Notes on the fly project

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September 16, 2016

1 Delivery of oligonucleotides

The oligonucleotides designed on 2016-06-09 were ordered to biomers.net, and delivered. They are dry. Table 1 specifies the yield and the corresponding amount of buffer required to dilute them to 100 pmol/μl.

2 DNA extraction test

On September 13$^{\text{th}}$ 2009, Dr. Carazo, Mrs. Sultanova, Mr. Andiç and I started the DNA extraction from 8 flies, following the GBS protocol. Table 2 summarizes the procedure. Not that we needed 4 people to run this, but they all were interested in going through the protocol, which is great. The protocol is applied to each fly individually, with the aim of measuring how much DNA we can get from one fly. Four of the flies had their oviduct previously removed by Mrs. Sultanova. We want to make sure that the ovariectomy does not significantly reduce DNA yield.

3 Literature review

Original motivation of classic life span QTL mapping studies was the elucidation of metabolic pathways involved in aging ?. I suspect that the biomedical interest in the mechanisms of aging preceded the interest in naturally occurring variation, as well as the real effect of the QTL identified in natural conditions. Several sex-specific life span QTL exist in autosomes of *D. melanogaster* ??. These QTL were originally identified using recombinant inbred lines (RIL) descended from two strains ?. In this design, the dominance of the QTL is not known, since only homozygous genotypes are produced (?, page 432). However, the quantitative complementation test with deficencies

Table 1: Name and available amount (yield) of oligonucleotides received from biomers.net. 'Volume' makes reference to the volume required to dissolve the corresponding oligonucleotides at 100 pmol/μl (μM).

Name	Yield (nmol)	Volume (μl)	Name	Yield (nmol)	Volume (μl)
Top1.1	82.6	826	Bot1.1	64.8	648
Top1.2	106.8	1068	Bot1.2	110.4	1104
Top1.3	94.9	949	Bot1.3	92.6	926
Top1.4	85.6	856	Bot1.4	75.8	758
Top2.1	78.9	789	Bot2.1	90.7	907
Top2.2	81.9	819	Bot2.2	97.4	974
Top2.3	100.5	1005	Bot2.3	84.2	842
Top2.4	88.4	884	Bot2.4	82.3	823
Top3.1	98.6	986	Bot3.1	87.1	871
Top3.2	95.2	952	Bot3.2	96.6	966
Top3.3	100.2	1002	Bot3.3	87.9	879
Top3.4	95.6	956	Bot3.4	78.7	787
A1.1	60.2	602	A2	65.9	659
A1.2	52.6	526	R1	78.7	787
A1.3	56.7	566	R2	60.0	600
A1.4	51.0	510			

Table 2: Summary of the DNA extraction test.

Sample	Treatment	Elution (μl)	Conc.(ng/μl)	Yield (ng)
1	–	100	1.690	169
2	–	100	0.590	59
3	–	100	1.540	154
4	–	100	0.574	57
5	ovariectomy	100	0.752	75
6	ovariectomy	100	1.850	185
7	ovariectomy	100	0.314	31
8	ovariectomy	100	0.418	42

used to refine the QTL **?** seems to assume that one of the alleles is at least partially recessive.

Crow **?** mentions the genetic basis of heterosis as one of the main mid-century controversies in population genetics. He is very clear that the debate between dominance and overdominance was resolved in favor of the dominance hypothesis. That is, both the inbreeding depression and the hybrid vigor (heterosis) are mostly due to recessive deleterious alleles that become either expressed upon inbreeding or concealed upon hybridization. A review **?** cites another work by James F. Crow that I cannot access (volume 9 of the Oxford Series in Evolutionary Biology), in which the author shows evidence of 30% of autosomes isolated from natural populations of *D. melanogaster* being lethal in homozygosis. The same cannot be true for sex chromosomes, of course. Among the 70% of natural chromosomes that are not recessive lethals, homozygosity reduces survival to adulthood in 84%.