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Characterization of bacteriophage P1 library containing inserts of Drosophila DNA of 75-100 kilobase pairs.

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Abstract.
A multiple-hit bacteriophage P1 library containing DNA fragments from Drosophila melanogaster in the size range 75-100 kb was created and subjected to a preliminary evaluation for completeness, randomness, fidelity, and clone stability. This P1 library presently contains 3840 individual clones, or approximately two genome equivalents. The library was screened with a small set of unique-sequence test probes, and clones containing the sequences have been recovered. In situ hybridization with salivary gland chromosomes indicates that the clones originate from the site of the probe sequences in the genome, and filter hybridization of restriction digests suggests that the clones are not rearranged in comparison with the genomic sequences. Approximately 1.7% of the clones contain sequences that hybridize with ribosomal DNA. A small subset of these clones was tested for stability by examination of restriction fragments produced after repeated subculturing, and no evidence for instability was found. The P1 cloning system has general utility in molecular genetics and may provide an important intermediate level of resolution in physical mapping of the Drosophila genome.