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## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=150 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.005 \AA$
$R$ factor $=0.024$
$w R$ factor $=0.065$
Data-to-parameter ratio $=19.3$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## trans-Dichlorodipyridinepalladium(II)

In the structure of the title compound, $\left[\mathrm{PdCl}_{2}\left(\mathrm{C}_{5} \mathrm{H}_{5} \mathrm{~N}\right)_{2}\right]$, determined at 150 K , the Pd atom is located on an inversion centre. The structure is a polymorph of a previously reported structure [Viossat et al. (1993). Acta Cryst. C49, 84-85].

## Comment

Our group is interested in the preparation of palladium complexes of $N$-heterocyclic carbene (NHC) ligands (Lee et al., 2004). A general synthetic method is via the in situ deprotonation of the corresponding imidazolium salt to generate the NHC ligand, which is then trapped by a suitable palladium precursor. In the course of preparing a palladium dichloride complex supported by a monodentate NHC ligand, we reacted the corresponding imidazolium salt, palladium dichloride, and pyridine as both solvent and base. Under unoptimized conditions, the title compound, (I), was the sole product.

(I)


Figure 1
The structure of (I), showing $50 \%$ probability displacement ellipsoids for non-H atoms. [Symmetry code: (A) $1-x, 1-y,-z$.]

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We present here the structure of (I) (Fig. 1). It crystallizes in the centrosymmetric space group $P \overline{1}$ with the palladium centre situated at a centre of inversion. The structure is a polymorph of a previously determined structure (Viossat et al., 1993). The marked difference between these two structures is the coplanarity of the two pyridine rings in (I); in the other polymorph, the two pyridine planes make an angle of $20.0(5)^{\circ}$.

## Experimental

The title compound is commerically available. Crystals were grown by slow diffusion of diethyl ether into a dimethylformamide solution of the compound.

## Crystal data

| $\left[\mathrm{PdCl}_{2}\left(\mathrm{C}_{5} \mathrm{H}_{5} \mathrm{~N}\right)_{2}\right]$ | $Z=1$ |
| :--- | :--- |
| $M_{r}=335.50$ | $D_{x}=1.955 \mathrm{Mg} \mathrm{m}^{-3}$ |
| Triclinic, $P \overline{1}$ | Mo $K \alpha$ radiation |
| $a=5.4624(3) \AA$ | Cell parameters from 2287 |
| $b=6.9863(4) \AA$ | reflections |
| $c=7.5977(5) \AA$ | $\theta=3.0-27.8^{\circ}$ |
| $\alpha=80.852(4)^{\circ}$ | $\mu=2.06 \mathrm{~mm}^{-1}$ |
| $\beta=84.578(4)^{\circ}$ | $T=150(2) \mathrm{K}$ |
| $\gamma=89.163(4)^{\circ}$ | Block, orange |
| $V=284.97(3) \AA^{3}$ | $0.12 \times 0.11 \times 0.07 \mathrm{~mm}$ |
|  |  |
| Data collection |  |
| Bruker SMART APEX-II | 1352 independent reflections |
| diffractometer | 1329 reflections with $I>2 \sigma(I)$ |
| $\omega$ scans | $R_{\text {int }}=0.013$ |
| Absorption correction: multi-scan | $\theta_{\text {max }}=27.9^{\circ}$ |
| $\quad(S A D A B S ;$ Sheldrick, 2003) | $h=-7 \rightarrow 7$ |
| $T_{\text {min }}=0.790, T_{\text {max }}=0.869$ | $k=-9 \rightarrow 9$ |
| 3106 measured reflections | $l=-9 \rightarrow 9$ |
|  |  |

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.024$
$w R\left(F^{2}\right)=0.065$
$S=1.14$
1352 reflections
70 parameters
H -atom parameters constrained

$$
\begin{aligned}
& w=1 /\left[\sigma^{2}\left(F_{\mathrm{o}}{ }^{2}\right)+(0.0193 P)^{2}\right. \\
& +0.8582 P] \\
& \text { where } P=\left(F_{\mathrm{o}}{ }^{2}+2 F_{\mathrm{c}}{ }^{2}\right) / 3 \\
& (\Delta / \sigma)_{\max }<0.001 \\
& \Delta \rho_{\text {max }}=1.08 \mathrm{e}^{\AA^{-3}} \\
& \Delta \rho_{\text {min }}=-0.52 \mathrm{e}^{-3}
\end{aligned}
$$

All H atoms were positioned geometrically $(\mathrm{C}-\mathrm{H}=0.95 \AA)$ and refined with a riding model, with $U_{\text {iso }}(\mathrm{H})=1.5 U_{\text {eq }}(\mathrm{C})$ for methyl H atoms and $1.2 U_{\text {eq }}(\mathrm{C})$ for all other H atoms. The highest peakin the electron-density map is $1.08 \AA$ from atom H 4 .

Data collection: APEX2 (Bruker, 2004); cell refinement: APEX2; data reduction: $A P E X 2$; program(s) used to solve structure: SHELXTL (Sheldrick, 1998); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

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