we figure if this is so with him, it's likely to happen with anyone else who finds new alleles. He gave it to de Busk (COPY) working on ~~tyrosine~~ mutants and this acted like a ~~bacterial~~ clear tyrosine mutant. de Busk sent us a letter saying it looked suspiciously like phen, chemically, just we found it unacceptable for linkage with leu-3 arg-1, because of it's growing on leucines.

I really should have checked when Dave first gave it to me, because the NM160 number meant that he must have keyed it out himself; but it didn't occur to me.

Incidentally, my data are all compatible with the idea that the ~~frameshift~~ modifier that prevents tal utilization is present in St. L. w.t.'s. If I ever get time I'll finish checking this out.

Best wishes,

Dot

Department of Biological Sciences
Florida State University
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U.S.A.

December 9, 1966

Dr. Raymond W. Barratt
Biology Department
Florida State University
Tallahassee, Florida 32306

Dear Ray:

I'm very sorry that we've caused you extra work. The only complication 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 PGSC to call NM160. At present it is listed in PGSC 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 pern. What do you think?

Sincerely,

Dorothy Newmeyer

DN:dm

cc: Dr. Raymond W. Barratt
Dartmouth College, Hanover, N.H.