7. J. J. Wolosewick and K. R. Porter, *ibid.* **82**, 114 (1979); J. Heuser and M. W. Kirschner, *ibid.* **86**, 212 (1980); M. Schliwa, K. B. Pryswansky, J. Van Blerkom, *Philos. Trans. R. Soc. London Ser. B* **299**, 199 (1982).
8. W. W. Graessley, *J. Chem. Phys.* **43**, 2696 (1965); *ibid.* **47**, 1942 (1967).
9. R. B. Bird, R. C. Armstrong, O. Hassenagen, *Dynamics of Polymeric Liquids* (Wiley, New York, 1977), vol. 1.
10. L. I. Rebhun, *Int. Rev. Cytol.* **32**, 92 (1972).
11. N. Kamiya, *Annu. Rev. Plant Physiol.* **32**, 205 (1981).
12. E. M. Purcell, *Am. J. Phys.* **45**, 3 (1977).
13. M. Willard, W. M. Cowan, P. R. Vagelos, *Proc. Natl. Acad. Sci. U.S.A.* **71**, 2183 (1974); P. N. Hoffman and R. J. Lasek, *J. Cell Biol.* **66**, 351 (1975).
14. M. W. Denny and J. M. Gosline, *J. Exp. Med.* **88**, 375 (1980).
15. S. MacLean-Fletcher and T. D. Pollard, *J. Cell Biol.* **85**, 414 (1980).
16. M. Doi and S. F. Edwards, *J. Chem. Soc. Faraday Trans. 2* **74**, 560 (1978).
17. S. Jain and C. Cohen, *Macromolecules* **14**, 759 (1981).
18. P. W. Anderson, *Basic Notions in Condensed Matter Physics* (Benjamin-Cummings, Menlo Park, CA, 1984), pp. 159–164.
19. J. A. Spudich and S. Watt, *J. Biol. Chem.* **246**, 4866 (1971); S. MacLean-Fletcher and T. D. Pollard, *Biochem. Biophys. Res. Commun.* **96**, 18 (1980).
20. M. L. Shelanski, F. Gaskin, C. R. Cantor, *Proc. Natl. Acad. Sci. U.S.A.* **70**, 765 (1973).
21. J. Meissner, *J. Appl. Polym. Sci.* **16**, 2877 (1972).
22. P. A. Valberg and D. F. Albertini, *J. Cell Biol.* **101**, 130 (1985).
23. I. Nemoto, *IEEE Trans. Biomed. Eng.* **29**, 745 (1982).
24. K. P. Sung *et al.*, *Biophys. J.* **39**, 101 (1982).
25. Y. Hiramato, *Exp. Cell Res.* **56**, 201 (1969).
26. M. King and P. T. Macklem, *J. Appl. Physiol. Respir. Environ. Exercise Physiol.* **42**, 797 (1977).
27. M. Sato, T. Z. Wong, R. D. Allen, *J. Cell Biol.* **97**, 1089 (1983).
28. F. H. C. Crick and A. F. W. Hughes, *Exp. Cell Res.* **1**, 37 (1950).
29. K. Yagi, *Exp. Biochem. Physiol.* **3**, 73 (1961).
30. We thank J. Sethna and D. Berry for alerting us to important modeling work, K. Jayaraman for the use of his equipment, C. Cohen and J. Condeelis for stimulating conversations, and J. R. McIntosh for comments on the manuscript. S.R.H. thanks J. Condeelis for the hospitality in his laboratory. Supported by NSF grant BNS 8401904. S.R.H. is a recipient of a Research Career Development Award from the National Institutes of Health.

21 August 1986; accepted 30 December 1986

Two Mammalian Genes Transcribed from Opposite Strands of the Same DNA Locus

JOHN P. ADELMAN, CHRIS T. BOND, JAMES DOUGLASS, EDWARD HERBERT*

This report describes the characterization of a genomic locus in the rat that encodes overlapping genes occupying both strands of the same piece of DNA. One gene (strand) encodes gonadotropin-releasing hormone (GnRH). A second gene, SH, is transcribed from the other DNA strand to produce RNA of undefined function. The RNAs transcribed from each DNA strand are spliced and polyadenylated, and share significant exon domains. GnRH is expressed in the central nervous system while SH transcripts are present in the heart. Thus, the genome of a mammalian organism encodes two distinct genes by using both strands of the same DNA.

INHERENT TO THE CONCEPT OF A EUkaryotic gene is that the function of the DNA strand opposite the transcribed strand is to serve as a necessary conduit for double-stranded, semiconservative DNA replication. Likewise, although the discovery of introns brought about modifications in the concept of genes as linear discrete units along the chromosome, introns have been regarded as raw genetic material susceptible to high levels of evolutionary drift with regard to nucleotide sequence and even to size fluctuation. Exons have been regarded as the biologically relevant portions of a gene, existing under varying degrees of selective pressure, reflective of the relative advantage they confer upon the organism possessing the particular allele. However, a number of recent reports have indicated a need to reexamine these concepts. The *Gart* locus of *Drosophila melanogaster*, known to encode three purine pathway enzymatic activities, has been shown to contain an entire gene encoding a cuticle protein, "nested," within the first *Gart* intron and transcribed from the opposite DNA strand (*1*). The cuticle protein gene itself is divided by an intron. Another Drosophila locus, encoding dopa decarboxylase, has been shown to share an 88-bp region at its 3′ end with the 3′ end of a transcript arising from an unknown gene on the opposite strand (*2*). A comparable situation has been described for a region of mouse DNA from tissue culture cells, BALB/cTS-A-3T3, which encodes two 3′ overlapping transcripts of undetermined functions (*3*). The data presented here extend these observations to describe the virtual cohabitation of a genomic locus within mammalian DNA by two distinct genes. Both DNA strands serve as templates for transcription, and the resulting polyadenylated [poly(A)$^+$] RNAs contain a significant amount of shared exonic sequences.

The gonadotropin-releasing hormone (GnRH) gene is a single-copy gene exhibiting a similar arrangement of four exons in both rats and humans (*4*). In the maturation of human placental preproGnRH messenger RNA (mRNA), the first intron is not removed and thus the human placental GnRH mRNA possesses an exceptionally long 5′ untranslated region (*5*). During experiments to characterize the hypothalamic form of GnRH mRNA, human placental GnRH complementary DNA (cDNA) was nick-translated and used as a hybridization probe to screen rat hypothalamic cDNA clones. DNA sequence analysis demonstrated that ten of the clones showing hybridization to this probe represented the hypothalamic form of preproGnRH mRNA. Surprisingly,

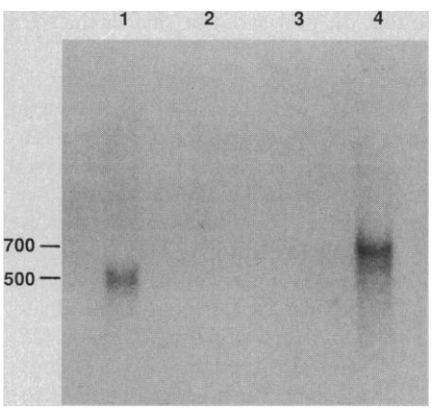

Fig. 1. Northern analysis of rat hypothalamic and heart poly(A)$^+$ RNA. Duplicate samples of heart (lanes 2 and 4) and hypothalamic (lanes 1 and 3) poly(A)$^+$ RNAs were prepared as a Northern blot and probed with an SP6-generated GnRH (lanes 1 and 2) or SH (lanes 3 and 4) strand-specific probe. In control hybridizations to M13 template DNAs of defined sequence the SP6 probes were shown to be completely strand-specific. Size markers are indicated to the left. Total cellular RNA was prepared from the indicated rat tissues by the guanidinium/CsCl method (*27*) and poly(A)$^+$ RNAs selected on oligo(dT)-cellulose. Glyoxal-denatured poly(A)$^+$ RNA (2.5 μg per lane) was fractionated on a 1.4% agarose gel, run in 10 m*M* $NaPO_4$ (*p*H 6.7) (*28*), and subsequently transferred to Nytran. SP6 strand-specific RNA probes were generated as described (*7*). Probes were labeled to a specific activity of 5×10^8 counts per minute per microgram of RNA. Blots were probed at 60°C in standard hybridization solution in the presence of 50% formamide. Filters were washed in .07× standard saline citrate/5 m*M* EDTA/0.5% SDS at 70°C and exposed to x-ray film for 10 hours.

The Institute for Advanced Biomedical Research, Oregon Health Sciences University, 3181 S.W. Sam Jackson Park Road, Portland, OR 97201.

*This work is dedicated to the memory of Edward Herbert.

one hybridizing clone of 250 bp, SH-0, represented a poly(A)$^+$ RNA that had been derived from a sequence within the intron between the exons (1 and 2) that code for hypothalamic GnRH mRNA (*6*). The location of a poly(A) tail, preceded 26 bp upstream by an AAUAAA polyadenylation signal sequence, indicated that the RNA represented by SH-0 was transcribed from the DNA strand opposite that used to generate the GnRH mRNA.

To examine whether the preproGnRH and SH clones represent full-length RNAs and to determine the tissue distribution of the transcripts defined by the two types of hypothalamic cDNA clones, the GnRH and SH cDNA sequences were subcloned into SP6 vectors. SP6-derived RNA probes are produced as unidirectional, single-stranded RNAs (*7*) and allow the detection of strand-specific RNAs when used to probe Northern blots. Hybridizations were performed with either probe on Northern blots prepared with poly(A)$^+$ RNA isolated from a spectrum of rat brain and peripheral tissues. PreproGnRH mRNA was detected in a variety of central nervous system areas, including the hypothalamus (Fig. 1). The size of the GnRH mRNA in the hypothalamus was ~500 bases, in agreement with previous estimates (*4*).

In contrast, a positive signal was observed only when an RNA probe, derived from SH-0 and specific for the SH RNA, was used with rat heart poly(A)$^+$ RNA (Fig. 1). The size of the hybridizing RNA was 650–750 nucleotides, significantly different from the size of either placental (~1500 bases) or brain (~500 bases) preproGnRH mRNA (*4, 5*). This Northern analysis also suggested the presence of multiple species of heart SH transcripts of similar size. Although the SH probe was initially derived from a hypothalamic cDNA clone, it remains to be determined why no hybridization signal was seen in poly(A)$^+$ RNA isolated from brain tissues.

Next, rat heart poly(A)$^+$ RNA was used to construct a cDNA library in λ phage. Eight clones showed hybridization to the SH-0 probe and DNA sequence analysis of the inserts revealed three distinct populations of cDNA clones. The RNA represented by the SH-4 cDNA (Figs. 2 and 3)

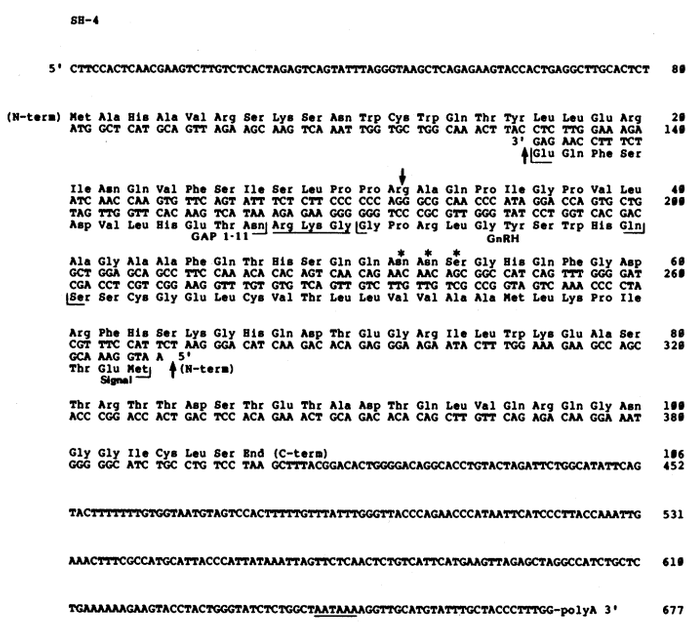

Fig. 2. Nucleotide sequences of SH cDNAs as isolated from rat heart tissue. The complementary nucleotide strand and amino acid sequence of preproGnRH is shown below the SH sequence in regions that serve as exons in both genes. Dots in the GnRH sequences indicate the continuation of the GnRH exon beyond the sequence found in the SH-1 or SH-2 cDNAs. The different functional domains of the GnRH precursor are indicated. Arrows indicate interruptions due to introns in the corresponding genomic DNA sequence. The polyadenylation signal sequence, AATAAA, is underlined. The arrow in the SH-4 sequence indicates the splice junction used as an acceptor site in the other classes of SH cDNA clones. A postulated glycosylation site (*9*) in the translated SH-4 sequence is indicated by asterisks. The Gly-Lys-Arg sequence used in proteolytic cleavage of preproGnRH and COOH-terminal amidation of the GnRH decapeptide (*4*) is underlined. An analysis of sequences involved in SH precursor RNA processing is shown underneath the SH-2 sequences. Nucleic acid strand polarity is indicated. Nucleotide sequences around splice donor sites in the SH-1 and SH-2 clones conform entirely to published consensus sequences (*10*), while the 3′ end of the intron sequence varies at only two of six positions. Polyadenylated RNA (5 μg) from rat heart tissue was converted into double-stranded cDNA by standard procedures (*4*), except that a specific cDNA size cut of 500 to 1200 bp was taken for cloning from a 6% acrylamide gel. The eluted cDNA was cloned with λgt10 as a vector as described (*29*). Recombinant phage (10^6) were screened with an SP6-derived probe specific for SH sequences. The probe was labeled to a specific activity of 5×10^8 counts per minute per microgram of RNA. Eight hybridizing λ clones were isolated and found to contain inserts of 600 to 750 bp. These cloned cDNAs were sequenced with single-stranded recombinant M13 DNA as template for primed DNA synthesis in the presence of dideoxynucleoside triphosphates (*30, 31*).

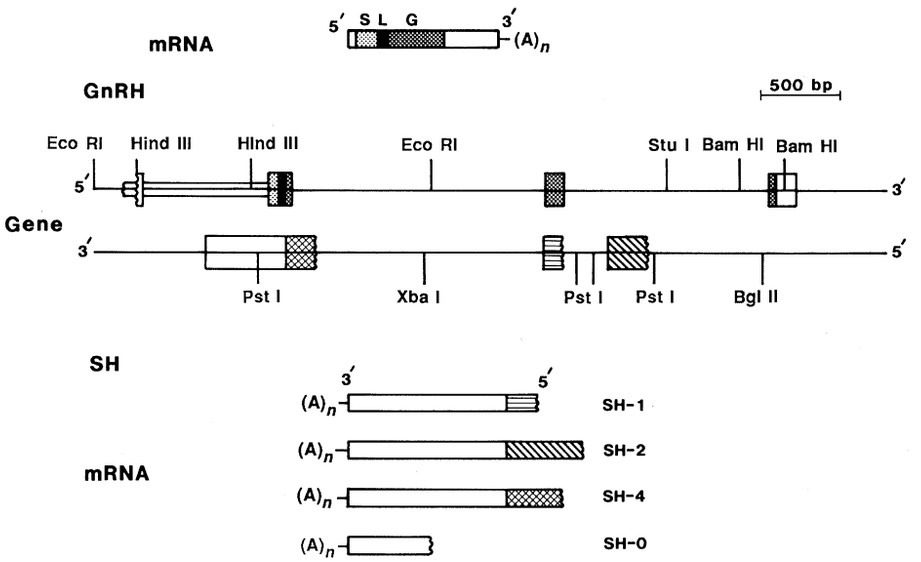

Fig. 3. Structure and restriction map of the GnRH-GAP:SH gene from rat. The information shown is derived from nucleotide sequences of the genomic locus (*4, 6*), and from cDNA nucleotide sequences (*4, 5*). Boxed areas are RNA-coding exons. The joining of exons from each gene, GnRH or SH, to yield the different RNAs is schematically represented. The open box 5′ to exon II in the GnRH gene corresponds to the 5′ untranslated sequence in the human placental GnRH mRNA. The coding regions that correspond to the precursor domains of signal sequence (S), LHRH or GnRH (L), and GAP (G) have the same shading in the gene and the GnRH RNAs. Likewise the SH coding regions are shaded alike in the gene and corresponding mRNAs. Wavy lines indicate that the exact 5′ nucleotide of the exon is not known. Note the different scale for gene and cDNA; bp, base pairs.

contains the entire sequence of the SH-0 clone and extends this sequence through the exon that encodes the GnRH precursor signal peptide, the GnRH decapeptide, and the initial 11 amino acids of GnRH-Associated Peptide (GAP). The cDNA insert is 673 bases long and is colinear with the gene sequence. The RNA identified by the SH-4 clone contains an open reading frame capable of encoding a peptide of 106 amino acids. The putative reading frame begins with the most 5′ AUG at nucleotide 77 and terminates with an ochre stop codon, UAA. The stop codon is followed by 276 nucleotides of a 3′ untranslated region, which contains an AAUAAA polyadenylation signal sequence (*8*) 26 nucleotides upstream of the poly(A) site. There is one possible site for *N*-glycosylation (Asn-X-Thr/Ser) (*9*) at amino acids 52–54. The sequence of the putative peptide shows no homology with any known protein.

The SH-1 cDNA clone contains the same 3′ nucleotide sequence that is present in the SH-4 sequence. However, an intron of ~1600 nucleotides is spliced from SH precursor RNA joining a 126-bp sequence from an upstream exon to the 3′ nucleotides shared by the SH-4 and SH-1 RNAs (Fig. 2). The upstream exon is encoded by DNA that contains exon 3 of the GnRH gene on the opposite DNA strand (Fig. 3). The SH-1 cDNA is 630 nucleotides in length and contains two of the protein-coding exons of the GnRH gene.

The SH-2 cDNA, 766 bp in length, shares the same 3′ sequences with SH-4 and SH-1 (Figs. 2 and 3). However, a different upstream exon, which is transcribed from a region of DNA 300 bases upstream of the start of the SH-1 sequence, is spliced to the common 3′ sequence. This DNA is part of an intron between GnRH exons 3 and 4, on the opposite DNA strand. As shown in Fig. 2, the splice acceptor junction is identical for the RNAs represented by clones SH-1 and SH-2 and the nucleotide sequence surrounding splice donor and acceptor sites is in excellent agreement with published consensus sequences (*10*). Neither SH-1 or SH-2 contain open reading frames of significant length (*11*). Thus, the SH clones represent heart RNAs of similar lengths that share a common 3′ sequence of nearly 500 nucleotides. However, the 5′ regions of the SH mRNAs are unique over a stretch of approximately 200 nucleotides. Although the lengths of the cDNA clones analyzed here are close to the size indicated by Northern analysis, S1 mapping (*12*) or primer extension (*13*) reactions have not yet been used to unambiguously map the cap sites of the SH RNAs. There may be an as yet undefined 5′ SH exon common to all SH transcripts. If this situation occurs, then the mature SH RNAs would probably be derived from a unique species of nuclear precursor RNA transcribed from a single promoter. The three species of mature SH RNAs would thus result from alternative splicing (*14, 15*). If, however, the cDNA sequences presented here represent virtually full-length RNAs, then the relative positions of the SH coding sequences within the genomic DNA would suggest that they could only arise from transcription initiating at three independent promoters (see Fig. 3).

Thus, we have found evidence for the use of both strands of a unique segment of genomic DNA to encode spliced poly(A)$^+$ RNAs in mammalian organisms. The SH clones show heterogeneous 5′ sequences joined to a common 3′ sequence. In all three categories of SH cDNA clones, at least one SH genomic exon also represents an exon in mRNA that is transcribed from the opposite strand and encodes preproGnRH.

The function of the SH gene product remains a mystery. Some or all of the SH RNAs may function as regulatory molecules. Among the prokaryotes, there are several examples of antisense RNAs that serve functional roles as regulatory molecules (*16–20*). In eukaryotes, the introduction of antisense RNA into cells has been shown to inhibit expression of the endogenous sense mRNA (*21–24*). In this way, the SH RNAs may be involved with the regulation of GnRH gene expression. While we have no evidence that the GnRH gene is transcribed in the rat heart, the discovery of a partial SH cDNA clone from a rat hypothalamic cDNA library suggests that both DNA strands are transcribed in that tissue.

It is equally possible that the SH and GnRH genes are functionally unrelated. The integrity of the GnRH gene is central to the reproductive capability of the mammalian organism (*25, 26*), and thus is under stringent selective maintenance. This implies that the SH gene product, whether RNA or protein, is also under considerable selective pressure. Thus, the organism maintains the SH gene by means of an evolutionary piggy-back. The availability of strand-specific probes may allow the discovery of analogous genetic arrangements at other loci. Indeed, this situation may be a significant form of molecular genetic evolution. By using both strands of the same conserved DNA, the information content (regulatory and/or structural) of a particular genetic segment becomes amplified, adding a new complexity to the concept of a eukaryotic gene.

REFERENCES AND NOTES

1. S. Henikoff, M. A. Keene, K. Fechtel, J. W. Fristrom, *Cell* **44**, 33 (1986).
2. C. A. Spencer, R. D. Gietz, R. B. Hodgetts, *Nature (London)* **322**, 279 (1986).
3. T. Williams and M. Fried, *ibid.*, p. 275.
4. J. P. Adelman, A. J. Mason, J. S. Hayflick, P. H. Seeburg, *Proc. Natl. Acad. Sci. U.S.A.* **83**, 179 (1986).
5. P. H. Seeburg and J. P. Adelman, *Nature (London)* **311**, 666 (1984).

6. J. P. Adelman and P. H. Seeburg, unpublished results.
7. D. A. Melton *et al.*, *Nucleic Acids Res.* **12**, 7035 (1984).
8. N. J. Proudfoot and G. G. Brownlee, *Nature (London)* **263**, 211 (1976).
9. P. V. Wagh and O. P. Bahl, *CRC Crit. Rev. Biochem.* **10**, 307 (1981).
10. B. Lewin, Ed., in *Gene Expression 2* (Wiley, New York, 1980).
11. P. Senapathy, *Proc. Natl. Acad. Sci. U.S.A.* **83**, 2133 (1986).
12. A. J. Berk and P. A. Sharp, *Cell* **12**, 721 (1977).
13. M. Houghton *et al.*, *Nucleic Acids Res.* **8**, 1913 (1980).
14. S. G. Amara, V. Jonas, M. G. Rosenfeld, E. S. Ong, R. M. Evans, *Nature (London)* **298**, 240 (1982).
15. H. Nawa *et al.*, *ibid.* **306**, 32 (1983).
16. J.-I. Tomizawa, T. Itoh, G. Selzer, T. Som, *Proc. Natl. Acad. Sci. U.S.A.* **78**, 1421 (1981).
17. R. M. Lacatena and G. Cesareni, *Nature (London)* **294**, 623 (1981).
18. J.-I. Tomizawa and T. Itoh, *Cell* **31**, 575 (1982).
19. T. Mizuno, M.-Y. Chou, M. Inouye, *Proc. Natl. Acad. Sci. U.S.A.* **81**, 1966 (1984).
20. J. Coleman, P. J. Green, M. Inouye, *Cell* **37**, 429 (1984).
21. D. A. Melton, *Proc. Natl. Acad. Sci. U.S.A.* **82**, 144 (1985).
22. J. T. Holt, T. V. Gopal, A. D. Moulton, A. W. Nienhuis, *ibid.* **83**, 4794 (1986).
23. J. G. Izant and H. Weintraub, *Science* **229**, 345 (1985).
24. S. K. Kim and B. J. Wold, *Cell* **42**, 129 (1985).
25. A. V. Schally *et al.*, *Biochem. Biophy. Res. Commun.* **43**, 393 (1971).
26. D. T. Krieger and J. C. Hughes, Eds., in *Neuroendocrinology* (Sinauer, Sunderland, MA, 1980).
27. J. M. Chirgwin, A. E. Przybyla, R. J. MacDonald, W. J. Rutter, *Biochemistry* **18**, 5294 (1979).
28. T. Maniatis, E. F. Fritsch, J. Sambrook, in *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1982).
29. T. Huynh, R. Young, R. Davis, in *DNA Cloning: A Practical Approach*, D. Grover, Ed. (IRL, Oxford, 1984).
30. J. Messing, R. Crea, P. H. Seeburg, *Nucleic Acids Res.* **9**, 309 (1981).
31. F. Sanger, S. Nicklen, A. R. Coulson, *Proc. Natl. Acad. Sci. U.S.A.* **74**, 5463 (1977).
32. We thank L. Calavetta for excellent technical assistance involving riboprobe vector constructions, Northern blots, and poly(A)$^+$ mRNA purifications; B. Thompson for help with initial Northern blot poly(A)$^+$ mRNA tissue distributions analysis; B. Hall for laboratory support; and D. Goeddel, P. H. Seeburg, and J. Hallum for enthusiastic and fruitful discussions. Supported by grants AM-16879 and AM-30155 from the NIADDK (E.H.) and grant DA-02736 from NIDA (E.H.).

6 October 1986; accepted 15 January 1987

Optical Trapping and Manipulation of Viruses and Bacteria

A. ASHKIN AND J. M. DZIEDZIC

Optical trapping and manipulation of viruses and bacteria by laser radiation pressure were demonstrated with single-beam gradient traps. Individual tobacco mosaic viruses and dense oriented arrays of viruses were trapped in aqueous solution with no apparent damage using ~120 milliwatts of argon laser power. Trapping and manipulation of single live motile bacteria and *Escherichia coli* bacteria were also demonstrated in a high-resolution microscope at powers of a few milliwatts.

WE REPORT THE EXPERIMENTAL demonstration of optical trapping and manipulation of individual viruses and bacteria in aqueous solution by laser light using single-beam gradient force traps. Individual tobacco mosaic viruses (TMV) and oriented arrays of viruses were optically confined within volumes of a few cubic micrometers, without obvious damage, and manipulated in space with the precision of the optical wavelength. The ability of the same basic optical trap to confine and manipulate motile bacteria was also demonstrated. We have used the trap as an "optical tweezers" for moving live single and multiple bacteria while being viewed under a high-resolution optical microscope. These results suggest that the techniques of optical trapping and manipulation, which have been used to advantage with particles in physical systems, are also applicable to biological particles. Optical trapping and manipulation of small dielectric particles and atoms by the forces of radiation pressure have been studied since 1970 (*1–4*). These are forces arising from the momentum of the light itself. Early demonstrations of optical trapping (*1*) and optical levitation (*5*) involved micrometer-size transparent dielectric spheres in the Mie regime (where the dimensions d are large compared to the wavelength λ). More recently optical trapping of submicrometer dielectric particles was demonstrated in the Rayleigh regime (where $d << \lambda$). Single dielectric particles as small as ~260 Å (*6*) and even individual atoms (*7*) were trapped with single-beam gradient traps (*8*).

Single-beam gradient traps are conceptually and practically the simplest. They consist of only a single strongly focused Gaussian laser beam having a Gaussian transverse intensity profile. In such traps the basic scattering forces and gradient force components of radiation pressure (*1, 3, 4, 8*) are configured to give a point of stable equilibrium located close to the beam focus. The scattering force is proportional to the optical intensity and points in the direction of the incident light. The gradient force is proportional to the gradient of intensity and points in the direction of the intensity gradient. Particles in a single-beam gradient trap are confined transverse to the beam axis by the radial component of the gradient force. Stability in the axial direction is achieved by making the beam focusing so strong that the axial gradient force component, pointing toward the beam focus, dominates over the scattering force trying to push the particle out of the trap. Thus one has a stable trap based solely on optical forces, where gravity plays no essential role as was the case for the levitation trap (*5*). It works over a particle size range of 10^5, from ~10 μm down to a few angstroms, which includes both Mie- and Rayleigh-size particles.

The sensitivity of laser trap effectiveness to optical absorption and particle shape is of particular importance for the trapping of biological particles. Absorption can cause an excessive temperature rise or additional thermally generated (radiometric) forces as a result of temperature gradients within a particle (*9*). In general, the smaller the particle size the less the temperature rise and the less the thermal gradients for a given absorption coefficient (*10*). Particle shape plays a larger role in the trapping of Mie particles than Rayleigh particles. For Mie particles both the magnitude and direction of the forces depend on the particle shape (*3*). This restricts trapping to fairly simple overall shapes such as spheres, ellipsoids, or particles whose optical scattering varies slowly with orientation in the beam. In the Rayleigh regime, however, the particle acts as a dipole (*6*) and the direction of the force is independent of particle shape; only the magnitude of the force varies with orientation. A significant conclusion of this work is that important types of biological particles in both the Mie and Rayleigh regimes have optical absorptions and shapes that fall within the scope of single-beam gradient traps.

As a first test for trapping of small biological particles we tried TMV, a much studied virus that can be prepared in monodisperse colloidal suspension in water at high concentrations (*11, 12*). Its basic shape is cylindrical with a diameter of 200 Å and a length of 3200 Å (*13*). Although its volume of about 470 Å^3 is typical of a Rayleigh particle, its length is comparable to the wavelength in the medium and we expect some Mie-like behavior in its light scattering. TMV particles have a negative charge in solution (*14*) and an index of refraction (*15*) of about 1.57. Our virus samples were prepared from the same batches used in experi-

AT&T Bell Laboratories, Holmdel, NJ 07733.