Metal complexes of some peptide derivatives. Part-XIV. Complex formation of copper(II) with *N*-benzenesulfonamides of some dipeptides

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Combined potentiometric and spectrophotometric investigation on the complex formation equilibria of Cu^{II} with *N*-benzenesulfonyl derivatives of some dipeptides, viz. glycylglycine, glycyl-*dl*- α -alanine, glycyl-*dl*-methionine, glycyl- β -alanine, β -alanylglycine (AH₂) in aqueous solution provides evidence of complexes of the types : $Cu(AH)^+$, $Cu(H_{-1}AH)$, $Cu(H_{-1}A)^-$, $Cu(H_{-1}A)(OH)^{2-}$, $Cu(AH)_2$, $Cu(H_{-1}AH)_2^+$, $Cu(H_{-1}A)_2^+$, $Cu(H_{-1}A)_2^+$, $Cu(H_{-1}A)_2^-$, $Cu(H_{-1}A)_2^$

Complex formation of metal ions of biological importance with amino acids, small peptides and their derivatives are of great significance, as many of these systems offer simple models of otherwise complex metal-protein equilibria occurring in enzymic processes. At low pH, the peptide group undergoes both protonation and metallation at the carbonyl oxygen atom. Metal ion coordination with the amide nitrogen atom takes place only upon substitution of the amide proton, for which a primary ligating site at a chelating position is, however, essential^{1,2} With a view to study the effect of a sulfonamide group at a chelating position on the modes of metal ion coordination by the amide group in dipeptides, the present paper describes the results of a systematic equilibrium study on the complex formation of Cu^{II} with a series of *N*-benzenesulfonyl derivatives (1),

C6H5SO2NH(CH2)x CONH(CHR)yCOOH

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of the following dipeptides, viz. glycylglycine, SGG (x = 1, y = 1, R = H), glycyl-dl- α -alanine, SGA (x = 1, y = 1. R = CH₃), glycyl-dl-methionine, SGM (x = 1, y = 1, R = CH₂CH₂SCH₃), glycyl- β -alamine, SGB (x = 1, y = 2, R = H) and β -alanylglycine, SBG (x = 2, y = 1, R = H) in aqueous solution, I = 0.2 M (NaNO₃) at 25 ± 1° by combined potentiometric and spectropho-tometric methods, coupled with computerized evaluation of the equilibrium constants³. Formation constants of the complexes are cor-

related with the modes of metal ion coordination by the amide and the sulfonamide moieties, size of the chelate rings and metal-ligand and ligand-ligand- π -interactions.

Results and Discussion

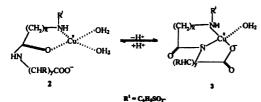
Proton-ligand equilibria : All the five sulfonamidodipeptide ligands, viz. SGG, SGA, SGM, SGB and SBG titrate as diprotic acids (AH₂) giving two wellseparated buffer regions, pH 2.5~4.4 and pH 8–11, corresponding to the deprotonation of the COOH and the SO₂NH groups in successive steps. In the absence of Cu^{II} the amide (CONH) group remains neutral in the entire pH range^{4,5}. The analogous ligand acetylglycine, CH₃CON-HCH₂COOH titrates as a monoprotic acid (AH) in the pH range 2.5–12.0. This supports the proposition of deprotonation of the SO₂NH group of the free ligands in the second step⁶.

 $1:1 Cu^{II}: AH_2 equilibria$: The initial buffer region (pH 2.5-5.5) in the pH-metric titrations of $1:1 Cu^{II}: AH_2$ mixtures (AH₂ = SGG, SGA, SGM, SGB and SBG) coincides with that due to deprotonation of the COOH group of the corresponding ligands (AH₂) in the absence of Cu^{II}. Thus, deprotonation of the COOH group of the ligands is not influenced by the presence of Cu^{II}. This is followed by two well-separated buffer regions, pH 5-7 and pH 8-11. Two moles of base (a = 2) per mole of Cu^{II} are consumed in the lower pH buffer region (pH 5-7) giving a sharp inflection

point, beyond which a third mole of base (a = 3) per Cu^{II} is consumed in the higher pH buffer region (pH 8–11). All the five ligands remain mainly in their COOH deprotonated monoanionic (AH⁻) forms in the first buffer region (pH 5– 7) of complex formation. Therefore, formation of 1 : 1 Cu^{II} : AH⁻ complexes with release of two protons per Cu^{II} obviously involves deprotonation of both SO₂NH as well as the CONH groups, according to equilibrium (1),

$$CH^{2+} + AH^{-} \Longrightarrow Cu(H_{-1}A)^{-} + 2 H^{+}$$
(1)

The λ_{max} (log \in) values of 1 : 1 Cu^{II} : AH⁻ mixtures at pH values corresponding to a = 0, 1 and 2 show a large blueshift from ~740 nm (1.5) at a = 0 to ~645 nm (2.05) at a =1 and a small blue-shift ~ 5 nm from a = 1 to a = 2. The observed λ_{max} values at a = 0 and a = 1 are close to the calculated values for square-planar Cull-dipeptide complexes with $[Cu(N,O), 2(H_2O)]$ and $[Cu(N,N,O), (H_2O)]$ coordination¹. This indicates the existence at a = 0, of a complex, $Cu(AH)(H_2O)^+$, in which the ligand AH^- ion coordinates Cu^{II} as a (N,O)bibentate ligand using the carbonyl O-atom of the amide group and neutral N-atom of the sulfonamide group, the remaining two positions around square-planar Cu^{II} are coordinated by two H₂O ligands (2). The carboxylate O-atom of AH- ions fails to coordinate Cull in these complexes due to angle strain in 7/8 - membered ring. The initial large blue-shift of λ_{max} with rise of pH may be attributed to substitution of the amide cabonyl O-atom in 2 by deprotonated amide N-atom, thereby transforming the ligand ion AH⁻, into H₋₁AH²⁻ ion, which coordinates Cu^{II} using the neutral N-atom of the sulfonamide group, deprotonated amide N-atom of the peptide group. The latter provides a stronger ligand field than the amide carbonyl O-atom and is obviously responsible for the blue-shift of the absorption maxima of Cu^{II} by ~90-100 nm. This structural change also brings the carboxylate Oatom of the ligand to a chelating position, making the $H_{-1}AH^{2-}$ ligand ions a (N,N⁻,O⁻)terdentate ligand in the resulting Cu(H₁AH)(H₂O) complexes (3).



A similar blue-shift of λ_{max} of Cu^{II} with increase of log \in has also been observed in case of conversion of Cu(AlaH)²⁺ into Cu(H₋₁AlaH)⁺, where AlaH = alaninamide⁷. On further increase of pH (i.e. in going from a = 1 to a = 2), the coordinated -SO₂NH- group in the Cu(H₋₁AH)(H₂O) complexes undergoes deprotonation to produce the complexes, Cu(H₋₁A)(H₂O)⁻ without any significant change of λ_{max} of Cu^{II}, as the strengths of the ligand fields provided by a neutral and a deprotonated sulfonamide N-atom are not very much different. The observed λ_{max} values of ~640 nm of 1 : 1 Cu^{II} : AH⁻ mixtures at a = 2 (pH ~7.25) are fairly close to the calculated value (~632 nm) for a square-planar Cu_{II} complex, Cu(H₋₁A) (H₂O)⁻, in which the ligand H₋₁A³⁻ ions coordinate Cu^{II} with deprotonated amide N-atom, deprotonated sulfonamide N-atom, carboxylate O-atom and a H₂O molecule. The higher pH-buffer region (pH 8–11) of 1 : 1 Cu^{II} : AH⁻ mixture obviously corresponds to deprotonation of the coordinated H₂O ligand in these Cu(H₋₁A)(H₂O)⁻ complexes according to equilibrium (2), since there are no other dissociable proton in these complexes,

$$Cu(H_{-1}A)(H_{2}O)^{-} \implies Cu(H_{-1}A)(OH)^{2-} + H^{+}$$
 (2)

The λ_{max} values of Cu^{II} remain practically unchanged in going from a = 2 to a = 3, as H₂O and OH⁻ are very closely placed in the spectrochemical series⁸.

 $1: 2 Cu^{ll}$ AH_2 equilibria : The initial buffer regions (pH 2.5-4.0) in the pH-metric titrations of 1: 2, 1: 5 and $1 : 10 \text{ Cu}^{\text{II}} : \text{AH}_2 \text{ mixtures (AH}_2 = \text{SGG, SGA, SGM and}$ SGB) coincide with those corresponding to the deprotonation of the COOH groups of the corresponding free ligands in the absence of Cu^{II}, similar to the 1 : 1 Cu^{II} : AH₂ systems. This is followed by two well-defined buffer regions, pH 4.5-6.5 and 7.5-11. In each of these regions, two moles of base (a = 2, a = 4) per mole of Cu^{II} are consumed. Mole ratio plots⁹ of the Cu^{II} : AH₂ mixtures at pH values corresponding to a = 0, 2 and 4 by spectrophotometric method at the appropriate λ_{max} values indicates the existence of both 1 : 1 and ! : 2 Cu^{II} : AH_2 complexes, as well as the absence of complexes higher than 1:2. As all these ligands in their lower pH-buffer region (pH 4.5-6.5) of complex formation remain in the forms of their COOH deprotonated monoanions (AH⁻), therefore, the formation of 1 : 1 and $1:2 \text{ Cu}^{II}: AH^{-}$ complexes involving the release of two to four protons per Cu^{II} in stepwise manner may be represented according to equilibria (3)-(6),

$$Cu^{2+} + AH^{-} \Longrightarrow Cu(H_{-1}AH) + H^{+}$$
(3)

$$Cu^{2+} + 2 AH^{-} \Longrightarrow Cu(H_{-1}AH)^{2-}_{2} + 2 H^{+}$$
(4)

$$Cu(H_{-1}AH)_2^2 \longrightarrow Cu(H_{-1}A)(H_{-1}AH)^{3-} + H^+$$
 (5)

$$Cu(H_{-1}A)(H_{-1}AH)^{3-} \Longrightarrow Cu(H_{-1}A)^{4-}_{2} + H^{+}$$
 (6)

in addition to equilibrium (1) described earlier. The λ_{max} (log \in) values of 1 : 5 Cu^{II} : AH₂ mixtures at pH values corresponding to a = 0, 1, 2, 3 and 4 show a large blue-shift by ~60-65 nm in going from a = 0 to a = 2 and a small blue-shift of ~5 nm in going from a = 2 to a = 4. The first blue-shift indicates a significant increase of ligand field stength around Cu^{II} in going from a = 0 to a = 2, which may be attributed to a change from [Cu(N,O)₂] to [Cu(N,N,O)₂] coordination^{1,6}. Thus, at a = 0, the 1 : 2, Cu^{II} : AH⁻ complexes may be Cu(AH₂) in which Cu^{II} is (N,O)biden

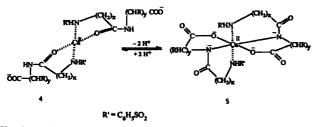
 Table 1. Formation constants of proton-ligand and Cu^{II}-ligand complexes with SGG, SGA, SGM, SGB and SBG (AH₂), and Cu^{II}-promoted deprotonation constants of coordinated CONH, SO₂NH and H₂O ligands*

| $1 \text{ cmp} = 25 \pm 1, 7 \pm 1$ | 0.2 m (14a1403), 1 | n aqueous solution | | | | | |
|--|--------------------|---|-------|-------|-------|-------|-------|
| Cu _p A _q (OH) _r | pqr | Constant | SGG | SGA | SGM | SGB | SBG |
| AH ₂ | 01–2 | –log К <mark>Н</mark> соон | 3.55 | 3.44 | 3.24 | 4.32 | 3.45 |
| АН | 0 1-1 | $-\log K_{SO_2NH}^{H}$ | 9.65 | 9.74 | 9.70 | 9.73 | 10.66 |
| Cu(AH) | 1 1–2 | log K ^{Cu} (AH) | 2.75 | 2.47 | 3.05 | 2.92 | 3.48 |
| Cu(H ₋₁ AH) | 1 1–2 | $-\log K_{(Cu+AH)}^{H}$ | 2.60 | 2.93 | 1.94 | 2.29 | 2.97 |
| Cu(H ₋₁ A) | 110 | $-\log K_{(Cu+AH)}^{2H}$ | 8.50 | 8.44 | 7 99 | 7.93 | 10.30 |
| Cu(H ₋₁ A)(OH) | 111 | $-\log K_{(Cu+AH+H_2O)}^{3H}$ | 17.75 | 17.79 | 16 99 | 17 13 | 19.80 |
| | | –log K _d | -1.55 | -2.15 | -2.32 | -5.08 | - |
| Cu(AH) ₂ | 1 2–4 | log K ^{Cu} (AH)2 | 4.80 | 4.34 | 5.50 | 5 24 | 6.36 |
| Cu(H ₋₁ AH)(AH) | 1 2-3 | $\log K_{(Cu+2AH)}^{H}$ | -0.40 | -1.06 | 1.00 | 0.76 | - |
| Cu(H-1AH)2 | 1 2–2 | –log K ^{2H} (Cu+2AH) | 6.40 | 6.60 | 5.49 | 7.13 | - |
| $Cu(H_{-1}A)(H_{-1}AH)$ | 1 2-1 | –log K ^{3H} Cu+2AH) | 15.20 | 15.93 | 14 82 | 16.93 | - |
| Cu(H ₋₁ A) ₂ | 120 | $-\log K_{(Cu+2AH)}^{4H}$ | 25.05 | 25.73 | 24.30 | 27.34 | - |
| Cu ^{II} : AH ₂ | Equilibria | | | | | | |
| 1:1 | (7) | pK ^H [Cu(CONH)] | 5.35 | 5 40 | 4.99 | 5 21 | 6.45 |
| 1:1 | (8) | $pK_{[Cu(SO_2NH)]}^{H}$ | 5.90 | 5.51 | 6.05 | 5.64 | 7 33 |
| 1:2 | (7) | pK ^H [Cu(CONH)2] | 5.20 | 5.40 | 4.50 | 6.00 | - |
| 1:2 | (7) | pK ^{2H} [Cu(CONH)2] | 11.22 | 10.94 | 10.99 | 12 37 | · _ |
| 1:2 | (8) | рК <mark>[Cu(SO2NH)2]</mark> | 8.80 | 9.33 | 9.33 | 9.80 | - |
| 1:2 | (8) | pK ^{2H} [Cu(SO ₂ NH) ₂] | 18.65 | 19 15 | 18.81 | 20.01 | - |
| 1:1 | (2) | р <i>К</i> [Си(Н_1А)(Н2О)] | 9.25 | 9 35 | 9.00 | 9.10 | 9.50 |
| | | | | | | | |

^{*}Limits of error = ± 0.02 ~0.05 in log unit. Changes are not shown for clarity.

Temp. = $25 \pm 1^{\circ}$, I = 0.2 M (NaNO₃), in aqueous solution

tate coordinated by the neutral N-atom of the neutral SO₂NH group and O-atom of the neutral CONH group (4), the O-atom of the COO⁻ group of AH⁻ fails to coordinate because of angle strain in 7/8-membered ring. In going from a = 0 to a = 2, these Cu(AH)₂ complexes certainly undergo a structural change involving substitution of the amide carbonyl O-atom by the deprotonated amide N-atom. This simultaneously brings the COO⁻ group at a chelating position making the H₋₁AH²⁻ ion a (N,N⁻,O⁻)terdentate ligand. Cu^{II} in the resulting amide deprotonated Cu(H₋₁AH)²₂⁻ complexes (5) is terdentate (N,N⁻,O⁻) chelated by the N-atom of neutral SO₂NH group, deprotonated amide N-atom and the carboxylate O-atom.



The large blue shift of λ_{max} in going from a = 0 to a = 2 is the result of substitution of the amide carbonyl O-atom by the deprotonated amide N-atom within the Cu^{II} coordination sphere. A similar blue-shift in the absorption maxima of Cu^{II} has also been observed in the case of conversion of $Cu(AlaH)_2^{2-}$ into $(Cu(H_{-1}AlaH)_2$, where AlaH = alamina $mid)^7$. Smaller shift in the present case may be due to axial coordination of Cu^{II} , possibly by the N-atoms of the SO_2NH groups in the $Cu(H_{-1}AH)_2^{2-}$ complexes (5). The observed absorption maxima ~640 nm (log $\in = 2$) of Cu^{II} at a = 2 are in good agreement with tetragonally distorted octahedral $Cu(N,N^-,O^-)_2$ geometry¹. The calculated λ_{max} for a square-planar $Cu(N,N^-)_2$ geometry with two neutral and two deprotonated amide N-atoms as donors, making allowance for acidity of the SO_2NH group, should be around 580 nm, which is about 60 nm lowar than the observed values (~640 nm) of the amide deprotonated $Cu(H_{-1}AH)_2^{2-}$ complexes (5). Such a difference strongly suggests axial coordination of Cu^{II} in the $Cu(H_{-1}AH)_2^{2-}$ complexes¹⁰.

The higher pH-buffer region (pH-7.5–11), a = 2 to a = 4, obviously involves deprotonation of the two coordinated SO₂NH groups of the Cu(H_AH)₂²⁻ complexes (5) according to eqlm. (5) and (6) to form the fully deprotonated Cu(H₋₁A)₂⁴⁻ complexes, in which Cu^{II} is (N,N⁻,O⁻)terdentate chelated by the N-atoms of deprotonated sulfonamide and amide groups and the O-atom of the carboxylate group of the ligand H₋₁A³⁻ ions. As the strengths of the ligand fields exerted by the N-atom of the neutral and deprotonated SO₂NH groups are not expected to be very much different, the λ_{max} (log \in) values of $1 : 2 \text{ Cu}^{\text{II}} : \text{AH}^$ mixtures remain practically unchanged in going from a = 2to a = 4.

The first step of complex formation (eqlm. 1 or 3 as the case may be) is found to be complete at pH values much lower than the buffer region corresponding to the hydrolytic equilibria of $Cu^{2+}(aq)$ ions, so the binary hydroxo complexes, $Cu(OH)^+$, $Cu(OH)_2$ etc. have been excluded in calculating the formation constants³ of Cu^{II} -AH₂ complexes. Formation constants of some of the 1 : 2 Cu^{II} -SBG complexes could not be determined due to the commencement of precipitation.

The overall formation constants of the complexes have been obtained as computer out-put, from which the Cu^{II}promoted deprotonation constants of coordinated amide (CONH), sulfonamide (SO₂NH) and H₂O ligands have been calculated (Tablet 1) using appropriate relations. Although the amide group in the free ligands remains neutral in the entire pH-range, metallation with amide N-atom takes place upon amide deprotonation¹¹ (eqlm. 7) in the presence of Cu_{II} in the pH range 4.5–6.5 {eqlm. (2) \implies (3) and eqlm. (4) \implies (5)) :

$$c_{u}^{2+} - c_{v}^{H}$$
 $H^{+} (Cu(CONH))$ $c_{u}^{2+} + H^{+} (7)$

Acidity of coordinated SO₂NH group in the Cu(H₁AH) complexes is enhanced by 3–4 log units over the acidity of uncoordinated SO₂NH group in the free ligands. The strongly suggests an equatorial disposition of the sulfonamide N-atom with the deprotonated amide-N and carboxylate O-atoms in the square-planar coordination geometry of Cu(H₁AH) complexes (3). However, such increase of acidity of SO₂NH group in the 1 : 2 complexes Cu(H₁AH)²⁻₂, (5) is quite small, ~0.1–0.5 log unit, suggesting a weak and possibly an axial coordination of the sulfonamide N-atom in these distorted octahedral Cu^{II} complexes. Further, it is observed that Cu^{II} promoted amide deprotonation (eqIm. 7) takes place at pH values much lower than the buffer region corresponding to deprotonation of coordinated sulfonamide group (eqIm. 8),

obviously due to favorable entropy effect arising out of a change from bidentate (N,O)mode of coordination by the ligand AH⁻ ions in Cu(AH)(H₂O)⁺₂ (2) and Cu(AH)₂ (4), to the terdentate (N,N⁻,O⁻)mode of coordination by the ligands $H_{-1}AH^{2-}$ ions in Cu(H₋₁AH)(H₂O) (3) and Cu(H₋₁AH)²₂ (5) complexes.

Stability constants of the (N,O)bidentate chelated

 $Cu(AH)(H_2O)_2^+$ and $Cu(AH)_2$ complexes fall in the ligand order : SBG > SGM > SGB > SGG > SGA. Higher stability of Cu(AH)(H₂O)⁺₂ and Cu(AH)₂ complexes derived from SBG may be due to lower angle strain in the six-membered chelate ring with a (C=O) double bond as compared to that in the corresponding complexes derived from the other ligands having five-membered chelate rings with (C=O) double bond. Comparatively higher stability of the complexes derived from SGM may be due to additional coordination by the methionine sulfur atom possibly in an intermolecular mode. Such intermolecular coordination of methionine sulfur in the $Cu(AH)(H_2O)_2^+$ and $Cu(AH)_2$ complexes possibly takes place at a position trans to the coordinated amide group, as is evident from the comparatively higher acidity of the amide proton (eqlm. 7) in the complexes derived from SGM, suggesting some metal $(d\pi) \rightarrow$ methionine $S(d\pi)$ back-bonding, which may enhance the acidity of amide proton. The resulting amide deprotonated complexes (3, 5) derived from SGM may be further stabilized through hydrophobic stacking interaction^{12,13} between the vacant $(d\pi)$ orbitals of methionine sulfur and the delocalized π -mo of the deprotonated amide (CON) moiety.

Deprotonation constants of coordinated H₂O molecule in $Cu(H_1A)(H_2O)^-$ complexes (eqlm. 2) are found to be fairly close to those of equatorially coordinated H₂O molecules in square-planar Cu^{II} complexes¹⁴. Formation of $Cu(H_1A)(OH)^{2-}$ complexes starts at pH \geq 7 and the solutions turn turbid around pH~10, where the concentration of the $Cu(H_1A)(OH)^{2-}$ complexes rise to $\geq 80\%$. Absorption maxima (~635 nm) of the clear filtrates are almost the same as the absorption maxima of $1:2 \text{ Cu}^{II}: \text{AH}^-$ mixtures are a = 4 (pH \approx 11). Calculation of the concentration of copper in the clear filtrates using the $\log \in$ values (~2.05) of the corresponding 1 : 2 Cu^{II} : AH⁻ mixtures at a = 4 provides evidence of formation of the fully deprotonated 1 : 2 Cu^{II}ligand complexes, $Cu(H_{-1}A)_2^4$ possibly through dissociation of the ternary hydroxo complexes, $Cu(H_1A)(OH)^{2-}$, according to eqlm. (9),

2
$$Cu(H_{-1}A)(OH)^{2-} \implies Cu(H_{-1}A)_{2}^{4-} + Cu(OH)_{2}$$
 (9)

of which the dissociation K_d may be calculated using the relation (10),

$$\log K_{\rm d} = \log K_{\rm (Cu+2AH)}^{\rm 4H} + K_{\rm Cu}^{\rm 2H} - 2 \log K_{\rm (Cu+AH+H_2O)}^{\rm 3H}$$
(10)

where, K_{Cu}^{2H} is the hydrolysis constant of Cu²⁺ (aq.) ion producing Cu(OH)₂. The log K_d values (Table 1) fall approximately in the reverse order of the formation constants of Cu(H₋₁A)(OH)²⁻ complexes. Comparatively higher stability of the Cu(H₋₁A)(OH)²⁻ complexes derived from SGB is possibly due to greater configurational flexibility of a combination of five- and six-membered chelate ring system in this complex over five-membered ring systems in the complexes derived from the other ligands. Due nonavailability of $K_{(Cu+2AH)}^{4H}$ value for the 1 : 2 Cu^{II} : SBG system, the corresponding K_d value could not be calculated.

Experimental

The ligands SGG, SGA, SGM and SGB were prepared by condensing N-benzenesulfonylglycyl chloride (0.02 mol) with the sodium salt (0.02 mol) of the corresponding amino acids (viz. glycine, α -alanine, *dl*-methionine and β alanine) at room temperature in aqueous solution at pH ≈ 9 maintained by adding 5% NaOH solution with constant stirring following the procedure as described earlier⁶. After stirring the reaction mixture for 1h, it was cooled in an icewater bath and acidified (pH \approx 2) with 2 M HCl. The resulting white crystalline needles were further purified by crystallization from hot water and air-dried. The ligand SBG was prepared by condensing N-benzenesulfonyl β -alanyl chloride with sodium glycinate following an analogous procedure. All the ligands were characterized by elemental analysis, equivalent weight determination and IR and UV spectral data. v_{max}^{15} for the COOH, amide (CONH) and sulfonamide (SO₂NH) groups were identified in the usual regions : 1740 ~ 1710 (COOH), 1640-1590 (amide I), 1565-1535 (amide II), 1285-1240 (amide III), 1350-1320 (sulfonamide I) and 1175-1155 cm⁻¹ (sulfonamide II). All the other reagents were of A.R. grade and their solutions were prepared in double-distilled CO2-free water. Cu(NO₃)₂ solution was standardized by combined ion exchange, acid-base and complexometric EDTA titrations¹⁶.

pH was measured with a Systronics 335 pH meter (accuracy ± 0.01 pH) using a special glass electrode in conjunction with a SCE. Electronic spectra were measured on a Hitachi U-3501 spectrophotometer and IR (KBr) on a Parkin-Elmer 681 spectrometer.

Experimental determination of the proton-ligand and Cu^{II}-ligand complex formation constants involved pHmetric titration¹⁷ of a series of aqueous solutions of known amounts (0.001 ~0.01 *M*) of the ligands (AH₂ = SGG, SGA, SGM, SGB and SBG as the case may be) containing known amount of (0.01 *M*) free HNO₃ in each case, in the absence and in the presence of known amounts (0.001 ~ 0.002) *M* Cu(NO₃)₂ with a carbonate-free standard (0.125 *M*) NaOH solution¹⁸ maintaining a constant ionic strength, I = 0.2 M(NaNO₃) at 25 ± 1°.

Analytical concentrations of hydrogen ion, correspond-

ing to the pH-meter reading were calculated by following the usual procedure¹⁹. Ionic product of water at the experimental temperature and activity coefficients of H^+ ion at the experimental ionic strength were obtained from literature^{20,21}. Formation constants were calculated with the aid of scogs computer programme³ using the pH vs volume of NaOH data as were the averages of three titrations, each time repeating the cycle of operation up to the minimum value of standard deviation.

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