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Brenda F. Baker^a

^a Isis Pharmaceuticals, Inc., Carlsbad, California, U.S.A.

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THE ROLE OF ANTISENSE OLIGONUCLEOTIDES IN THE WAVE OF GENOMIC INFORMATION

Brenda F. Baker

Isis Pharmaceuticals, Inc., 2292 Faraday Avenue,
Carlsbad, California 92008

ABSTRACT

Technologies which efficiently dissect gene function and validate therapeutic targets are of great value in the post-sequencing era of the human genome project. The antisense oligonucleotide approach can directly use genomic sequence information, in a relatively time and cost effective manner, to define a gene's function and/or validate it as a potential therapeutic target. Antisense oligonucleotide inhibitors of gene expression may be applied to cellular assays (*in vitro*) or animal models of disease (*in vivo*). Information generated by this approach may then direct or supplement traditional drug discovery programs, or support development of the antisense oligonucleotide inhibitor, used to validate the target, as a drug.

Significant progress in the chemical synthesis and biological applications of modified antisense oligonucleotides (ASOs) in the last decade has yielded a technology which has the potential to play a pivotal role in decoding the underlying function of the wave of genetic information now available (1–3). Through direct usage of sequence, this technology may be used to determine the function of genes in the context of cell processes (4) and pathological conditions (5), as well as identify and validate targets for future therapeutics.

The ASO opportunity is supported by those oligonucleotide modifications which have proven to impart greater nuclease resistance, enhance RNA hybridization, and have suitable bioavailability and pharmacokinetic profiles. These attributes, in conjunction with the development of multiple modes of administration, have allowed broad usage and characterization of this class of compounds *in vitro* (6) and *in vivo* (6–9).

Biological applications are now further facilitated by the ease of synthesis and identification of antisense oligonucleotides that sequence specifically reduce target messenger RNA levels (10). Evolution of automated oligonucleotide synthesis and the process of ASO lead identification has lead to a rapid turn around time (days) from design to application, and consequently the ability to quickly sift through a relatively high volume of sequence space.

The sequence fidelity of the ASO technology allows for regulation of a single gene from a family of genes (11, 12) or a single ribotype (13) from one gene (14, 15). Oligonucleotides which sterically interfere (16) with the processes of mRNA metabolism, *e.g.* splicing (17, 18) and translation (19, 20), provide the opportunity to determine and direct gene function that is regulated at the RNA level.

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