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V. RECURRENT ALTERNATION OF PHASE IN SAL. TYPHIMURIUM.

Report by Tetsuo Iino (Dec. 1, 1957)

THE THIRD STRAIN WHICH HAS NON-MOTILE 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, suggesting the contribution of a similar factor as Ah_1 in SW1061 and SW629.

Transduction was performed from SW547 to Sal. heidelberg SW1092 Fla^-(r:1.2). Motile 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 Fla_1-H_1 transductions , 8 are phase-2 monophasics, which produce non-motile phase in place of phase-1, whereas the remaining 3 are diphasics. Thereofore, it is inferred that the gene which inactivate the function of H_1 in SW547 is linked to H_1 as in SW1061 and SW629. The monophasic factors in SW1061, SW629 and SW547 will be given symbols Ah_{1a}, Ah_{1b} and Ah_{1c} correspondingly.

To test allelism of Ah_{1a}, Ah_{1b} and Ah_{1c}, 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 supplemented anti-1,2 serum. As a control, diphasic Sal. typhimurium TM2 was used as a donor. The results were summarized in table 2a. They are parallel with the results previously obtained between SW1061 and SW629 (c.f. the Report 1956-j), indicating 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 are substracted from the data in table 2a, and the numbers of transductions are expressed by % of the yield in which TM2 was used as a donor, the results are represented as in table 2b. The data present a rule that the yield of the recombinant is higher in between Ah_{1a} and Ah_{1b} than in between Ah_{1b} and Ah_{1c} when the donor or the recipient is the same. Samely, the yield between Ah_{1b} and Ah_{1c} is higher than that between Ah_{1a} and Ah_{1c}. If the assumption that the number of recombinant between two loci is a function of the linkage distance can be applied to these results, the sequence of Ah_{1a}, Ah_{1b} and Ah_{1c} may be a--c--b. However,

genetic background of these three strains are considerably different, and the possibility that some factors other than linkage distance affect the yield of the recombinant type is not excluded. Consequently, the proposed sequence must be examined by a more appropriate analysis in future (for example, $H_1^r\ Ah_{1a}\ Ah_{1b}\ H_2^{1,2}$ ---x $H_1^i\ Ah_{1a}\ Ah_{1b}\ H_2^{1,2}$ anti-1,2 serum NGA screening test whether major type is i or r.).

Table 1

Transductions from Fla⁻(i):1,2 monophasic variants of *Sal. typhimurium* to *Sal. heidelberg* Fla⁻(r:1,2).

Transductional types	Donors SW1061	SW629	SW547	Transduced loci
r : 1,2	152	145	81	Fla_1
r : 1,2	189	161	32	Fla_1
i : 1,2	0	2	3	Fla_1, H_1^i
i : 1,2	6	1	0	Fla_1, H_1^i
(r): 1,2	0 } 3*	2	0	Fla_1, Ah_1^-
(i): 1,2	6 }	30	8	Fla_1, H_1^i, Ah_1^-
Total	356	341	127	

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

Table 2

Mutual transduction between Ah_1^- strains. Recombinants between Ah_1 loci were scored by counting the number of i-type swarms on NGA plates. In each combination, 5×10^8 cells and 8×10^8 phages were used. T indicates trail production.

(a)

Donor	Recipient	SW1061 (Ah_{1a})	SW629 (Ah_{1b})	SW547 (Ah_{1c})
TM2	(+)	266 + T	321 + T	235 + T
SW1061	(a)	0	230	50
SW629	(b)	86	106	58
SW547	(c)	72	193	2

(b)

Donor	Recipient	SW1061 (Ah_{1a})	SW629 (Ah_{1b})	SW547 (Ah_{1c})
TM2	(+)	100	100	100
SW1061	(a)	0	58	21
SW629	(b)	32	0	24
SW547	(c)	27	40	0