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Edwin Southern is Whitley Professor of Biochemistry in the University of Oxford, a post he has held since 1985.

Previously, he worked in the Medical research Council (MRC) Mammalian Genome Unit in Edinburgh for eighteen years, first as a Research Assistant and then as Director. He was also Associate Director of the Clinical and Population Cytogenetics Unit. His major research has been in the analysis of sequences in mammalian genomes. In 1970, he sequenced the major satellite of the guinea pig, which turned out subsequently to be derived from the now familiar telomeric repeat.

In 1975, he published the first of the "blotting" methods for testing for the presence of specific sequences among nucleic acid fragments separated by gel electrophoresis. In recent years, he has maintained his long-standing interest in genome analysis and contributed methods, based on oligonucleotide arrays, for the analysis of sequence variation and for antisense reagent development.

Microarrays for basic studies of nucleic acid hybridization and selection of antisense reagents

Microarrays of oligonucleotides which represent the complete set of complements to a target RNA are readily made by a simple automated method. These 'scanning' arrays can be used for basic studies of the hybridization reaction, which is the basis of all microarray techniques. We have studied the influence of secondary and tertiary structure in the RNA and found that it is mainly this which determines the extent of hybridization, rather than base composition or sequence. We also find that the folded structure is formed during transcription process, which indicates that computer-based prediction of RNA folding by finding the structure with the minimum global free energy is over-simple.

In addition to these fundamental studies, 'scanning' arrays are useful for the selection of antisense reagents, which are increasingly used for gene ablation to discover the functions of genes emerging from sequencing programmes. Antisense methods are very simple, but only a fraction of potential sequences provide effective targets. These can be found by hybridization of the transcript to a complete set of complements represented on the array.