Kremer H, Pinckers A, Van den Helm B, Deutman AF, Ropers HH, Mariman ECM (1994) Localisation of the gene for dominant cystoid macular dystrophy on chromosome 7p. Hum Mol Genet 3:299–302

Moore AT, Fitzke FW, Jay MR, Arden GB, Inglehearn CF, Keen TJ, Bhattacharya SS, et al (1993) Autosomal dominant retinitis pigmentosa with apparent incomplete penetrance: a clinical, electrophysiological, psychophysical and molecular genetic study. Br J Ophthalmol 77:473–479

Nichols BE, Sheffield VC, Vandenburgh K, Drack AV, Kimura AE, Stone EM (1993) Butterfly-shaped pigment dystrophy of the fovea caused by a point mutation in codon 167 of the Rds gene. Nature Genet 3:202–207

Wells J, Wroblewski J, Keen TJ, Inglehearn CF, Jubb C, Eckstein A, Jay MR, et al (1993) Mutations in the human retinal degeneration slow (RDS) gene can cause either retinitis pigmentosa or macular dystrophy. Nature Genet 3:213–218

0002-9297/94/5503-0020$2.00

Am. J. Hum. Genet. 55:582–583,1994

The Exact Numbers of Possible Microsatellite Motifs

To the Editor:

Microsatellites can be defined as tandemly repeated DNA with lengths of repeat units of ≤6 bp (Litt and Luty 1989; Beckmann and Weber 1992). Microsatellites have been shown to be very useful in gene mapping (e.g., see Weber and May 1989; Weissenbach et al. 1992), because of their high abundance, widespread distribution, and high heterozygosities in the genomes of various organisms (Stalling et al. 1991).

Several efforts have been made to study the distributions and frequencies of microsatellites in the genomes of various organisms by searching the existing GenBank sequences (Weber and May 1989; Weber 1990; Beckmann and Weber 1992; Kalaitsidaki et al. 1992). This is even more important for trinucleotide repeat sequences, since several diseases (e.g., fragile X syndrome, Huntington disease, etc.; Riggins et al. 1992) have now been described to be due to triplet expansions. However, the numbers of possible microsatellite motifs (repeats) in several publications are inconsistent with each other (Edwards et al. 1991; Beckmann and Weber 1992; Kalaitsidaki et al. 1992), and this may raise questions on the accuracy of the results of such study. For example, Beckmann and Weber (1992) stated that there are 10 trinucleotide motifs and 32 tetranucleotide motifs, while Kalaitsidaki et al. (1992) showed that there are 14 possible trinucleotide motifs and 56 tetranucleotide motifs. Here we give the exact number of possible microsatellite motifs and list all those motifs for mono-, di-, tri-, tetra-, and pentanucleotide microsatellite loci.

Theoretically, there are 4, 16, 64, 256, 1,024, and 4,096 possible motifs for mono-, di-, tri-, tetra-, penta-, and hexanucleotide repeats, respectively. However, because microsatellites are tandemly repeated, some motifs are actually equivalent to others. Two rules can be used to identify whether motif A is equivalent to motif B. Motif A is considered equivalent to motif B when (1) motif A is inversely complementary to motif B or (2) motif A is different from motif B or the inversely complementary sequence of motif B by frameshift. For example, $(GAAA)_n$ is equivalent to $(AGAA)_n$ or $(AAGA)_n$, to $(AAAG)_n$ or $(TTTC)_n$, to $(TTCT)_n$ or $(TCTT)_n$, or to $(CTTT)_n$. In other words, the eight motifs are equivalent. Note that $(AGAG)_n$ is considered a dinucleotide motif instead of a tetranucleotide motif, and the same logic is used to identify the motifs in this report.

The repeat units and the numbers (in parentheses) of possible mono-, di-, tri-, tetra-, and pentanucleotide motifs are listed in the Appendix. The "alphabetically minimal" form of listing, followed in this Appendix, is recommended for a general description of microsatellite repeats, since it provides uniformity of nomenclature. Furthermore, homology of repeats at different disease loci (e.g., CCG in the FRAXA locus vs. GGC in the FRAXE locus) may be traced by adopting the nomenclature used in this Appendix. The number of hexanucleotide motifs is 350, but the repeat units are not listed because of the space limit (it is available on request). Likewise, theoretical numbers of different hepta- and octanucleotide repeat motifs would be 1,170 and 4,140, respectively.

LI JIN, YIXI ZHONG, AND RANAJIT CHAKRABORTY
Center for Demographic and Population Genetics
Graduate School of Biomedical Sciences
University of Texas at Houston Health Science Center
Houston

Acknowledgments

This research was supported by U.S. Public Health Service research grants GM 41399 and GM 45816 from the U.S. National Institutes of Health and by grant 92-IJ-CX-K024 from the National Institute of Justice.

Appendix

List of Possible Microsatellite Motifs

Mononucleotide motif (2):

A	C

Dinucleotide motif (4):

AC	AG	AT	CG

Trinucleotide motif (10):

AAC	AAG	AAT	ACC	ACG	ACT	AGC	AGG
ATC	CCG						

Tetranucleotide motif (33):

AAAC	AAAG	AAAT	AACC	AACG	AACT	AAGC	AAGG
AAGT	AATC	AATG	AATT	ACAG	ACAT	ACCC	ACCG
ACCT	ACGC	ACGG	ACGT	ACTC	ACTG	AGAT	AGCC
AGCG	AGCT	AGGC	AGGG	ATCC	ATCG	ATGC	CCCG
CCGG							

Pentanucleotide motif (102):

AAAAC	AAAAG	AAAAT	AAACC	AAACG	AAACT	AAAGC	AAAGG
AAAGT	AAATC	AAATG	AAATT	AACAC	AACAG	AACAT	AACCC
AACCG	AACCT	AACGC	AACGG	AACGT	AACTC	AACTG	AACTT
AAGAC	AAGAG	AAGAT	AAGCC	AAGCG	AAGCT	AAGGC	AAGGG
AAGGT	AAGTC	AAGTG	AATAC	AATAG	AATAT	AATCC	AATCG
AATCT	AATGC	AATGG	AATGT	AATTC	ACACC	ACACG	ACACT
ACAGC	ACAGG	ACAGT	ACATC	ACATG	ACCAG	ACCAT	ACCCC
ACCCG	ACCCT	ACCGC	ACCGG	ACCGT	ACCTC	ACCTG	ACGAG
ACGAT	ACGCC	ACGCG	ACGCT	ACGGC	ACGGG	ACGTC	ACTAG
ACTAT	ACTCC	ACTCG	ACTCT	ACTGC	ACTGG	AGAGC	AGAGG
AGATC	AGATG	AGCAT	AGCCC	AGCCG	AGCCT	AGCGC	AGCGG
AGCTC	AGGAT	AGGCC	AGGCG	AGGGC	AGGGG	ATATC	ATCCC
ATCCG	ATCGC	ATGCC	CCCCG	CCCGG	CCGCG		

References

Beckmann JS, Weber JL (1992) Survey of human and rat microsatellites. Genomics 12:627–631

Edwards A, Civitello A, Hammond HA, Caskey CT (1991) DNA typing and genetic mapping with trimeric and tetrameric tandem repeats. Am J Hum Genet 49:746–756

Kalaitsidaki M, Cox T, Chakravarti A, Antonarakis E (1992) Cloning and linkage mapping of three polymorphic tetranucleotide $(TAAA)_n$ Repeats on human chromosome 21. Genomics 14:1071–1075

Litt M, Luty JA (1989) A hypervariable microsatellite revealed by in vitro amplification of a dinucleotide repeat within the cardiac muscle actin gene. Am J Hum Genet 44:397–401

Riggins GL, Lokey LK, Chastain JL, Leiner HA, Sherman SL, Wilkinson KD, Warren ST (1992) Human genes containing polymorphic trinucleotide repeats. Nature Genet 2:186–191

Stallings RL, Ford AF, Nelson D, Torney DC, Hildebrand CE, Moyzis RK (1991) Evolution and distribution of $(GT)_n$ repetitive sequences in mammalian genomes. Genomics 10:807–815

Weber JL (1990) Informativeness of human $(dC\text{-}dA)_n$-$(dG\text{-}dT)_n$ polymorphisms. Genomics 7:524–530

Weber JL, May PE (1989) Abundant class of human DNA polymorphisms which can be typed using the polymerase chain reaction. Am J Hum Genet 44:388–396

Weissenbach J, Gyapay G, Dib C, Vignal A, Morissette J, Milasseau P, Vaysseix G, et al (1992) A second-generation linkage map of the human genome. Nature 359:794–801

0002-9297/94/5503-0021$2.00

Am. J. Hum. Genet. 55:583–585, 1994

The Y-associated XY275G (*Low*) Allele Is Common among the Portuguese

To the Editor:

In previous issues of the *Journal,* two sets of haplotype and genotype data at the pseudoautosomal XY275 polymorphic site have been reported that presented alternative views of the origin and spread of modern man. Ellis et al.