	nce is 25 map t						-	he top. The <i>Gr-Rc</i> hree genes may be	
(6	s(1)Gr	(25)	Rc						
Oi (I	r b) <i>Gr</i> (1) <i>S</i>	(24)	Rc						
The table, however, tells us that the distance S-Rc is 26 units. Therefore, alternative (a) must be correct, i.e., Gr is between S and Rc. Step 2. The Gr-Y distance is 19 units. Again, two alternatives are possible:									
(0	s) <u>S(1)Gr</u>	(19)	Y	(6)	Rc				
0	r f) Y	(18)	S(1)Gr	(25)	Rc				

In the table we find that the distance Y-Rc=6. Hence, possibility (c) must be correct, i.e., Y lies between the

Step 3. The distance Gr-P is 7 map units. Two alternatives for these loci are

loci of Gr and Rc.

(e)
$$S(1)Gr$$
 (7) P (12) Y (6) Rc or (19) P (6) $S(1)Gr$ (19) Y (6) Rc

The distance P-S is read from the table, and thus alternative (f) must be correct.

Step 4. There are 20 units between Gr and oa. These two genes may be in one of two possible relationships:

(g)	<u>P</u>	(6)	S(1)Gr	•	(19)	Y(1)0a		(5)	Rc
or									
(h)	oa	(13)	P	(6)	S(1)Gr	(19)	Y	(6)	Rc

The table indicates that Y and oa are 1 map unit apart. Therefore, (g) is the completed map.