Research on DNA

Publication/Creation

1951-1953

Persistent URL

https://wellcomecollection.org/works/uus54sbp

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Rob Waddell
1951

Century

NOTE BOOK

Sept. 1951

Signer N.A., ~~tot~~ bundle of fibres selected dumped over sat. $KClO_3$ + straightened + slightly extended.

Micro-camera. Fluorescent screen. No filter

1. 1st small specimen, over $KClO_3$ 2 hrs 10 mm

2. New specimen 10 mm
~~Pack v. wet, drop of water in camera~~

3. Same, dried, over sat. $KClO_3$ "

4. Stacked ~ 50% of its length, over $KClO_3$ "

5. Same specimen, over sat. NH_4Cl, 15 mm
19.9.51 3 p.m. in camera, H_2 flow started. Sat. NH_4Cl in camera
New filament
20.9.51 Exposure 2.15 - 5.45

80%.

6. 20.9.51 6.30 p.m. Same specimen in camera, over Na_2CO_3 in camera ± H_2 flow
21.9.51 exposure 3½ hours
~~23.9.51 Exposure 10.15~~ 92%

7. ~~As 6. 21.9.51 6 p.m. H_2 flow, Na_2CO_3~~
~~24.9.51 Exposed 3 hrs~~
~~specimen was stuck~~ ~~[illegible]~~

~~7~~ ~~26.9.51 12 p.m. $NaNO_2$ equil. @ 78%~~
~~24.9.51 5 p.m. H_2 flow, Na_2CO_3~~
26.9.51 Exposed 3 hrs (3–6 p.m.)

~~8 26.9.51 7 p.m. over $NH_4Cl + KNO_3$~~
~~Na_2CO_3 92%~~

8. 27.9.51
5 p.m. over sat $CaNO_3$ → equil @ ~~51~~ 49%
5.30 – 6.00 (49–53%)
1.10.51 11.30 – 5.00
(6 hrs)

9. Specimen built up from ~ 30–35 Silver fibres, stuck together by keeping wet.

1.10.51 6 p.m. over H_2, sat NH_4Cl
2.10.51 10.15 – 12.30

10. 2.10.51 Over Na_2CO_3 (92%)
1 hr to equilibrate, 4 hrs exposure
– sample moved: it was wet

10.10.51

Single fibre of Signer DNA, fairly thick, ~~which~~ part selected ~~as~~ giving better extinction than most thick fibres, though not perfect

Micro camera

100μ collimator (fibre diameter ≈ ¼ collimator diameter)

Ni filter

Specimen stretched over collimator using holder, the other set glued to collimator on other side of hole

0.26 m.a. 36–38 kV

2 p.m. H_2 through sat. NH_4Cl through camera, sat. NH_4Cl in camera

3.30 p.m. tube on

12.10.51

11 a.m.

NH_4Cl sol^n found in camera (specimen unharmed)

Films developed ∴ no good

(10) A B & C

12.10.51

Some specimen & cond°, repeat

2 p.m. camera set up w H_2 & NH_4Cl sat.

3 p.m. tube on (filament 69 hrs)

13.10.51 4 p.m. Filament burnt out

15.10.51 11.30 a.m. tube on (New Filament)

Filament burnt out during night of 16–17, & leak developed

17.10.51 Leak in window patch w glass cement

Target cleaned, new filament

→ much brighter beam (as bright w Ni as previously without)

5 p.m. tube on

18.10.51 Some again, during night

Tube cleaned, new filament 4 p.m.

19.10.51 Stopped for 6 hrs to renew brass can

20.10.51 H_2 stopper blown off during night. Stopped 7 hrs

21.10.51 ✓

22.10.51 Filament burned out during night.

Renewed & target cleaned. Started 2 p.m.

23.10.51 2 p.m. ff - developed

25 hrs

31–43

2–15

53–77

24

Total exposure 135 – 184 hours

23.10.51 Yougoslav carbon ③ 2.30 – 5.30

(11) β Coli 6 p.m. (NH_4Cl, filter)

24.10.51 12 p.m. stopped (18 hrs)

(12) 24.10.51 4 p.m. embryo rat tail collagen

H_2 through sat. $Ca(NO_3)_2$, not in camera

exposed 1 hr

25.10.51 10.30 – 1.00

3.30 – 10.00 } 10 hrs

3 films, thick specimen ∴ distance ~ 1

Equatorial are 3.8 in mm

$\tan 2\theta = \frac{1.9}{13.5} = .14$ $\theta = 4° 0'$

$d = 11.0$ A

Diffuse ring 8 to 13 mm

$\tan 2\theta = .30$ to $.48$ $\theta = 8° 21'$ to $12° 48'$

$d = 5.3$ to 3.5 A

Meridional are 17 mm

$\tan 2\theta = .63$ $\theta = 16° 6'$

$d = 2.8$ A

30.10.57

Pin-hole photographs on Ehrenberg tube

Pinhole size - 5 divisions on micrometer scale
$= \frac{5}{80} = .0625$ mm

Distance pin-hole → tube $\sim 1.15" = 29$ mm

Distance " → film 12", 20" and 29"
i.e. 305, 510 and 740 mm

Size of image. Ø 29" 1.5 → 2.3 mm × 3.2 → 5.5 mm
Ø 20" 1.0 → 1.6 mm × 2.3 → 3.7 mm

∴ geometric Ø 29" $\frac{0.5}{2} \times \frac{2.3}{2} = 0.4 \times \frac{1.15}{}$ mm

" " 20" $\frac{0.6}{2} \times \frac{1.4}{2} = 0.3 \times 0.7$ mm

∴ focal size (given by 29" image) $= \frac{1.15}{29} \times 0.4 \times \frac{1.15}{29} \times \frac{1.15}{0.046}$
$= .016 \times$ ~~.024~~ mm²

Beaudouin filament field

int. dia. 15.55mm

Length 70 mm

(13)

2.11.51

Bundle of Sigrex fibres (prepared Sept'51) in micro-camera on Beaudouin tube. Strapped to collimator near hole w. narrow 0.1mm Al strips

Ni filter 2½ ma., 37 KV, bias

$NaClO_3$ sol^n, H_2 ∠ in camera

11.00 a.m. camera set up, H_2 over

11.45 tube on

5.45 Off } 6 hours

(13A) As above, with Na_2CO_3 sol^n (92%)

2.11.51 6.30 p.m. specimen in camera, H_2 flow

7 p.m. tube on

3.11.51 Filament burnt out during night

5.11.51 Transferred to threaded tube

11.45 tube on

Good beam, 2.6 amps through filament (sub. protruded ~1mm through tube)

5.45 Off

→ "wet" photo

Filament slip 33-45 hrs

(15) As above

5.11.51 6.30 over H_2, $NaClO_3$

6.11.57 4.00 – 9.45 } 10½ hrs

7.11.57 10.45 – 3.30 }

→ "crystalline"

(16) 7.11.51 4.00 over $Ca(NO_3)_2$, H_2

6.00 on

8.11.57 Switched off during night

on 11.30 – 3.00

→ "crystalline"

(17) As (16). 8.11.51 6.00 on 9.11.51 10.00 off

Specimen broken – no photo

(18) 9.11.57 Same specimen, pumped down with Al strips one end broke pumped down with Al strips A.K.

10.30 over $CaCl_2$, H_2

11.45 – 3.00. (filament burned ~ 3 hrs)

10.11.57 New filament

10.30 on (switched off some time between 12.30 & 1.30 & on again 1.30)

3.00 off

(19) As above

P_2O_5 in camera H_2 through 98% H_2SO_4

10.11.51 H_2 3.30 p.m.

12.11.51 10.45 on } 7¼ hrs

6.00 off

P_2O_5 in camera got v wet. film blackened probably ∴ acid vapour

(20) As above

H_2 through 98% H_2SO_4, over KOH and P_2O_5

P_2O_5 in camera

13.11.51 4 p.m. H_2 through camera

5.45 take on off } 22 hrs

Specimen moved

14.11.51 4 p.m. — 15.11.51 12 noon

(21) As above Na_2CO_3

15.11.51 12.45 in camera, H_2 'drug photo

5.30 on

16.11.51 3.30 off } 22 hrs

Filament 5 5 hrs so far

19½
22½
30
7½
89½

Filament 145 hrs so far

(22)

Ar above 16.11.57 4.30 over Na_2CO_3
6.30 on
17.11.57 2.00 off } 19½ hrs
"dry" photo v good resolution

(23) 17.11.57 4 p.m. over $K_2Cr_2O_4$ (99%) ~~to~~ wet
18.11.57 12.00 specimen has visibly wetted
18.11.57 12.~~35~~ 45 ~~camera~~ over Na_2CO_3
12.45 on
19.11.57 11.15 off } 22½ hrs
"dry" photo
Hydrogen flow stopped during night

(24) Specimen wetted by standing over $K_2Cr_2O_4$, then of Na_2CO_3 ~~camera~~ 48 hours the exposed
30 hrs

(25) French rods, specimen A. Bundle of fibres straight from tube placed over 100% collimator
26.11.57 3.30 ~~camera~~ over $NaClO_3$
27.11.57 5.00 on } 17½ hrs
28.11.57 10.30 off } 17½ hrs
Top flm, fine grain
2nd flm, monocrocite
(liquid got into camera at start)

DNA fibres suspended in alcohol-water-alkali mixtures

6.12.51 6 p.m. Bundle of fibres, as received (paper non-pulling)

1. Wt bottle + suspended fibre 64.4 g
   " " + alcohol 75.4 g
   " " " + water 76.1 g
   + ~ 0.01 g KOH

8.12.51 + more water ~ 72.7 g
   nearly dissolved
   Ca little left clinging to nylon fibre

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2. Fibre bundle tied w fine Cu wire, suspended in 70% alcohol
   → v highly swollen gel
   added little alcohol (~ 5%)
   - still v swollen gel
   added ~ 0.03 g solid KOH (to ~ 18 cc liquid)
   fibre bundle immediately shrinks & transparent gel becomes opaque
   Shrunk to ~ ⅓ length (in ~ 10 mins)
   Removed from liquid shown to be still gelatinous
   - left to stand - liquid

10.12.57 10 a.m.

K-specimen apparently unchanged. (Sol yellow, prob. : smeared from Cu wire)

Specimen removed, and gelatinous piece of length ~ 3 in. stretched to fibre 30 - 70 μ, ~ 2 cm long

- stretching v easy and smooth → +ve fibre

∴ repeat

3. ~~Pd~~ 3 g.m. bundle of fibres suspended in 10 cc 70% + 10 cc 80% alcohol.

3.35 Still opaque (but gelatinous). Transferred to 70% alcohol

5.30 Added 0.05 gm KOH

- specimen broke

4. Added fibre bundle, room dry, to KOH-alcohol mixture used for 3. Shrinkage observed as in 2.

Pulled out to +ve fibre

N.B. these +ve fibres when smeared or when pulled to ± ve fine fibres always remain +ve

11.12.57 Repeated above expts omitting KOH, & use of alcohol does affect stretching properties. → Gels/threads now behaving as normal material. Not easy to pull as thick fibres as after KOH treatment, but not → rod at any stage

Sinned to thin fibres + sheets → always weakly −ve

13.12.51 Bundle of ~20-30 Signer pulled fibres tied together with fine Cu wire & suspended in ext. KCl - H_2O - alcohol mixture 11 a.m.
- mixture made up to give extensive swelling
3.30 p.m. put to wash in 70% alcohol
Stretched and broken

Now specimen 20-30 fibres put in KCl - H_2O - alcohol ~5.30 p.m.
14.12.57 11 a.m. put to wash in 70% alcohol
5 p.m. dried over P_2O_5
17 ~~14~~.12.57 11~~3~~ a.m. in camera

(26) 6 fibres (+ve) of KOH-treated DNA in adapted Guinier camera (specimen over lead guard-hole on Hilger plate of new micro-camera) No filter. 75% humidity ($NaClO_3$)
12.12.57 7 p.m. on. 11 p.m. still on
13.12.57 10 a.m. off during night. Switched on
5 p.m. developed → black film
Repeat with slits more closed (washer ~~gap~~ less)
6 p.m. → 11 a.m. (14.12.51) (17 hrs)

(27) Bundle of KCl-treated Signer fibres
17~~/12~~.57 11.30 in camera over H_2, ext. $NaClO_3$ (75%)
(adapted Guinier camera, specimen on brass plate / over guard-hole)
12.00 On
~~finis~~

20.12.51

Swelling of fibres

Fibres of "non-pulling" Signer DNA, swelling observed under coverslip

① Small fibre ~ 0.6 scale divisions (i.e. 8 μ) at narrowest but oriented part
enclosed in 92% humidity (sat. Na_2CO_3)
Rapid swelling ≈ 2× diameter - well-oriented part rather less

② Fibre of unsigned quality, finest at best part ~ 8 μ,
Enclosed by water
Rapid swelling → ~ 2× diameter
then slow
after 2 hours, diameter increased ~ × 10 ;
length increase small (straight, stretched fibre, with ends fixed
→ only slightly wavy)

Small drops of undersat water visible everywhere except
immediately on either side of fibre (showing that even
for 10-fold linear swelling reduction of VP is appreciable)

11.12.51 → 28.12.51

2 attempts to photograph single fibres ~ 10 μ after
baking over, one exposure 2 weeks; one 1 week
→ v poor intensity, much impurity and only
described DNA (used new "non-pulling" Signer specimen)

(28)

27.12.51 Single fibre of old Signer DNA after 3 weeks
over P_2O_5 (pulls v well) ~~0.01~~ 0.001" Al over ½ film 3 films
Baked over-night at > 50° (6 p.m. - 10 a.m.)

28.12.51 5 p.m. in camera, H_2, $NaClO_3$
6.00 tube on (new filament)

29.12.51 12 noon beam v weak

31.12.51 10 a.m. beam invisible. Developed
→ wet photograph
∴ specimen baked over overnight before next photograph

(29) 67% RH 3 films
Poor resolution

(30) As (29) 68% RH 1 film
still poor resolution

(31) 7.1.52

~70% RH, one fibre ~ 40μ

Beaudouin tube, Chromium target, no filter

on 7.30 p.m.

8.1.52 2.30 off. Blank film

- fibre moved : not stuck directly on collimator

(photo under-exposed, & resolution on equator v poor)

(32) 22.1.52

Bundle of ~10 fibres of Signer DNA 2

Micro-camera, Ni

Specimen dried 3 hrs over P_2O_5. Then @ 75% RH

22.1.52 6 p.m. → 23.1.52 11 a.m.

wet diagram

(33) 24.1.52 6 p.m. → 25.1.52 10.30 a.m.

3 30-40μ fibres Signer DNA 2. Dried 50°

no filter, 73% RH

→ wet diagram (with badly fogged centre)

25.1.52 → 1.2.52 Series of photographs with Signer DNA 1 and 2 humidities 60 - 80%, always → "wet" photo

is this ∵ specimens were heated in air? (40 - 60°c)

(34) as above, Signer 1, no filter, 65% RH

→ "wet" photo 1.2.52. 16 hrs

(35) New specimen dried room T over P_2O_5 Ni filter 6 fibres

→ "wet" photo 2.2.52 16 hrs

(36) 3.2.52 4 30μ. fibres

New Signer DNA Ni filter. 74% RH

3.2.52 2 p.m. → 5.2.52 11 a.m.

→ "wet" photo

(37) New filament. Bundle of Signer (1) fibres (not really!) wetted & stretched to ~ 2 x length

$NaClO_3$ sol^n. radiograms. No filter

5.2.52 2.30 → 6.2.52 10 a.m.

→ "Xtalline" photo, v weak exposure & poor resolution

10.15 specimen on camera in oven at 50°c till 2.30

~~38~~ Specimen as above, after 4½ hrs @ 50°. Ni filter
7.2.52 3.00 – 8.2.52 3.00 24 hrs
→ "crystalline", apparently better oriented. Resolution slightly better but still poor. Temperature ~ 80°.
Left over 3.30, exposed 3 days – forgot

38 ~6 Spicules 1 fibres // but converging
~½mm in depth from surface of collector. Ni. $Ni(CO)_3$
12.2.52 9.30 on
→ photo showing some well-oriented strong amorphous ring. Specimen contained 1 fat +ve fibre – presumably +ve fibre gave amorphous ring

39 2 fibres Spicule ② ~20–30μ 8 strong
no filter, 75% RH
18.2.52 3 p.m. on. 19.2.52 12 a.m. off
→ "wet" type photo v thin diffuse spots on equator

40 4 Spicules (2 fibres, 18–30μ. Dried 6 hrs over P_2O_5
Ni, 75% RH
20.2.52 5.30 → ? (tube off during night – probably spicules fallen)
→ v weak. Xtalline, oriented apparently good, resolution doubtful

41 Same specimen, reused w 3 fibres & smaller hole Ni
21.2.52 11.00 on } 48 hrs
23.2.52 11.00 off }
→ v good, even good, resol" moderate.
Repeat longer exposure

42 New filament (filter not burned), clean target. Ni. 3 fibres
23.2.52 1.00 on
26.2.52 off for 1 hr to clean target } 116 hrs
28.2.52 10.00 off

43 Same specimen, 92% RH
(test for 1 h over 92% showed fibres don't move)
28.2.52 12.00 on.
29.2.52 2.30 a.m. off (CCl_4 ff) } 14½ hrs
→ X Tedious

44 Same specimen but now only 3 fibres (fattest first)
29.2.52 5 p.m. on
10.30 p.m. filament burned out
1.3.52 12.30 p.m. on. 3.3.52 12 a.m. off
3.3.52 11 a.m. on

Adsorption water by DNA

4 specimens (3 French caravans rats / Sigler fibre-pulling) in weighing bottles in vacuum dessicator

9. 11. 57 4 p.m. Weighing bottles and specimens (in specimen tubes) evacuated over P_2O_5

10. 11. 57 1.30 p.m. Bottles weighed empty + DNA
12. 11. 57 11 a.m. re-weighed 5 p.m. re-weighed
5.30 evacuated over sat. KOH
13. 11. 57 10.15 weighed 5 p.m. re-weighed
5.30 p.m. over sat. $CaCl_2$
14. 11. 57 10.30 a.m. Humidity 40% (hygrometer-determination) weighed, then left over sat $CaCl_2$. not evacuated
5 p.m. 39% re-weighed
5.30 p.m. over $Ca(NO_3)_2$
15. 11. 57 11.45 77%
2.30 re-weighed 76.5%
2.45 over sat. $NaNO_2$
6.30 71% weighed

Specimen	S	F	C	B
Weighing bottle	1	2	3	4
Wt bottle	8·3959	8·0993	9·5953	7·9100
Bottle + specimen	8·4318	8·1291	9·7185	7·9425
14/11/51				
Specimen 14/11/51	0·0359	·0293	0·1232	0·0325
12.11.51 11 a.m.	8·4289	8·1288	9·7173	7·9425
" 5 p.m.	8·4291	8·1287	9·7175	7·9421
	8·4290	8·1287	9·7174	7·9423
Specimen	0·0331	·0289	0·1221	0·0323
13.11.51 10.15 a.m.	8·4314	8·1303	9·7216	7·9443
" 5 p.m.	8·4313	8·1303	9·7215	7·9442
Wt H_2O	·0023	·0016	·0041	·0019
	7·0%	5·5%	3·4%	5·9%
14.11.51 10.30	8·4341	8·1321	9·7256	7·9470
5 p.m.	8·4341	8·1321	9·7254	7·9470
Wt H_2O 3½ hrs	·0051	·0034	·0081	·0047
	15·4%	11·9%	6·6%	14·6%
15.11.51 11.45	8·4428	8·1372	9·7377	7·9555
Wt H_2O 77 hrs	·0138	·0086	·0203	·0132
	41·7%	29·8%	16·6%	40·8%
2.30	8·4425	8·1370	9·7376	7·9552

	S	F	C	B
	1	2	3	4
15.11.51 6.30 p.m.	8·4413	8·1363	9·7362	7·9541
H_2O (mean) 71 hrs	0·0125	0·0076	0·0188	0·0118
	37·8%	26·2%	36·4% 15·4%	36·6%
16.11.51 10.15	8·4416	8·1363	9·7360	7·9573
" 3 p.m.	8·4428	8·1372	9·7375	7·9554
78½ hrs H_2O	·0138 = 41·7%	·0086 = 29·8%	·0201 = 16·6%	·0131 = 40·6%
" 5.45	—	8·1380	9·7388	7·9564
Wt H_2O		·0093	·0214	·0141
81½ hrs		32·2%	17·5%	43·7%
17.11.51 2.45	—	8·1476	9·7614	7·9691
Wt H_2O		·0189	·0440	·0268
96%		65·4%	36·0%	83·0%
18.11.51 12.30	—	8·1502	9·7749	7·9740
Wt H_2O	—	·0215	·0575	·0317
98%		74·5%	47·1%	98·2%
19.11.51 10.15	—	8·1457	9·7743	9·7690
Wt H_2O 81½		·0170	·0569	·0267
		58·9%	46·6%	82·7%

16.11.51 10.15 weighed 71%
10.45 over sat. NH_4Cl
3 p.m. 78.5 - weighed
gives same results as $NaNO_2$
3.15 p.m. over Na_2CO_3
5.45 weighed 87.5% -
17.11.51 2.45 96% weighed
3.00 over $K_2Cr_2O_7$
18.11.51 12.30 98% weighed
12.45 over sat. KCl
19.11.51 10.15 87.5% - weighed
10.30 over sat. $NaClO_3$
2.15 76.5 - weighed
20.11.51 10.30 76.5% weighed
" 3.30 74.5% "
" 3.45 over $NaNO_2$
" 7.00 weighed (forgot hygrometer. Should be 71%)
over $CaCl_2$
21.11.51 10.30 40.5% weighed
" 3 p.m. over sat KOH
22.11.51 10.30 weighed
23.11.51 11.30 "
" 11.45 evacuated over P_2O_5 26.11.51 11.30 weighed

		S	F	C	B
		1	2	3	4
Dry wt		0.0331	0.0289	0.1221	0.0323
" + bottle		8.4290	8.1287	9.7174	7.9423
19.11.51	2.15	8.4427	8.1423	9.7706	7.9657
20.11.51	10.30	8.4447	8.1398	9.7629	7.9580
"	3.30	8.4441	8.1391	9.7610	7.9569
H_2O, 10.30 76.5%		.0157	.0111	.0455	.0157
		47.5	38.4%	37.3	48.6%
20.11.51	7.00	8.4425	8.1379	9.7577	7.9552
71% (?)		.0135	.0092	.0403	.0129
		40.8%	31.8%	33.0%	40.0%
21.11.51	10.30	8.4374	8.1347	9.7318	7.9503
40.5%		.0084	.0060	.0144	.0080
		25.4%	20.9%	11.8%	24.8%
22.10.51	10.30	8.4328	8.1317	9.7236	7.9455
23.10.51	10.30	8.4327	8.1317	9.7236	7.9455
		.0038	.0030	.0062	.0032
		11.5%	10.4%	5.1%	9.9%
26.11.51	11.30	8.4289	8.1285	9.7175	7.9418

26.11.57 6 p.m. over H_2SO_4 - H_2O ~ RH 60%

27.11.57 10.15 59% weighed

" 12.00 over H_2SO_4, water

" 3.30 62% - weighed

3.45 over H_2SO_4 ~ 70% RH

" 6.15 71.5% - weighed

" 6.30 over sat. ~~$NaClO_3$~~ ?

28.11.57 11.00 45.5% (wrong sol?)

11.00 just over $NaClO_3$

1.45 74% - weighed

29.11.57 12.45 78.5% weighed. Put over H_2SO_4 ~ 80

3.12.57 12.00 81% - weighed. Store H_2O & H_2SO_4

6.20 82% - weighed 1 and 4

6.30 evacuated over P_2O_5

4.12.57 12.00 over H_2SO_4 ~ 82% RH

Results for S1 adsorption not left overnight

~~27~~ 27.11.57	6.15	71.5%	24.8%
28.11.57	1.45	74%	25.7%
5.12.57	2.00	71.5%	24.8%
"	1.00	83.5%	36.6%
4.12.57	4.30	71.5%	28.4%
"	6.50	82.5%	32%

	S	I	C	B
	1	2	3	4
	0.0331	0.0289	0.1221	0.0323
	8.4290	8.1287	9.7174	7.9423
26.11.57 16.15	8.4357	8.1331	9.7272	7.9487
Wt H_2O 59%	.0067	.0044	.0098	.0064
	20.2%	15.2%	8.0%	19.8%
27.11.57 3.30	8.4362	8.1335	9.7278	7.9491
Wt H_2O 62%	.0072	.0048	.0104	.0068
	21.8%	16.6%	8.5%	21.1%
27.11.57. 6.15 71.5%	8.4372	8.1341	9.7290	7.9502
	~~8.4375~~ 24.8%	18.7%	9.50%	24.5%
28.11.57 Pass 74%	8.4375	8.1344	9.7292	7.9505
	25.7%	19.7%	9.65%	25.4%
29.11.57 12.45	8.4434	8.1381	9.7398	7.9563
78.5%	0.0144	.0094	.0224	.0140
	43.5%	32.6%	18.3%	43.4%
3.12.57 12.00	8.4456	8.1396	9.7557	7.9585
x%	0.0168	0.0109	0.0383	0.0162
(but after wkd week-end)	50.8%	37.7%	31.4%	50.2%
3.12.57 6.20 82%	8.4450	—	—	7.9576

4.12.57	4.30	74.5% - weighed
	4.40	over H_2SO_4, wetter
	6.50	82.5% - weighed
	7.00	over P_2O_5
5.12.57	10.30	over H_2SO_4
	2.00	71.5% - weighed 2.15 over H_2SO_4, wetter
	6.00	83.5% - weighed
6.12.57	11.00	over sat. KCl Equ. 65%
8.12.57	4.15	87.5% - weighed
	5.00	over P_2O_5

	S	F	C	B
	1	2	3	4
	0.0331	0.0289	0.1221	0.0323
	8.4290	8.1287	9.7174	7.9423
4.12.57 4.30	8.4384	8.1353	9.7300	7.9573
74.5%	0.0094	0.0066	0.0126	0.0090
	28.4%	22.8%	10.3%	27.9%
4.12.57 6.50	8.4396	~~i~~	—	7.9526
	32.0%			32.5%
5.12.57 2.00 71.5%	8.4371	8.1345	9.7285	7.9499
	24.5%			28.5%
" 6.00 83.5%	8.4411	8.1372	9.7335	7.9541
	36.6%			36.5%
8.12.57 4.45 87.5%	8.4475	8.1410	9.7518	7.9599

Adsorption of water by DNA at 28°

Weighing bottle ① Sigma batch ② not pre-heated
② " " pre-heated ~~4 hrs~~ 75° in P_2O_5
③ as ②
④ Fresh rats B, treated as ② & ③

Specimens sealed overnight over P_2O_5 in ①
weighed 10.30 a.m. ~~4.1.52~~ 4.1.52
11.10 in thermostat, 26° over sat. KOH
2.45 weighed 2.55 replaced in thermostat
6.15 re-weighed
6.30 ~~in~~ over 18° over H_2SO_4-H_2O
7.1.52 10 a.m. to dry (< 20%) in charged H_2SO_4 sat^n
7.15 18 % RH weighed
7.30 put over water H_2SO_4
8.1.52 10.30 a.m. RH 42 % weighed
2.30 put over water H_2SO_4
9.1.52 10.30 a.m. 67 % weighed
11.00 put over water H_2SO_4
7.00 75 % weighed over water H_2SO_4

10.1.52 3.00 78 % weighed Left for 10 days over same sol^n

Dry wt DNA		·0920	·0614	·0318
	1	2	3	4
Bottle + lid	7·3623	8·0998	9·5953	7·9100
4.1.52 10.30 a.m. Bottle + specimen	~~7·4603~~ (7.4603)	8·1918	9·6567	7·9418
4.1.52 2.45	7·4797	8·1962	9·6596	7·9435
" 6.15	7·4763	8·1973	9·6604	7·9439
Wt H_2O		·0055	·0037	·0021
% H_2O		6·0%	6·0%	6·6%
7.1.52 7.15	7·4698	8·1972	9·6601	7·9437
Wt H_2O	·0096	·0054	·0034	·0019
% H_2O 18%		5·9%	5·5%	6·0%
8.1.52 10.30	7·4740	8·2005	9·6625	7·9449
Wt H_2O	·0138	·0087	·0058	·0031
% H_2O 42%		9·5%	9·4%	9·7%
9.1.52 10.30	7·4829	8·2095	9·6688	7·9487
Wt H_2O	·0227	·0177	·0121	·0069
% H_2O 67%		19·3%	19·7%	21·7%
9.1.52 7.00	7·4858	8·2119	9·6707	7·9502
75%	·0256	0·0201	0·0140	0·0084
		21·9%	22·8%	26·4%
10.1.52 3.00	7·4942	8·2195	9·6759	7·9533
Wt H_2O	·0340	0·0277	~~0·0208~~ 0·0192	0·0115
% H_2O 78%		~~30·1%~~	~~31·3%~~	~~36·2%~~
		30·1%	31·3%	36·2%

22.1.52 5 p.m. 78.5% (still at 23°C since 10.1.52)

23.1.52 10.30 a.m. 85%

25.1.52 6 p.m. 86%

30.1.52 4.30 p.m. 85% Left to dry over P_2O_5.

12.2.52 10 a.m. weighed. Put over H_2SO_4 ~ 40%

14.2.52 3 p.m. 39.5%

18.2.52 5.30 p.m. 40% weighed
added little water

Dry wt	0979	0920	0714	0318
	1	2	3	4
Bottle+dry DNA	7.4602	8.1918	9.6567	7.9418
		8.1905	9.6557	7.9412
22.1.52. 5 p.m. 78.5%	7.4990 ~~7.4796~~	8.2257	9.6796	7.9540
Wt H_2O 78.5%	.0388	.0339	.0229	.0122
% H_2O	39.6%	36.9%	37.3%	38.4%
23.1.52 10.30 a.m. 85%	~~7.5042~~ 7.5042	8.2304	9.6832	7.9564
85%	.0440	.0386	.0265	.0146
% H_2O	45.0%	42.0%	43.2%	45.9%
25.1.52 6 p.m.	7.5083	8.2346	9.6859	7.9574
86%	.0482	.0426	.0292	.0156
% H_2O	49.2%	46.3%	47.5%	49.0%
30.1.52 4.30	7.5080	8.2343	9.6856	7.9571
% H_2O 85.5%				

12.2.52 10 a.m.	7.4602	8.1905	9.6557	7.9412
14.2.52 3 p.m.	7.4721	8.2011	9.6630	7.9455
18.2.52 5.30	7.4720	8.2010	9.6628	7.9453
Wt H_2O	.0118	.0105	.0071	.0041
% H_2O 40%	11.9%	11.4%	11.6%	12.9%

20.2.52	6.30	47.5%	weighed. H_2O added
21.2.52	12 p.m.	61.5%	weighed. replaced
23.2.52	5 p.m.	66%	weighed. Added little H_2O
25.2.52	2.30	73.5%	re-placed
27.2.52	11.30	74%-	weighed. Added 10 drops water
28.2.52	2.30	76%+	weighed + replaced
29.2.52	12.00	75%	weighed (4) and replaced
1.2.52	4 p.m.	76%+	weighed added 8 drops, replaced
4.2.52	5.30	78%	weighed

Empty	.0979	.0907	.0604	.0312
	1	2	3	4
Bottle+dry salt	7.4602	8.1905	9.6557	7.9412
20.2.52. 6.30	7.4734	8.2023	9.6636	7.9456
Wt H_2O	.0132	.0118	.0079	.0044
% H_2O, 47.5%	13.5%	13.0%	13.1%	14.1%
21.2.52 12.00	7.4801	8.2086	9.6682	7.9483
23.2.52 5.00	7.4811	8.2094	9.6686	7.9484
Wt H_2O	.0209	.0189	.0127	.0072
H_2O, 66%	21.4%	20.8%	21.0%	23.1%
25.2.52	7.4854	8.2134	9.6715	7.9503
27.2.52	7.4858	8.2138	9.6717	7.9506
Wt H_2O	.0256	.0233	.0160	.0094
% 74%	26.1%	25.7%	26.5%	30.1%
76% 29.2.52	7.4875	8.2154	9.6729	7.9514
75% 29.2.52	~~7.4885~~ 7.4875	~~8.2164~~ 8.2154	~~9.6735~~ 9.6729	7.9520
78% 1.2.52	~~7.4885~~ 7.4875	8.2164	9.6735	7.9514
~~4.2.52~~				
4.2.52 5.30	7.4921	8.2194	9.6753	7.9530

ARITHMETICAL TABLES

NUMERATION TABLE

Units	1
Tens	1 2
Hundreds	1 2 3
Thousands	1, 2 3 4
Tens of Thousands	1 2, 3 4 5
C. of Thousands	1 2 3, 4 5 6
Millions	1, 2 3 4, 5 6 7
Tens of Millions	1 2, 3 4 5, 6 7 8
C. of Millions	1 2 3, 4 5 6, 7 8 9

STERLING MONEY TABLE

4 Farthings	1 Penny (*d.*)
12 Pence	1 Shilling (*s.*)
2 Shillings	1 Florin
2 Shillings & 6 pence	1 Half Crown
5 Shillings	1 Crown
10 Shillings	1 Half Sov.
20 Shillings	1 Sov. or 1 Pound (£)
21 Shillings	1 Guinea

ARITHMETICAL SIGNS

+	Plus: Sign of Addition
—	Minus: Sign of Subtraction
×	Sign of Multiplication
÷	Sign of Division
=	Sign of Equality
::	Signs of Proportion
√	Sign of the Square Root
∛	Sign of the Cube Root
°	Degree, ′ Minute, ″ Second
∴	Therefore

TROY WEIGHT—For Gold & Silver

24 Grains	1 Pennyweight (*dwt.*)
20 Pennyweights	1 Ounce (*oz.*)

Precious Stones are weighed in Carats
(1 Metric Carat = 200 Milligrammes)

APOTHECARIES' WEIGHT
For Mixing Medicines

20 Grains	1 Scruple (*scr.*)
3 Scruples	1 Drachm (*dr.*)
8 Drachms	1 Ounce (*oz.*)

AVOIRDUPOIS WEIGHT
For all Goods, except Gold, Silver and Jewels

16 Drams	1 Ounce (*oz.*)
16 Ounces	1 Pound (*lb.*)
14 Pounds	1 Stone (*st.*)
28 Pounds	1 Quarter (*qr.*)
4 Quarters	1 Hundredweight (*cwt.*)
20 Cwt.	1 Ton

HAY AND STRAW WEIGHT

36 lbs. Straw	1 Truss
56 lbs. Old Hay	1 Truss
60 lbs. New Hay	1 Truss
36 Trusses	1 Load

LONG OR LINEAR MEASURE

12 Lines	1 Inch (*in.*)
12 Inches	1 Foot (*ft.*)
3 Feet	1 Yard (*yd.*)
6 Feet	1 Fathom (*f.*)
5½ Yards	1 Pole (*pl.*)
40 Poles	1 Furlong (*fur.*)
8 Furlongs or 1760 Yards,	1 Mile

CLOTH MEASURE

2¼ Inches	1 Nail
4 Nails	1 Quarter of a Yard
4 Quarters	1 Yard

SOLID OR CUBIC MEASURE

1728 Cubic Inches	1 Cubic Foot
27 Cubic Feet	1 Cubic Yard
11¼ Cubic Yards or 306 Cubic Feet	1 Rod of brickwork

IMPERIAL HEAPED MEASURE

	Avoird. of Water lbs.	
8 Gallons	1 Bushel	= 80
3 Bushels	1 Sack	= 240
12 Sacks	1 Chaldron	= 2880

IMPERIAL DRY MEASURE

		Avoird. of Water	lb.	oz.
2 Glasses	1 Gill	=	0	5
4 Gills	1 Pint	=	1	4
2 Pints	1 Quart	=	2	8
4 Quarts	1 Gallon	=	10	0
2 Gallons	1 Peck	=	20	0
4 Pecks	1 Bushel	=	80	0
8 Bushels	1 Quarter	=	640	0

SQUARE MEASURE

144 Square Inches	1 Square Foot
9 Square Feet	1 Square Yard
30¼ Square Yards	1 Square Pole
40 Square Poles	1 Rood
4 Roods	1 Acre
640 Acres	1 Square Mile

TABLE OF MOTION

60″ Seconds	1 Minute
60′ Minutes	1 Degree
30° Degrees	1 Sign
12s Signs or 360°	the circle of the earth

TABLE OF TIME

60 Seconds	1 Minute
60 Minutes	1 Hour
24 Hours	1 Day
7 Days	1 Week
4 Weeks	1 Lunar Month
365 Days	1 Year
366 Days	1 Leap Year
52 Weeks	1 Year
12 Calendar or 13 Lunar Months	1 Year

Days in the Months

Thirty days have September
April, June and November
All the rest have thirty-one,
Excepting February alone,
Which has but twenty-eight days clear,
And twenty-nine in each leap year.

MULTIPLICATION TABLES

2 TIMES	3 TIMES	4 TIMES	5 TIMES	6 TIMES	7 TIMES	8 TIMES	9 TIMES	10 TIMES	11 TIMES	12 TIMES
1 are 2	1 are 3	1 are 4	1 are 5	1 are 6	1 are 7	1 are 8	1 are 9	1 are 10	1 are 11	1 are 12
2 — 4	2 — 6	2 — 8	2 — 10	2 — 12	2 — 14	2 — 16	2 — 18	2 — 20	2 — 22	2 — 24
3 — 6	3 — 9	3 — 12	3 — 15	3 — 18	3 — 21	3 — 24	3 — 27	3 — 30	3 — 33	3 — 36
4 — 8	4 — 12	4 — 16	4 — 20	4 — 24	4 — 28	4 — 32	4 — 36	4 — 40	4 — 44	4 — 48
5 — 10	5 — 15	5 — 20	5 — 25	5 — 30	5 — 35	5 — 40	5 — 45	5 — 50	5 — 55	5 — 60
6 — 12	6 — 18	6 — 24	6 — 30	6 — 36	6 — 42	6 — 48	6 — 54	6 — 60	6 — 66	6 — 72
7 — 14	7 — 21	7 — 28	7 — 35	7 — 42	7 — 49	7 — 56	7 — 63	7 — 70	7 — 77	7 — 84
8 — 16	8 — 24	8 — 32	8 — 40	8 — 48	8 — 56	8 — 64	8 — 72	8 — 80	8 — 88	8 — 96
9 — 18	9 — 27	9 — 36	9 — 45	9 — 54	9 — 63	9 — 72	9 — 81	9 — 90	9 — 99	9 — 108
10 — 20	10 — 30	10 — 40	10 — 50	10 — 60	10 — 70	10 — 80	10 — 90	10 — 100	10 — 110	10 — 120
11 — 22	11 — 33	11 — 44	11 — 55	11 — 66	11 — 77	11 — 88	11 — 99	11 — 110	11 — 121	11 — 132
12 — 24	12 — 36	12 — 48	12 — 60	12 — 72	12 — 84	12 — 96	12 — 108	12 — 120	12 — 132	12 — 144

Ref. No. D24

R. D. Franklin

1952

Century

NOTE BOOK

March - April, 1952

Long series of microphotographs at >75% RH (not preserved) in which trial short-exposure films were generally good — specimen subsequently went non-crystalline during long exposure. Twice drying at room T over P_2O_5 in attempt to recover photograph apparently spoilt specimen. Specimen non-crystalline at >75% was never re-converted to crystalline

Tilting camera

Series of setting photographs and minor adjustments to camera.

All specimen eight thick fibres (40-70μ) 75% R.H.

18.4.52

(45) 75% N_2 filter
3 films. Exposure unknown (3–7 days, ∴ Exists)
Single fibre ~40μ
→ good photo, showing some double orientation

(T0) specimen previously X-rayed, now gives "wet" diagram
(2 films, ~3 days)

(T1) Single fibre, ~50μ. 16 hrs
Tilt ~14° (edge set to 61)

(T2) Chromium 21 hrs, thin V filter
Tilt as above

(T3) As T2. 2 films
On 18.4.52, 6 p.m. (Friday)
Still running Sat., filament burned out before Mon. 21st
Developed 21.4.52 3 p.m. Dirty centre.
~~Black~~ Specimen deteriorating → "wet" ∴ changed

(46) As (45), but Cr and V filter
Exposure as for T3 – result blank films

(T4) Exposure 16 hrs, 1 film, no filter Tilt ~18°
→ "wet" diagram v well oriented. Dirty centre
∴ specimen transferred to Unicam

T4 specimen was dried 4 hrs over P_2O_5 ∠ this apparently destroyed x-talinity. ∴ New specimen not dried

(T5) New specimen. Beam centred ~~photographically~~
Tilt ~18°. Lead pinhole removed from tube. No filter
X specimen moved. V dirty centre ∴ replace pinhole

(47) As (46). On 7 p.m. 21.4.52
Exposure to 26.4.52 10 a.m. ~~10 a.m. 22.4.52~~
Result – X-tal diffraction pattern of foreign body + diffuse ring
Specimen has "necked" over collimator hole → ~⅔ diameter of needle

(T6) Black paper over film ∴ dirty centre believed
due to soft radiation scattered from glass collimator
– shadow of DNA fibre (~50μ) appears sharply
on dirty centre. Specimen as in T5, no filter
Exposure 3 days. Weak x-talline diagram ∴

28.4.52 Copper target replaced

(48) 3 rolled fibres viewed edge on, Industrial G film,
no filter, exposure 16 hrs
→ mainly wet photo, v strong exposure
– no trace of X-tals shown by (47) although
collimator had not been cleaned meanwhile
∴ X-tals were decomp. product of DNA fibre

Filament life ~ 250 hrs

(49) Specimen from TO (which gave good "wet" photo)
re-exposed at 75% RH. 2 films, Ni
29.4.52 11 a.m. — night of May 1-2 (filament burned out)
i.e. exposure 33 – 44 hrs
NB Film 8 back to front. V good "wet" photo
New filament

(50) Rolled fibre, 75%, no filter, Industrial G
2.5.52 3.20 p.m. – 5.00
⇒ wet photograph, mod. well oriented
∴ put specimen 8 days over P_2O_5

(51) Specimen as in (49) with holder centred over collimator so as to include both 3.4 Å ares
2.5.52 7.30 p.m. — 6.5.52 5 p.m. with interruption of 32 hrs i.e. 62 hrs

(50) Streaks = outer pair of diagram (( ))) are v strong and differently shaped from normal "wet" diagram, being more rounded. Is this an effect due to double orientation of e.g. elliptical lattices?

(47) $2l = 2 \times 14.2$ cm 2θ 5

Strong rings of spots. Diameters measured across specimen-film distance 14.2 mm

$2l$ (cm)	strength	$\tan 2\theta$	θ	d	$\log d$
1.65	m	.581	15°5′	4.38	.6415
1.89	v w	.665	16°48′	3.95	.597
2.13	m	.750	18°26′	3.64	.5575
2.29	w	.806	19°26′	3.43	.535
2.63	s	.926	22°24′	3.13	.4955
2.70	w	.951	21°47′	3.08	.489
3.14	s	1.106	23°56′	2.82	.450

Also four diffuse rings at 8–9 Å
Cell spots too small to be photographed
Wyckoff gives As_2PO_4 cubic, $a = 6.00$
KH_2PO_4 tetrag. $a = 7.43$, $c = 6.97$
$(NH_4)H_2PO_4$ " 7.53 7.54
Li_3BO_3 orthorhombic 4.86, 6.10, 26, $c = 6.07$

$NaHCO_3$ $a = 7.51$, 6.79 $c = 3.53$ $\beta = 93° 19'$
NH_4HCO_3 7.29 10.79 8.76

(49) 49B

Rough measurements on projection drawing (2.5.52) (gypsum layer-lines straight)

Layer-line spacings, mm: — (= 23)

14·8, 30·5, 46, –, 79, –, –, 131

Suppose specimen-film distance = 14·4 mm

3·4 A reflexion are less 23 = 164 mm, $\theta = 13°4'$, $\tan 2\theta = .491$

~~$\tan 2\theta = \frac{23}{2 \times 164}$~~

∴ Specimen-film distance for projection = $\frac{164}{2} \times \frac{1}{.491} = 167$ mm

∴ $\tan 2\theta$ for layer-lines = $\frac{23}{2 \times 167} = \frac{23}{334}$

= ·0443, ·0914, ·1378, –, ·2365, –, –, ·392, –, ·504

θ = 1°16', 2°37', 3°55', –, 6°39', –, –, 10°52', 13°23'

d = 34·8, 16·8, 11·3, –, 6·64, –, –, 4·14

Multiplying by 1, 2, 3, –, ~~5~~, ~~6~~, –, –, 8, 10 gives:

34·8, 33·6, 33·9, 33·2, 33·2, 33·2

∴ layer-line spacing = 33 – 34 A

3·4 are ~ corresponds to 10th layer-line

(if helix is non-integral no. ~~reflexions~~ residues per turn, 3·4 are not necessarily lie on a layer-line)

Equator strong doublet at 20·8, 23·2 mm

On above approx (using 3·4 one) this gives 24·6 A, 22·1 A

This suggests co-existence of 2 phases differing only by 1 molecular layer of water separating chain units

Taking mean pos^n of 1st doublet and centre of diffuse equatorial spot gives 23·3 A, 13·8 A, 9·3 A, 5·42 A

~~These do not fit hexag. close-packing~~

this fact, together with the 3·4 are lying on a layer-line, suggests that there is an integral no. (or right fractional no.) of residues per turn of helix (if there is a helix) even in the "wet" state.

In passing from "crystalline" to "wet" the predominant equatorial spacing is approximately doubled, and the fibre-axis period is extended by ~ 25%

(27 A → 34 A)

(52) As 51, with Na_2CO_3
on 6.5.52 6 p.m.

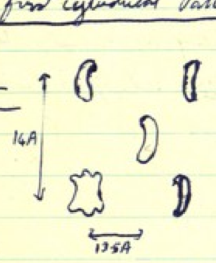
<u>51A</u>

Measuring on projection, and taking meridional axis ? to be 3.5
gives equatorial spots <u>24.5</u> and 9.83 (weak and diffuse)

2. 7. 52

Notes on first cylindrical Patterson

General form



There is no indication of an helix of diameter 11A.
The central banana-shaped peak fits curve calc. for helix of diameter 13·5A having 2 turns / unit cell
If a helix there is only one strand
(2-strand helix would give )
If a helix, it is v far from continuous uniform density. Has deep trough for r 6-7 A.
Helix does not explain vertical short vector ~ 4A (this is superimposed on peak at origin, so represents true distance of > 4A) (i.e. not 3·4A). But if there is a flat banana-like unit in structure, with banana axes ∥ fibre axis this vector is explained.

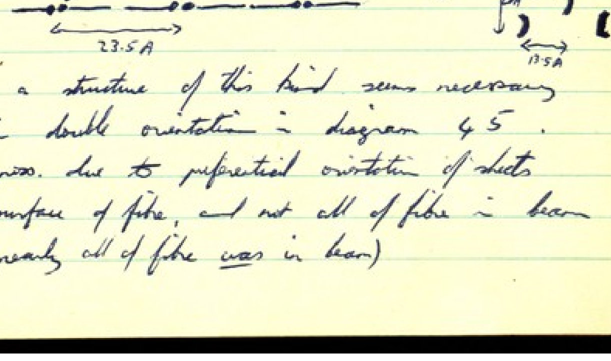
Cylindrical Patterson should give unit cell. Projections of a and b axes on plane ⊥ fibre axis being ~ 13·5 and 23·5A. γ differs little from 60°.

~~If bananas are flat and vertical, not helical, this explains why those at 23·5A are less curved — they are~~

i.e. triclinic cell ~ ½ size of previously considered primitive cell of monoclinic face-centred lattice.

Again, the dimensions of this cell make a helical structure improbable — if helices of 13·5A diameter how is the remaining space in the long period filled?

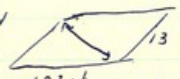
Suggests rather a double-sheet structure



Also a structure of this kind seems necessary to explain double orientation in diagram 45. Effect poss. due to preferential orientation of sheets w.r.t. surface of fibre, and not all of fibre in beam (though nearly all of fibre was in beam)

July 7th

Pattern max. of $x \sim 13A$, $z \sim 7A$ can not be lattice point

∴ projected cell  would have a lattice vector with both x and z values intermediate between those of the 2 vectors observed. No trace of this.

∴ Pattern was extended to 46 A

This shows a large peak of $x \sim 35$ A, $z \sim 7$

i.e. it is to the peak of 23 A as in the 13 A peak to the origin

∴ this is not a lattice point

It seems probable that both lattice vectors are contained in the 23 A peak. Banana-like form might be due to one peak on x-axis and one slightly off — nearer origin. This would give $\beta \sim 93°$, which seems reasonable for measured z value

There is no lattice peak between 24 A and, at the nearest 36 A. ∴ the cell is strongly anisodimensional

July 15th

G. Pett. has no cross mer. // fibre axes between 4-5 A
and ~14 A

∴ there is no narrow straight chain of high density // axis
i.e. high-density regions are discrete regions, not continuous
Gap between x = 6 — 1 x = 10

14.8.52

(60) Fine fibre of Sigma 10 scale divisions (~120μ) covering ½ of 80μ aperture, to look for double orientation due to edge effect
14.8.52 12.15 p.m. – 15.8.52 10.45
Film grey. Trace of double orientation?

(61) Sigma (2), fibre ~15μ ∴ no white Xtalline
15.8.52 11.45 – 18.8.52 9.45
→ wet diagram (v weak)

(62) Sigma (3). Pulling properties resemble (1) rather than (2). Fibre ~50μ
18.8.52 4 p.m. – 19.8.52 3.30 p.m.
→ Xtalline photograph (poor)

(63) 19.8.52 6 p.m. – 25.8.52 11 a.m.
As (60), same fibre, covering ~⅓ hole
no double orientation

(64) Fibre Sigma (1) ~40μ, 75% RH
25.8.52 12 p.m. – 26.8.52 6 p.m.
Good photograph, but with strong trace of Xtalline impurity
– collimator blocked

(65) Fibre used in (60) and (63) replaced. 75% RH
26.8.52 7 p.m. – 27.8.52 3 p.m. – 20 hrs

(66) As above, using $Ca(NO_3)_2$ sol.
27.5.52 4 p.m. – 28.8.52 2 p.m. – 22 hrs
→ similar to (65) but with one Xtalline impurity

(67) As above, using $CaCl_2$ (in jar: blocks sintered bubbler)
Start over with this!
25.8.52 6.30 p.m. – 29.8.52 3 p.m.

(68) Over $Ca(NO_3)_2$ 3.30 p.m. 29.8.52
29.8.52 Exposed 5 p.m. – 30.8.52 12 p.m. – 19 hrs
→ photograph similar to 67

(69) Over P_2O_5 in hydrogen, 12.30 p.m. 30.8.52
1.30 p.m. on → 31.8.52 8 a.m.
Film fogged ∴ repeat

(70) As (69)
1.9.52 10.30 a.m. – 2.9.52 2 p.m.
oxygen fogged (through bars)
– this also to avoid oxygen?

(71) Repeat as (70). On 2.9.52 4 p.m. → 3.9.52 4.30
fogged again
- must be acid again. Why?

(72) $NaClO_3$
3.9.52 4.45 in camera
Exposed 6.15 - ~~eg~~ 2.15 4.9.52

(73) Na_2CO_3
4.9.52 5.30 in camera
Exposed 6.30 — 5.9.52 2.30
→ X-ray photo

(74) Wetted by standing ~10 minutes over dil. soln $NaClO_3$
→ length change, moved off collimator hole
then exposed to air till came back over hole &
exposed to Na_2CO_3 in camera 4 p.m. 5.9.52
Exposed 5 p.m. - 6.9.52 11 a.m.
Fibre has flowed - too wet

from Spool (3)

(75) New fibre, ~100 μ, light blue when close to collimator hole (~0.2 mm fibre exposed)
In camera, with Na_2CO_3 1 p.m. 6.9.52
Exposed 3 p.m. — 8.9.52 10 a.m.
→ wet photo with trace of crystalline

(76) Same fibre as (75), with $NaClO_3$ 11 a.m.
exposed 11.40 — 3.30
→ "wet" photo
∴ specimen dry third over P_2O_5 - before
exposing to $NaClO_3$

(77) 9.9.52 exposed 1.20 — (?)
→ wet photograph

(78) 14.10.52 New fibre, 60-70 μ. Over $NaClO_3$
Exposed 48 m. —

Notes by A.K (45) Some double orientn 18 Apr 52
(49) V. Good B night of May 1–2

April 1952 Tilting (camera) photos devoted by T

(50) elliptical helices? "eff^{ve} helix"

(49) 10 residues / turn of helix

2-7-52 cyl. Patt

"make a helical structure improbable"

July 7 cell strongly anisodimensional

July No "Zickzack" straight chain of deos. (?) [illegible]

14-8-52 trying to repeat double orientation

Went on taking pictures till 9-9-52, & one extra on 14-10-52
(mostly A fibres 75% RH & $CaCl_2$ or $Ca(NO_3)_2$

May 22, 1952 REF was in Belgrade

ARITHMETICAL TABLES

NUMERATION TABLE

Units	1
Tens	1 2
Hundreds	1 2 3
Thousands	1, 2 3 4
Tens of Thousands	1 2, 3 4 5
C. of Thousands	1 2 3, 4 5 6
Millions	1, 2 3 4, 5 6 7
Tens of Millions	1 2, 3 4 5, 6 7 8
C. of Millions	1 2 3, 4 5 6, 7 8 9

STERLING MONEY TABLE

4 Farthings	1 Penny (*d.*)
12 Pence	1 Shilling (*s.*)
2 Shillings	1 Florin
2 Shillings & 6 pence	1 Half Crown
5 Shillings	1 Crown
10 Shillings	1 Half Sov.
20 Shillings	1 Sov. or 1 Pound (£)
21 Shillings	1 Guinea

ARITHMETICAL SIGNS

+	Plus: Sign of Addition
—	Minus: Sign of Subtraction
×	Sign of Multiplication
÷	Sign of Division
=	Sign of Equality
::	Signs of Proportion
√	Sign of the Square Root
∛	Sign of the Cube Root
°	Degree, ′ Minute, ″ Second
∴	Therefore

TROY WEIGHT—For Gold & Silver

24 Grains	1 Pennyweight (*dwt.*)
20 Pennyweights	1 Ounce (*oz.*)

Precious Stones are weighed in Carats
(1 Metric Carat = 200 Milligrammes)

APOTHECARIES' WEIGHT
For Mixing Medicines

20 Grains	1 Scruple (*scr.*)
3 Scruples	1 Drachm (*dr.*)
8 Drachms	1 Ounce (*oz.*)

AVOIRDUPOIS WEIGHT
For all Goods, except Gold, Silver and Jewels

16 Drams	1 Ounce (*oz.*)
16 Ounces	1 Pound (*lb.*)
14 Pounds	1 Stone (*st.*)
28 Pounds	1 Quarter (*qr.*)
4 Quarters	1 Hundredweight (*cwt.*)
20 Cwt.	1 Ton

HAY AND STRAW WEIGHT

36 lbs. Straw	1 Truss
56 lbs. Old Hay	1 Truss
60 lbs. New Hay	1 Truss
36 Trusses	1 Load

LONG OR LINEAR MEASURE

12 Lines	1 Inch (*in.*)
12 Inches	1 Foot (*ft.*)
3 Feet	1 Yard (*yd.*)
6 Feet	1 Fathom (*f.*)
5½ Yards	1 Pole (*pl.*)
40 Poles	1 Furlong (*fur.*)
8 Furlongs or 1760 Yards,	1 Mile

CLOTH MEASURE

2¼ Inches	1 Nail
4 Nails	1 Quarter of a Yard
4 Quarters	1 Yard

SOLID OR CUBIC MEASURE

1728 Cubic Inches	1 Cubic Foot
27 Cubic Feet	1 Cubic Yard
11½ Cubic Yards or 306 Cubic Feet	1 Rod of brickwork

IMPERIAL HEAPED MEASURE

	Avoird. of Water lbs.	
8 Gallons	1 Bushel	= 80
3 Bushels	1 Sack	= 240
12 Sacks	1 Cheldron	= 2880

IMPERIAL DRY MEASURE

		Avoird. of Water	lb.	oz.
2 Glasses	1 Gill	=	0	5
4 Gills	1 Pint	=	1	4
2 Pints	1 Quart	=	2	8
4 Quarts	1 Gallon	=	10	0
2 Gallons	1 Peck	=	20	0
4 Pecks	1 Bushel	=	80	0
8 Bushels	1 Quarter	=	640	0

SQUARE MEASURE

144 Square Inches	1 Square Foot
9 Square Feet	1 Square Yard
30¼ Square Yards	1 Square Pole
40 Square Poles	1 Rood
4 Roods	1 Acre
640 Acres	1 Square Mile

TABLE OF MOTION

60″ Seconds	1 Minute
60′ Minutes	1 Degree
30° Degrees	1 Sign
12s Signs or 360°	the circle of the earth

TABLE OF TIME

60 Seconds	1 Minute
60 Minutes	1 Hour
24 Hours	1 Day
7 Days	1 Week
4 Weeks	1 Lunar Month
365 Days	1 Year
366 Days	1 Leap Year
52 Weeks	1 Year
12 Calendar or 13 Lunar Months	1 Year

Days in the Months

Thirty days have September
April, June and November
All the rest have thirty-one,
Excepting February alone,
Which has but twenty-eight days clear,
And twenty-nine in each leap year.

MULTIPLICATION TABLES

2 TIMES	3 TIMES	4 TIMES	5 TIMES	6 TIMES	7 TIMES	8 TIMES	9 TIMES	10 TIMES	11 TIMES	12 TIMES
1 are 2	1 are 3	1 are 4	1 are 5	1 are 6	1 are 7	1 are 8	1 are 9	1 are 10	1 are 11	1 are 12
2 — 4	2 — 6	2 — 8	2 — 10	2 — 12	2 — 14	2 — 16	2 — 18	2 — 20	2 — 22	2 — 24
3 — 6	3 — 9	3 — 12	3 — 15	3 — 18	3 — 21	3 — 24	3 — 27	3 — 30	3 — 33	3 — 36
4 — 8	4 — 12	4 — 16	4 — 20	4 — 24	4 — 28	4 — 32	4 — 36	4 — 40	4 — 44	4 — 48
5 — 10	5 — 15	5 — 20	5 — 25	5 — 30	5 — 35	5 — 40	5 — 45	5 — 50	5 — 55	5 — 60
6 — 12	6 — 18	6 — 24	6 — 30	6 — 36	6 — 42	6 — 48	6 — 54	6 — 60	6 — 66	6 — 72
7 — 14	7 — 21	7 — 28	7 — 35	7 — 42	7 — 49	7 — 56	7 — 63	7 — 70	7 — 77	7 — 84
8 — 16	8 — 24	8 — 32	8 — 40	8 — 48	8 — 56	8 — 64	8 — 72	8 — 80	8 — 88	8 — 96
9 — 18	9 — 27	9 — 36	9 — 45	9 — 54	9 — 63	9 — 72	9 — 81	9 — 90	9 — 99	9 — 108
10 — 20	10 — 30	10 — 40	10 — 50	10 — 60	10 — 70	10 — 80	10 — 90	10 — 100	10 — 110	10 — 120
11 — 22	11 — 33	11 — 44	11 — 55	11 — 66	11 — 77	11 — 88	11 — 99	11 — 110	11 — 121	11 — 132
12 — 24	12 — 36	12 — 48	12 — 60	12 — 72	12 — 84	12 — 96	12 — 108	12 — 120	12 — 132	12 — 144

Ref. No. D24

MADE IN GREAT BRITAIN

REF 1951 notebook
& 1952

(12) moved. 2-8 A ?

30.10.51. Chem lab

2.11.51.

(14) "wet" 92% RH

(15) same specimen "crystalline"

(22) dry photo
(23) dry photo
/ even though ~~[illegible]~~ < RH

6.12.51 alcohol water - alkali washes

10.12.51. fibres always remain positive when pulled

Use of "non-pulling" Signer fibre

31.12 "wet"

25.1.52–1.2.52. Series of photos with Signer DNA 1 RH
~~#~~ wet & cryst.

Aug 1952 (74) wetter
fibre moved off roller
- length change

March-April 1952. long series of ~~photos~~.
Used short exposure films good → ~~specimen~~
Event non crystalline specimen non crystalline
at 75% never ~~[illegible]~~ converted to crystalline

Tilly camera

(49) 49b B photo

Roger 7 cryst → wet transit

10.12.52

Volume of complete unit cell ~~24450~~ A^3

In Page 31 of Notebook

KBP Needs to know no. of chains per lattice pt. for interpretation of Patterson (page 71B photo A-form

Wt of nucleotide 330

Volume of dry nucleotide 336 A^3 ($d = 1.63$)

Density wet ~ 1.55

Using this approx. value for wet density,

M. Wt of wet unit cell = $1.55 \times 2.4845 \times 10^4 / 1.66 = 2.285 \times 10^4$

M. Wt per primitive cell = 1.143×10^5

Suppose whole number of water molecules per nucleotide, ~1 in between 6 & 8

the MWt per unit cell is 402, 420, 438, 456 or 474

And no. nucleotides/primitive cell: 284 272 261 251 241 220

% H_2O 21.8% 27.3% 33.6% 38.2% 43.6%

If phosphates are 2 pairs, ~~there~~ there are 24, 26 or 28 per primitive cell

If 2 chains = primitive cell are equivalent,

there are 24 or 28 nucleotides = primitive cell

If odd no. pairs per chain (it occurs for peaks of 13, 14 & not 15)

there are 28 nucleotides per unit cell.

This is also suggested by 71B

Density 1.52

M. Wt wet cell $: 22.4 \times 10^3$

M. Wt primitive cell 11.2×10^3

$\therefore$ for 22 nucleotides, wt/unit: $\frac{11.2 \times 10^3}{22} = 509$

Wt water = 509 − 330 = 179

~~10~~ : 10 molecules/nucleotide

or 54% of dry weight

for density 1.67, MWt wet cell, primitive $11.2 \times \frac{1.67}{1.52} = 10.82 \times 10^3$

wt/unit: $10.82 \times 10^3 / 22 = 492$

Wt water = 492 − 330 = 162

= 49%

R. E. F.

DNA. Cristallographie Calcas. etc 1953

19. 1. 53

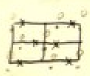
Results of superposition of 3-dimensional Patterson of crystalline

Na DNA

__Space group__ C 2

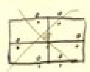
- axes found in superposition function
- mirror planes impossible ∵ asymmetric C

__Axial sections__

one axial section contains principal maxima (c.0) 

the other no important maxima (c + ½)

__Peaks at heights 13/30 and 17/30__

v strong, also in pseudo-hexagonal array 

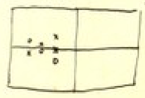
[N.B. hexagons appear centred, ∵ superposition method is not capable of eliminating central peak. But 1. can't reconcile centring w density
2. would have pseudo-cell of side a ~ b ~ 13 A]

__Possible structure having chains along a - c diagonal__

but fibres can't be built this way - unreasonable

∴ search for alternative - gives:-

__Figure of 8 structure__ (in projection). 7 peaks on chain in one cell.



2 pairs of chains / primitive cell
(4 pairs / full cell)
i.e. 56 nucleotides / full cell

Consistent w density data if
1. ~25% H_2O
2. __2 P atoms per peak__
i.e. 2 chains 'back to back'

A.K.
[illegible] p45 [illegible]

i.e. chains are ∴ pairs, one upside-down w.r.t the other

Patterson peaks representing Zphosphates

If pairs are all ∴ "oriented" and record is poor, maxima will give distances between most ∴ of pairs

i.e. : : : : gives ⋮ ⋮

If pairs in one another, no central maxima

i.e. : : : : gives ⋮ ⋮

does this indicate that pairs at c=8 are inclined to other pairs at ∴ give weaker peaks?

Peak at 6·3Å in section c=2 would then be P-P distance with pair?

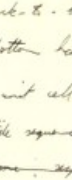
but in that case Na is not directly between P-P, or resolution would be destroyed by 2 Na-P peaks

Peak at height 0 lies on axis

∴ 2 P atoms attacked to similar nucleotides

- apart from this, symmetry does not control nucleotide sequence

except that ∴ a "back-to-back" pair of chains top half of one is similar to bottom half of other



Each chain of peaks is unit cell

∴ can't reconcile nucleotide sequence with Chargaff's analysis

~~If all chains are same, sequence must be A B C D D C B~~

N.B. Symmetry axis does not affect sequence within one chain

Distance between neighbouring peaks 5·7Å (= 3 dimension)

Nearest to agreement with Chargaff analysis would be

4 purines, 3 pyrimidines, with 2 purines & 2 pyrimidines occupying equivalent positions

- c.f. Broomhead, ∨ similar X-ray structures of adenine + guanine

Construction of models

Scale $\frac{1}{2}'' : 1\text{Å}$ (as for Patterson diagrams)

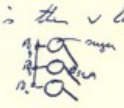
Backbone chain

PO_4 tetrahedra – wooden balls, tetrahedrally pierced (Fraser) glued in contact.
Sugar ring constructed (wire) on Furberg model

Constructed models using only phosphates and sugar rings show that it is possible to construct straight-chain model with P-P = 5·7 Å, all sugar rings in identical position

Pyrimidines for one of both chains, are then inclined at 25–30° to backbone – this would have inter-base plane spacing ~ 5·0 Å

Base planes can be tilted on this model to give inter-plane spacing 3·4 Å but then there is very little overlap, i.e. very little van der Waals attraction



∴ if P-P distance 5·7 Å, not straight chain

– this (among other things) eliminates a-c diagonal structure

Putting pyrimidine rings ⊥ and in full contact we can have 3 phosphates in straight line, at P-P distance ~ 5·7 Å but 4th must lie well off this line to bring 4th pyrimidine into contact

(system involves some distortion of N_3 bonds)

[taken to Sugar]

If next base is a purine then next P out of line would bring 6-ring of purine into contact with pyrimidine

This arrangement for 1 or 3 P has sugar ring nearly ∥ to P chain

⇒ 3 base rings either ⊥ or inclined to chain

Backbone chain and symmetry at c = 0

Consider 2 pairs of chains 1, 1′ and 2, 2′ separated by b = 1/3

1 is related to 1′ and 2 to 2′ by dyad axis

1 —— 2 and 1′ to 2′ by rotation through 180°

Constant rise modelled of chain corresponding to Patterson peaks

i.e. 7 steps of each 5.7 Å, with 3 successive sets of 3 [illegible] at reasonable angles

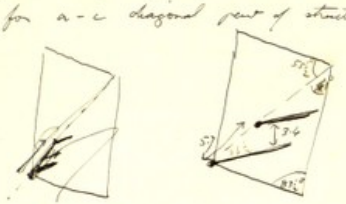
⇒ angle 0-1-2 ~ 100°

angle 2-3-3′ ~ 110°

For accurate model these angles would be regularly, since 33′ ÷ 11 ÷ 07

∴ angles 100 - 110°

Suppose length of pyrimidine nucleotide is in a-c plane
Then for a-c diagonal part of structure (i.e. peaks 1'-0-1)

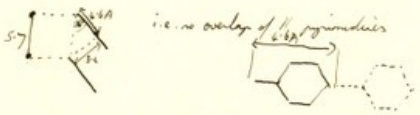


$\sin^{-1} \frac{3.4}{5.7} = 36\frac{1}{2}°$

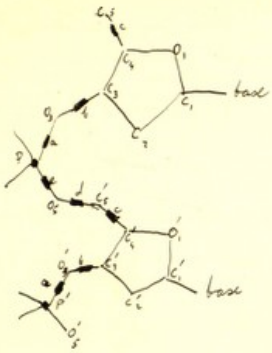
∴ if plane of pyrimidine is ⊥ a-c plane, it makes
$\angle 36\frac{1}{2}°$ with phosphate chain
and $36\frac{1}{2} + 61 = 77\frac{1}{2}$ with fibre axis

Unlikely the ∠ between base + backbone is so small
- more probable base is also inclined to a-c plane
- this would make its length more nearly ⊥ to both backbone chain + fibre axis

In general, if all P-sugar are equivalent, then $c_1 - c_1' = 5.7 A$



∴ sugar rings must be skew to one another,
with ⊥ distance between bonds C,N and C'N' ~ 3.4 A
- closer than ∥ one another but differently oriented



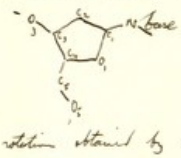
Free rotation at a, b, c, d, e

Wire model of backbone chain and sugar rings

Scale 1" = 1Å

Sugar ring constructed as in Furberg and Beevers & Cochran

i.e. 4 atoms coplanar and C_3' ½Å out of plane, bringing O_3 into plane



All free rotation obtained by making joint with centre ring ~~[illegible]~~

PO_4 tetrahedra

Requirements

1. Neighbouring P on chain 5·7° apart
2. 2 un-bound O of PO_4 facing away from sugar
3. $P<^{O}_{O}-$ near vertical plane (Fraser, but this was not for structure A)
4. Possibility of placing neighbouring bases parallel and ~3·4 Å between planes

Observations

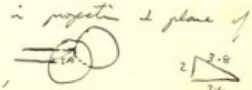
Distance apart of P P′ determined by rotations d, c, about axis c

Distance apart of C_2 C_5' —— —— —— a, b, e

(closest approach ~ 1·2")

Fully extended chain gives P – P ~ 6·8 Å

If v d w contact d ~ 3·6 Å between bases, rise perpendicular are ~3Å ∴ diameter of C,N bonds, seen in projection ⊥ plane of rings, must be > ~2Å apart



∴ ~~equation~~ distance between N and N′ > 3·8 Å

29.1.53

It doesn't seem to be possible to put 3 P gps in s.l. in spacing 5.7 A and have C.N bonds in posi for 11 bases at 3.4 A sepn

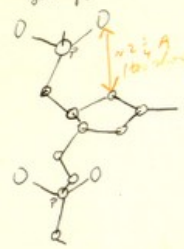
Is it possible for 3 P making bend of 110°?

If so, perhaps structure has groups of 2 or 3 bases in 11 contact, and break of contact when chain turns a corner

in this confign it is easy to avoid steric hindrance of sugar rings. Not easy for P $\underline{5.7}$ P $\underline{5.7}$ P

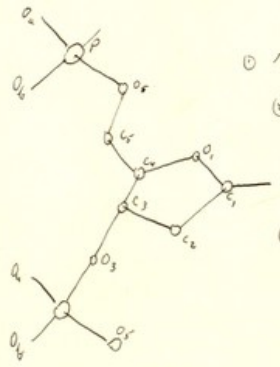
Arrangements of backbone chain with P-P: 5·7

1. Sugar rings ~ ⊥ P–P makes it easier to avoid steric hindrance



This leaves $P\overset{O}{\underset{O}{<}}$ directed to one side of sugar ring

2. Sugar rings ~ ∥ P–P — again $P\overset{O}{\underset{O}{<}}$ to one side



Steric factors

① Make C_5 equidistant from O_3 and O_b

② C_3 tilted away from O_a, but not equidistant btw. O_a and O_5 ∴ this would make C_2 approach O_5 ∴ compromise

③ $P\text{-}O_5\text{-}C_5\text{-}C_4$ coplanar
This keeps O_5 as near (∠ equal) distance from O_1 and C_3

MgB

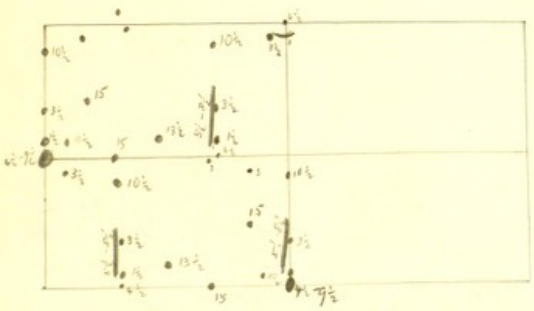


Figure of eight A.K. 2.2.53 17

Objection to 2D structure

Part of Lein -1, 0, 1 lies along a-c diagonal
P-P of ~~#~~ pair at 0 must lie in a-c plane. A
Patterson shows that this must be ∥ along a-c diagonal
i.e. in same direction as Lein
∴ impossible

Superposition

To obtain function which gives maxima of atom-pairs
at their centres, must take account of four that
V_g is not strictly in zero section but on either side of it
Suppose P-P distance in join = 4.5 A
& corresponds to peak in section $\frac{3}{}$ a = 5 cms
the axes at c = 1½, a = 2½ cms

This is MgB

3.2.53

MgB doesn't help solve the problem of how
the a-c diagonal streak is related to the ¼-cell
heavy peak nor does it show any alternative form
for Lein

<u>M29</u>

Peak at height 13 repeats at $\frac{1}{3}b$ away. ∴ try ~~four~~ combining M2 and M9 by placing V_9 <u>not</u> at height 0 but at height 13

i.e. put OM9 on 0/13 M2, and giving

M9 displacement ÷ 8.3 cms, and M_2 $\frac{1}{2}$ shift where necessary

axes are then at height −13 in M9 (and a = 0)
∠ (x.7)

∴ draw <u>M9C</u> derived from M9 with axes at height 17

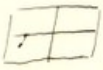
and M2B " " M_2 with axis at 0/17

Principal positions of c:2 vectors : Patterns

Sections 0-2 (twice)

N.B. not at 0
∴ not 11 pairs

Sections 10-12



Sections 3-5
(& 2-4)

Sections 14-16

Sections 12-14

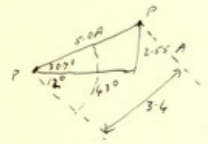
If there are 11 nucleotides per chain

rean inter-P spacing along c-axis is 2·55 A

If P.P : 5·0 A

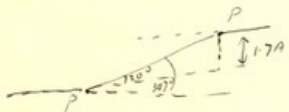
and inter-nucleotide base spacing 3·4 A

the inter bases inclined at ~12° to ⊥ to fibre axis



but then no contact ∴ bases too small

or if chain ⫫



bases inclined ~ 11° to fibre axis

but only 20° to P-P chain

∴ impossible

5.2.5.3 23

Possible steps in chain

Predominant near-origin peaks in P are ~5A

① section 2 peak 122 - strongest of all but c=5 (∴ in general use)

∴ suppose this is important step in chain

also ② step along a·c diagonal (section 3

or ③ with ⫫ 2, peak 75 (written to ①, with a-glide reversal)

If there are the 3 poss. chain steps, then total number of ② + ③ is equal to no. of ①

∴ total translation in 'a' = 0

There is no horizontal translation of ~5A

2 consecutive ① can occur (sections 2½ and 5)

or 3 " ①

or ① followed by ③ i.e.  possible

but not ① followed by ② but not  or

N.B. angle of ① in a·b plane is somewhat variable - probably some peaks the nearer 'b' axis, to account for resolution power in 'b' axis than 'a' although 'b' axis is further from main maxima

in by

② can be followed by ③ but not by ①

and ③ can be followed by ① (directly) but not by ②

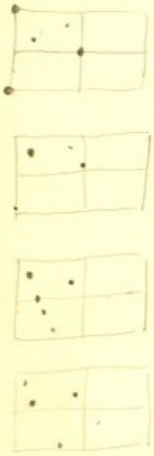
but ② ③ following ① giving peak c~5, b~½ which fulfils ∴ hole

Possible sequences of peaks ① ② ③

① - ① - ① ② - ② - ② ③ - ③ - ③

① - ① - ③

M12



(cont'd from opp.)
The suggested Harker peak c=b ~~a = 8·0 cms~~

M 11

Peak on section 2, a = -4·8 cms b = 3·3 cms
Possible posⁿ of peaks in -ve region of Patterson marked in, and ~~mark~~ when they coincide with +ve region of 2nd sheet, they were marked with dotted lines on M11

M12

Suppose M11 atom occurs twice consecutively. Then M11 is multiple, 2 structures being related by V_{11}
∴ M12 is M11 displaced V_{11} on itself
a = -5·5 b = ~~3·3~~ 3·5

M12 Axes on section 7, with a ≈ -2·0 cms?

7.2.53

Try M13, using peak at height 4, a = 3·0 cms b = 0 in M11
distance of this peak from peak in section 1 ?

9.2.53

Possible posⁿ of ones in M11

c=4	a=3·5 cms	c=11	a=-3·5 cms
c=7	a=-0·5	c=8	a=+0·5
c=1	a=-2·5	c=14	a=+2·5 ~~-2·5~~ ∴ gives peak in wrong a-c diag. in section 4
c=4½	a=0	gives Harker peaks	c=7 a=4·8 } v. general
		at	c=11 a=-4·8 }

V_{11} gives 2 Harker peaks differing by c=4, a=10 cms
∴ superposition of a-c sections on itself, with displacement c=4, a=10 gives pseudo-Harker peaks + false pseudo posⁿ of ones

10.2.53

Structure B

Evidence for 2-chain (or 1-chain helix) ?

69c - general trend is as for right contravin helix
(which differs from right dextrarotatory chain in integral no. residues/turn
only - contrib^{n} of high order $\bar{J}_n$ to the latter)

and this is indistinguishable from double helix with residues on
each having same ζ value, since 2nd chain has opp. signs in
$\xi < \eta$ terms (eg $1-2$), and eq^{n} 2 contains only
$R^2 \sin^2 \xi \eta^2$ and tan $\phi = \frac{\sin \xi \eta}{\cos \xi \eta}$

13.3.53.
Axes derived from 0 other possible positions of VII' derived from V II

$\frac{1}{2}(a-5)$	$\frac{1}{2}(c+2)$	$a-10$	$c+4$	Harker peaks
-4·7	6	-14·4	14	~~✓~~ ✓✓
-4·0	6½	-13·0	15	~~✓~~ ✓
7·0	6½	9·0	15	~~✓~~ ?
4·8	7	4·6	16	~~✓~~ ?
1·0	3	7·0	8	×
0	3	-5	8	×

Possible pos^{n}s of Harker peaks of V_{II} and axes in M_{11}

Harker peaks are a , c
and a-10 , c+4
then axes is at $\frac{1}{2}(a-5)$ and $\frac{1}{2}(c+2)$

Observed	a-10 (av)	c+4	$\frac{1}{2}(a-5)$	$\frac{1}{2}(c+2)$	
✓ good (weight)	14	6½ +	3·2	(1¼) 1½	
no V' ✗	21·0	6½ -	13·0	(2¼) 2	
	11·6	9½ +	8·3	(3¾) 4	II D tries a = 8·0 c = 9½
✗	23·0	10½ -	14·0	(4¼) 4	II C try 4½ no good - origin peaks too
✓ good but unreliable	12·8	13½ -	8·9	(5¾) 5½	III E
✓ v good	26·0	13½ +	15·5	(5¾) 6	
	19·8	20	12·4	9	✓ II B

M911

M9 shows a vector V11 having one end in common with end of V9

∴ put M9 on M11 with origin at a = 2·4 c = 6·6·8

and OM911 is OM9 on 2 9 M11

i.e. axes on M11 at a = 2·4 c. 1
if true axes are M9 axes

M911 blue for axes on M9 axes

M. Wt

Wt. monoclinic unit cell 11.2×10^3

Vol. " " " $12230\ \text{Å}^3$

Suppose partial sp. vol. DNA is 0.55 (as did Riley)

Vol. of 22 nucleotides in $\frac{0.55 \times 330 \times 22 \times 10^{24}}{6.03 \times 10^{23}} = 6620\ \text{Å}^3$

$\therefore$ vol. some water $= 12230 - 6620 = 5610\ \text{Å}^3$

$\sim 45.8\%$ of volume

$\therefore$ Wt % of water is $\frac{45.8}{45.8 + 54.2 \times \frac{1}{0.55}} = \frac{45.8}{45.8 + 98.7} = \frac{45.8}{144.5} = 31\%$

Density of water in Na DNA

Dry density 1.63 sp. vol. .615

Density + 35% (wgt) of water = 1.52 (wgt) i.e. sp. vol. .658

vol. 1.35 g of mixture wet DNA = .889 cc

$\therefore$ vol. of .35 g water = .274 cc if vol. DNA is wet.

i.e. density of water = 1.28 g/cc

Suppose density of water = 1.00 g/cm³

Vol of 1.35 g wet Na DNA: .615 + 0.35 = .965 cc

Suppose density of water 1.00 density $= \frac{1.35}{.963} = 1.40$ g/cc

and of mixture 1.52 i.e. vol 1.35 g : $\frac{1.35}{1.52} = 0.89$ cc

sp. vol. DNA: 0.89 − 0.35 = 0.54

Suppose partial sp. vol. DNA 0.55

and " H_2O 1.00

Then for 40% H_2O, 1.4 g occupies 0.55 + 0.60 = 0.95 cc

$d = \frac{1.4}{.95} = 1.475$

35% H_2O $d = \frac{1.35}{0.90} = 1.50$

30% H_2O $d = \frac{1.30}{0.85} = 1.53$

12.12.53 52 33

a - c diagonal

All Patterson peaks streak along forward a - c diagonal

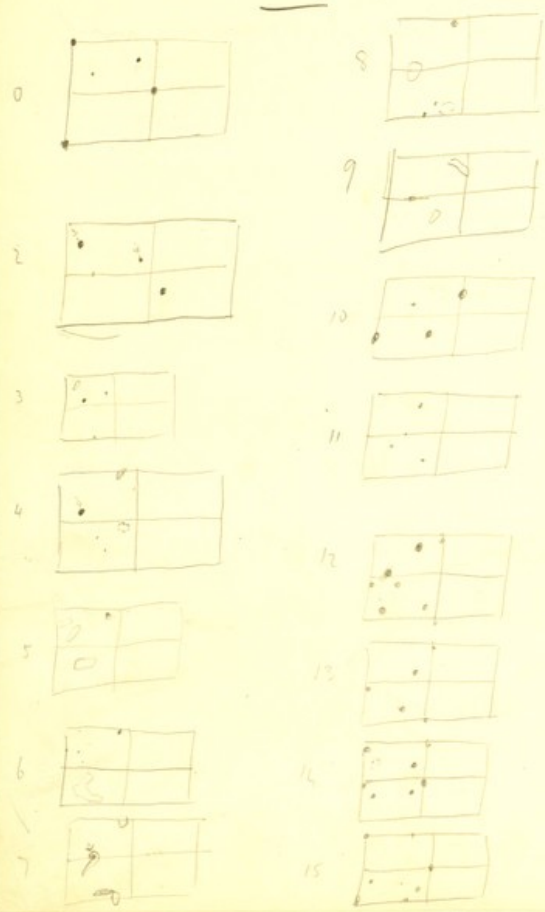
- this suggest possibility of disorder in direction of diagonal

M11C

No good

- beats 1 - 4 almost nothing

M12 (first 15 states only)



M 13.11

O M 13 on 1711, with M13 reflected across B plane ~~B~~
(i.e. turned over about axis)

points used are 2 on vertex 0
and 1 on each 2 8
(marked with red crosses)

M 13.11

Possible position of axes

Search for V_{13}' with view to position. Then axis lies ½ way between this and sheet 0

Section 16 — no . 7 + 8 not used

Section 13 -> bad axial sections

25 "

26 "

5 less bad axial sections 2/3, 17/8

See preliminary notation of Structure B on 10-2-53 p. 28

A.K.

23.2.53

Structure B

Photograph 51 C

3.4 A are – 158.5 mm on projection

$\therefore$ 158.5 = 2R tan 2θ where R is effective specimen-film distance for projection

For d = 3.40 A, θ (calcd) = 13° 4′ tan 2θ = 0.491

$R = \frac{158.5}{2 \times 0.491} = 161.4$ mm   2R = 322.8

Equator mm	tan 2θ	θ	d (Å)	$\frac{1}{d}$	λ/d	θ/π on Bernal chart	Conversion factor
20.2	.0625	1° 48′	26.5	.041	.0629	12.6	(.626 ~~.639~~)
54.7	.1695	4° 49′	9.16	.109	.168	33.6	.614
82	.254	7° 8′	6.19	.162	.249	50.7	.618
to 100	to .310	8° 37′	to 5.13	.195	.300	61.7	.617
						mean	.616
120	.372	10° 12′	4.34	.230	.355		
to ~~152~~ 152	to .470	12° 36′	3.52	.284	.438		

These equatorial maxima do not correspond to maxima in $J_0^2(x)$,

which are approximately at 0, a, 2a, 3a | min. $J_0(x)$ for x 3.83 10.18 / max. $J_0(x)$ for x 7.02 13.32

But if, assume 1st max. is missing (9.16 A reflexion is v. weak)

Then max. at $\frac{\lambda}{d}$ = .27, ~~.405~~ .391, and .149

gives $2\pi R r$ = ~~[illegible]~~ 7.0 for $R = \frac{2\sin\theta}{\lambda} = \frac{1}{d} = \frac{\lambda}{2\theta}$ .27/λ ~~[illegible]~~ .175

$\therefore r = \frac{7.0}{2\pi \times .175}$ = ~~[illegible]~~ 6.36

5th layer-line

1st diffuse spot

2l = 88 to 100 mm   tan 2θ .2725 to .310,   θ 7° 37′ to 8° 37′

d = 5.80 to 5.10 $\frac{1}{d^2}$ = .0298 to .0385

$c^{*2} = \frac{1}{c^2}$ = $\left(\frac{5}{34}\right)^2$ = .02165

$\therefore \left(\frac{\xi}{\lambda}\right)^2$ = .0082 to .0169 ξ/λ = .0905 to .130

ξ = ~~[illegible]~~ .139 to .200

1st max. for $J_5^2(x)$ has x ~ 6.5

$\therefore$ if r = 6.36A, $R = \xi/\lambda = \frac{6.5}{2\pi \times 6.36}$ = .163

– fits better with max. in $J_3(x)^2$,

or J_5, and r = 9.4A, giving ξ/λ = .113

3rd layer line

1st streak of spots

2l = 49 to 65 mm   tan 2θ = .152 to .201   θ = 4° 19′ to 5° 41′

d = 10.26 to 7.76 $\frac{1}{d^2}$ = .00953 to .01665

$\frac{l^2}{c^2} = \left(\frac{3}{34}\right)^2$ = .00780

$\therefore \left(\frac{\xi}{\lambda}\right)^2$ = .00153 to .00885, ξ/λ = .0391 to .0940

1st max. for $J_3^2(x)$ has x ~ 4.2

$\therefore R = \xi/\lambda = \frac{4.2}{2\pi \times 6.36}$ = .105

for r = 9.4A $R = \xi/\lambda$ = .071

but equator, taking r = 9.4A

should have maxima at $\frac{1}{9.4 \times 2\pi}$ (3.83, 7.02, 10.18, 13.32) in ξ/λ and zero at 2.40

i.e. at .065, .119, .172, .226 and zero at .0406

or ξ = .100, .183, .265, .368

and zero at ξ = .0625 i.e. exactly on observed strong peak

2 helices of different radius for single case of whole number of residues per turn.

Following Cochran Crick + Vand (Acta Cryst. 5 581 1952)
term $J_n(2\pi R r)e^{in(\psi+\frac{1}{2}\pi)}$ becomes $J_n(2\pi R r)e^{i(n\psi - n\phi + \frac{1}{2}n\pi + 2\pi l z/c)}$
(in present case, $l = n$)

For equator $I = \left[J_0(2\pi R r_1) + J_0(2\pi R r_2)\right]^2 = J_0^2(2\pi R r_1) + J_0^2(2\pi R r_2) + 2J_0(2\pi R r_1)J_0(2\pi R r_2)$

for n^{th} layer line, $I = FF^* = J_n^2(2\pi R r_1) + J_n^2(2\pi R r_2) + J_n(2\pi R r_1)J_n(2\pi R r_2)\left(e^{in(\phi - 2\pi z/c)} + e^{in(\phi - 2\pi z/c)}\right)$

$= J_n^2(2\pi R r_1) + J_n^2(2\pi R r_2) + 2J_n(2\pi R r_1)J_n(2\pi R r_2)\cos\left[n(\phi - 2\pi z/c)\right]$

Here terms in $J_n J_n'$ may give negative contribution to intensity

but on any layer-line, moving out from the meridian, when the first maxim appears in a J_n contribution (i.e. for the J_n term corresponding to largest value of r) there is no negative term in I, since all other J_n terms are small and +ve

∴ even for complex helical structures, first maxima should give maxim diameter.

On equator, first max. (in J_0^2), excluding central max, neither -ve J_0, ∴ max. diameter can't necessarily be got from equator

In general

$$F_n = e^{in(\psi + \frac{\pi}{2})}\left[\sum_1 J_n(x_1)e^{in\alpha_1} + \sum_2 J_n(x_2)e^{in\alpha_2} + \ldots + \sum_p J_n(x_p)e^{in\alpha_p}\right]$$

where $\alpha_s = \phi_s - 2\pi z_s/c$
and $x_s = 2\pi R r_s$

and $I = FF^* = \sum_1^p J_n^2(x_p) + \sum_{p \neq q}^{rs} J_n(x_p)J_n(x_q)\cos(\alpha_p - \alpha_q)$

and same argument applies
i.e. first max give outside radius
but later max. of equatorial non-central max complicated

2-strand helix with pairs of groups at opp. ends of diameter

~~Equator~~ ~~$J_0 + J_0$~~ $x_1 = x_2$, $\alpha_1 - \alpha_2 = n\pi$
∴ layer-lines absent for n odd
and $I = 4J_n^2(x)$ for n even

Conclusion

Structure B does not fit right helical theory, even for low layer-lines. ζ-values of first observed are too small for right-stranded helix, & even more so for multi-stranded.

Doing radius of helix so that layer-line measured fit for right-stranded (i.e. $r = 9{\cdot}4A$) gives v bad fit for equator

Outer shape / \ \ / suggesting from 3·4 reflection indicates repeat at 3·4 A is v important — i.e. inner \ / / \ represents structure further of main figure, which exists only for $c = n \times 3{\cdot}4$, & figure repeats from 3·4 A apart as for helix

1st J_5 on 5th l.l (In R E F's terminology there could still be two sheets, unrelated by the symmetry) See P. 46 A K

Structure B if helix is right-stranded helix

i.e. 2-strand, fitting 5th layer-line max. to $J_{10}(x)$, not requires $r = 17A$ which is much too big

Suppose ~~diameter~~ radius of outer helix 8·5 A

This gives 3rd layer-line max. at $\zeta/\lambda = .0805$

at 5th ——— $\zeta/\lambda = .122$

– these values are reasonable, because max. $\simeq J_3$ & J_5 is near outer edge of peak

For equator, we then have max. at $\zeta/\lambda = .072, .132, .190, .250$

not 1 zero for $\zeta/\lambda = .045$

– this still has zero rather near the 2·5A equator spot

Length of helix of ~~diameter~~ radius 8·5A & pitch 34A

$l^2 = 34^2 + (8{\cdot}5 \times 2\pi)^2 = 1156 + 2850 = 4006$

$l = 63{\cdot}3$

∴ distance between atoms on 8·5A radius helix $= \frac{63{\cdot}3}{10}$

$= 6{\cdot}3A$

Intensity of inner \ / / \ compared with rest of photograph suggests that outer helix (~8·5A) is heavy part of structure, i.e. P

For radius 10A

$l^2 = 1156 + 3950 = 5106$ $\quad l = 7{\cdot}15A$

For radius 9·4A $l^2 = 1156 + 3690 = 4666$ $\quad l = 6{\cdot}82A$

If right-hand helix as above is basis of structure B, the structure A is probably similar, with P–P distance along fibre axis < 3·4 A, probably 2–2·5A

(c.f. 2A indicated by posⁿ of P-P peaks in Patterson at 2·5A ... 11th layer-line reflection)

Wardlaw and A.K.

24.2.53 45

Single-stranded helix for structure B rules out also pairing for structure A (with 7 pairs in fibre period)

∴ right-hand helix 3·4 A in c between neighbouring P

∴ structure A has less

There is correct A.K.

If suppose important translation in Patterson is

$c = \frac{1}{11}$ $b = \frac{1}{11}$ $a = \frac{2}{11}$ (corresp. approx. to Patterson peaks)

Then important reflections are those for which

$$h\left(-\tfrac{2}{11}\right) + k\left(\pm\tfrac{1}{11}\right) + l\,\tfrac{1}{11} = 1$$

$$-2h \pm k + l = 11$$

$$-2h \pm k = 11 - l$$

i.e. on 11th layer-line and experiment only 9.0.11

and mass of reflections on layer-lines 6, 7, 8, whether (001)'s does not indicate steps of $\sim\frac{1}{5}$ in c

These reflections due to the bases. REF missed this. A.K.

Structure B

7th layer-line

$2l$: 122 – 138 mm in 2θ : 378 to 427

θ : 10° 21′ to 11° 34′ d : ~~4·28~~ 4·28 to 3·84 A

$\frac{1}{d^2}$: ·0566 to ~~·0677~~ ·0678

$\left(\frac{Rd}{c}\right)^2$: $\left(\frac{7}{34}\right)^2$: ·0624 ∴ $\left(\frac{s}{\lambda}\right)^2$: ·0122 to ·0254

$\frac{s}{\lambda}$: ·110 to ·159

1st max. for $J_7(x)$ has $x \sim 9{\cdot}0$

∴ for $r \sim 8{\cdot}5$,

$R = \frac{s}{\lambda} = \frac{9}{2\pi \times 8{\cdot}5}$: ·168

for r : 9·4 $\frac{s}{\lambda}$: ·152

N.B. Here we expect observed max. to be displaced inwards ∴ Lorentz etc

7th layer-line should also have max. of same value as 3rd

i.e. $\frac{s}{\lambda}$: ·039 to ·094

– this is apparently absent

3-chain v 2-chain helix?

Chains are not equally spaced, ∴ this 3rd max. of 7th layer-line contains 321

∴ 3-chain helix is highly improbable

∴ chains must be non-equivalent (2 chains ~~must~~ would be equivalent)

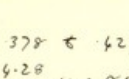
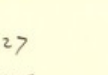
Also ∴ structure A believed to have 2 chains / unit cell

RFF. would like making the correct correlation between A and B

A K.

N.B.

Outer Pattern emerging from 3·4 spot is not equator of pattern from origin. If it were they would cross on 5th layer-line

Inner  melts  on 5th layer-line

$J_{10}(x)$ has first max. for $x \sim 11{\cdot}8 = 2\pi Rr$

Observed max. on equator, R : ·162 to ·195

∴ r : 11·6 to 9·6

Here observed max. is displaced inwards ∴ 3rd max. of J_0 for r : 9·4 has R ·172

Density

Volume of cylinder radius 10A height 34 A : $\pi \times 100 \times 34$: $\frac{10700}{\text{~~21400~~}}$ A^3

Vol. dry nucleotide (density 1·63) : 336 A^3

∴ no. nucleotides / cylinder : $\frac{10700}{336}$: 32

Since some fairly dry fibres give structure A density of cylinder is prob. near density of dry Na DNA, water lying mainly outside cylinder.

∴ this suggests 3 chains

but not easy to reconcile w structure A

For helix of radius 8·5A Vol. cylinder : $\pi \times 8{\cdot}5^2 \times 34 \simeq 7700$ A^3

no. nucleotides : $\frac{7700}{336}$: 23

A form superposition map

5. 3. 53

M 11

Uses peaks on section Z which, it seems, must be a P-P peak. Other superpositions may be fruitless ∴ much part of Pattern not due to P-P

V 11 is clearly multiple – or, more probably, peak is due to agglomeration of near-equal vectors. ∴ should be several valid positions for axes (as described 9.2.53)

∴ take M11B and M11D and look for possible chain common to each – allowing shift in b-direction of one relative to other

To find correct posn of M11B wrt M11D, look for the 4 origin peaks in each

– these are at heights 8 and 10 in M11B and 3, 5 in M11D

(M11c no good, as shown by fact that origin peaks are lost)

M11B can be put on M11D in 4 ways

1) axes at 0 in 11B may correspond height 15 in 11D

∴ ~~rotate through 180°~~ and put 0-7 on 15-22
i.e. on 15-8 upside-down

2) 11B and 11D may give different enantiomorphs

– this corresponds to 0-7 on 0-7 rotated and upside-down

i.e. possns are
i) 0-7 on 0-7
ii) 0-7 on 0-7 rotated and upside-down
iii) 0-7 on 15-8 upside-down
iv) 0-7 on 15-8 rotated

M11D 0-7 on M11B 15-8 upside-down

11D 0-7 at ~~c – 11 cms – gives good fit for 3-5, quite good for 10~~
– 16.3 3, 5, 8, 10 all fit, and general fit good ~~but bad for 8~~

∴ Impossible ∵ peaks at 5 not coincident with peaks at 0

M11D 0-7 on M11B 15-8 ~~rotated~~ rotated

11D 0-7 at ~ +3.5 cms – gives 5-10 nearly coincident (2.7 cms apart), 3 & 8 quite good

11D 8-15 on 11B 0-7 rot. general fit good

M11D 0-7 on M11B 0-7

M11D at – 15.7 cms → good fit for 3, 5, 8, 10 but using v small peaks

general fit good in 0-7, bad on 15-8

M11D at – 8.7 cms

M11D 0-7 on M11B 0-7 rotated and upside-down

~~11D 0-7 at ~ 21.5 cm gives 3 & 5 good~~
~~general fit poor~~

Presumably during the period REF was preparing MS. ~~excerpt~~ on the B form. "Rough draft"
Later 17 March 1953

M11 superpositions 18.3.53

~~All B and M11E both have origin peaks at height 8 and 10~~
~~Thus have different 'a' values, ∴ must relate to different chains~~

~~How can M11E 8-15 be fitted to M11B?~~

M11B has origin peaks at 8 & 10. M11E at 5, 7
Thus have different 'a' values, ∴ ~~either~~ belong to diff. chains
= to diff parts of same chain

A. Diff. chains, same light

M11E 0-7 on M11B 8-15 upside-down

a: 0 b: +7.9 cms
general fit — other peaks less good

M11E 0-7 on M11B 8-15 rotated

a: b/2, b: 11.8 cms good — full chain

M11E 0-7 on M11B 0-7

a: ½ b: −10 cms

a: 0 b: −8.2 cms ~~high~~ 0 peaks good
a: 0 b: +8.5

M11E 0-7 on M11B 0-7 rotated and upside-down

20.4.53

53

Is structure A triclinic?

2-axis can't pass through DNA chain ∵ asymmetric sequence

but superpositions always show peak on axes

If peaks are P, axis can't only be pseudo-axis

i.e. array of P monoclinic, but true symmetry triclinic

In this case, whole Patterson is wrong

∵ each reflection is unresolved pair, (hkl) and ($h\bar{k}l$)

[If structure is triclinic and P's ~ monoclinic will Patterson give ~ correct P-P vectors?]

If structure truly monoclinic

either chains don't go through axes

i.e. no peaks on axes

or sequence of phospho-ester links is 3 3 5 5 3 3 . etc

∴ this is symmetric about phosphorus atom

but unsuitable a) ∵ evidence from enzymatic degradation

b) ∵ prob. impossible to get 3.4 equally spaced bases, distance ≈ 3.4Å

21. 4. 57

Intensities of structure P suggest equally spaced chains (pseudo-halving of cell)

Then unit has true diad $\frac{1}{2}$-way between planes

+ pseudo-diad through chain, relating phosphates only

- can we arrange units so that pseudo-diad applies to whole structure and true diad does not?

Pseudo-diad passing through P is only possible if chains are equally spaced.

Vertical distance between 2 chains would then be ~ same as shorter vertical distance in Crick model.

Sharpness of Patterson peaks

All peaks are stretched along a.c axis

- can this be due to P···Na in that direction ?
- well-resolved ~~peak~~ peaks on C=2 suggest that Na does not lie half-way between 2 P's

Sharpness of P-P, Na-Na, and P-Na peaks were calculated by approximating f^2 curve (or $f_P f_{Na}$) by $e^{-a^2 s^2}$ & taking account of artificial temperature factor used

Results

P-P	r(Å)	0	0·5	1·0	1·5	2·0	2·5	3·0
P-P	P(r)	115·2	108·0	88·8	66·0	40·4	22·6	10·9
Na-Na		66·3	59·4	42·6	24·1	11·4	6·3	1·3
P-Na		85·2	78·5	61·8	41·3	23·5	11·4	4·7
P-P + Na-Na		181·5	167·4	131·4	88·1	51·8	26·9	12·2
2 (P-Na)		170·4	157·0	123·6	82·6	47·0	22·8	9·4
Sharpness of peaks for P-Na distance 3·0Å		190·9	190·2	178·4	170·7	175·4	183·9	182·6
Sharpness of peaks for P-Na 2·5Å		204·3	214·4	213·0	211·7	208·8	~~197·3~~	4169·2
Sharpness of peaks for P-Na 2·0Å		228·5	250·0	255·0	245·1	222·2	183·9	135·8

Isolated Patterson peaks mostly have max. dimension approx. twice min. dimension

½-peak width of P-P + Na-Na (Patterson) ~ 1·5 × 2 Å

for this is minimum dimension.

∴ ½-peak width of P—Na combination must be ~ 3·0 × 2 Å

& this requires P-Na distance ~ 2·0 Å

7.5.53

Attempt to adapt Watson and Crick model to structure A

Modifications introduced

1/ P–P distance decreased from 7·0 A to 5·3 A
(as suggested by peaks on sections 2·3)

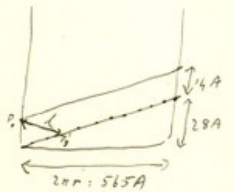
2/ 11 nucleotides per turn instead of 10
(as suggested by reinforced peak on 11th layer-line)

3/ 2 chains of helix ~~a~~ equally spaced
(as suggested by pseudo-halving of cell
ed indication on Patterson that only part of structure
repeats at half-cell height

4/ P on radius 9A instead of 10A
(as indicated by cylindrical Patterson)

Suppose chains equally spaced
and P's vertically above one another on chain

Draw schematically un-wrapped helix



Suppose $P_0 P_3'$ are linked through
their C_3's to same purine-pyrimidine
complex. Then on W & C model
$P_0 - P_3' = 15·2A$

To obtain length of arc (on un-wrapped helix, consider helix of
same ~~pitch~~ radius, of which $P_3' P_0$ are in a part
Then this helix makes 3/11 of a turn ∴ height $\left(\frac{1}{2} - \frac{3}{11}\right) \times 28A = \frac{5}{22} \times 28A$
i.e. whole turn ∴ height $\frac{5}{22} \times \frac{11}{3} \times 28 = \frac{5}{6} \times 28 = 23·6A$
∴ length of whole turn $= \sqrt{56^2 + 23·6^2} = \sqrt{3192 + 548} = \sqrt{3740} = 61·2A$
∴ length of arc $l = 3/11 \times 61·2 = 16·8A$

Length of P - P' bonded through C_3's to same P_0 - P_3 complex

Crick says 15.2 A
but this is inconsistent with other data of his model - too small

$C_1 - C_1' = 11A$
$C_1 - P \sim 3.5A$ (from wire model)
and these are fairly nearly co-linear

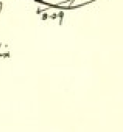
$\therefore PP' \sim 18A$
- this is consistent with other W & C data

When chain contracts to form structure A, $P - C_3$ can't decrease much - contraction must occur between C_3 and P on other side

$\therefore PP'$ still ~ 18 A

If $P_0 P_0'$ are vertically above one another, distance 15 A

xy proj of $P_0 P_3'$ is 16.18
z proj $(15.0 - 3 \times 3.4) = 4.8A$



$\therefore P_0 P_3' = \sqrt{16.18^2 + 4.8^2} = \sqrt{261.8 + 23.0} = 16.8A$

If P_0 rotated $\sim 1A$ behind P_0' on helix
$P_0 P_3' \sim 17.6A$

11-residue helix = structure A

Difficulties

Can dry have one helix / primitive cell

∴ how account for 13 Å vector = c plane?

and how account for pseudo-beams

Density

Vol. dry nucleotide, density 1·63 g/cc, = 336 Å^3

Partial sp. vol. 0·55 (Kekker, J. Phys. Coll. Chem. 52 1948 676)

Suppose partial sp. vol. = structure A is 0·55

Then 330 g occupy 0·55 × 330 = 181·5 cc

1 nucleotide occupies $\frac{181·5 \times 10^{24}}{6·03 \times 10^{23}}$ Å^3 = 296 Å^3

1 molecule H_2O occupies $\frac{18 \times 10^{24}}{6·03 \times 10^{23}}$ = 29·85 Å^3

Vol. of complete unit cell 2465 Å^3

1 nucleotide + 4 H_2O	= 415 Å^3	giving 59 nucleotides / unit cell
5 "	465	55
6	475	51·5
7	505	48·5
8	535	45·7
9	565	43·3

Structure B. Suppose 24·5 Å reflection = (100) of hexag. close packed rods

Then vol. unit cell: $\frac{2}{\sqrt{3}} \times 24·5^2$ ~~1694 Å^3~~ × 34 = 694 × 34 Å^3

Suppose this contains 20 nucleotides, i.e. M.W. 20 × 330 = 6600

~~If suppose~~ then density due to nucleotides only is

$$\frac{6600}{6·03 \times 10^{23} \times 694 \times 10^{-24} \times 34} = 0·465 \text{ g/cc}$$

∴ if the density is 1·52 g/cc

water content must be $\frac{1·52 - 0·465}{0·465} \times 100$ = 227% of dry weight!

If 40 nucleotides = unit cell

water content is $\frac{1·52 - 0·93}{0·93}$ = 63·5% of dry weight

still high, but more reasonable

11.5.53

Equatorial reflection in structure B

Main reflection ~ 24·5 A

If this is inter-helical distance, density is much too low

Some inter-penetration of helices in one direction might be possible, the spacing in other direction being 24·5 A

but nucleo-protein gives ~ same spacing, 24·5 A

and in this case, on W & C model, inter-penetration quite impossible

- spacing measured on R & W's published photo

Distance in A

	① R & W	② Structure B	Ratio ①/②
equatorial	15·4	7·5	2·05
2nd layer line	21·7	10·3	2·1
3·4 A reflection	111	57	1·95

12.5.53

65

Density calculation (see above) suggest packing is such that there are 2 helices per unit cell

(i.e. not hexag. close-packing

- reasonable ∵ helix hasn't got hexag. symmetry

M.Wt. of 20 nucleotides 6600

+50% H_2O 9900

∴ X-section of unit cell, for density 1·50 is

$$\frac{9900 \times 10^{16}}{6.03 \times 10^{23} \times 1.50 \times 34 \times 10^{-8}} \text{ Å}^2 = 322 \text{ Å}^2$$

If hexag. close-packing, $\frac{\sqrt{3}}{2} a^2 = 322$ $a^2 = 372$

$a = 19.3$

If distorted, $a\, b \sin\gamma = 322$

and $b \sin\gamma = 24.5$ (∵ strong reflection)

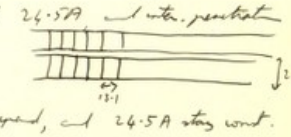
∴ $a = 13.1$ A impossible for W & C model

or Unit cell contains 2 helices

and $a = 26.2$ A.

This is only slightly distorted from graphite-like structure, giving inter-helical distance ~ 16 A

∴ Helices in sheets, with inter-sheet spg 24·5 A and inter-penetration giving other direction $\frac{323}{24.5} = 13.1$ A



In nucleo-protein, then 13·1 A will have to expand, and 24·5 A stay same.

W & C modified for structure A

Cylindrical Patterson ~~has~~ suggests helix of diameter 18 Å
∴ suppose P'_0 on helix of radius 9·0 Å
and 11 residues per chain (∵ 11th layer-line reflection)

Horizontal spt of P–P on 10 Å, 10-residue helix : $20 \sin 18° = 6{\cdot}18$ Å
9 Å 11-residue helix : $18 \sin \frac{32{\cdot}73°}{2} = 5{\cdot}07$ Å

P–P for B : $\sqrt{6{\cdot}18^2 + 3{\cdot}4^2} = \sqrt{38{\cdot}19 + 11{\cdot}56} = \sqrt{49{\cdot}65} = 7{\cdot}05$ Å
A : $\sqrt{5{\cdot}07^2 + 2{\cdot}55^2} = \sqrt{25{\cdot}70 + 6{\cdot}53} = \sqrt{32{\cdot}23} = 5{\cdot}68$ Å

If near inter-base distance is const. ∠ of tilt ~40° ?
Suppose ∠ of tilt 40° and $C_1' - C_1'$ const. at 11 Å
then horiz. spt of $C_1' - C_1' = 11 \cos 40° = 8{\cdot}4$ Å
∴ ~~C_1' lies on O of radius 8·2 Å~~

Suppose P_n and P'_n lie vertically above one another
(∵ equator peak suggests this is approx. true)

Then on O containing all C_1''s, ~~then~~ chord subtending $\frac{3 \times 360°}{11}$
at centre is of length 8·4 Å

radius : $\frac{4{\cdot}2}{\sin 69{\cdot}1°} = 5{\cdot}55$ Å $\frac{6{\cdot}29}{\sin 49°} = 5{\cdot}67$ Å

[for structure B, equivalent radius is $\frac{5{\cdot}5}{\sin 54°} = 6{\cdot}8$ Å
∴ radial extension of oxy + phosphate is same in both cases]

Horizontal spt of $C_1' - C_1'$ in this $5{\cdot}55 \times 2 \sin \frac{360}{2 \times 11} = 3{\cdot}12$ Å
Total $C_1' - C_1' = \sqrt{3{\cdot}12^2 + 2{\cdot}55^2} = \sqrt{9{\cdot}73 + 6{\cdot}53} = \sqrt{16{\cdot}26} = 4{\cdot}03$ Å

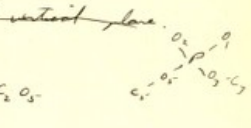
Model giving approx right distances & reasonable v d W

C_2 equidistant from O_1, O_5-

~~P - O_5 - C_5 - C_2 cyclo planar, & in vertical plane~~

~~Also option with O_1~~

giving rea. v d W distances for $C_2 O_2$ & $C_2 O_5$



P - O_5 - C_5 - C_4 ~ planar

P - P 3.7 Å $C_1' - C_1'$ 4.0 Å

C_1' N points ~ 40° upwards (when O_3 - C_3 in plane P)

Helix of radius 9.0 ~~→~~ Å Pitch 28.1 Å

Length of one turn $= \sqrt{(2\times9\cdot17)^2 + 28\cdot1^2} = \sqrt{56\cdot35^2 + 28\cdot1^2} = \sqrt{3178 + 790}$

$= \sqrt{3968} = 63\cdot15$ Å

x-pt of vector on cylindrical Patterson

$= 2 \times 9$ in $\frac{360 \times n}{11 \times 2} = 18$ in $16\cdot35$ n

$x_1 = 18 \times \cdot2815 = 5\cdot07$

$x_2 = 18 \times \cdot5407 = 9\cdot74$

$x_3 = 18 \times \cdot7559 = 13\cdot60$

$x_4 = 18 \times \cdot9098 = 16\cdot37$

$x_5 = 18 \times \cdot9858 = 17\cdot80$

Distances of atoms from axis projected with base tilt 40°

① r	② 2πr	③ 2πr × 0·88	$J_0(3)$
0·76	4·9	0·43	·95
1·31	8·2	0·72	·87
1·88	11·8	1·04	·75
2·28	14·3	1·26	·65
2·63	16·5	1·45	·55
2·73	17·2	1·51	·51
2·88	18·1	1·59	·66
3·06	19·2	1·69	·60
3·11	19·5	1·72	·39
(½)3·35	21·0	1·85	(·31)·16
3·86	24·3	2·14	·16
3·92	24·6	2·16	·13
4·09	25·7	2·26	·08
4·10	25·8	2·27	·07
4·12	25·9	2·27	·07
4·44	27·9	2·45	·02
4·54	28·5	2·51	$\overline{\cdot 05}$
4·55	28·6	2·51	$\overline{\cdot 08}$
(½)4·90	30·8	2·71	$(\overline{\cdot 15})\ \overline{\cdot 08}$
5·10	32·1	2·82	$\overline{\cdot 19}$
5·67	35·6	3·13	~~$\overline{\cdot 21}$~~
5·67	35·6	3·13	$\overline{\cdot 21}$
Total 21			

19.5.53 71

Intensities in structure A

If one helix per lattice point, then ~~intensities~~, intensities depend only on structure factor of helix

∴ can't explain large diff. I for (130) and (200)
is this wrong, → large error in Patterson?

To calculate equatorial intensities, only require radial distance of each atom.

Suppose base complex tilted 40°.

Drawing (1" : 1Å) gives $C_1' - C_1' = 11{\cdot}2$ Å

∴ (see 2 pages back) these lie on helix of radius 5·67 Å

Suppose tilt is about "chord" of complex. Then draw foreshortened complex by reducing distance of each atom from chord by factor ~~cos~~ cos 40° = 0·766. This gives projection

Then measure distance of each atom from axis

Intensities & position of 1st equatorial reflection

Continuous transition from ~17 Å in very dry DNA through 19 Å for structure A → >24 Å

This suggests that reflection has same significance in 2 cases i.e. related to inter-unit distance in both cases

Intensity appears to have min. at ~19 Å

- c/ dry rather dry photo 34 : mid reflection ~17-18 Å is stronger than round 19 Å : structure A

[Dry photo 34 has reciprocal arc of larger spacing than structure B (at ~36 Å) ?]

Spacing on photos showing B+B (e.g. 75, 5,) ~20 Å : intensity high

52 & 53 as same specimen as 51, at higher RH (92%)

- they have same equatorial spacing

4.6.53 Tilt of bores in structure A

6, 7, and 8 longer-lines suggest ~ 25°

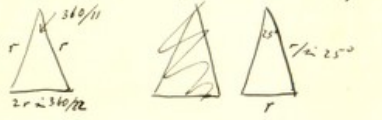
∴ ~~B/H~~ B/S mean values are 0·56, 0·48, ·46 for the longer lines

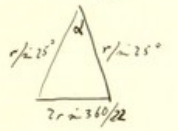
i.e. $\tan^{-1}$ 29°, 26°, 24°

Suppose tilt 25°, find ∠ between planes of neighbouring bores

i.e. ∠ between ⊥'rs to planes of bores

These lie on cone of semi-vertical angle 25°



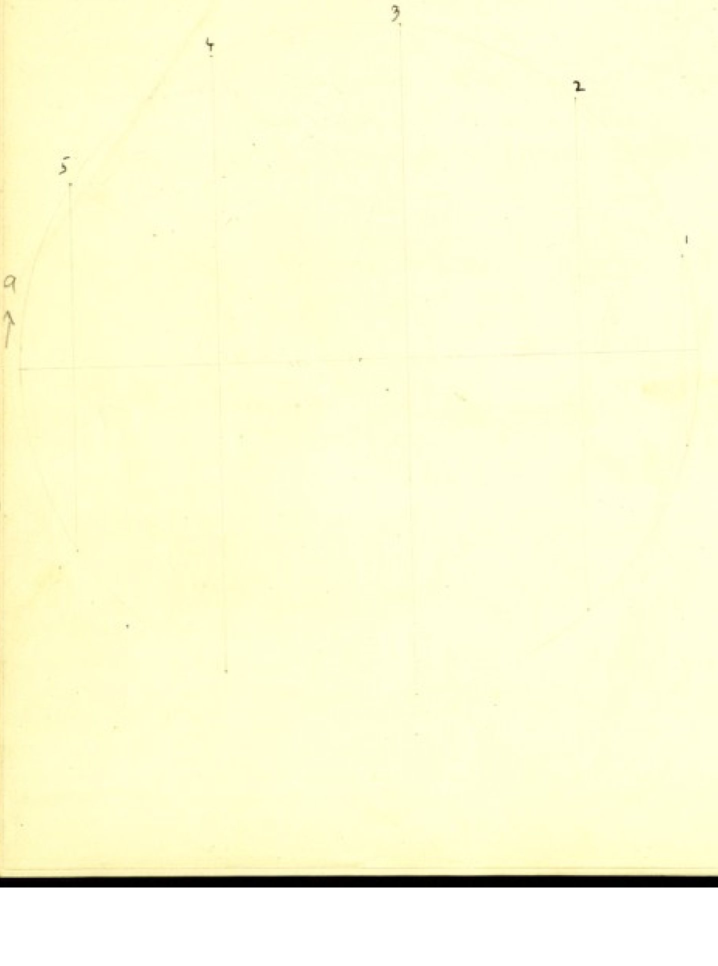


$\alpha = 2\sin^{-1}\left(\sin\frac{360}{22}\sec 25\right)$

$= 2\sin^{-1}\cdot 2818 \times \cdot 4226 \sim 2\sin^{-1}\cdot 11.9$

$\sim 2 \times 6°\,50'$

$\simeq 13\frac{1}{2}°$



Harker peaks for helix of radius 9Å (structure A)

	'a'	'c'	δ $= \frac{'a'}{22}\times 2.54$	c corrected Å	c section
1.	$18 \sin \frac{360}{22} = 18 \sin 16.36° = 18 \times .2818 = 5.07$	$c/11$	0.6	3.2	17.2
2.	$18 \sin 360 \times \frac{3}{22} = 18 \sin 49.1° = 18 \times .7559 = 13.6$	$3c/11$	1.6	9.3	23.2
3.	$18 \sin 360 \times \frac{5}{22} = 18 \sin 81.85° = 18 \times .9899 = 17.8$	$5c/11$	2.1	14.9	0.8
4.	$18 \sin 360 \times \frac{2}{11} = 18 \sin 65.5° = 18 \times .9100 = 16.4$	$7c/11$	1.9	19.8	5.8
5.	$18 \sin 360 \times \frac{1}{11} = 18 \sin 32.72° = 18 \times .5404 = 9.74$	$9c/11$	1.2	26.2	10.1

δ is ∵ a-b sections are not ⊥ to fibre axis.

± δ depending on orientation (or hand) of helix

Examination of inter-helical vectors on 3-dimensional shows orient^n & hand to be as indicated opposite, & this gives + δ

26.7.53

Suppose the 2 helices on which P atoms lie are related by vector V_1

and suppose a vector v on Patterson is a P – X interaction, where X is any atom ~~other than P~~ (e.g. N_a)

then there is a similar vector $V_1 - v$

Suppose V_1 has $x = -1$ A
$y = 0$
$z = 13$ A (= section 14)

then find which Patterson peaks, un-accounted for by P-P vectors, occur in pairs v and $V_1 - v$. These will be P – X vectors

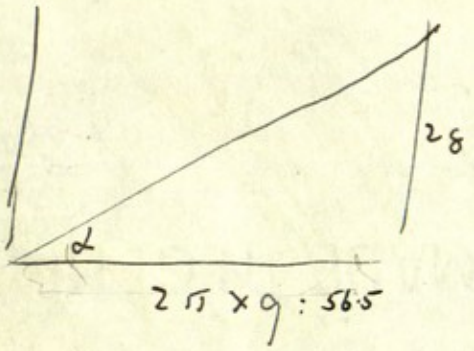
e.g. ~~xxx~~ v ~~section 10,~~ ~~$x = 6$ A~~ $y = 0$
$V_1 - v$ ~~section 4~~

v section 12 $x \sim 8$ A, $y \sim 7$ A
given section 2 $x \sim -9$ A $y \sim -7$

28.7.53

"Slope" of DNA helix

for structure A



$$\alpha : \tan^{-1}\frac{28}{565} : \tan^{-1} \cdot 495 : 26^\circ\ 20'$$

11th layer . line reflect

2 chains are out of phase, even for P atoms

- this explains why reflection is weak

c.f. Burn $(C_2F_4)_n$, equivalent reflection is strong

Temperature factor ∴ Pattersons, ∴ effect exaggerates el. importance of P's.

∴ reduces 6, 7, 8 layer-lines, supposed due to bases

Between pages 50 & 51

a - b superpositions

No direct way of finding how M_i shd be placed on M_j

- those using peaks on $b = 0$ (M_2 and M_3) did not have axes at origin
  [shown later that these are not Harker peaks]
- other sections show many similar regions

Patterson suggests axes rather than plane of symmetry

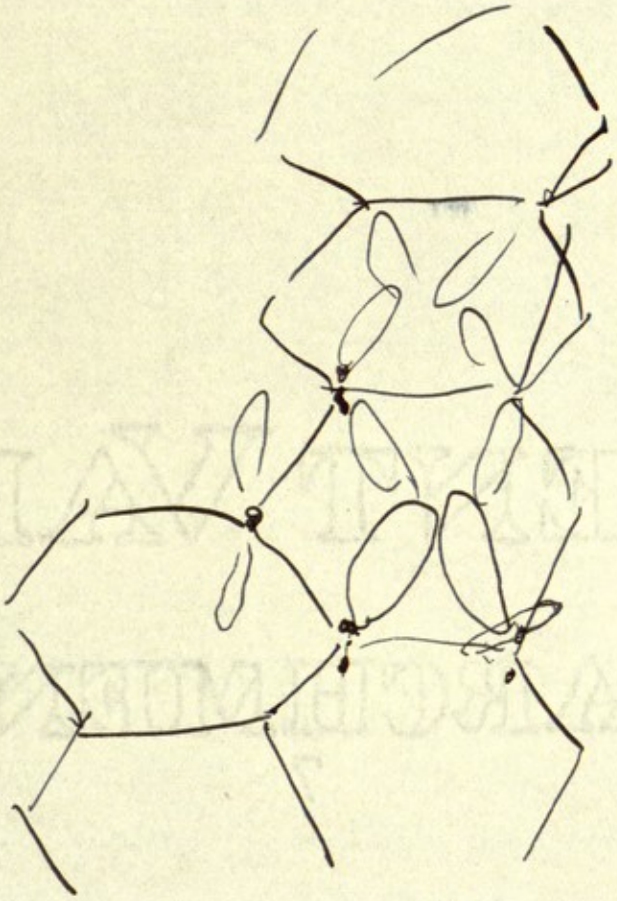
∴ a - c plane rich, b-axis poor

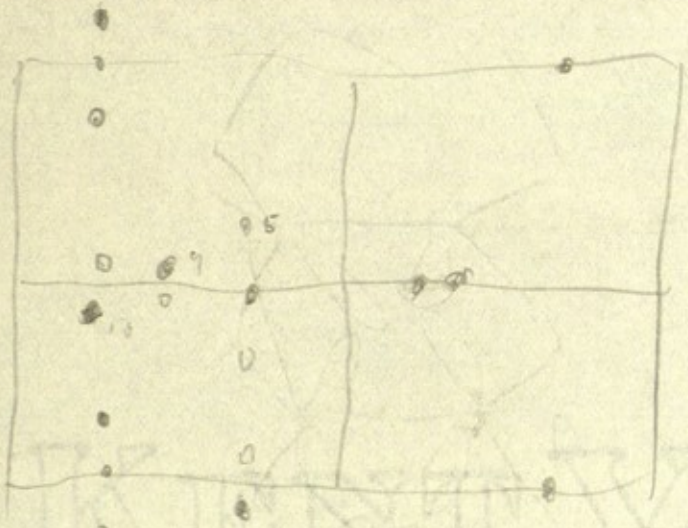
Vector hunt

To place M_i on M_j search for V_i in M_j by doing superposition V_i of M_j on itself

In this way obtained M56 which very clearly had axes

but clearly not whole truth - some parts obviously unreasonable.





1 symmetric

$F \propto 2\cos 2\pi l x + 1$

zero for $l = 4$

$\therefore \cos 2\pi l x = -\frac{1}{2}$ for $l = 4$

$\cos 8\pi x = -\frac{1}{2}$ $\quad 8\pi x = \frac{2\pi}{3}$ or $\frac{4\pi}{3}$

$x = \frac{1}{12}$ or $\frac{1}{6}$

for $l = 6$ $\quad 2\pi l x = 12\pi x$

for $x = \frac{1}{12}$ $\quad \cos 2\pi l x = -1$ $\quad F = 4 - 1$

$x = \frac{1}{6}$ $\quad \cos 2\pi l x = 1$ $\quad F = 3$

---

2 dips $\quad F \propto 2\cos 2\pi l \frac{x}{2}$

for $x = \frac{1}{8}$ this is zero for $l = 4, 12$

for $x = \frac{3}{8}$ ——— $l = 4, 6\frac{2}{3} \sim 1\frac{1}{3}$

between pages 56 & 57

Other Mg [illegible] with axes with feature in common for

one 2 [illegible] are in revealing structure obviously

Mg certainly correct

~~All have [illegible]~~ All have one rich and one poor

axial section, rich one with [illegible] (peak O)

Peck 1 along along a-c along, giving 2 peaks

on a-c section, - at distance from those of Mg

Mg 97 shows clearly that all peaks have $k = \frac{n}{12}$

∴ can express everything on 6 a-c sections

2nd [illegible] feature is '13' peaks

i.e. 0, 5, ... 13, 17

suggests one to look for at c ~ 9

giving 7 [illegible] along chain

which fits in realistically if each peak contains 2 P

N.B. 2 chains / primitive cell

- my proportions tend to show 3, but this is

property of Patterson and only be checked by absolute

values, and 3 does not fit density

Found between pages 40147

Structure B, 51 c

Layer. line	1st max ξ/λ obs	ξ/λ for r: 9.4	ξ/λ for r: 8.0	ξ/λ for r. 85
0	0.041 ~~0.905 – 0.130~~	.065 zero ∅ .0406	.076 zero ∅.048	zero 0.045
1				
2				
3	0.391 - 0.940	0.071	.083	.0805
5	0.905 - 0.130	0.113	.133	.0122

Zone sheet
Probably A K
1953 Post-Graduate

Analysis of A-form
– 11th Cycle-line
(see nature July 1953)

Attempt to explain (00,11) by arrangement of phosphate groups

$$F_{00l}^{hkl} = \sum_3 f^2 \cos 2\pi l z$$

Suppose 7 groups at heights $0, \frac{5}{30}, \frac{10}{30}, \frac{13}{30}, \frac{17}{30}, \frac{20}{30}, \frac{25}{30}$

Take amplitudes 20 for $\frac{5}{30}, \frac{10}{30}, \frac{13}{30}$ (strips 10, 20, 26)

and " 10 " 0

and vary heights (z-values) to find: –

Possible arrangements giving strong 00l

① Heights $0, 5, 8\frac{1}{2}, 13\frac{1}{2}$ $F_{0011} = 54$ $F_{007} = 52$ $F_{004} = 19$ $F_{008} = -18$

② " $0, 5\frac{1}{2}, 11, 13\frac{1}{2}$ $F_{0011} = 78$ $F_{005} = 36$ $F_{006} = 25$

③ $0, 5\frac{1}{2}, 10\frac{1}{2}, 13\frac{1}{2}$ $F_{0011} = 60$ $F_{006} = 36$ $F_{005} = 26$ $F_{009} = 30$

two ④ Heights $0, 10, 20, 26$ gives $F_{0011} = 12$, $F_{00,12} = 46$ $F_{005} = 20$ $F_{006} = 34$ etc

① ② and ③ fit Pattern less well than ④

∴ conclude that (00,11) is not due to phosphate groups

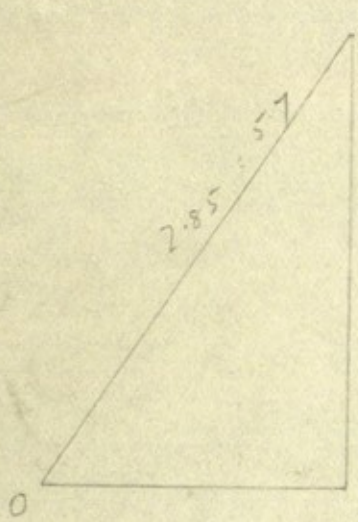
Consider each peak having 2 cpts. ~2A apart = c

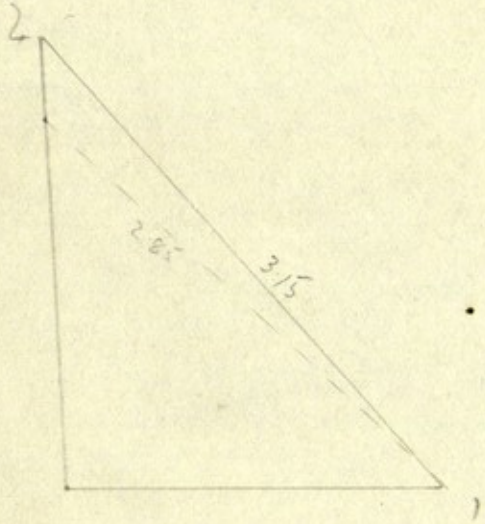
Then heights $1, 4, 0, 7\frac{1}{2}, 9\frac{1}{2}, 12\frac{1}{2}, 14\frac{1}{2}$

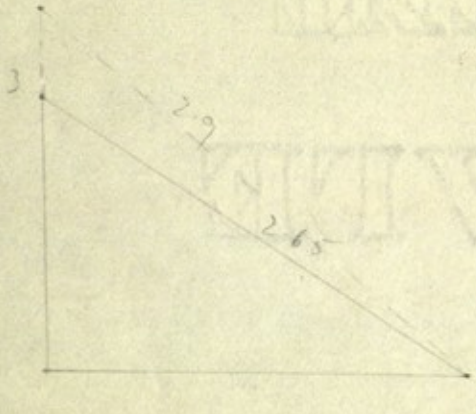
gives $001 = \bar{3}$ $002 = \bar{2}$ $003 = \bar{8}$ $004 = \underline{13}$ $005 = 1$ $006 = 5$ $007 = 6$

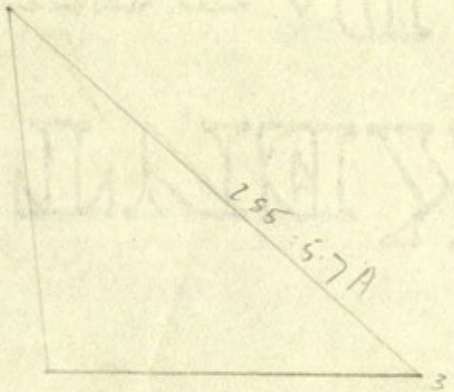
$008 = 2$ $009 = 3$ $0,10 = 5$ $\underline{00,11 = \bar{37}}$ $0012 = 4$ $0013 = \bar{22}$ $0014 = \bar{13}$ $0015 = 4$

Distance between neighbouring groups for '8' structure





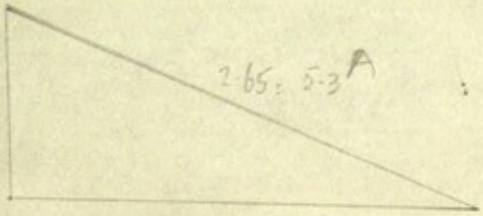


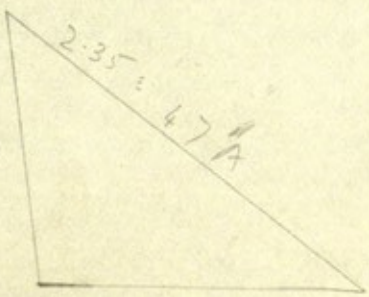


rear-origin peaks

① c: 2 : 2·4 cms a - b: 6·1 cms

② c = 3: 4·6 cms a: 4·3 cms b: 0





'8' structure & structure B

Vertical P-P distance on one molecule is 4·0 A (28/7)

Structure B must have other distance

- has inter-base height 3·4 A

∴ inter-leaved bases of 2 chains, & vertical P-P height on one chain is 6·8 A

but this involves length-change (70%) >> observed

[may be ∵ structure B is not fully extended - generally more disoriented than structure A - e.g. helical form imposed on 4-chain group. This would explain elastic properties of gelatinous (wet) fibres]

[[would it explain shocks?]]

Suppose 4-chain group persists in structure B, it will probably take up helical configuration. Unit cell corresponds to half-turn of helix (∵ 2 adjacent groups are on different level from opp. 2). i.e. fibre-period of 34 A contains 5 nucleotide on each chain, and complete turn of helix corresponds to 10 nucleotides

Found in notebook, undated
?Feb 1953? A.K.

See p 46 where this is repeated

3 chains

Non-equivalent unlikely

if equivalent must be equally spaced, & this is ruled out

But density indicates 2

2 chains

suggested by projections : 2 chains – structure A

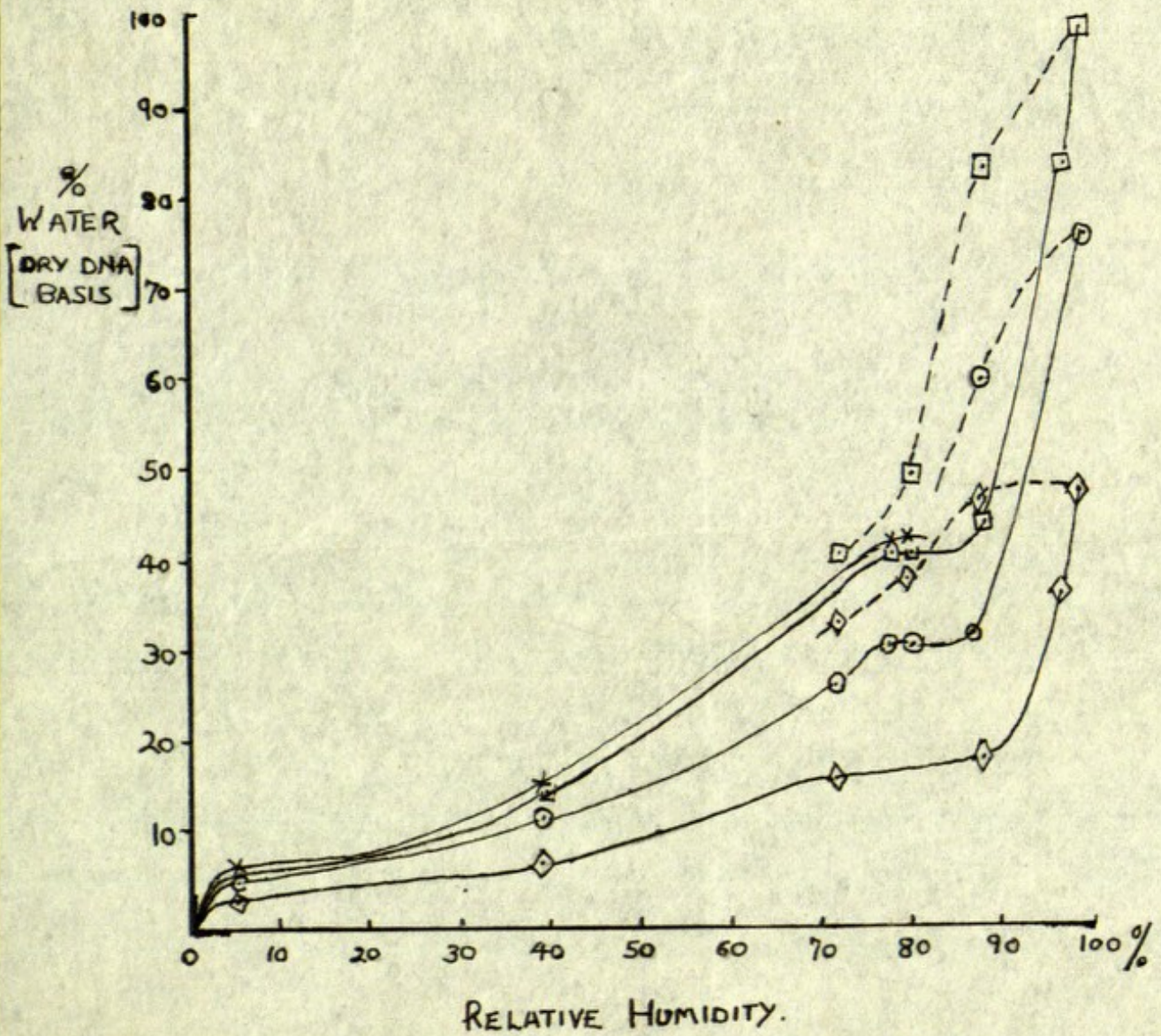
equally spaced ruled out

but unequally spaced 2 are still equivalent

RH	Sojer S	French Rats 2	3	4
5%	7.0	5.5	3.4	5.9
39	15.4	11.9	6.6	14.6
71	37.8	26.2	15.4	36.6
77	41.7	29.8	16.6	40.8
78.5	41.7	29.8	16.5	40.6
87.5	~~37.2~~ –	~~17~~ 32.2	17.5	43.7
96	–	65.4	36.0	83.0
98	–	74.5	47.1	98.2
87.5	–	58.9	46.1	82.7
76.5 78.5?	–	38.4	37.3	48.6
71	(40.8)	31.8	33.0	40.0

⊙ ~~Water Uptake~~ ◇ □

Grams Water per 100 gms Dry ~~Wt~~ DNA.


%
WATER
[DRY DNA BASIS]
100
90
80
70
60
50
40
30
20
10
0
10
20
30
40
50
60
70
80
90
100 %
RELATIVE HUMIDITY.