Practice trihybrid crosses

phenotype	count	phenotype	count	phenotype	count	phenotype	count
+ + +	208	g i m	364	+ + +	350	i g n	275
e i n	200	+ + +	356	a g m	338	+ + +	265
+ i +	135	+ + m	92	a + m	90	i g +	176
e + n	137	g i +	88	+ g +	82	+ + n	184
+ i n	100	g + m	44	a + +	60	+ g +	33
e + +	92	+ i +	36	+ g m	52	i + n	27
+ + n	68	g + +	12	+ + m	18	i + +	16
e i +	60	+ i m	8	a g +	10	+ g n	24

A) The four sets of data above form a continuous map over six loci.
   1) Determine the locus order and distances among loci for each set of data.
   2) Determine the gene order and the distances between all six loci.

In each case, a triple dominant homozygote (**ABD // ABD**) parent has been crossed with a triple recessive homozygote **tester** (**abd // abd**) to produce an **F1** triple heterozygote (**AaBbDd**). The heterozygote was then back-crossed to the tester stratin (**abd // abd**), and the numbers of resultant progeny counted. A '**+**' symbol indicates the phenotype corresponding to the dominant allele at each locus. [So, each parental cross could also be written in the form **+++ // +++** X **abd // abd**].

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phenotype	count	phenotype	count	phenotype	count	phenotype	count
a M R	338	a I R	430	N i R	416	e i N	366
a M r	16	a I r	46	N i r	38	e i n	94
a m R	5	a i R	3	N I R	5	e I N	7
a m r	142	a i r	20	N I r	44	e I n	34
A M R	146	A I R	16	n i R	48	E i N	30
A M r	7	A I r	1	n i r	3	E i n	9
A m R	12	A i R	50	n I R	34	E I N	90
A m r	334	A i r	434	n I r	412	E I n	370

B) The four sets of data above form a continuous map over six loci.
   1) Determine the locus order and distances among loci for each set of data.
   2) Determine the gene order and the distances between all six loci.

Each of the **P1** parents is a **triple homozygote** as above, however the *cis / trans* phase relationships among the three loci in the various crosses are not as simple as in the first set of examples. The **F1** offspring were crossed with a triple recessive homozygote, as above.

Hints: First determine the Parent and Double Recombinant phenotypes. All distances in both maps should work out to round numbers. The correct gene order should spell a word.

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