Interaction of cis-Pd(guo)₂Cl₂ with Amino Acids

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Abstract

The reactions of the complex cis-Pd(guo)₂Cl₂ with the sodium salts of the amino acids gly, L-ala, L-val, L-ileu, L-pro and L-phe, were studied in methanolic solutions. Complexes of the general formulae cis-[Pd(guo)₂(amac)]Cl, with the amino acids coordinated to Pd(II) with the N atom of their amino groups and the O atom of their carboxylate groups were isolated from these reactions. These were further reacted with dilute hydrochloric acid to produce complexes of the formulae cis-[Pd(guo)2-(amacH)Cl]Cl, with the amino acid coordinated only through the --NH₂ group. All the isolated complexes in the solid state were characterized with elemental analysis, conductivity measurements, IR and ¹H NMR spectra. Many isomers corresponding to 'head to head', 'head to tail' and 'tail to tail' orientations of the nucleosides, with two major ones called 'closed' and 'opened' forms in 1:1 ratio, with strong and weak inter- or intra-molecular ligand-ligand hydrophobic interactions were observed with ¹H NMR, in D_2O solutions, for the complexes. In DMSO-d₆ the 'opened' form with weak ligand-ligand interactions is favored (~80-90%). Possible ligand-ligand interactions are detected in the ¹H NMR spectra of the compounds. The anti conformation of the sugar moiety of guo is found to increase in the 'closed' forms of the *cis* ternary complexes, indicating that the model DNA-Pt-protein crosslink may be responsible for the toxicity of the platinum drugs, increasing with increase of the DNA-protein hydrophobic interactions.

Introduction

The significance of DNA-protein interactions that take place *in vivo* through the interactions of metal

ions, has been recognized in many cases [1, 2]. The antitumor drug *cis*-DDP, which exhibits its antitumor action through a direct interaction with DNA during its replication, is known together with its *trans* congener, to form DNA-Pt-protein crosslinks in the body [3-7]. The significance of such crosslinks is not presently well understood.

Such crosslinks caused by Pt(II) drugs can be studied *in vitro* by making the simplest models of them, constituted by the metal or the analogous Pd(II) and nucleobases or nucleosides—nucleotides and amino acid—peptides.

Studying such models, we recently reported the ternary complexes formed from the interactions of cis-Pt(ino)₂Cl₂ [8,9], together with a preliminary account of the interaction of cis-Pd(guo)₂Cl₂ with amino acids of increasing aliphatic side chain, e.g. gly, L-ala, L-val, L-ileu, L-pro and L-phe [8]. In the case of the Pd(II) complexes of guo and amino acids, we had noticed the presence of many rotational or other isomers in D₂O solutions, with ¹H NMR spectra.

In the present paper we report details of these interactions, trying to identify the various species existing in solution, to detect ligand—ligand interactions and correlate the results with other similar systems [10, 11].

Results and Discussion

Ternary complexes of Pd(II) with guo and am-acH, were synthesized as follows. After the synthesis of the starting material cis-Pd(guo)₂Cl₂, according to a known method [12], a similar method to the one employed for the corresponding Pt(II) complexes [8,9] was employed, consisting of treatment of the starting Pd(II) complex, with the sodium salt of the amino acids, in methanolic solutions. The amino acids used were: glycine (glyH), L-alanine (alaH), L-proline (proH), L-valine (valH), L-isoleucine (ileuH) and L-phenylalanine (pheH).

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cis-Pd(guo)₂Cl₂ + amacNa \xrightarrow{MeOH}

$$cis$$
-[Pd(guo)₂(amac)]Cl + NaCl (1)

When the cis-[Pd(guo)₂(amac)]Cl complexes were treated with dilute solutions of hydrochloric acid, they underwent the reaction

cis-[Pd(guo)₂(amac)]Cl + HCl \rightarrow

$$cis$$
-[Pd(guo)₂(amacH)Cl]Cl (2)

The elemental analysis of the complexes given in Table 1, agree with the assigned formulae.

The molar conductance values of the first series of complexes correspond to 1:1 electrolytes in aqueous solutions, while they are somewhat larger in the second series, increasing further with time, due to both the chloride and the hydrolysis of the free --COOH group of the amino acid (see Table 1).

IR Spectra

The characteristic IR bands of the complexes are given in Table 2.

The region of 2800–3600 cm⁻¹ is covered by a very strong and broad band with various submaxima, due to the ν NH of guo and the amino acids, the ν OH of the sugar of guo and the aliphatic and aromatic ν CH motions. Deuteration of the complexes results to the appearance of a new strong and broad band at 2300–2550 cm⁻¹, due to ν N–D and ν O–D motions (ν NH₂/ ν ND₂ = 1.33).

The region of $1500-1700 \text{ cm}^{-1}$ for all the complexes is characterized by a strong band at about 1690 cm⁻¹, due to the free ν C=O of the 6th position of guo [10, 12] (see Table 2). Bands attributable to the ring ν C=C and ν C=N motions of guo are also shown almost invariably at about 1590 and 1530 cm⁻¹ for all the complexes.

The $\nu_{COO^-}^{\alpha}$ of the coordinated carboxylate group coincides with the δNH_2 of guo at 1629 cm⁻¹ for the

complex cis-[Pd(guo)₂(gly)]Cl, at 1635 cm⁻¹ for cis-[Pd(guo)₂(ala)]Cl and cis-[Pd(guo)₂(phe)]Cl, at 1638 cm⁻¹ for cis-[Pd(guo)₂(pro)]Cl and cis- $[Pd(guo)_2(val)]Cl$ and at 1637 cm⁻¹ for cis-[Pd(guo)₂(ileu)]Cl. This band diminishes in intensity upon deuteration of the complexes, or in the second series of complexes of the type cis-[Pd(guo)2-(amacH)Cl]Cl where the protonated free carboxylate group (-COOH) contributes to the increase of the intensity of the band near 1690 cm⁻¹, due also to the $\nu C=0$ of the carbonyl group at the 6th position of guo. These findings give good indications for the bidentate coordination $(-NH_2, -COO^-)$ of the amino acids in the first series of complexes and for the monodentate $(-NH_2)$ coordination in the second [8, 9], the latter also supported by the appearance of a medium band, due to the vPd-Cl near 330 cm⁻¹ and absent in the first series of complexes.

The $\Delta \nu = \nu_{COO}^{\alpha} - \nu_{COO}^{\delta}$ is found at 217 cm⁻¹ for the complex *cis*-[Pd(guo)₂(gly)]Cl, 220 cm⁻¹ for *cis*-[Pd(guo)₂(ala)]Cl and *cis*-[Pd(guo)₂(val)]Cl, 224 cm⁻¹ for *cis*-[Pd(guo)₂(pro)]Cl, 225 cm⁻¹ for *cis*-[Pd(guo)₂(phe)]Cl and 239 cm⁻¹ for *cis*-[Pd(guo)₂-(ileu)]Cl. This difference, which reflects the degree of covalency of the metal-oxygen bond [13], follows the order ileu > phe > pro > val ~ ala > gly, e.g. increases with the bulkier side substituent of the amino acid. A similar behavior was also found with analogous Pt(II) complexes [14].

Free guo shows medium intensity bands at 824 and 801 cm⁻¹ [15–17]. These two bands were found to be associated with the percentage of the C₃'-endo and C₂'-endo conformation of the sugar. Thus, the intensity of the first decreases and of the second increases as the C₃'-endo conformation of the sugar increases upon coordination of Pt(II) with guo at N₇ [15–17]. Similar behavior is observed in all the complexes of the present study, showing a decrease of the band at 820 cm⁻¹ and an increase of the one at 798 cm⁻¹ (see Table 2), compared to free guo. This indicates an increase of the C₃'-endo conformation of

TABLE 1. Elemental analysis and conductivity values of the complexes

Complexes	Pd (%)		Cl (%)		C (%)		N (%)	_	H (%)		Λ_{M}
	Calc.	Found	Calc.	Found	Calc.	Found	Calc.	Found	Calc.	Found	$(\text{cm}^2 \ \Omega^{-1} \text{mol}^{-1})$
cis-[(guo) ₂ Pd(gly)]Cl	13.60	13.71	4.53	4.25	33.74	33.70	19.68	19.62	3.83	3.80	119.0
cis-[(guo) ₂ Pd(ala)]Cl	13.36	13.55	4.45	4.34	34.65	34.60	19.33	19.31	4.02	4.22	121.0
cis-[(guo) ₂ Pd(pro)]Cl	12.94	13.08	4.31	4.20	36.48	36.30	18.72	18.57	4.13	4.26	111.0
cis-[(guo)2Pd(val)]Cl	12.91	12.82	4.30	4.19	36.39	36.25	18.68	18.54	4.36	4.55	95.2
cis-[(guo) ₂ Pd(ileu)]Cl	12.69	12.85	4.23	4.00	37.20	37.00	18.40	18.20	4.60	4.68	93.8
cis-[(guo) ₂ Pd(phe)]Cl	12.19	12.40	4.06	4.00	39.89	39.80	17.65	17.52	4.24	4.33	122.0
cis-[(guo)2Pd(alaH)Cl]Cl	12.77	12.96	8.51	8.19	33.13	33.00	18.49	18.30	3.96	4.06	168.0
cis-[(guo)2Pd(proH)Cl]Cl	12.39	12.55	8.25	7.89	34.93	34.80	17.93	17.70	4.07	4.17	165.0
cis-[(guo)2Pd(valH)Cl]Cl	12.36	12.48	8.23	7.94	34.85	34.62	17.89	17.68	4.30	3.41	147.8
cis-[(guo)2Pd(ileuH)Cl]Cl	12.16	12.22	8.10	7.88	35.68	35.49	17.60	17.51	4.45	4.62	122.8

Complexes	$\nu_{\alpha}(\mathrm{NH})$	$\nu_{\alpha}(\text{NH}) \nu_{\mathbf{S}}(\text{NH}) \nu(\text{CH})$	ν(CH)	$\nu_{\alpha}({\rm C=O})$ of guo	$ \nu_{\alpha}(C=0) $ $ \nu_{\alpha}(C=0) $ of guo of amacH	$\delta(\mathrm{NH_2})$	$\delta(\mathrm{NH}_2) \ \nu(\mathrm{C=C}, \mathrm{C=N}) \ \delta_{\mathrm{s}}(\mathrm{CH}_3) \ \rho_{\mathrm{w}}(\mathrm{CH}_2) \ \delta(\mathrm{CH}) \ \rho_{\mathrm{t}}(\mathrm{CH}_2) \ \mathrm{conformula}$	δ s (CH ₃)	$\rho_{\rm w}({\rm CH_2})$	δ(CH)	$\rho_{\rm t}({\rm CH_2})$	Sugar $\nu_{\alpha}(COO)$ conformation $\nu_{s}(COO)$	$\nu_{\alpha}(\text{COO}) - \nu\text{Pd}-\text{Cl}$ $\nu_{s}(\text{COO})$	-CI
cis-[(guo)2Pd(gly)]Cl	3210b	3210b 3160b	2930sh	1690s	1629b	1629b	1597s 1528s		1324sh		914m	820sh 803 m	217	
<i>cis</i> -[(guo) ₂ Pd(ala)]Cl	3230b	3230b 3120b 2940sh	2940sh	1695s	1635b	1635b	1590s 1540s	1385m		1280w		821sh 700m	220	
cis-[(guo)2Pd(pro)]Cl			2940sh	1690s	1638b		1590s 1533s		1330sh		905w	820sh	224	
cis-[(guo)2Pd(val)]Cl	3230b	3230b 3140b	2950w	1691s	1638b	1638b		1370sh		1252sh		823sh 700m	220	
cis-{(guo)2Pd(ileu)]Cl	3230b	3140b	2960w	1695s	1637b	1637b		1380m	1330w			821sh 798m	239	
<i>cis</i> -[(guo) ₂ Pd(phe)]Cl	3240b	3140b		1690s	1635b	1635b	1590s 1540s					820sh 797w	225	
<i>cis</i> -[(guo) ₂ Pd(alaH)CI]CI	3230b	3120b	2942sh	1698s	1700s	1630b		1385m		1278w		820sh 795m	340w	M
cis-[(guo)2Pd(proH)Cl]Cl			2940sh	1695s	1700s		1589s 1534s		1330sh		906w	820sh 797m	335w	M
cis-[(guo)2Pd(valH)Cl]Cl 3230b		3140b	2948w	1690s	1798s	1630b		1370sh		1250sh		820sh 799.m	339sh	hs ⁶
cis-[(guo)2Pd(ileuH)CI]Cl 3230b		3140b	2950m	1695s	1700s	1629b	1589s 1534s	1380sh	1330sh	1260w		820sh 798w	340sh	lsh
<i>cis-</i> (guo) ₂ PdCl ₂				1702s			1590s 1540s					822sh 800m	335w	M
ong				1730s			1630s					823m 800m		

b = broad; sh = shoulder; s = strong; m = medium; w = weak.

TABLE 2. Characteristic IR bands of the complexes

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the sugar in the complexes, also confirmed with the ¹H NMR spectra (see below).

Other characteristic bands of the compounds with their assignments can also be seen in Table 2.

¹H NMR Spectra

The ¹H NMR spectra of the compounds have been taken in D_2O and DMSO-d₆ solutions and are given in Tables 3 and 4 respectively. The chemical shifts of the complexes are compared with the ones of the free amino acids in their zwitterionic forms and are given in parentheses. Negative values correspond to chemical shifts of the protons of the coordinated ligands downfield as compared to the free ones, while positive values correspond to upfield shifts.

The ¹H NMR spectra of the complexes of both series cis-[Pd(guo)₂(amac)]Cl and cis-[Pd(guo)₂-(amacH)Cl]Cl showed the presence of two major isomers, besides a few minor ones, which are more in the second series with the monodentate amino acid. An attempt was made to characterize the various isomers observed and this is outlined in detail in the case of the complexes cis-[Pd(guo)₂(val)]Cl and cis-[Pd(guo)₂(valH)Cl]Cl.

The H₈ proton of guo in the ¹H NMR spectrum of the complex cis-[Pd(guo)₂(val)]Cl in D₂O, shows three resonances at 8.4287, 8.4080 and 8.1218 ppm, all downfield shifted, as compared to free guo, by 0.4420, 0.4210 and 0.1350 ppm respectively, with a relative intensity of 1:0.2:0.9. This result confirms the retention of the $Pd-N_7$ bonds in the ternary complex [12]. The two major peaks at 8.4287 and 8.1218 ppm, in a 1:0.9 relative intensity, are assigned to two different isomers with strong and weak interactions of the aliphatic side chain of the chelated amino acid and the aromatic rings of guo respectively, in equilibrium. These are the so called 'closed' and 'opened' forms observed also in similar M-nucleotide-amino acid ternary systems by Sigel et al. [1, 18, 19] (see Fig. 1). They were also observed in the ternary systems trans-[Pd(ino)₂- $(peptide)_2 Cl_2 [10].$

'Closed' and 'opened' form isomers have also been assigned in the complex cis-[Pd(guo)₂(ala)]Cl, presenting two peaks at 8.4123 and 8.1656 ppm in D₂O solutions, in about a 1:1 ratio of relative intensities. The position of the methyl group of ala may justify a hydrophobic interaction with the aromatic rings of guo, only when the latter are oriented in a 'head to head' position. The phenomenon of the presence of the 'closed' and 'opened' isomeric forms, however, with strong and weak ligand—ligand interactions can also be intermolecular [20], since the distance between the guo molecules and the methyl group is quite large even with such an orientation [14], as is also evidenced with molecular models.

The peak at 8.4080 ppm of cis-[Pd(guo)₂(val)]Cl, on the other hand, is undoubtedly due to rotational

isomers around the Pd-N₇ bond, which may give rise to relative orientations of the two guo molecules, such as 'head to head', 'head to tail' and 'tail to tail' [8, 21-26]. The two peaks are coalesced at 50 °C with $\Delta G^{\neq} = 72.8$ kJ/mol.

a

In DMSO-d₆ solutions only two resonances are observed for the H₈ of guo in the complex *cis*- $[Pd(guo)_2(val)]Cl$, in 1:6.3 relative intensity at 8.6010 and 8.0440 ppm respectively. They are assigned to the 'closed' and 'opened' forms. A relatively higher degree of intramolecular guo-guo interaction could justify the smaller downfield shift (8.0440 ppm) of the H₈ in the 'opened' form. The latter is favored in DMSO-d₆ solution, since the intermolecular stacking effects are minimized [10]. The downfield shifts of the H₈ protons of both isomers, as compared to the free guo (Table 4), shows again the retention of the Pd-N₇ coordination [12].

The H₈ of the 'opened' form of cis-[Pd(guo)₂-(val)]Cl (Fig. 2(a)) in D₂O solutions, shown at 8.1218 ppm in $c = 2.72 \times 10^{-3}$ mol/l, shifts more upfield with increasing concentration, due to the increase of the intermolecular stacking effect of the aromatic rings of guo. The H₈ of the 'closed' form on the other hand (Fig. 2(b)) shows exactly the opposite effect; this can be explained with the increase of the intermolecular hydrophobic interactions between the aliphatic side chain of the amino acid and the aromatic rings of guo, with increasing concentration.

The valine protons, on the other hand, are as follows: The α -CH proton of the amino acid shows two doublets at 3.5965 and 3.6384 ppm, the first almost unshifted (-0.005 ppm) and the second shifted downfield by -0.037 ppm, relative to the zwitterionic form of the val [27] (see Table 3). Two bands with opposite shifts (upfield, downfield), compared to the zwitterionic form of the amino acid show also the protons of γ and δ carbons of val while the β protons show a multiple resonance centered at 2.2441 ppm, upfield by +0.0164 ppm. The upfield shifts of the methyl protons are +0.024 and +0.025 ppm respectively for the γ and δ protons and the corresponding downfield shifts are -0.091and -0.097 ppm (see Table 3). They are assigned to the 'closed' and 'opened' forms respectively. Since the two methyl groups of the amino acid should lie closer to the guo molecules in the 'closed' form, the largest upfield shifts observed for their protons are justified [1, 18].

The complex cis-[Pd(guo)₂(valH)Cl]Cl in D₂O, shows five resonances for the H₈ of guo, at 8.5589, 8.4496, 8.4296, 8.3207 and 8.1384 ppm, all shifted downfield compared to the free ligand. This confirms again the retention of the Pd-N₇ bonds [12]. The three bands at 8.4496, 8.4296 and 8.3207 ppm are assigned to the rotational isomers around the Pd-N₇

Complexes	Guanosine protons	protons						Amino acid protons	rotons			
	H ₈	H ₁ ′	H ₂ ′	Н ₃ ′	H4'	Η ₅ ′	H ₅ "	αCH	βCH	γCH	۶CH	¢СН
Guanosine [36]	7.9870	5.8950	4.7120	4.3940	4.2150	3.8450	3.8450					
cis-(guo)2PdCl2 [12]	9.1700 (-1.183)	6.0700										
<i>ci</i> s-[(guo) ₂ Pd(gly)]Cl	8.4252 (-0.438) 8.1800 (-0.193) 7.9699	5.8224d 5.8654d		4.2882				3.5399 (+0.002) 3.5755 (-0.033)				
<i>cis</i> -[(guo) ₂ Pd(ala)]CI	8.4123 (-0.425) 8.1656 (-0.179)	5.8245d 5.8719d	4.5105t 4.5871t	4.2973t 4.3410t				3.6281	1.4682 (+0.010) 1.5084d (-0.030)			
<i>cis</i> -[(guo) ₂ Pd(pro)]Cl	8.4986 (-0.5116) 8.3469 (-0.359) 8.2788 (-0.292)) 5.8326d 5.8499d	4.5054t 4.5635t	4.2769t 4.3168t					2.1390 (+0.294) 2.2876 (+0.046)	1.6839 (+0.345)	2.8017t (+0.559) 3.0362t (+0.324)	
<i>cis</i> -[(guo) ₂ Pd(val)]Cl	8.4287 (-0.442) 8.4080 (-0.421) 8.1218 (-0.135)	5.8067d 5.8879d	4.5038t 4.6051t	4.2787t 4.3531t	4.1409 4.1930	3.7254 3.8253	3.7254 3.8253	3.5965d (-0.005) 3.6384d (-0.037)	2.2441m (+0.016)	1.0141 (+0.024) 1.1276 (-0.091)	0.9625 (+0.025) 1.0851 (-0.097)	
<i>cis-</i> (guo) ₂ Pd(ileu)]Cl	8.4319 (-0.445) 8.4109 (-0.424) 8.1219 (-0.135)	5.8119d 5.8842d	4.5023t 4.5998	4.2776	4.1482 4.1839	3.7209 3.8226	3.7209 3.8226	3.6667d (-0.015)	1.9355 (+0.030)	1.3079 (+0.053)	0.9733 (+0.028)	0.8778 (+0.055)
<i>ci</i> s-[(guo) ₂ Pd(proH)Cl]Cl	8.5450 (-0.558) 8.4192 (-0.432)								2.0621 (+0.271)	1.7046m (+0.324)	2.8157 (+0.545)	
												(continued)

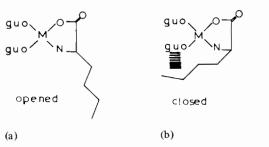
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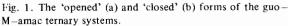
Complexes	Guanosine protons	protons						Amino aci	Amino acid protons			
	H ₈	H ₁ ′	H ₂ '	Н3′	Η4'	Hs′	H ₅ "	αCH	βCH	γCH	۶CH	€CH
	8.3468								2.3061		3.0328	
	(-0.360) 8.3048								(+0.027)		(+0.328)	
	(-0.318)											
	8.2716											
	(-0.284)											
cis-[(guo)2Pd(valH)C1]C1	8.5589											
	(-0.572)											
	8.4496	5.7703										
	(-0.463)											
	8.4296	5.8258							2.2394m		1.1086	
	(-0.443)											
	8.3207	5.8971										
	(-0.333)											
	8.1384											
	(-0.151)											
cis-[(guo)2Pd(ileuH)Cl]Cl	8.5606											
	(-0.0574)											
	8.4492	5.7713										
	(-0.462)											
	8.4312	5.8280							1.9417m			0.9306
	(-0.444)								(+0.023)	(-0.036)	(-0.014)	(+0.003)
	8.3232	5.8995										
	(-0.336)											
	8.1335											
	(-0.146)											

14 17 17 13 14 15 14 15 14 15 14 15 14 15 14 15 14 15<	Complexes	Guanosine protons	protons						Amino acid protons	otons			
1300 5890 14120 13903 1		Н _в	H1'	H2′	Н3′	H4'	Hs'	H ₅ "		1	γCH	۶CH	€CH
8.8900 (-0.242) (-0.242) (-0.242) (-0.243) (-0.243) (-0.243) (-0.243) (-0.243) (-0.203)	Guanosine	7.8000	5.8950						I				
8.0016	<i>cis</i> -[(guo) ₂ Pd(ala)]Cl	8.5800 (-0.780) 8.0420 (-0.242)	5.8095	4.5150	4.1955	3.9903			10.8980	1.3940 1.3140			
8.001 3.8125 4.5120 4.2033 3.9893 10.7820 2.2000m 1.1030m 0.0241 8.8028 4.5120 4.2035 3.9893 10.7820 2.3000m 1.1030m 8.602 8.8039 4.5074 4.1952 3.9893 3.7041 3.6548 11.2050 1.5337 1.0679 8.6030 6.0.2430 8.8110 4.5140 4.1952 3.9840 1.03490 1.3320d 1.0679 8.6390 8.810 8.810 3.9840 3.9840 1.03490 1.3100d 1.3320d 1.3320d 8.6390 8.810 4.5140 4.2090 3.9940 1.12370 1.3100d 1.3100d 8.6393 8.810 4.5090 4.1865 3.9905 1.12240 1.1240 1.1300d 1.130	<i>cis</i> -[(guo)2Pd(pro)]Cl	8.6916 (-0.892) 8.6060 (-0.806) 8.0626 (-0.203)	5.8060	4.5130	4.2057	3.9890			11.2470 10.8541	2.0543		2.9038m	
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	<i>cis</i> -[(guo)2Pd(val)]Cl	$\begin{array}{c} 8.6010\\ (-0.801)\\ 8.0440\\ (-0.244)\end{array}$	5.8125	4.5120	4.2035	3.9893			10.7820	2.2000		.030m	
8.5830 11.2370 (-0.783) 8.0420 5.8110 4.5140 4.2090 3.9840 10.8490 8.0420 5.8110 4.5140 4.2090 3.9840 10.8490 (-0.242) 8.6290 10.2310 4.5140 4.2090 11.2240 8.6290 (-0.783) 8.6975 11.2240 11.2240 (-0.245) 8.6975 10.8420 10.8420 8.6975 (-0.2898) 8.6975 10.8420 8.6975 4.0863 3.9905 10.8420 8.6975 8.6108 10.8420 10.8420 8.6975 1.0288 8.6975 10.8420 8.6975 1.0288 8.6975 10.8420 8.6975 1.0286 8.6968 10.8420 8.6975 1.0288 8.6975 10.8420 8.6108 1.0286 10.84855 11.2540	<i>cis</i> -{(guo) ₂ Pd(ileu)]Cl	8.6092 (-0.809) 8.0546 (-0.255)	5.8058	4.5074	4.1952	3.9805	3.7041	3.6548	11.2050 10.7886	1.88951		1.0679	0.9960
8.6290 (-0.829) 8.5830 (-0.783) 8.0450 5.8110 4.5090 4.1865 3.9905 10.8420 (-0.8420 (-0.245) 8.6975 (-0.245) 8.6975 (-0.245) 8.6975 (-0.245) 8.6975 (-0.881) 8.6975 (-0.811) 8.6108 (-0.811) 8.4855 (-0.686) 11.2540	<i>cis</i> -[(guo) ₂ Pd(alaH)Cl]Cl	8.5830 (-0.783) 8.0420 (-0.242)	5.8110	4.5140	4.2090	3.9840			11.2370 10.8490	1.39200			
8.6975 (-0.898) 8.6108 (-0.811) 8.4855 (-0.686)	<i>cis</i> -[(guo) ₂ Pd(proH)Cl]Cl	8.6290 (-0.829) 8.5830 (-0.783) 8.0450 (-0.245)	5.8110	4.5090	4.1865	3.9905			11.2240 10.8420	2.0120	F		
	cis-[(guo)2Pd(va1H)Cl]Cl	8.6975 (-0.898) 8.6108 (-0.811) 8.4855 (-0.686)							11.2540				

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Complexes	Guanosine protons	rotons						Amino acid protons	protons			
	H ₈	H1'	H ₂ '	H ₃ ′	Η4'	H _S ′	Hs"	ΗN	αCH βCH	уCH	۶CH	éСН
	8.3666 (-0.567) 8.0630	5.8076	4.5232	4.5232 4.2000	3.9858			10.8538	2.1868		1.0646	
cis-[(guo),Pd(ileuH)C]]C]	(-0.263) 8.6854											
	(-0.885)											
	8.6094 (-0.809)							11.2100				
	8.4850											
	(-0.685)											
	8.3567											
	(-0.557)											
	8.0562	5.8060	5.5079	5.5079 4.1958	3.9879			10.7921	1.8800m	m 1.5090m	1.0668	0.9946
	(-0.256)											





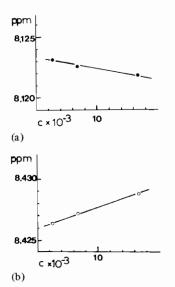


Fig. 2. Chemical shift of the H_8 proton of the 'opened' (a) and 'closed' (b) forms of the complex *cis*-[Pd(guo)₂(val)]Cl, as a function of concentration.

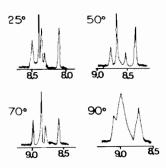


Fig. 3. The region of the H₈ proton in the ¹H NMR spectrum of the complex cis-[Pd(guo)₂(valH)Cl]Cl, as a function of temperature.

bonds of the two guo molecules corresponding to their relative orientations ('head to head', 'head to tail' and 'tail to tail') [8, 21–26] of the 'closed' form. This is confirmed with the spectra taken at 50 °C where the first two bands coalesce with $\Delta G^{\neq} = 72.86$ kJ/mol. All the three bands coalesce to one at 90 °C, with $\Delta G^{\neq} = 74.4$ kJ/mol (Fig. 3).

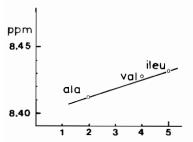


Fig. 4. Chemical shift of the H_8 proton of the 'closed' form of the complexes *cis*-[Pd(guo)₂(amac)]Cl, where amac is L-ala, L-val and L-ileu.

The resonance at 8.5589 ppm is assigned to the hydrolysis product cis-[Pd(guo)₂(valH)(H₂O)]Cl₂, which is then converted to cis-[Pd(guo)(guo-H⁺)-(valH)]Cl containing a possible N₇O₆ chelate of guo [12, 28, 29]. It should be noted that at pH = 6.2 the cis-[Pd(guo)₂(val)]Cl precipitates out the complex of the empirical formulae cis-[Pd(guo)(guo-H⁺)(val)]. Finally the 8.1384 ppm resonance may be due to the 'opened' isomer.

In DMSO-d₆ solutions five resonances are observed at 8.6975, 8.6108, 8.4855, 8.3666 and 8.0630 ppm in an intensity ratio 0.4:1:0.2:0.3:7.5, all shifted downfield, compared to free guo, implying Pd-N₇ bonds. The assignment of the bands is the same as in D₂O solutions. The band at 8.0630 ppm which increases in intensity in DMSO-d₆, is assigned to the 'opened' form.

The behavior of the other complexes of both series is similar. It is worthwhile noting that the chemical shifts of the H_8 proton of the 'closed' form, observed more downfield than the corresponding 'opened' form in D_2O solutions, in the chelated complexes of the amino acids with aliphatic side chain, e.g. ala, val, ileu, increase with an increase of the aliphatic side chain (Fig. 4), reflecting a stronger ligand—ligand hydrophobic interaction [1]. The more upfield shifted H_8 of the 'opened' form, on the other hand, shifts slightly upfield with an increase of the aliphatic side chain of the amino acids.

Conformations around the $C\alpha$ -C β Bond of the Amino Acids

The percentage of the three possible conformations around the $C\alpha$ -C β bond in the complexes *cis*-[Pd(guo)₂(val)]Cl and *cis*-[Pd(guo)₂(ileu)]Cl (Fig. 5) can be calculated from their ¹H NMR spectra [30-33]. The results are included in Table 5.

The percentage of the g + h conformers directing the aliphatic side chains of the amino acids towards the metal ion, is thus 89% in the 'closed' form of the complex *cis*-[Pd(guo)₂(val)]Cl and 83% in the 'opened' form. In the complex *cis*-[Pd(guo)₂(ileu)]Cl the percentage of only the 'opened' form could be calculated and found to be more than 90%. In com-

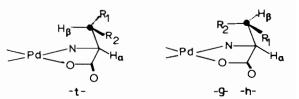


Fig. 5. The h, g and t conformers of L-val and L-ileu.

TABLE 5. Percentages of the t, g and h rotational isomers of the complexes with L-val and L-ileu

Complexes	J_{AB}	t (%)	(g + h) (%)	Solvent
cis-[(guo) ₂ Pd(val)]Cl 'closed' 'open'		11.0 17.0		D ₂ O
cis-[(guo) ₂ Pd(ileu)]Cl 'open'	3.45	10.0	90.0	D ₂ O

plexes of Pd^{2+} with dipeptides containing val and ileu [20, 30], the sum of g + h isomers was also found larger than 90%. The same percentage was also found in the ternary systems IMP or GMP-Pd-dipeptide [20], while in the complex GHL-Pd-nucleotide, the h isomer was more than 80% [11].

The existence or not of hydrophobic interactions between the aliphatic side chain of the amino acids and the aromatic rings of guo, in the same complex molecule, is therefore determined by the relative position of the two *cis*-guo molecules. If they are oriented 'tail to tail', the two guo molecules are far from the aliphatic side chains of the amino acids ('opened' form) and the interactions between them are minimum, while in a 'head to head' orientation, the two ligands are closer together and their interaction possible ('closed' form). The ligands however, may also interact intermolecularly [20].

Finally the largest percentage of the h + g isomers in the ileu complex, reflects the stronger ligand ligand interaction in this complex, possessing a longer side chain than val.

Sugar Conformations

The percentage of the ³E conformation of the sugar moiety of guo, being 38% in the free ligand [34], is known to increase by about 10% upon coordination with Pt(II) or Pd(II) at N₇ [10, 15, 16]. The same is true with ino [9]. A slight decrease was further observed in the ternary systems of *cis*-[Pt(ino)₂(amac)]Cl upon amino acid coordination [9] which was larger in the amino acids with longer aliphatic side chains. A similar trend was also observed here for the systems *cis*-[Pd(guo)₂(amac)]Cl in D₂O solutions, being 55% for the gly derivative, 53% for the ala and pro, 50% and 49% for the 'closed' and 'opened' forms respectively of both the val and ileu derivatives. In DMSO-d₆ solutions on the other

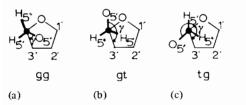


Fig. 6. Sugar conformation around the $C_4'-C_5'$ bond; (a) gg, (b) gt and (c) tg.

hand, the percentage of the ${}^{3}E$ conformation is comparable to the one of the free ligand, varying from 38-40% in the complexes of the present study and the systems *trans*-[Pd(guo)₂(dipeptide)₂]Cl₂ [10].

The conformation around the $C_{4'}-C_{5'}$ bond of the sugar moiety, described with the gg, gt and tg conformers (Fig. 6) was calculated only for the complexes *cis*-[Pd(guo)₂(val)]Cl and *cis*-[Pd(guo)₂(ileu)]-Cl, where the values of the coupling constants ³J(HH) could be estimated and the Carplus equation subsequently applied [35–38]. The results were 75% and 77% gg conformer for the 'closed' form and 65% and 68% for the 'opened' forms of the two complexes respectively, in D₂O solutions. A 69% gg conformer is retained upon coordination of *cis*-DDP with guo [15, 17], as well as in the series *trans*-[Pd(guo)₂-(dipeptide)₂]Cl₂ [10].

The chemical shift of the $H_{2'}$ proton of the nucleosides is related to the relative percentage of the *syn-anti* conformation of the sugar moiety and was observed at 5.073 ppm in t-Bu⁸guo with a supposed 100% *syn* and at 4.608 ppm in the *cis*-Pt(NH₃)₂⁷(G⁵_P)₂²⁺ with a supposed 100% *anti* conformation [17]. The relative ratio of the *syn-anti* conformation of nucleosides was then calculated from their observed H'₂ chemical shifts [17] and the relation [39]

$$\delta_{\rm obs} = P_{\rm syn} \delta_{\rm syn} + P_{\rm anti} \delta_{\rm anti} \tag{3}$$

In the present case however, the $H_{2'}$ proton of the sugar moiety of guo is always found more upfield than the value of 4.608 ppm of the *cis*-Pt(NH₃)₂⁷- $(G_{P}^{5'})_{2}^{2^{+}}$ with a supposed 100% *anti* conformation [17], for both the 'closed' and 'opened' forms, with the former even more upfield (see Table 3). The relation (3) cannot therefore be applied and it can only be said that the *anti* conformation predominates and it increases linearly with the increasing aliphatic side chain of the amino acid (see Fig. 7), in the 'closed' form of the complexes. In the 'opened' form, on the other hand, although again the *anti* conformation is favored, its ratio does not depend on the amino acid (Table 3).

Finally, in DMSO-d₆ the chemical shift of the $H_{2'}$ values observed, is at almost constant frequency (Table 4) for all the complexes, though again more upfield than the value of 4.608 ppm of the complex

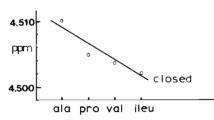


Fig. 7. Variation of the *anti* conformation of sugar in the complexes cis-[Pd(guo)₂(amac)]Cl, based on the chemical shift of the H₂' proton.

cis-Pt(NH₃)₂⁷($G_P^{5'}$)₂²⁺ [17]. These results are similar to the ones observed for the systems *trans*-[Pd(guo)₂-(dipeptide)]Cl₂ [10], though the relative ratio of the *anti* conformation was larger in these last systems.

Conclusions

The cis ternary complexes of the types cis-[Pd(guo)₂(amac)]Cl and cis-[Pd(guo)₂(valH)Cl]Cl, with amino acids of increasing aliphatic side chain show:

(i) Two main isomers with strong and weak ligand-ligand interactions, called 'closed' and 'opened' forms respectively, in D_2O solutions. These interactions can be inter- or intramolecular and decrease in DMSO-d₆ solutions, where the 'opened' form is favored.

(ii) The increase of the aliphatic side chain of the amino acids results in an increase of the percentage of the 'closed' form and to a decrease of the 'opened' form (see Fig. 8).

(iii) The hydrophobic interactions between the protons of the aliphatic side chain and the aromatic rings of guo in D_2O solutions increase with increasing distance of the protons from the bonding site with Pd(II), contrary to what is observed in the series *trans*-[Pd(guo)₂(dipeptide)₂]Cl₂ [10].

(iv) The ³E conformation of the sugar moiety in the complexes cis-[Pd(guo)₂(amac)]Cl decreases slightly upon coordination of amino acids with increasing aliphatic side chain, in D₂O. In DMSO-d₆, the percentage of ³E is comparable to the one of the free ligand and does not depend upon the amino acid.

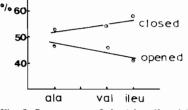


Fig. 8. Percentages of the 'closed' and 'opened' forms of the complexes cis-[Pd(guo)₂(amac)]Cl with L-ala, L-val and L-ileu.

(v) The gg conformer increases by 6-8% in the 'closed' form as compared to the free ligand and decreases by 1-4% in the 'opened' form.

(vi) The *anti* conformation of the sugar of guo increases with an increase of the aliphatic side chain of the amino acid in the 'closed' form of the complexes. The *anti* conformation of the 'closed' form is larger than the one of the 'opened' form.

(vii) The relative ratio of the *anti* conformation in these systems appears to be less than in the systems trans-[Pd(guo)₂(dipeptide)₂]Cl₂ [10].

In the DNA-Pt-protein model, it could be said that the *anti* conformation increases with an increase in the DNA-protein hydrophobic interaction, while the ³E conformation of the sugar decreases, though to a lesser extent. The toxic effects of the platinum drugs could therefore be due to such DNA-Ptprotein crosslinks.

Experimental

Materials

Glycine, L-alanine, L-valine, L-proline, L-isoleucine, L-phenylalanine and guanosine were purchased from Aldrich Chemical Company and Sigma Chemical Company. Palladium chloride was purchased from Degusa A.G. (F.R.G.). They were all used without further purification.

Methods

(i) The elemental analyses of Pd and Cl were performed in our laboratory, those of C, H and N in the Laboratoire de Chimie de Coordination in Toulouse. (ii) The conductivity measurements were performed in an E365B Conductoscope, Metrohm Ltd., Herisau, Switzerland. (iii) The IR spectra were recorded on a Perkin-Elmer model 580 spectrophotometer. (iv) The ¹H NMR spectra were obtained on a Brucker WM-250 spectrometer equipped with an Aspect 3000 computer. ¹H NMR chemical shifts were measured in parts per million with DSS or TMS as internal reference.

Preparation of the Compounds

The preparation of the starting complex cis-Pd(guo)₂Cl₂ was carried out according to a literature method [12]. The sodium salts of the amino acids were prepared by mixing equivalent amounts of each one of them with 0.1 NaOH solution and allowing the water to evaporate slowly in the water bath, washing the white residue with acetone and drying it at 110 °C under vacuum.

Preparation of cis-[Pd(guo)₂(amac)]Cl

One mmol of cis-Pd(guo)₂Cl₂ was mixed in the solid state with 1:1 mmol of the corresponding sodium salt of the amino acid (amacNa) and 150 ml

of methanol were added. The suspension was stirred for 8 h at 25 °C, filtered and the yellow filtrate obtained. This was evaporated to dryness and the residue dissolved in DMF, filtered and reprecipitated with a mixture of acetone and ether (1:1), in excess. The light yellow precipitate was filtered and washed with acetone and ether. It was then recrystallized in a mixture of ethanol:water (8:2). After subsequent drying in a dessicator at room temperature, followed by drying at 110 °C under vacuum, in the presence of CaCl₂, the yield varied from 40–75%, depending on the amino acid.

Preparation of cis-[Pd(guo)2(amacH)Cl]Cl

One mmol of the complex cis-[Pd(guo)₂(amac)]Cl was dissolved in an equivalent amount of a dilute HCl solution (0.1 N) and left to react at room temperature under stirring, for a few minutes. After filtration the complex was precipitated with an excess of isopropanol. The precipitated complex was filtered and washed with acetone and ether. It was then dried, first in a dessicator at room temperature, followed by drying at 110 °C under vacuum, in the presence of CaCl₂. Yield 80–85%.

Preparation of the Deuterated Derivatives

One hundred mg of the corresponding complex were dissolved in a few ml of D_2O and stirred for 5 min at room temperature. The deuterated complex was then reprecipitated with acetone and ether, filtered and dried *in vacuo*.

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