I. THE THIRD STRAIN WHICH HAS NON-MOTIIE PHASE-1.
II. MONOPHASIC NAIURE OF SAI. ABORTUS-EQUI.
III. ARE $H_{2}$ AND PHASE CONTROLLER SEFARABLE BY RBCOMBINATION ?
IV. PHASE-I MONOPHASIC VARTANTS OF SAL. IYPHIMURIUM AND SAL. PAPATYYHI B.
V. RECURRENT ALIEPLVATION OF PHASE IN SAL. TYPHIMURIUM.

```
Report by Tetsuo Iino
    (Dec. 1, 1957)
```

THE THIRD SIRAIN WHICI HAS NON-WOTILE PHASE*1.

SW547 is a phase-2 monophasic variant of Sal. typhimurium. A mass culture of the strain segregates swarms (motile clones) and colonies (non-motile clones) on a NGA plate. The change from motile to non-motile and the reverse occurres as frequently as phase variation, suegesting the contribution of a similar factor as $\mathrm{Ah}_{1}$ in SW1061 and SW629.

Transduction was performed from SW547 to Sal. heidelberg SWl092 Fla-(r:1.2). Hotile transductional clones were screened on NGA plates, and antigen type was examined. The methods emploied are the same as those described in the Report 1956-i. The results were listed in table 1 together with the results on SW1061 and SW629. Among 11 Flal- $\mathrm{H}_{1}$ transductions, 8 are phase-2 monophasics, which produce non-motile phase in place of phase-1, whereas the remaining 3 are diphasics. Theresfore, it is inferred that the gene which inactivate the function of $H_{1}$ in SW547 is linked to $\mathrm{H}_{1}$ as in SW1061 and SW629. The monophasic factors in SW1061, SW629 and SW547 will be given symbols $A h_{1 a}, A h_{1 b}$ and $A h_{1 c}$ correspondingly.

To test allelism of $A h_{1 a}, A h_{1 b}$ and $A h_{1 c}$, mutual transductions were made between SW1061, SW629 and SW547. Non-motile phase was used as both donor and recipient, and i-type swarms were screened on NGA plates which were supplizemented anti-1,2 serum. As a control, diphasic Sal. typhicurium MT2 was used as a donor. The results were summarized in table 2 a . They are parallel with the results previously obtained between SW1061 and gW629 (c.f. the Report 1956-j), indicatimg that they are not allelic but closely linked each other and presumably belong to a cistron.

When the number of swarms which occurred by spontaneous reversion area substracted from the data in table $2 a$, and the numbers of transductions are expressed by $\%$ of the yield in which $7 T 2$ was used as a donor, the results are represented as in table $2 b$. The data present a rule that the yield of the recombinant is higher in between $A h_{l a}$ and $A h_{1 b}$ than in between $A h_{1 b}$ and $A h_{l c}$ when the donor or the recipient is the same. Samely, the yield between Ahlb and $A_{l c}$ is higher than that between $A h_{1 a}$ and $A h_{l c}$. If the assumption that the number of recombinant between two loci axe a function of the Tinkage distance can be applied to these results, the sequence of $A h_{l a}, A h_{l b}$ and $A h_{l c}$ may be $a--c--b$. However,
genetic background of these trree strains are considerably different, and the possibility that some factors other than linkage distence affect the yield of the recombinant type is not excluded. Consequently, the proposed sequence must be examined by a more appropriate anelysis in future (for example,
 test whether major type is $i$ or r.).

Table 1
Transductions from Fla-(i):1,2 monophasic variants of Sal. typhimurium to Sal. heidelberg $\mathrm{Fla}^{-}(\mathrm{r}: 1,2)$.

| Transductional types | SW1061 | $\begin{aligned} & \text { Donors } \\ & \text { SW629 } \end{aligned}$ | SW547 | Transduced loci |
| :---: | :---: | :---: | :---: | :---: |
| $\underline{r}: 1,2$ | 152 | 145 | 81 | $\mathrm{Fla}_{1}$ |
| $r: 1,2$ | 189 | 161 | 32 | Flal |
| i : 1,2 | 0 | 2 | 3 | $\mathrm{Fla}, \mathrm{H}_{1}{ }^{\text {i }}$ |
| i : 1,2 | 6 | 1 | 0 | Flal, $\mathrm{H}_{1}{ }^{\text {i }}$ |
| (r) : 1,2 |  | 2 | 0 | $\mathrm{Fla}_{1}, \mathrm{Ah}_{1}{ }^{-}$ |
| (i): 1,2 | 6 | 30 | 8 | $\mathrm{Fla}_{1}, \mathrm{H}_{1}{ }^{\text {i }}$, $\mathrm{Ah}{ }^{-}$ |
| Total | 356 | 341 | 127 |  |

* The cultures were lost before hidden antigen type is determined.

Table 2
Hutual transduction between $\mathrm{Ah}_{1}{ }^{-}$strains. Recombinants between $\mathrm{Ah}_{1}$ loci were scored by counting the number of i-type swarms on NGA plates. In each combination, $5 \times 10^{8}$ cells and $8 \times 10^{8}$ phages were used. $T$ indicates trail production.
(a)

| Donor | Recipient | $\begin{aligned} & \text { SW1061 } \\ & \left(\mathrm{Ah}_{1 \mathrm{a}}\right) \end{aligned}$ | $\begin{aligned} & \hline S W 629 \\ & \left(A h_{1 b}\right) \end{aligned}$ | $\begin{aligned} & S W 547 \\ & \left(\mathrm{Ah}_{1 \mathrm{C}}\right) \end{aligned}$ |
| :---: | :---: | :---: | :---: | :---: |
| TM2 | (t) | $266+$ T | $321+\mathrm{T}$ | $235+T$ |
| SW1061 | (a) | 0 | 230 | 50 |
| SW629 | (b) | 86 | 106 | 58 |
| SW547 | (c) | 72 | 193 | 2 |
| (b) |  |  |  |  |
| Donor | Recipient | $\begin{aligned} & \operatorname{SWIO61}^{\left(\mathrm{Ah}_{1 a}\right)} \end{aligned}$ | $\begin{aligned} & \text { SW629 } \\ & \left(\text { Ah1b }^{2}\right) \end{aligned}$ | $\begin{aligned} & S W 547 \\ & \left(\mathrm{Ah}_{10}\right) \end{aligned}$ |
| TM2 | ( + | 100 | 100 | 100 |
| SW1061 | (a) | 0 | 58 | 21 |
| SW629 | (b) | 32 | 0 | 24 |
| SW547 | (c) | 27 | 40 | $\dagger$ |

