## Crystal Structure

## Communications

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# 2-Aminopyridinium-succinatesuccinic acid (2/1/1) 

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In the title compound, $2 \mathrm{C}_{5} \mathrm{H}_{7} \mathrm{~N}_{2}{ }^{+} \cdot \mathrm{C}_{4} \mathrm{H}_{4} \mathrm{O}_{4}{ }^{2-} \cdot \mathrm{C}_{4} \mathrm{H}_{6} \mathrm{O}_{4}$, cyclic eight-membered hydrogen-bonded rings exist involving 2-aminopyridinium and succinate ions. The succinic acid and succinate moieties lie on inversion centres. Succinic acid molecules and succinate ions are linked into zigzag chains by $\mathrm{O}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds, with $\mathrm{O} \cdots \mathrm{O}$ distances of 2.6005 (16) $\AA$.

## Comment

Hydrogen bonding plays a key role in molecular recognition (Goswami \& Ghosh, 1997) and crystal engineering research (Goswami et al., 1998). The design of highly specific solid-state structures is of considerable significance in organic chemistry, due to their important applications in the development of new optical, magnetic and electronic systems (Lehn, 1990). Our investigation of the title compound, (I), shows that the 2-aminopyridinium ions are linked to the succinate ions through $\mathrm{N} 1-\mathrm{H} \cdots \mathrm{O} 3$ and $\mathrm{N} 2-\mathrm{H} 2 \mathrm{~N} A \cdots \mathrm{O} 4$ hydrogen bonds, resulting in the formation of cyclic eight-membered hydrogenbonded rings.



(I)

Each amino H atom in (I) is involved in a single hydrogen bond, one in the cyclic eight-membered hydrogen-bonded ring system and the other to another succinate ion (Fig. 1). The 2-aminopyridinium-succinate-succinic acid units are arranged so that a two-dimensional network of intermolecular $\mathrm{N} 2-$ $\mathrm{H} 2 \mathrm{~N} B \cdots \mathrm{O} 4$ and $\mathrm{O} 2-\mathrm{H} 6 \cdots \mathrm{O} 3$ hydrogen bonds exists on each nearly perpendicular 2-aminopyridinium-succinatesuccinic acid unit [dihedral angle $=84.34(8)^{\circ}$ ] (Fig. 2).

2-Aminopyridine, like other organic bases, is protonated in acidic solutions. The bonding of the H atom to the ring N atom of 2-aminopyridine, but not to the amino N atom, gives an ion


Figure 1
A view of the three moieties of (I), with the atom-numbering scheme and $50 \%$ probability displacement ellipsoids. H atoms are shown as small spheres of arbitrary radii [symmetry codes: (i) $-x,-y,-z$ ].
for which an additional resonance structure can be written. As this monocation has more resonance energy (additional ionic resonance) than 2-aminopyridine itself, 2-aminopyridine is a strong base, like amidines (Acheson, 1967).

The present investigation clearly shows that the positive charge in (I) is on the amino group in the crystal. The $\mathrm{C} 1-\mathrm{N} 2$ bond length is 1.3272 (19) $\AA$, and this is approximately equal to a previously reported $\mathrm{C}=\mathrm{N}$ double-bond length (Shanmuga Sundara Raj, Fun, Lu et al., 2000). The location of the positive charge on the amino group is also supported by the $\mathrm{C} 1-\mathrm{N} 2-\mathrm{H} 2 \mathrm{~N} A$ angle of $118.4(11)^{\circ}$ and by the fact that atoms $\mathrm{C} 1, \mathrm{~N} 2, \mathrm{H} 2 \mathrm{~N} A$ and $\mathrm{H} 2 \mathrm{~N} B$ lie in the pyridine plane, with a maximum deviation of 0.04 (2) $\AA$ for atom H2NB. Similar $\mathrm{C} 1-\mathrm{N} 2$ bond lengths have also been observed in other 2-aminopyridine-containing molecules (Yang et al., 1995; Grobelny et al., 1995; Shanmuga Sundara Raj, Fun, Zhao et al., 2000).


Figure 2
A packing diagram for (I), viewed along the $b$ axis.

## Experimental

The title compound was prepared by mixing 2-aminopyridine and succinic acid in a 1:1 molar ratio in water at 353 K . Crystals of (I) were obtained by slow evaporation of the solvent.

## Crystal data

$2 \mathrm{C}_{5} \mathrm{H}_{7} \mathrm{~N}_{2}{ }^{+} \cdot \mathrm{C}_{4} \mathrm{H}_{4} \mathrm{O}_{4}{ }^{2-} \cdot \mathrm{C}_{4} \mathrm{H}_{6} \mathrm{O}_{4}$
$D_{x}=1.436 \mathrm{Mg} \mathrm{m}^{-3}$
$M_{r}=424.41$
Monoclinic, $P 2_{{ }^{1}} / c$
$a=10.228$ (2) $\AA$ 。
$b=5.1840(10) \AA$
$c=19.047$ (4) A
$\beta=103.60(3)^{\circ}$
$V=981.6(4) \AA^{3}$
$Z=2$

## Data collection

Siemens $P 4$ diffractometer $\omega$ scans

## 2362 measured reflections

2362 independent reflections
1690 reflections with $I>2 \sigma(I)$
$\theta_{\text {max }}=28^{\circ}$

$$
h=-13 \rightarrow 13
$$

$$
\begin{aligned}
n & =0 \rightarrow 6
\end{aligned}
$$

$l=0 \rightarrow 25$

$$
\text { Mo } K \alpha \text { radiation }
$$

Cell parameters from 35 reflections
$\theta=5-25^{\circ}$
$\mu=0.11 \mathrm{~mm}^{-1}$
$T=153$ (2) K
Rectangular, light yellow
$0.3 \times 0.2 \times 0.2 \mathrm{~mm}$

1 standard reflection frequency: 120 min intensity decay: none

Table 1
Selected geometric parameters ( $\left({ }^{\circ},{ }^{\circ}\right)$.

| C1-N2 | $1.3272(19)$ | $\mathrm{O} 2-\mathrm{C} 6$ | $1.3123(17)$ |
| :--- | :---: | :--- | :---: |
| C1-N1 | $1.3500(18)$ | $\mathrm{O} 3-\mathrm{C} 8$ | $1.2747(16)$ |
| $\mathrm{N} 1-\mathrm{C} 5$ | $1.3578(19)$ | $\mathrm{O} 4-\mathrm{C} 8$ | $1.2413(16)$ |
| $\mathrm{O} 1-\mathrm{C} 6$ | $1.2038(17)$ |  |  |
|  |  |  | $122.95(12)$ |
| $\mathrm{O} 1-\mathrm{C} 6-\mathrm{O} 2$ | $123.44(14)$ | $\mathrm{O} 4-\mathrm{C} 8-\mathrm{O} 3$ |  |
|  |  |  | $11.1(3)$ |
| $\mathrm{N} 2-\mathrm{C} 1-\mathrm{N} 1-\mathrm{C} 5$ | $178.53(14)$ | $\mathrm{O} 4-\mathrm{C} 8-\mathrm{C} 9-\mathrm{C} 9^{\mathrm{ii}}$ | $-169.72(18)$ |
| $\mathrm{O} 1-\mathrm{C} 6-\mathrm{C} 7-\mathrm{C} 7^{\mathrm{i}}$ | $2.6(3)$ | $\mathrm{O} 3-\mathrm{C} 8-\mathrm{C} 9-\mathrm{C} 9^{\mathrm{ii}}$ |  |
| $\mathrm{O} 2-\mathrm{C} 6-\mathrm{C} 7-\mathrm{C} 7^{\mathrm{i}}$ | $-177.09(18)$ |  |  |

Symmetry codes: (i) $-x, 1-y, 1-z$; (ii) $1-x, 1-y, 1-z$.

Table 2
Hydrogen-bonding geometry ( $\AA,{ }^{\circ}$ ).

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| N1-H1N $\cdots \mathrm{O} 3$ | $0.969(18)$ | $1.751(18)$ | $2.7185(16)$ | $176.0(17)$ |
| N2-H2N $A \cdots \mathrm{O} 4$ | $0.929(18)$ | $1.936(19)$ | $2.8521(18)$ | $168.2(16)$ |
| N2-H2N $B \cdots \mathrm{O}^{\mathrm{i}}$ | $0.84(2)$ | $2.11(2)$ | $2.9447(19)$ | $167.7(17)$ |
| O2-H6 $^{\mathrm{H}} \mathrm{O}^{\mathrm{Hi}}$ | $0.89(2)$ | $1.72(2)$ | $2.6005(16)$ | $178(2)$ |

Symmetry codes: (i) $1-x, y-\frac{1}{2}, \frac{3}{2}-z$; (ii) $x, y-1, z$.

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.037$

$$
\begin{aligned}
& w=1 /\left[\sigma^{2}\left(F_{o}{ }^{2}\right)+(0.0496 P)^{2}\right. \\
& +0.0805 P \text { ] } \\
& \text { where } P=\left(F_{o}{ }^{2}+2 F_{c}{ }^{2}\right) / 3 \\
& (\Delta / \sigma)_{\text {max }}=0.001 \\
& \Delta \rho_{\text {max }}=0.29 \mathrm{e}^{-3}
\end{aligned}
$$

$S=1.02$
2362 reflections
185 parameters
All H-atom parameters refined
Extinction correction: SHELXL97

Extinction coefficient: 0.015 (3)
All H -atom parameters were freely refined, with $\mathrm{C}-\mathrm{H}$ distances in the range $0.92(2)-0.982(15) \AA$ and $U_{\text {iso }}(\mathrm{H})$ values in the range 0.039 (4)-0.075 (6) $\AA^{2}$.

Data collection: XSCANS (Siemens, 1991); cell refinement: XSCANS; data reduction: SHELXTL (Bruker, 2001); program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEPIII (Burnett \& Johnson, 1996); software used to prepare material for publication: WinGX (Farrugia, 1997).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: FR1391). Services for accessing these data are described at the back of the journal.

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