Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 150 KMean σ (C–C) = 0.013 Å Disorder in solvent or counterion R factor = 0.063 wR factor = 0.099 Data-to-parameter ratio = 16.5

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

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In the title compound, $[PdCl_2(C_{26}H_{24}P_2)]\cdot 3CDCl_3$, the $[PdCl_2(dppe)]$ molecule adopts a distorted square-planar metal coordination and an asymmetrical twist conformation

of the five-membered metallocycle. The structure contains

infinite channels filled with deuterochloroform of crystal-

lization and displays an (a, b/2, c) subcell.

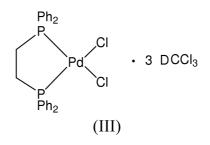
[1,2-Bis(diphenylphosphino)ethane-P,P']dichloro-

palladium(II) tris(deuterochloroform) solvate

Received 14 May 2001 Accepted 29 May 2001 Online 15 June 2001

Comment

[PdCl₂(dppe)] [dppe is bis(diphenylphosphino)ethane], (I), was first studied crystallographically by Steffen & Palenik (1976) in the form of its 1:1 solvate with CH_2Cl_2 , (II). Later, Singh *et al.* (1995) determined the crystal structure of pure (I). In the course of our studies of organopalladium phosphine complexes, we found that recrystallization of (I) from deuterochloroform gives a stable 1:3 solvate [PdCl₂(dppe)]- $3CDCl_3$, (III), the structure of which is reported herein.



The asymmetric unit of (III) comprises two [PdCl₂(dppe)] molecules (A and B) and six molecules of deuterochloroform (Fig. 1). The [PdCl₂(dppe)] molecules are related to each other by an approximate translation of b/2. Atoms related by this pseudo-translation are given the same numbers with letters A or B added. The Pd atoms deviate from the ideal b/2translation by 0.54 Å, P by 0.50 and 0.56 Å, Cl by 0.62 and 0.70 Å, and C atoms by 0.09-1.10 Å with the average 0.55 Å (Fig. 2). These deviations are relatively small, compared to the length of the translation (b/2 = 9.2 Å). The [PdCl₂(dppe)] molecule A has three molecules of deuterochloroform attached to it through C-D···Cl-Pd hydrogen bonds. Two of these molecules, A1 and A3 (see Fig. 1), are hydrogenbonded to the chloride ligand Cl2A, while molecule A2 forms a bifurcated hydrogen bond with both Cl1A and Cl2A. The positions of deuterochloroform molecules B1, B2 and B3 are roughly related respectively to those of A1, A2 and A3. Molecule B2 also forms a bifurcated hydrogen bond, with Cl1B and Cl2B. Molecule B1 is hydrogen-bonded to Cl2B but, unlike A1, molecule B1 is disordered (see below). In molecule B3, the C5B, Cl9B and Cl0B atoms are related by pseudotranslation to the C5A, Cl9A and Cl0A of molecule A3, but

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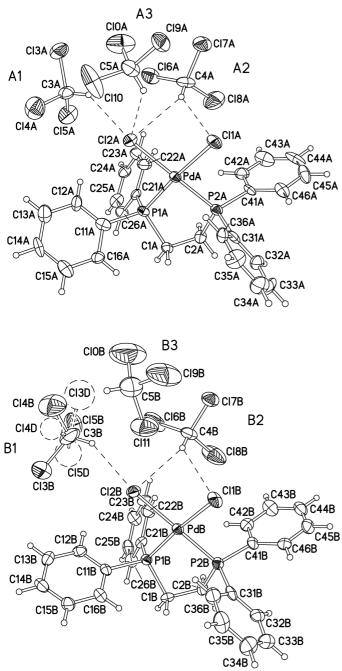


Figure 1

Two independent formula units of $[PdCl_2(dppe)]$ ·3CDCl₃ (III), showing hydrogen bonds. Displacement ellipsoids are drawn at the 50% probability level. Note different orientations of deuterochloroform molecules A3 and B3.

Cl11 is not related to Cl10. Thus B3 can be described as a pseudo-equivalent of A3 with the deuterium and Cl11 atoms exchanged. Consequently, the deuterium atom of B3 does not point towards the $[PdCl_2(dppe)]$ molecule B, but instead forms a weak hydrogen bond with the Cl7A atom of the A2 molecule, related to the original one by the crystallographic translation b.

Thus structure (III) has an (a, b/2, c) subcell, which is manifested in the diffraction pattern: reflections with even k

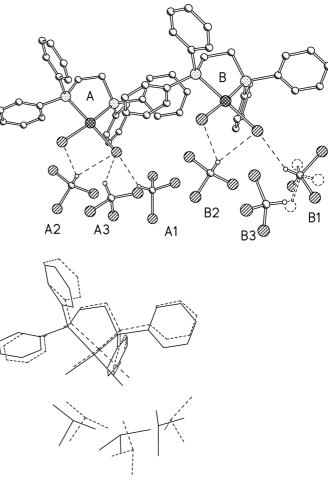


Figure 2

Top: asymmetric unit in the crystal of (III) (H atoms omitted); bottom: its convolution by the b/2 pseudo-translation (molecules A in solid, B in dashed lines; minor components of disordered Cl atoms as well as H and D atoms have been omitted).

indices have intensities on average twice as high as those with odd k. The crystal packing can be described as a clathrate (host–guest complex), in which deuterochloroform molecules occupy infinite channels (parallel to the b axis) in the packing of [PdCl₂(dppe)] molecules (Fig. 3).

The molecular structure of [PdCl₂(dppe)] in (III) is similar to those found in structures (I) and (II). The palladium atom has a slightly distorted square-planar coordination. In molecule A, the PdA, P1A, P2A and Cl1A atoms are coplanar, while Cl2A deviates from their mean plane by 0.160(4) Å. Probably because of this asymmetric distortion, the Pd-P bond lengths differ by 0.018 Å, or 9 s.u.'s. In molecule B, the distortion is of tetrahedral mode: the the PdCl₂ plane is twisted by 6.4 (1)° with respect to the PdP_2 plane, and the Pd-P distances are identical. In any case, the distortion is probably due to steric strain in the chelating ligand (Steffen & Palenik, 1976). In both [PdCl₂(dppe)] molecules of (III) the five-membered metallocycle adopts an asymmetric twist conformation: the C1 and C2 atoms are displaced from the PdP_2 plane in opposite directions, by 0.48 (1) and -0.29 (1) Å in molecule A, 0.50 (1) and -0.28 (1) Å in molecule B.

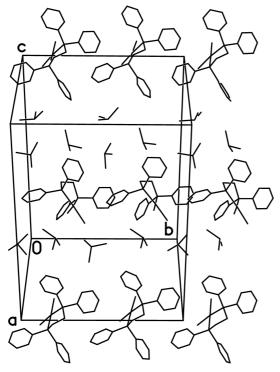


Figure 3

The crystal packing of (III) projected onto the (101) plane.

The average Pd-P and Pd-Cl bond distances of 2.242 (7) and 2.364 (3) Å in (III) are essentially the same as in (II), viz. 2.230 (4) and 2.359 (2) Å (Steffen & Palenik, 1976).

Experimental

[Pd₂(dba)₃]·CHCl₃ (0.10 g, 0.11 mmol), where dba is dibenzylideneacetone, and dppe (0.08 g, 0.20 mmol) were dissolved in toluene (50 mol) under nitrogen and stirred for 2 h. ClCO₂Me (0.02 g, 0.23 mmol) was added and the solution (which turned yellow) was stirred briefly. The solvent was removed in vacuo, the residue was identified as (I) and re-crystallized from deuterochloroform by slow evaporation at room temperature.

Crystal data

$[PdCl_{2}(C_{26}H_{24}P_{2})] \cdot 3CCl_{3}D$ $M_{r} = 936.81$ Orthorhombic, $P2_{1}2_{1}2_{1}$ a = 16.292 (1) Å b = 18.404 (1) Å c = 25.317 (2) Å V = 7591 (1) Å ³ Z = 8 $D_{x} = 1.634$ Mg m ⁻³ Data collection	Mo $K\alpha$ radiation Cell parameters from 447 reflections $\theta = 12-23^{\circ}$ $\mu = 1.37 \text{ mm}^{-1}$ T = 150 (2) K Plate, yellow $0.34 \times 0.25 \times 0.08 \text{ mm}$
SMART 1 K CCD area-detector diffractometer ω scans Absorption correction: by integra- tion (<i>XPREP SHELXTL</i> ; Siemens, 1995) $T_{\min} = 0.701, T_{\max} = 0.920$ 41 687 measured reflections	12 994 independent reflections 9802 reflections with $l > 2\sigma(l)$ $R_{int} = 0.083$ $\theta_{max} = 25.0^{\circ}$ $h = -18 \rightarrow 19$ $k = -21 \rightarrow 21$ $l = -30 \rightarrow 27$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + 5.0304P]$
$R[F^2 > 2\sigma(F^2)] = 0.063$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.099$	$(\Delta/\sigma)_{\rm max} = 0.005$
S = 1.78	$\Delta \rho_{\rm max} = 1.36 \text{ e } \text{\AA}^{-3}$
12994 reflections	$\Delta \rho_{\rm min} = -0.98 \text{ e} \text{ Å}^{-3}$
787 parameters	Absolute structure: Flack (1983)
H-atom parameters constrained	Flack parameter = -0.02 (3)

Table 1

Selected geometric parameters (Å, °).

PdA-P1A	2.254 (2)	PdB-P1B	2.238 (2)
PdA - P2A	2.236 (2)	PdB - P2B	2.238 (2)
PdA - Cl1A	2.363 (2)	PdB-Cl1B	2.365 (2)
PdA - Cl2A	2.361 (2)	PdB-Cl2B	2.367 (2)
P1A-C1A	1.840 (7)	P1B-C1B	1.841 (7)
P1A-C11A	1.815 (8)	P1B-C11B	1.820 (8)
P1A-C21A	1.818 (8)	P1B-C21B	1.810 (8)
P2A-C2A	1.816 (7)	P2B-C2B	1.846 (7)
P2A-C31A	1.811 (9)	P2B-C31B	1.818 (9)
P2A-C41A	1.818 (7)	P2B-C41B	1.813 (7)
P2A - PdA - P1A	85.63 (8)	P2B-PdB-P1B	85.77 (8)
P2A - PdA - Cl2A	176.27 (8)	P2B-PdB-Cl1B	90.47 (8)
P1A - PdA - Cl2A	92.98 (8)	P1B-PdB-Cl1B	174.30 (8)
P2A - PdA - Cl1A	89.68 (8)	P2B-PdB-Cl2B	173.73 (8)
P1A - PdA - Cl1A	175.26 (8)	P1B-PdB-Cl2B	90.45 (8)
Cl2A - PdA - Cl1A	91.74 (8)	Cl1B - PdB - Cl2B	93.66 (8)
C21A-P1A-C11A	104.4 (4)	C21B-P1B-C11B	106.0 (4)
C21A - P1A - C1A	106.6 (4)	C21B-P1B-C1B	105.7 (4)
C11A - P1A - C1A	106.6 (4)	C11B-P1B-C1B	107.2 (4)
C21A - P1A - PdA	110.6 (3)	C21B-P1B-PdB	113.0 (3)
C11A - P1A - PdA	121.0 (3)	C11B-P1B-PdB	116.6 (3)
C1A - P1A - PdA	106.8 (2)	C1B - P1B - PdB	107.7 (3)
C31A-P2A-C2A	104.6 (4)	C41B-P2B-C31B	109.1 (4)
C31A-P2A-C41A	108.1 (4)	C41 <i>B</i> -P2 <i>B</i> -C2 <i>B</i>	106.6 (3)
C2A-P2A-C41A	104.7 (3)	C31 <i>B</i> -P2 <i>B</i> -C2 <i>B</i>	103.6 (4)
C31A - P2A - PdA	113.7 (3)	C41B - P2B - PdB	113.7 (3)
C2A - P2A - PdA	108.4 (3)	C31B-P2B-PdB	114.3 (3)
C41A - P2A - PdA	116.4 (3)	C2B - P2B - PdB	108.7 (3)

Table 2

Hydrogen-bonding geometry (Å, °).

$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$					
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$C3A - D3A \cdots Cl2A$	1.00	2.62	3.452 (9)	141
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$C4A - D4A \cdots Cl1A$	1.00	2.81	3.649 (10)	141
$C3B-D3B\cdots Cl2B$ 1.002.613.501 (10)148 $C4B-D4B\cdots Cl1B$ 1.002.963.759 (9)137 $C4B-D4B\cdots Cl2B$ 1.002.703.513 (9)138	$C4A - D4A \cdots Cl2A$	1.00	2.88	3.717 (9)	142
C4B-D4B···Cl1B 1.00 2.96 3.759 (9) 137 C4B-D4B···Cl2B 1.00 2.70 3.513 (9) 138	$C5A - D5A \cdot \cdot \cdot Cl2A$	1.00	2.76	3.534 (10)	135
$C4B - D4B \cdots Cl2B$ 1.00 2.70 3.513 (9) 138	$C3B - D3B \cdots Cl2B$	1.00	2.61	3.501 (10)	148
	$C4B - D4B \cdots Cl1B$	1.00	2.96	3.759 (9)	137
$C5B - D5B \cdots CI7A^{i}$ 1.00 2.98 3.967 (13) 170	$C4B - D4B \cdots Cl2B$	1.00	2.70	3.513 (9)	138
	$C5B - D5B \cdots Cl7A^{i}$	1.00	2.98	3.967 (13)	170

Symmetry code: (i) x, 1 + y, z.

All H atoms were treated as riding, with Csp^2 -H and Csp^3 -H bond distances of 0.95 and 1.00 Å, $U_{\rm iso}$ equal to $1.3U_{\rm eq}$ of the carrying C atom for the methylene H atoms and $1.2U_{eq}$ for the deuterium atoms and phenyl H atoms. Molecule B1 shows rotational disorder around the threefold molecular axis. The disorder was approximated by two sets of chlorine positions: Cl3B, Cl4B, Cl5B with occupancies 0.85 and Cl3D, Cl4D, Cl5D with occupancies 0.15, but the high residual electron density (up to $1.36 \text{ e} \text{ Å}^{-3}$) may indicate a continuous rotational disorder. All C-Cl bonds in both orientations of molecule B1 were restrained to similar lengths. Anomalous distribution of reflection intensities, due to the sublattice and the disorder

of relatively heavy (Cl) atoms, results in high S and/or weighting scheme parameters. The actual weighting scheme was optimized for the data set, excluding non-positive F^2 .

Data collection: *SMART* (Siemens, 1995); cell refinement: *SMART* (Siemens, 1995); data reduction: *SAINT* (Siemens, 1995); program(s) used to solve structure: *SHELXS*86 (Sheldrick, 1990); program(s) used to refine structure: *SHELXL*93 (Sheldrick, 1993); molecular graphics: *SHELXTL* (Siemens, 1995); software used to prepare material for publication: *SHELXTL*.

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