SALMONELLA INDEX

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Organized summary.

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Pedigrees :

—x Sw578	1151
FA12—x Sw666.	1131-2-3-4-6-~~7~~8-41 ; 1212
FA60—x Sw666	1142-3-4-7-8-9-50
—x Sw967	1137
Planting's	1140-3
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Segregation 1033.

INCIDENCE 1073 1075 990 (flax) 987 1212 981

(in H1 x) 1044

Serum effect 975 1003

O-CROSSES 1149? 988

Motility methods 1048 980

X_p' age 1047 972 942

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$H_1^{1,2}$ and H_1H_1 dupl. strains and macrophage pairs. 1002 1074 1053 991-2 1036-38-46 1051. 1049 976

Misc ϕ —X 1071 978 1063-8 1024 1016. 983

Som. antigens 1869 1034 1062 980

$H_{1,2}$ X— 989 1044 (tails)

TM2 Macrophage 1026e 1067 1053

SW666 X— 1067 1030 (autoant.) 985 984 1001 988 992-3 971 974 (993) 999

Galv 993 977 1032

SW967 X— 1027

Index notes on Salmonella
9/52 – 1/55.

Pedigrees: 1212 (① → swarms; ①$_S$ → 20, 11, 9, 9, 8; 12 → ≯1). 18 isolated; TM2 × 666 ; T/S

Details on T/S 1212-14 (FA37 × SW666 (Jan 55).

Apr 54.

1151 Pedigri × SW578 (paralytic). ; ca = T/S.

1150 FA60 × SW666 (40) cool. ① → swarms; ⑪ 12, 17, 4, 36, 50, 20, 12, 24, 26, 27, 12 (28) ≯1.

1149 60B × SW666 (37) [+ pool (11).] → swarms. ② → swarms; ⑥ → "large amicbaes" Remainder ≯1.
DCC also looked for crossovers.

1148 " " (10) 2 inv., 4 ≯1, (20), (30).

1147. " " (2) ①≯1; (5).
(35): 3 inv; 4 swarms; 27 ≯1; (+8).

1149. Dot also noted that SW967 × SW666 gave swarms (Gal+, gen) ambiguity of 60C! Presumably these were all saved.
But all isolates seemed idiotypic. Question of crossing over, esp. in swarm sites, should be reviewed.

1146 9 × SW967. "This gives largest tracks". Only (7). ; 6 $^{0}/_{10^3}$; 1 $^{2}/_{10^3}$...

1144. 60B × SW666. (10). 1×; (2); (1); (16); (46); SW, (+14).

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1143 60-xsw666 – Some isolations of motiles to plates
16 isolates, no trails.

other isolates pdyzd: see protocol

1142 60-x sw666 Some isolations to plates. No clear trails.
also (9): 0,0,1,1,2,3,10,>50 (++). → but not swarms!

1141 FA12-x 666 (1); 1 (14); others ∄1.

Note FA92 expt., no Pla⁺ seen microscopically.

1140 (1) platings: 130 (1) plated → 2 swarms, 7 cols. ∄ motility

1139 ∅OH ~~tactic~~ taxis

1138 12-x 666 mostly d. do not count, though some pdyzes useful.

1137 9-x 967. (12): all ∄ (1)

1136 Plant 12-x666: 1 swarm; 4 colonies/5.

1134 12-x666 detailed pdyzes
1133 " " mil. 1 swarm (not cross-over)
1131-2 " "

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1073, 1075 / 1043 — S. gallinarum + pullorum for H_1 identity = gm — 8 / 10/53.

→x SW967 "few long trails, 1 swarm"; φ1→x "single trails".

→x 957 "numerous trails; few swarms".

N97: H_1, H_1, H_2 tests (inconclusive) 1074. see also ~~[illegible]~~ 1000 ?

1071 "φR"→x . Note FA84→x SW666: ~~4~~ 1 5-6 swarms } Mustke→x 0901 ca 100 trails. }

1069 Vi+ S. typhi x— and —x
Misc. phages 978

8/53. S. bungendorf; and misc nonsp. φ from them. 1068, 1063
paraB phages: BAOR
TM2 monophasic SW1067. ~~SW 1067~~ 1067 of 1063 / 1026e (SW986)
Note: SW1067→x SW666 gave only H_1^b's.
TM2→x SW1061 gave no non-1,2.

UV, heat / phase variation: inconclusive 1065

S. abortus-equi (and bovis) 1042 / 1062, 1052

Somatic selection (inconclusive) 1034 1062

Resumé at 1053:

SW1047 (N97...) H_1 H_1 1046 1038 1036 992–991

Misc. on S. wien etc. inconcl. (cf Aleuts; PRE)

× SW1061 → stellmanyphasic env: —

but SW1055 × SW1061 (same?) did give c:1,2

S

1049; misc para B strains.

1045 S. para A.

1051 : H_1 – H_1 – Fla linkage

Used duplication stocks → × . No clear result.

1048 Motility agar changes – inconcl

1047 χ phage

1044 H_1, H_2 transductions (TM: miami abony) × ; note of trailstrue!

1041 – Phase variation = resume 1035 979

1037 S. napoli

1033 Fla segregations in trailer tested. Some data on T:S ratio. Serum effects (975)

SW967 Fla linkage. Ratios of gen: i etc.

1032 Galv? Looks for Hft (misguided). 977 973B1

1031 Resumé

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1031 – Resume

Fla$_1$-H$_1$,... linkage tests 1008.; crossovers?
Monophasics (976)
abortus equi, javiana, pullorum
z_{33}, z_6

1030 "autoantibody" – inhibition of Fla$^+$ H$_1^b$ by Fla$^-$ H$_1^b$?

1027 9–×967 "extensive teach" (This is probably the one saved)

"numerous T, no S" "numerous T, 1S".
has list of Fla$^-$ types. typing of SW970, 972...

Statement that 9–×967: numerous T, rare swarms } linkage?
10–×967: " and " . }

[Has there ever been adequate test for Fla$_1^-$ in 9–×967?]

1024 S. choleraesuis, javaica Felix antigen; 1020
Misc & tests + stability tests

1019 1/53. Citrunellus for inactivating phage n.g.

1018 "Cooperation of phage"; lysogenization 1009 994/998 protection – transduction 1017, 1012

1016 Felix O phage. n.g.

1014/ PLT22V. 1006

1013 host adaptation

1011 adsorption

1010 999 UV'd PLT22; TM2 Val-mutants;

1008 S. para A

1007 XRay PLT22

1003 Serum

1002 buffers 999

1001 b/i ratios: Fla⁻ linkage? Bais? 993, 992 986

0993 UV'd phage → Fla⁻. Val⁺/Fla⁺/infectivity

990 Flares + Tracks.

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7

989. Sendai x—
Eastbourne x—

988 "O form crosses" Never completed. Cf. OCG eq 3/53.

987 SW905-908 FA21-x908 "Tumorally long + prolific".
—FA9 : good yield of T+S. (better parabytic?)

985 SW666 (rough?) - b agglutinable?
984 " lysogenic? FA26-x666 28T/0S!
64T/2S!

983 Boyd phages. & h.r. tests

982 Rectify SW534 series

981 T/S/Cal+

980 Methods for O forms

974/ SW666x— back crosses ; 971

972 Xphage

992 5/6 → typhi H901 → 3/3 SW930 1,2: —

→ abony 7/7 1,2: eux

1000 Edwards N25 (SW942?)

and wi FA15 → SW942b → 1,2 -gam!

1023M Misr m Manchanco; ; 5216 → miami → 1,2; 1,5
SW973

1025 z33

1031 Expts on N97, N25 same xns 6: 1,2)

SW942 /b → 7/7 z33: — only

do 959-960-961

1036 N97 = SW1007, /b → 1036B1 → 1,2 !
Messstab 1,2 slowly

∴ reversible ! } reputable mutation

1036E i → SW1007 → i: b and cycled

1038 Homology ~~tests~~ N97 → miami → 6: 1,5 } H_1^b ~~H~~
→ TM2 → 6: 1,2 } incl $H_2^b H_1^{1,2}$

E TM2 → SW1007 → 3/3 i: b

→ 942 → i: —

10385 SW1026x — serdai → a:b:a SW1031
:b

Check 1026i → x mains → 1/2 i:1,5 mi. sluggish

nob's reformed

see summary at 1044

1046 Fresh N97 = SW1043 —b→ 1,2 1046A1

and check single colonies 6/6 —b→ 1,2

↙ 1046B1 = b → SW1043(1,2)
(SW1043b)

1,2's poorly reversible.

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c) TM2 → x SW 1043 2/2 i:1,2:(i)

Salmonella notes 1/61

Is there any turnover?

H_2 protein as repressor of H_1 synthesis.

Iino found a stock which was permanently in the phase-1 state.

$Ph_2^+ H_2^{1.2} Ah_2^-$ ↕ $Ph_2^- H_2^{1.2} Ah_2^-$ or $Ph_2^- H_2^{1.2} Ah_2^-$ ⇸ vh_2^-. or $Ph_2^- H_2$ stable allele.

? Can $Ph_2^+ Ah_2^-$ be obtained by recombination.

$Ah_2^- Ph_2^- H_2^{1.2}$ × ⟵ $Ph_2^+ H_2^{enx} Ah_2^+$

↓

$H_2^{enx} Ph_2^+ Ah_2^-$ i.e. stable phase 2.

how select ~~in presence of~~ $H_2^{enx} Ph_2^+ Ah_2^+$ variable phase 2.

? Is phase variation going on?

$Ah_2^- Ph_2^+ H_2^{1.2}$ ↕ $Ah_2^- Ph_2^- H_2^{1.2}$ × ⟵ $Ah_2^+ Ph^{del} H_2^{del}$ ⟶ both phases.

about 5
APR ~~12~~ 1955

A loves duplications in Salmonella

Genetics of phases. (Z[33])

① Phases of Salmonella ② CDC - ... as (H,).
992 → (for SW534)
b

989 SW546

91 Tal2 × 546 → (11) i: —
16
27 i: —

b: — × → 3 b: —

b: end → b: —
↘ end: 1,2 × — i: 1,2
↳ i: end

Tal2 × 937 12 i: —

All IPD

CDC 137 behaves as $H_1^{1,2}$ H_2^{0}.

+ caused by N25 → CDC 137 by mutation of $H_1^{b} \rightarrow H_1^{1,2}$

{ contra other pseudo B's + monophasic 1,2's: