Construction of repetitive DNA libraries from the genomes of two hamster species, *Phodopus sungorus* and *Phodopus roborovskii* (Cricetinae)

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We report the construction of two libraries of repetitive sequences from genomes of *Phodopus sungorus* to *Phodopus roborovskii*. For this, a series of experimental steps were performed: restriction of *P. sungorus* or *P. roborovskii* total genomic DNA, cloning of the restriction products and colony lift hybridization using the restriction products as probes. Sequencing of these repeats revealed 20 different sequences of *P. sungorus* and 17 of *P. roborovskii*. Moreover, blast searches revealed that only one of *P. roborovskii* sequences shares similarity with a known repetitive sequence, a chromosome-specific satellite DNA of the Chinese hamster (*Cricetulus griseus*, Cricetinae). The remaining sequences seem to correspond to new repetitive DNA elements, isolated for the first time in this work. All the sequences were physically mapped by fluorescent in situ hybridization on chromosomes of species of origin. C banding performed after in situ hybridization revealed that hybridization patterns of these sequences are consistent with the distribution of C-positive bands. Here, we present results that show different and diverse chromosomal distributions of these sequences: some of them are almost chromosome-specific, while some are distributed genome-wide, displaying (peri)centromeric, interstitial or telomeric locations in several autosomal pairs and/or sex chromosomes.

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