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Kim, W., J.M. Kim, and D.J. Shin. Department of Biology, Dankook University, Cheonan-Si, Choong-Nam 330-714, Korea. Molecular analysis for specific *hobo* deletion derivatives in the Korean population of *Drosophila melanogaster*.

On the basis of our results of *in situ* and Southern blot hybridization using *Xho*I restriction enzyme (Kim and Kim, 1996), the Korean population of *D. melanogaster* appeared to have a low copy number of 3.0 kb putative full-size *hobo* elements and a high copy number of internally deleted *hobo* elements. This result is somehow comparable with the earlier reports detected from American and Eurasian populations of *D. melanogaster* (Periquet *et al.*, 1989a, b; Pascual and Periquet, 1991; Boussy and Daniels, 1991). Periquet *et al.* (1989a, 1990) reported the presence of two major classes of *hobo* elements, a 3.0 kb element class and one particular deletion derivative class of elements called the *Th* element, which have accumulated in all naturally-occurring strains throughout the Eurasian continent. They suggested that the presence of *Th* element might be interpreted as potential regulatory elements of the *hobo*-induced hybrid dysgenesis.

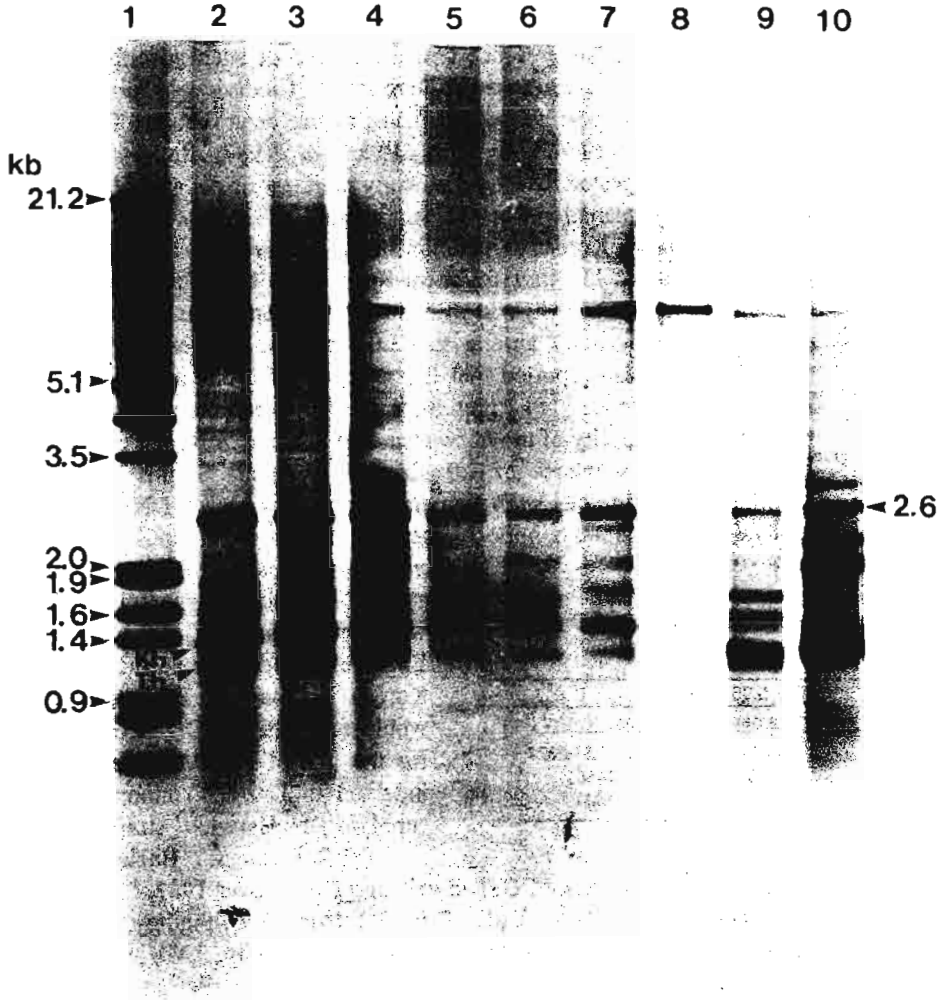

Figure 1. Southern blot analysis for the structure of *hobo* elements from Korean lines of *D. melanogaster*. Genomic DNAs were digested with *Xho*I, and hybridized with the 2.6 kb *Xho*I restriction fragment of the pH108 plasmid as a probe. Lanes are as follows: (1) Dig-labelled DNA marker III, (2) Cheonan 96-33 (H^+), (3) Cheju 96-29 (H^+), (4) Cheonan 96-15 (H^0), (5) Cheju 96-12 (H^0), (6) Cheonan 96-6 (H^-), (7) Cheju 96-9 (H^-), (8) Basc (E), (9) Harwich^Y (E), (10) 23.5*/Cy (H). H^+, H^0, and H^- strains were classified by reference tests of Pascual and Periquet (1991).

Based on the result of Southern blot hybridization, a specific 1.7 kb *hobo* deletion derivative (1.3 kb *Xho*I restriction fragment in Figure 1) is the most preserved in all of the Korean lines tested and is termed *Kh* element. The 1.5 kb *Th* element, giving a 1.1 kb fragment and 3.0 kb full-size *hobo* element (2.6 kb fragment) are also observed in these lines (Figure 1). The entire 1.7 kb sequence of four *Kh* elements derived from Korean lines have been obtained by polymerase chain reaction (PCR) and DNA sequencing. PCR amplification of *Kh* element sequence was performed on the genomic DNA using the following two primer sequences in pH108 (Streck *et al.*, 1986): #1, 5'-CAGAGAACTGCAAGGGT GGC-3' (1-21), and #2947,

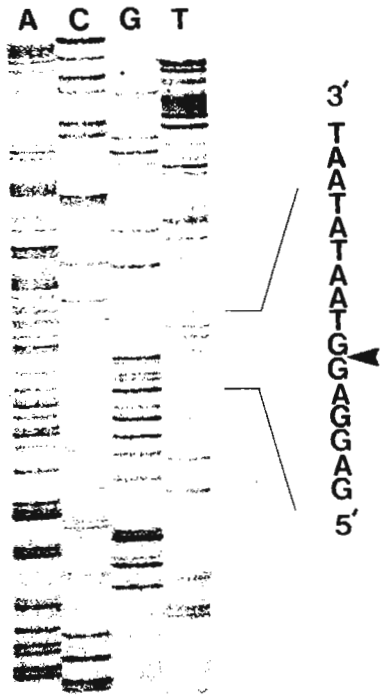

Figure 2. Sequencing gel autoradiograph of a segment of the 1.7 kb *Kh* element from a Korean line. The arrow shown is that of the breakpoint (938/2192) of the *Kh* element from an autonomous 2959 bp HFL1 *hobo* element.

5'-GCCCGCCACTCGCACTCTAC-3' (2947-2928) by the method of Kim and Kidwell (1994). The 1.7 kb fragments of individual *Kh* elements were cloned into pCR™II vector plasmids, and subsequently sequenced by the dideoxy-chain-termination method (Sanger *et al.*, 1977) using the Sequenase kit (U.S. Biochemical, Cleveland) according to the supplier's protocol. We also determined the sequences of *Th*1 and *Th*2 elements isolated from these lines, to compare the breakpoint to *Kh* element.

The sequence of all *Kh* elements tested in these populations suggested that they might have been derived from the autonomous *hobo* element HFL1 (Calvi *et al.*, 1991) by a 1253 bp internal deletion between positions 939 and 2191 (Figure 2). The sequences of *Th*1 and *Th*2 elements appeared to be identical to that of the HLF1 with the exception of internal deletions of 1442 bp and 1455 bp removing nucleotides 940-2381 and 923-2377, respectively (Table 1). Therefore, all of these *hobo* deletion derivatives seem to be derived from the HLF1 *hobo* element, not from pH108.

The massive presence and the spread of such specific deletion derivatives might be due to a selective favor of individuals carrying high copy numbers of these deleted elements, as has been reported for the *KP* element in the P-M hybrid system (Black *et al.*, 1987; Rasmusson *et al.*, 1993). It is suggested that the high copy numbers of *Kh* and *Th* elements provides an explanation for the suppression of *hobo*-mediated hybrid dysgenesis in the Korean population of *D. melanogaster*. However, the presence of a 2.6 kb *Xho*I fragment by itself in this study cannot be a sufficient prediction of hybrid dysgenesis or autonomous because of the sequence heterogeneity among the 3.0 kb *hobo* element. Bazin and Higuet (1996) also reported that the structure of the S region where an amino acid sequence (TPE) presents a repetition polymorphism could be specific to the activity of the *hobo* element. Further work will be required to identify the sequence of 3.0 kb *hobo* elements in this population whether an autonomous *hobo* element is present or not. A DNA sequence analysis of the 3.0 kb *hobo* element in the Korean population of *D. melanogaster* is in progress.

Table 1. Comparison of sequence differences between deletion derivative *Kh* and *Th* element derived from Korean lines of *D. melanogaster*.

	HFL1 (2959 bp)		
	Kh element (bp)	*Th* (1) element (bp)	*Th* (2) element (bp)
Internal deletion site	939-2191	940-2381	923-2377
Deletion size	1253	1442	1455
Size in genome	1706	1517	1504

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