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Y: waving, not drowning

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The human Y chromosome contains 60 million base pairs (Mb) of DNA, it is haploid, and 95% of it is nonrecombining. Helen Skaletsky from the Whitehead Institute for Biomedical Research and colleagues report in the first of two papers in the June 19 Nature that the 23Mb euchromatic region in the Y chromosome comprises eight massive palindromic sequences and that these regions are rich in genes that are functional and testis-specific (*Nature* 2003*,* **423:**825-837.

In the second paper, they describe both comparative sequencing of the great ape Y chromosome, and the mechanism of gene conversion by which the Y chromosome repairs mutations that occur within these genes (*Nature* 2003, **423:**873-876). The results raise important questions about the molecular clock dating of segmental duplications in the human genome and the rate of human-chimpanzee divergence in these regions.

Skaletsky *et al.* sequenced 97% of the male-specific region of the Y chromosome (MSY) from one man, and observed that it contained at least 156 transcription units, all located within euchromatic sequences, and identified 24 MSY-specific families to account for 125 of these. Half of the transcription units encode 27 distinct proteins or protein families, 12 of which are expressed ubiquitously, and 11 of which are testis-specific, confirming a previous model proposing two distinct functional classes of MSY genes.

They also showed that three different classes of sequences comprised the euchromatin: the X-transposed class, the X-degenerate class, and the ampliconic segments, the latter being composed of sequences that demonstrated intrachromosomal identities of at least 99.9%, and which contained the eight palindromic segments. The palindrome arms range from 9 kb to 1.4 Mb, are symmetrical and identical within a palindrome, and six of them contain the testis-specific genes as gene pairs in the palindromic arms, as well as inverted repeats and long tandem arrays. In the light of these findings, Skaletsky *et al.* propose a model for the evolution of the MSY.

"The occurrence of MSY gene pairs that are subject to frequent gene conversion might provide a mechanism for conserving gene functions across evolutionary time in the absence of crossing over," conclude the authors, debunking the previously held theory of the Y as a genetic wasteland of dead and dying genes that will rot away over the next few million years. "We have a new way of understanding how the rotting tendencies of the Y are counteracted," commented lead researcher David Page.

"Although the sex chromosomes provide the strongest case for a special relationship between genome organization and the unique biology of chromosomes, the other chromosomes shouldn't feel left out. […] Piecing together these [evolutionary] events remains a worthwhile challenge, for among the flotsam and jetsam of each chromosome lie clues to our history," writes Huntington F. Willard of Duke University in an accompanying News and Views article.

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