ON INVERTED REPEAT SEQUENCES IN CHROMOSOMAL DNA

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ABSTRACT

It is suggested that chromosomal DNA should contain a class of palindromic reverse repeats, comparable in number to that of genes themselves, which are formed as follows: (1) a transcription-termination signal that follows the gene plus (on the complementary strand and located as near to the "anti-gene" as possible); (2) a second termination signal which actively prevents the accidental transcription of the anti-gene. Thus, the adjacent termination-anti-termination region of one strand would complement the anti-termination-termination region of the other.

IN an exceptionally fine study, SCHMID, MANNING and DAVIDSON (1975) report that genome of *Drosophila melanogaster* contains 2000–4000 inverted repeat pairs. Their techniques, as they point out, do not permit them to infer the function of these regions which are also known as "palindromes".

Certain functions, on the other hand, have seemingly called for the existence of palindromes. WALLACE and KASS (1974), for example, were forced by a model they developed to postulate the existence of overlapping palindromes in gene control regions in order that transcription initiation sites might move about within these regions with little risk of being excised and lost. They were also forced by their model to suggest that transcription initiation sites themselves are palindromic; this suggestion was demanded by the rotation of these sites that occurs whenever they change position within gene control regions.

We would like to point out the need for still another class of palindromes in the chromosomes of higher organisms; the number of palindromes described here could compare with that of genes, themselves.

If a gene occupies one strand of the chromosomal DNA, the complementary strand carries what might be called an "anti-gene". Following the gene, there must be a section of DNA carrying a transcription termination signal; preceding the anti-gene on the other strand, then, would be a corresponding "anti-termination" segment.

In order that the anti-gene not be transcribed in error, it should also be preceded by a termination signal. If this signal is far removed from the anti-gene, spontaneous rearrangements within the genome would frequently separate the anti-gene from its protective terminator, thus allowing the anti-gene's (meaningless) transcription. Consequently, the protective terminator should be close to the anti-gene, thus making the accidental separation of the two highly unlikely.

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Assuming that the transcription termination signal is constant for a species, the above argument leads to the prediction that many, if not most, genes should be followed by a termination-anti-termination palindrome as shown below; this is true whether or not the cruciform configuration of palindromic DNA plays a special role in transcription termination:

gene	termination	anti-termination
anti-gene	anti-termination	termination

These should number in the thousands; depending upon the extent to which termination signals are juxtaposed to anti-genes, there may or may not be non-palindromic spacers found in these post-gene inverted repeat sequences.

LITERATURE CITED

Schmid, C. W., J. E. Manning and Norman Davidson, 1975 Inverted repeat sequences in the Drosophila genome. Cell **5:** 159–172.

Wallace, Bruce and T. L. Kass, 1974 On the structure of gene control regions. Genetics **77:** 541–558.

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