zero-crossing structure of the stimuli, we do not mean to imply that zero-crossings are explicitly represented. Other descriptions of the pattern structure are possible (including the centroids of zero-bounded regions[5]), and we have no doubt that the positions of peaks of local energy[14] would give a similar picture. The critical question is whether d_{max} is determined by the statistical structure of the pattern, and if so, at what spatial scale or scales. Bex *et al.* do not provide a quantitative model of d_{max} based on 'motion energy', and until one is available it would be premature to reject an existing model that has made some successful predictions.

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Mariner transposons in humans

SIR — The *mariner-Tc1* gene superfamily represents a diverse collection of DNA-based transposable elements with broad phylogenetic distribution[1]. We have now identified two *mariner* transposons in the human genome which share both structural and sequence similarity to elements previously described in arthropods, nematodes and planaria[1–3]. The two human elements are members of divergent *mariner* subfamilies, suggesting multiple instances of horizontal transfer of these elements into the human genome.

Mariner elements, first described in *Drosophila*[4], consist of a transposase gene flanked by two short terminal inverted repeats. This structure is similar to a variety of other DNA-based transposable elements[5], including the *Ac* element in maize. The autonomous *Ac* elements are associated with a family of non-autonomous *Ds* elements[6]. Whereas *Ac* and *Ds* elements are defined by the same 11-base-pair (bp) inverted repeats, the *Ds* elements vary considerably in both size and internal sequence. Small, divergent, non-autonomous elements that share sequence similarity with the autonomous forms only within the terminal inverted repeats are a commonly observed feature in DNA-based transposons[5].

The human *mariner* transposons were detected by identifying two families of putative non-autonomous transposons in the genome. These elements were identified as short, conserved, inverted repeated domains present in multiple loci[7]. The members of the first of these families are defined by a 45-bp inverted repeated domain designated *hum1* (*a* in the figure). Small putative transposable elements can be easily identified in a variety of human genes by screening the available databases with the consensus *hum1* repeat[8]. Two oligonucleotide primers were designed using this repeat, and used to direct two rounds of polymerase chain reaction (PCR) amplification with human genomic DNA as a template. A 1.4-kilobase amplification product from these reactions was sequenced and found to be a *mariner* transposable element, designated *humar1* (GenBank locus HSU38613; *b* in the figure). The same element has also been cloned from a human genomic library using *humar1* PCR product sequences as probes.

The structure of *humar1* is similar to previously described *mariner* elements. As shown in the figure (*b*), the *hum1* repeats defining the element flank smaller (29 bp) imperfect inverted repeated domains. We have sequenced two additional genomic clones containing *humar1* elements (GenBank loci HSU38614 and HSU38615) which are defined only by the internal 29-bp repeats and lack the *hum1* domains. This suggests that the internal repeats represent the authentic terminal repeats of this transposon. The transposase pseudogene is interrupted by four frameshifts and numerous stop codons. The deduced amino-acid sequence of the transposase is similar to that of the *mariner* transposase from lacewing (*Chrysoperla plorabunda*; PIR locus S36925), indicating that this element is a member of the irritans subfamily of *mariner* elements[9].

We have identified a second human *mariner* element, a member of a second subfamily. Similar to *humar1*, this element was found by first identifying a second family of small, putative, non-autonomous transposons defined by inverted repeated domains (designated *hum7*, consensus inverted repeated domain sequence: TGGTGCAAAAGTAATGCAGTTTT-TGCCA)*. When this sequence was used as a database query[8], one of the returned sequences (GenBank locus HUMTCRB, positions 495,300–497,513) was found to contain a *mariner* element defined by two *hum7* repeats. The DNA sequence of the transposase pseudogene at this locus is interrupted by four frameshifts, numerous stop codons and a 950-bp insertion. The deduced amino-acid sequence of the putative transposase is similar to that of a planarian (*Dugesia tigrina*) *mariner* transposase (GenBank locus DTPM9), suggesting that this element is derived from the cecropia subfamily of *mariner* elements[9].

The two *mariner* elements described here represent two divergent subfamilies, consistent with multiple horizontal transfer events involving *mariner* transposons[1]. We have not yet identified intact (mobile) human *mariner* elements, which would represent potential sources of transformation vectors.

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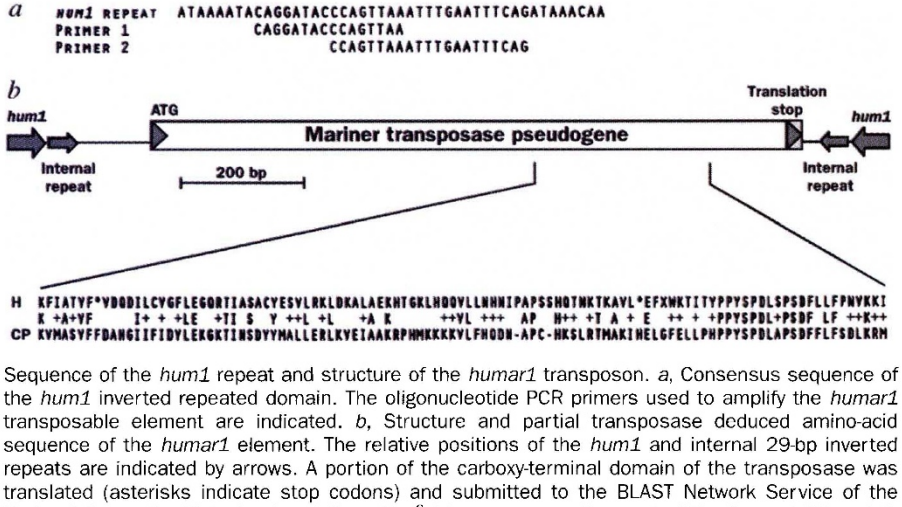

Sequence of the *hum1* repeat and structure of the *humar1* transposon. *a*, Consensus sequence of the *hum1* inverted repeated domain. The oligonucleotide PCR primers used to amplify the *humar1* transposable element are indicated. *b*, Structure and partial transposase deduced amino-acid sequence of the *humar1* element. The relative positions of the *hum1* and internal 29-bp inverted repeats are indicated by arrows. A portion of the carboxy-terminal domain of the transposase was translated (asterisks indicate stop codons) and submitted to the BLAST Network Service of the National Center for Biotechnology Information[8]. The sequence alignment of the *humar1* (H) and *C. ploribunda* (CP) transposase was returned. Positions of identity are shown; + indicates a conservative change.

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*During the preparation of this manuscript, we became aware that the *humar7* element described here was also identified by Hugh Robertson, University of Illinois, using *mariner*-transposase-specific sequences (H. M. Robertson, personal communication), and that partial *mariner* transposase sequences have been reported[10].