Bill - File these in Mosley Book between 1294 and 1295

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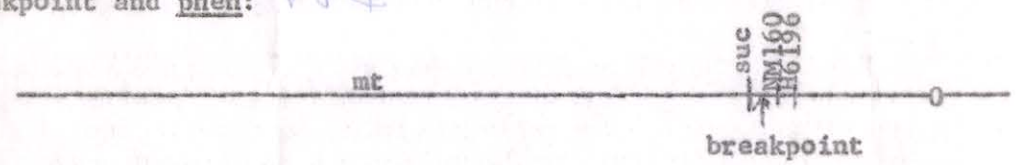
TYR(NM160)

December 9, 1966

Dr. A. Gib DeBusk
Biology Department
Florida State University
Tallahassee, Florida, 32306

Dear Dr. DeBusk:

We've got the results of the allelism test between phen-1 (H6196) and the new tyrosine mutant which David sent you (NM160, erroneously called tyr-4). The two mutants are extremely closely-linked and probably allelic. We got only 2 sure w.t. and 2 possible w.t. (not picked because of heterocaryosis with neighboring spores) out of an estimated 4000 germinated spores. This alone would not completely convince me, because this is essentially the same w.t. frequency we got between phen-1 (H6196) and suc; this is a very elastic region and we haven't succeeded in getting either phen or suc into a high crossover stock. However the mating type of the two phen$^+$tyr$^+$ wild types indicates that NM160 is left of H6196. A separate cross shows that tyr is not covered by the duplication produced by H4250; this duplication begins just left of phen, between phen and suc. Therefore, if we can trust two crossovers, tyr must be located in the extremely small region between breakpoint and phen:



I'm very sorry that we've caused you extra work. The only consolation is that tyr seems more vigorous than phen, which may make it easier to work with. I had no trouble getting them to cross well, so they might be complementers. This raises the possibility that they are adjacent genes concerned with related functions like me-7 me-9, but I doubt that it's worth your while to check this more than you have already.

If you decide that they are biochemically identical, David wants to know what we should instruct FGSC to call NM160. At present it is listed in FGSC as tyr (NM160). It's misleading to call it a phen allele when it can't use phenylalanine. And as long as the locus is called phen, everyone else who finds a new allele is going to make the same mistake. He suggests getting together with Ray Barratt to change the name of phen-1 perhaps to tyr-4 or perm. What do you think?

Sincerely,

Dorothy Newmeyer

DN:dm
cc: Dr. Raymond W. Barratt
Dartmount College, Hanover, N.H.

Ray: What happened was that Dave kept out NM160 with Atwood's antiserum test mixtures. It didn't respond to Val, and leucine response wasn't realized because it is in over of some mixtures as tyrosine. Initial genetic tests made it seem most likely to be in I R near centromere, so he tested it with the tyr there. When they weren't allelic, he labelled it tyr-4 subsequently found it was left of centromere and gave it to me to locate in I L. When anyone gives me a mutant with a locus number on it, I assume it's been tested for allelism with anything it could be allelic with, so it never occurred to me it hadn't been tested for growth on leucine etc. Somehow Dave has never latched onto the idea that some phen strains won't use Val, in spite of my talking about it. So-