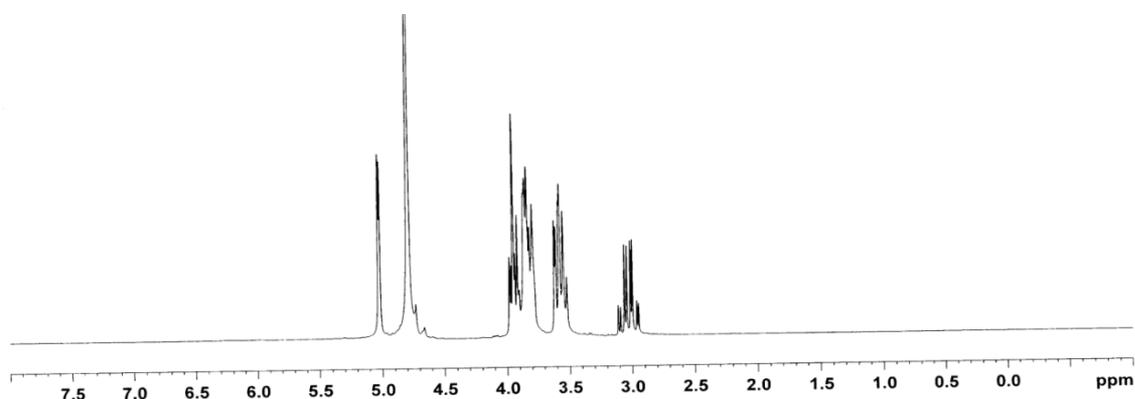
Amino acid	Conc. of α -CD/mM	Conc. of amino acid/mM	Surface tension γ^a /mNm ⁻¹
cysteine	5.27	4.73	70.77
	Conc. of β -CD/mM	Conc. of amino acid/mM	γ^a /mNm ⁻¹
	4.79	5.20	69.91
	Conc. of α -CD/mM	Conc. of amino acid/mM	κ^a / μSm^{-1}
	4.72	5.28	112.76
	Conc. of β -CD/mM	Conc. of amino acid/mM	κ^a / μSm^{-1}
	5.20	4.8	114.52



(a)



(b)



(c)

Figure 1: ^1H NMR spectra of (a) cysteine (b) α -CD and (c) 1:1 M ratio of α -CD & cysteine in D_2O at 298.15 K.

whereas H1, H2 and H4 are situated in the exterior of CD molecules. Among H3 and H5, H3 are near to the wider rim and H5 are closer to the narrower rim (Caso. et al., 2015). As most of the guest molecules are inserted through the wider rim, the H3 proton is more shifted compared to H5. In the present study the ^1H -NMR spectra of the CDs, L-cysteine inclusion complexes, the H3 and H5 protons of CD and the protons of acid show considerable shift. (Figure 1 and Figure 2) The other protons of CD show little shift in the spectra. This fact is in agreement with the formation of inclusion complex [11]. As indicated by chemical shift data the interaction of the H3 proton with cysteine is much higher than H5 probably due to insertion of the amino acid through the wider rim.

3.2 Surface tension study supports inclusion

Surface tension gives valuable information about the nature and formation of inclusion complex [12]. The aqueous solution of CD does not show any considerable change of surface tension. The amino acid shows the existence of NH_3^+ and COO^- in their zwitterionic forms [13]. Thus side group being non polar L- cysteine show surfactant like behaviour and it has a tendency to decrease the surface tension of aqueous solutions like other surfactants [14].

Here surface tension (γ) is measured for a series of solution with increasing concentration of both host α and β cyclodextrin at 298.15K. The γ values shows increasing trend in case of both the guests. (Table 1) Perhaps it is due to the formation of inclusion complex between L- cysteine and CD because due to the removal of the surface active type L-cysteine molecule from the surface of the solution into the hydrophobic cavity α and β cyclodextrin. In the two surface tension plots appearance of single break point indicates formation of inclusion complex (Figure 3).The values of surface tension with corresponding concentration of α and β cyclodextrin and concentration of cysteine at each break has been listed in table 1 .Over all variation of γ and one beak point clearly show that at certain concentration of amino acid and CD where their concentration ratio in solution was almost 1:1, thus the study proves 1:1 ratio in both α and β CD[15] (table 3)

3.3 Conductivity study informs inclusion

The conductivity measurement also gives valuable information not only about the inclusion phenomena but also the stoichiometry of the inclusion complex formed [16-17]. If inclusion complex is formed by L-cysteine with α and β CD, the conductivity of the solutions distinctly affected. The amino acid L- cysteine exists as zwitterions and due to the existence of this charged structure, it shows considerable conductivity. With addition of both the host α and β -CD the conductivity gradually decrease indicating the amino acid molecule enters into the hydrophobic cavity of α or β CD. (Table 2) The conductivities of a series of solution having 10 mmolL⁻¹ concentration of aqueous solution of cysteine with increasing concentration of cyclodextrins have been measured. The trend of conductivity regularly declining which indicates formation of the inclusion complex between CD and amino acid.

A sharp single break is found in the conductivity curve in each case. (Figure 4). This is again in agreement with the fact that 1:1 host – guest inclusion complex is formed between L-cysteine and CD's [18-20] a dynamic equilibrium is attained between the guest amino acid and host CD molecules. The break point is that at which maximum inclusion takes place.

3.4 Structural influence of cyclodextrin

Cyclodextrins are molecules with inner hydrophobic cavity and hydrophilic rims which provide an opportunity to act as host molecules. The guest molecule's apolar part resides inside the cavity and polar part of the guest molecule makes association with the polar rims, thereby forming stable inclusion complex. The apolar cavity diameter of α -CD is 4.7-5.3Å and β -CD is 6-6.5 Å respectively [21]. The size of natural amino acid L-Cysteine is within the range which can be easily encapsulated inside the cavity of CD. There is no covalent bond formation or breaking during the formation of inclusion complex [21]. The polar water molecules are present inside the slightly apolar cavity of cyclodextrin. This is generally energetically unfavoured. So the polar water molecules are readily substituted by hydrophobic chains of the amino acids. This results a more stable energy state. The stoichiometry of the inclusion complex is found as 1:1, which is supported by conductivity and surface tension measurements. So after inclusion of one amino acid molecule the zwitterionic part blocks the rim by making hydrogen bonding with the rim -OH groups, so second molecule cannot enter. Hydrophobic part of L- cysteine was found to be inserted through the wider rim of cyclodextrin.

4. Conclusion

The $^1\text{H-NMR}$ spectra, surface tension and conductivity study shows that the natural amino acid L-cysteine forms host-guest inclusion complex with both the CDs. The surface tension and conductivity study suggests the inclusion complex formation and 1:1 stoichiometry of the complex while the NMR data confirms the inclusion. These two inclusion complexes have vast applications in the field of bio-chemistry.

Figures:

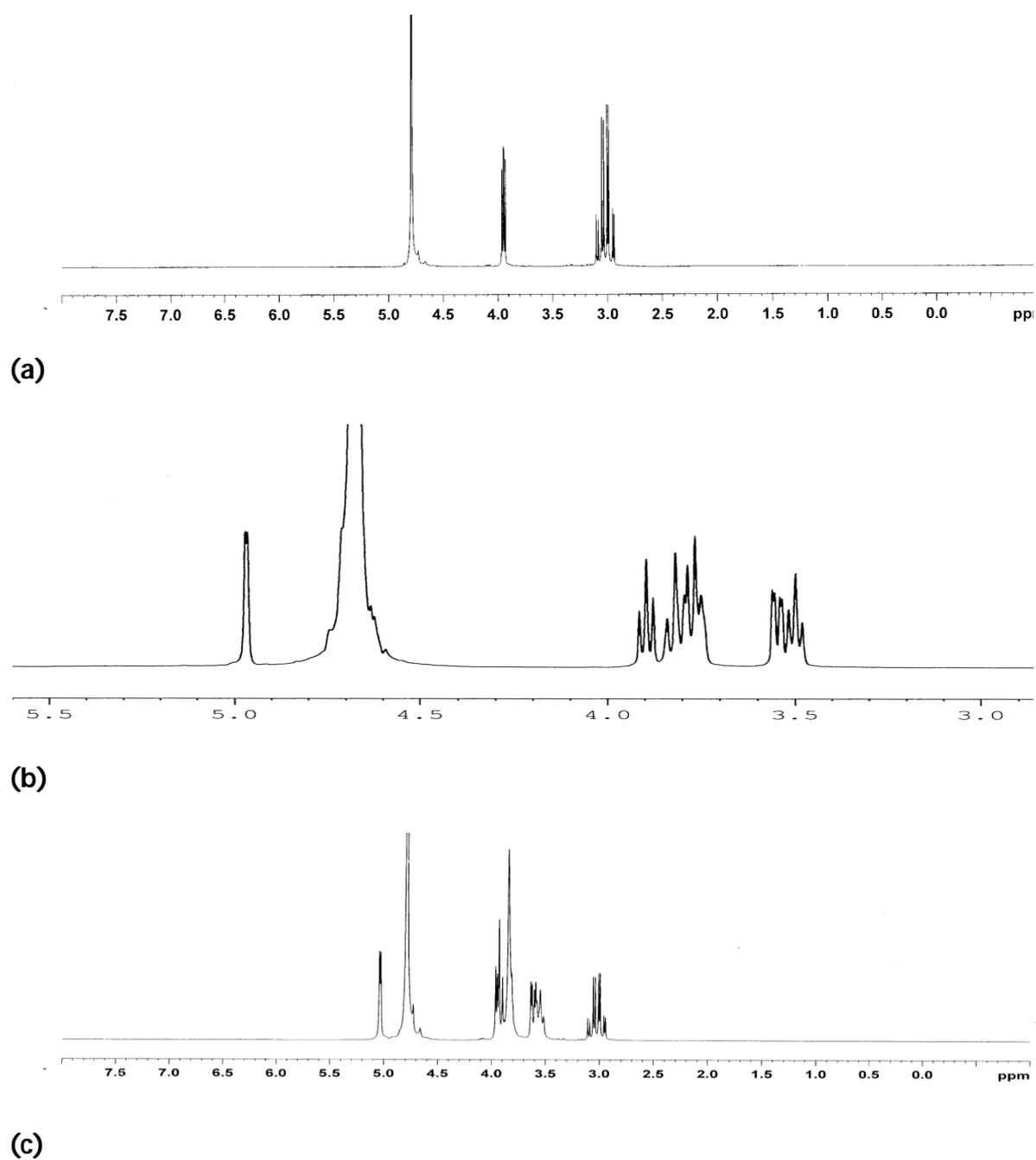


Figure 2: ^1H NMR spectra of (a) cysteine (b) β -CD and (c) 1:1 M ratio of β -CD & cysteine in D_2O at 298.15 K.

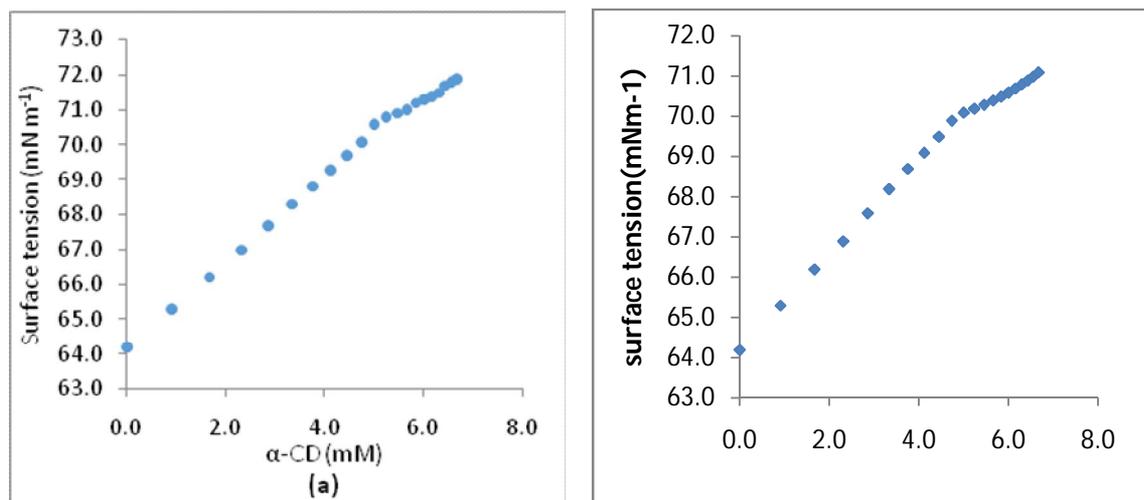


Figure 3: Variation of surface tension of aqueous (a) cysteine-α-CD and (b) cysteine-β-CD systems respectively at 298.15 K.

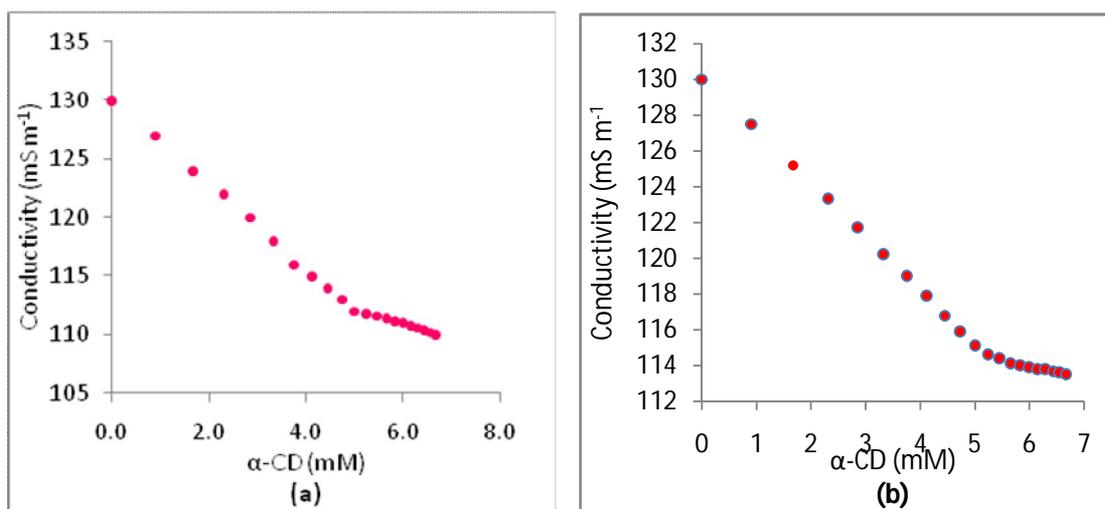
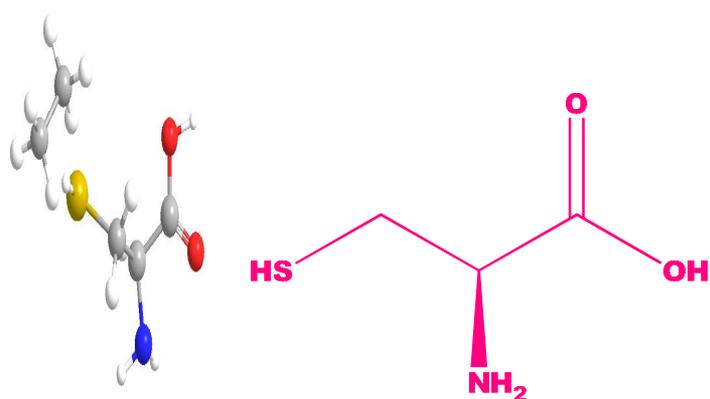
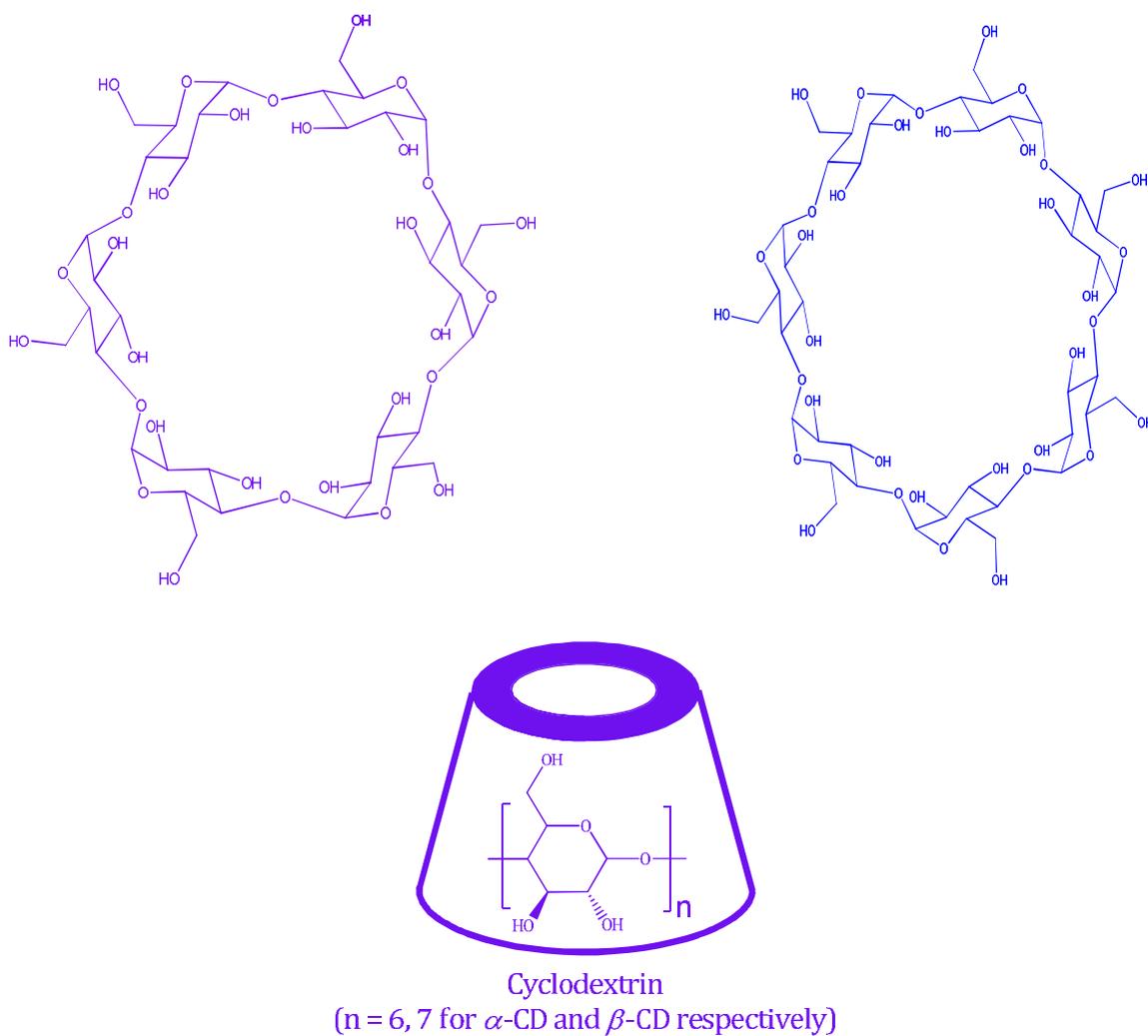


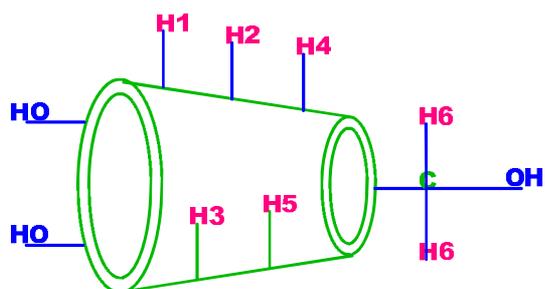
Figure 4. Variation of conductivity of aqueous (a) cysteine-α-CD and (b) cysteine-β-CD systems respectively at 298.15 K.

Schemes:

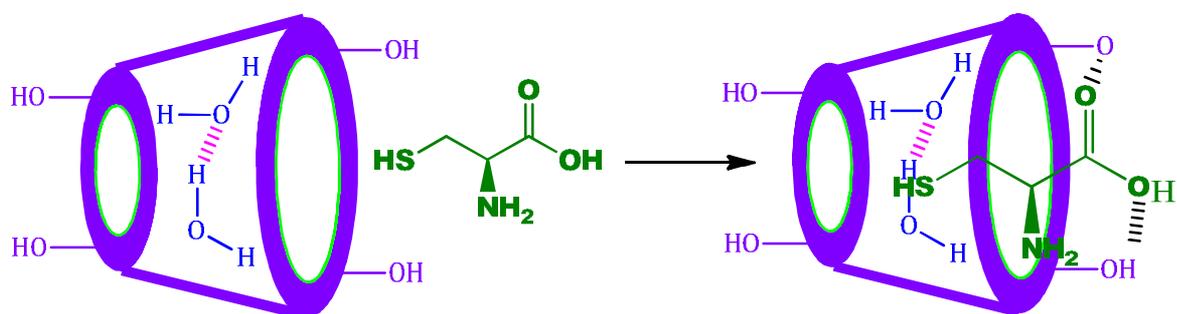
Scheme1. Molecular (a) Three dimensional and (b) Two dimensional structure of amino acid cysteine.



Scheme 2. Structure of cyclodextrin molecules.



Scheme 3: Truncated conical structure of α and β -cyclodextrin



Scheme 4 Plausible Schematic representation of mechanism for the formation of (1:1) inclusion complex of cysteine with both α and β -cyclodextrin.