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Amplification of DNA from 30-year-old aceto-orcein stained salivary gland squash slides.

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Salivary gland squash slides have been used since the early days of genetics to visualize the fruit fly's polytene chromosomes. These slides represent an immense archive of genetic material for *Drosophila* and other genera. Aceto-orcein is commonly used to stain salivary gland preparation, as well as other cytological specimens, especially when trying to visualize chromosomal material. However, aceto-orcein stained tissue proves recalcitrant to yielding DNA for amplification. I describe here a simple procedural modification of a basic DNA extraction protocol that yields PCR-amplifiable DNA from aceto-orcein stained salivary glands.

The slides in question were made over 30 years ago from *Drosophila melanogaster* strains with presumptive tandem duplications of the maroon-like (*mal*) locus. These were apparently the result of spontaneous non-homologous unequal crossing over (Johnson and Smith, 1976; Johnson, 1977). These slides were prepared using a standard protocol involving 1) coating one slide with a gelatin subbing solution, 2) squashing salivary glands in 45% acetic acid between two slides using a bench vice, 3) freezing the slides on dry ice then popping them apart, 4) staining with aceto-orcein, 5) dehydration in alcohol, serial toluene treatment, and mounting a coverslip with CoverBond (Harelico). Various protocols to recover DNA were attempted repeatedly, including using the Pinpoint Slide DNA Isolation System™ (Zymo Research), all yielding no detectable DNA after PCR.

The key that made DNA isolation possible was a brief acidification step, presumably to remove the DNA-bound aceto-orcein. The successful protocol below is a modification of the Wizard® Genomic DNA Purification Kit procedure (Promega). The use of toluene here is to remove CoverBond which is toluene soluble.

Protocol

- 1) Carefully scrape salivary gland tissue off the slide with a new razor blade then soak the tissue in toluene for 5 minutes.
- 2) Add an excess of 95% ethanol and mix gently.
- 3) Centrifuge briefly to pellet the tissue flake then discard the supernatant.
- 4) Wash three more times with 95% ethanol (repeat steps 2 and 3).
- 5) Remove remaining ethanol in a vacuum centrifuge.
- 6) Dissolve the flake (as much as possible) in 600 µL Wizard Nuclei Lysis Solution.
- 7) Incubate at 65°C for 30 minutes.

8A21	1	TAGATGTGAAAACGAATTTAATGTTCTGTAGTTAAAAACATTTTATAAATGTTTAAAT	60
AE014298.4			
8A21	61	AATAAGATTGTAGTTTCCAAAAATTATTGTCATACAATTGGCCAATTAGCCATTAGCAAC	120
AE014298.4			
8A21	121	CATTTTCCTAACACCAATTGTTTGCCAACTCAGAACATATGTTTGAATAGCCATGCAA	180
AE014298.4			
8A21	181	AGTGCAACGACTAGTTAATACCGTACAATTTGAGTTTAAAATTCTATGCAATTCAGAG	240
AE014298.4			
8A21	241	TTAATAATTGGAAAAGATTGGTAAAATGCTACATCTATAATATTGGTGAGCAGTGTGAG	300
AE014298.4			
8A21	301	AATATGATATATATATTACAATAAGCAAACATAATGCACAAGAAGCTTAATAAATTGAGC	360
AE014298.4			
8A21	361	TTCGTAAAATGTGTAGGGTGGAGTAAGTTCAAAGAGAAGTCAAAGCAAATGCTCAACTGA	420
AE014298.4			
8A21	421	ACGTGATAGTTGATGTATACTGTCCGTGGCTTTTTCAGCGAAGAAGAGTATGGCGCAAC	480
AE014298.4			
8A21	481	AAATGCAAGCCGGTCGCAAATAAATAAGCCCGCTTTCAGCCAACACGAATAGTTAGTT	540
AE014298.4			
8A21	541	CCCAACATGACATCATATCGGCCGGAGTTCTCCGCATCGGAGCAGTCGCAAATAGACGCG	600
AE014298.4			
8A21	601	GAATTCTCTAGATTGGCCAGTAAGTGGAGAACCATGGTGAAATACCCAGCGCAAACAGAT	660
AE014298.4			
8A21	661	AACGAACCTAACCATCCGTCTATCGAACAGGCAACA	696
AE014298.4			

Figure 1. Alignment the entire fragment amplified from a slide (8A21) and the *Drosophila melanogaster* chromosome X *mal* region DNA (AE014298.4).

- 8) Add 10 μ L of Wizard RNase and 10 μ L of Proteinase K (20 mg/mL) and incubate at 37°C for 20 minutes.
- 9) Incubate at 95°C for 5 minutes to denature Proteinase K.
- 10) Add 200 μ L of Wizard Protein Precipitation Solution and vortex for 20 seconds.
- 11) Chill on ice for 5 minutes.
- 12) Centrifuge for 4 minutes at 13,000-16,000 $\times$ g.

- 13) Transfer supernatant to a clean 1.5 mL microfuge tube containing 600 μ L of isopropanol.
- 14) Gently mix by inversion.
- 15) Centrifuge for 1 minute at 13,000-16,000 $\times$ g.
- 16) Carefully remove isopropanol with a pipette and discard.
- 17) Add 600 μ L of 70% ethanol and gently mix by inversion.
- 18) Centrifuge for 1 minute at 13,000-16,000 $\times$ g.
- 19) Carefully remove ethanol with a pipette and discard.
- 20) **Add 100 μ L 45% acetic acid and mix gently; let stand for 2 minutes.**
- 21) **Add 300 μ L Wizard Rehydration Solution and 1/10 volume 7.5 M ammonium acetate and mix gently.**
- 22) **Add 2 volumes 95% ethanol and mix gently.**
- 23) **Incubate at 70°C for 5 minutes.**
- 24) **Centrifuge for 1 minute at 13,000-16,000 $\times$ g.**
- 25) **Carefully remove supernatant with a pipette and discard.**
- 26) **Add 1000 μ L ethanol, mix gently, and centrifuge for 1 minute at 13,000-16,000 $\times$ g.**
- 27) **Carefully remove supernatant with a pipette and discard.**
- 28) Invert tube on a paper towel and air-dry the pellet for 10–15 minutes.
- 29) Add 40 μ L of Wizard DNA Rehydration Solution and incubate at 65°C for 1 hour.
- 30) Store DNA at 2–8°C.

PCR was performed on these extracts using GoTaq® (Promega) and primers that amplify an approximately 744 nt segment at the beginning of the *mal* mRNA (primers: 5'CAGCTGTATGTGTAGGCTATCGTC3' and 5'CCGCATGATCCAGGTAAACACTCT3'). Longer extension times were used (94°C for 1 minute, 55°C for 1 minute, 72°C for 3 minutes for 33 cycles) and hot start PCR was performed using AmpliWax® PCR Gem wax beads (Applied Biosystems). A typical reaction used 10.5 μ L of DNA in the lower layer and 12.5 μ L of GoTaq and 1 μ L of each primer in the upper layer. DNA amplified from two slides using these primers was indistinguishable on agarose gels from similarly amplified DNA from wild-type flies. PCR products were cloned using the TOPO® TA method (Invitrogen) and sequenced (Macrogen, Korea). As shown in Figure 1, this amplified DNA is from the *mal* locus of *Drosophila melanogaster*. All clones from the two slides gave similar results.

It is my hope that this report will make such archived *Drosophila* DNA more accessible.

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An organizational strategy for deficiency mapping: A computational approach.

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Introduction

Deficiency mapping provides *Drosophila* geneticists with the unique ability to physically map mutations by studying a single generation of animals. By crossing a lethal mutation in an unknown