Novel repeats in the genome of the woodchuck *Marmota monax*

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Infection of woodchucks from the Eastern United States (*Marmota monax*) with the woodchuck hepatitis virus (WHV) has proven to be an excellent animal model system for the study of hepatitis B virus infection of humans. Woodchucks infected experimentally with WHV develop acute virus infections which can become chronic infections leading to hepatocellular carcinoma (1–7). However, understanding hepatocarcinogenesis using this model system is limited by a general lack of information on the host genome.

In this study we cloned DNA from the genome of an uninfected woodchuck to search for unique, repeated DNA sequences. Genomic DNA was isolated from woodchuck number 809, digested with restriction endonuclease HindIII, and cloned into the HindIII site of pUC13 DNA. Independent recombinants were selected for analysis. Recombinant W220172, a 318 bp HindIII fragment, was found to occur 20 times in the woodchuck genome using standard hybridization techniques (8). Recombinant W87, a 249 bp repeat, was found to be repeated approximately 1,000 times in the woodchuck genome. Both repeats lack significant open reading frames and are AT rich (Table 1). Computer analysis (9) indicates that there are no sequences in the EMBL 25 or the GenBank 66 databases that possess statistically significant sequence similarity with the two repeats. Thus, these repeats appear to be unique. Repeat W87 may be useful as a probe to identify woodchuck specific DNA sequences in mouse NIH 3T3 cell assays in the search for oncogenes responsible for liver tumor formation in WHV-infected animals.

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Table 1.

	W220172		W87	
A	80	(25.2%)	96	(38.6%)
C	74	(23.2%)	48	(19.3%)
G	52	(16.4%)	26	(10.4%)
T	112	(35.2%)	79	(31.7%)