

## Optical Communication: Heterodyne Detection Scheme

I should like to add a small contribution to R. Kompfner's discussion of optical communications (1):

With respect to the heterodyne detection scheme, Kompfner says that the practical realization depends on precise alignment of two independent light beams. Actually, a greater difficulty than this exists. An optical maser, or laser, has a frequency when free-running that is critically dependent on the distance between the two mirrors used to form the optical cavity. For a laser operating at  $0.6328\text{-}\mu$  wavelength (He-Ne) (approximately  $5 \times 10^{14}$  cy/sec), for example, and having a mirror separation of 1 m, a change in length of  $10^{-7}$  cm would cause a frequency shift of about 0.5 Mcy. Such changes in length are easily caused by thermal variations or vibrations, and if not tracked exactly by a local oscillator result in prohibitive noise in the detected signal. These problems have both been recently solved (2).

The common type of gas laser operates with Brewster angle windows, which eliminate oscillation in one polarization plane of the laser. Thus, laser light is commonly plane polarized.

It has been demonstrated that a laser can operate in two different modes in the same space simultaneously, at different frequencies (3), if the laser is caused to move in such a way that the light in the two modes takes different times to make a circuit through the laser. I have since suggested use of two modes which are basically the two directions of polarization, separating them over part of the path, passing one of them through a plasma, and then from the beats (heterodyne detection) deriving the plasma density (4). Such a laser interferometer would be more sensitive than the previously described instruments (5) used for plasma diagnostics.

In the present case, special separation of the two beams is unnecessary. Instead, an electroactive crystal is put into the laser cavity (flat rather than Brewster windows are used), and the information signal is imposed on the crystal. The signal (a varying electric field) causes the crystal to have different optical lengths to the two light beams having different polarizations, and this difference in effective path

length causes oscillation of the differently polarized beams at different frequencies, the frequency difference being dependent only on the field strength imposed on the crystal. The light beams occupy at all times the same space, and may be focused and transmitted together. Since the mirrors and other parts of the system are common, noise frequency changes track perfectly in the "local oscillator" beam, which is no longer generated locally at the receiver but at the transmitter. Perhaps it should be renamed; "reference" oscillator seems appropriate. The beams may be separated if desired by polarization film, a Glan-Thomson prism, or other means, but for communications this is not likely to be desirable. The system operates, of course, by frequency modulation.

I have written at length on this scheme because it is such an elegant solution to two of the important problems of laser communications and is not nearly so well known as it ought to be.

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### References

1. R. Kompfner, *Science* **150**, 149 (1965).
2. W. M. Doyle and M. B. White, *Proc. I.E.E.E. (Inst. Elec. Electron. Engrs.)* **52**, 1353 (1964).
3. W. M. Macek and D. T. M. Davis, Jr., *Appl. Phys. Letters* **2**, 67 (1963).
4. H. Malamud, *J. Sci. Instr.*, in press.
5. D. E. T. F. Ashby and D. F. Jephcott, *Appl. Phys. Letters* **3**, 13 (1963).

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## Single Point Mutation or Chromosomal Rearrangement

Titani, Whitley, Avogardo, and Putnam (1) summarize their own findings and those of Hilschmann and Craig (2) on the amino acid sequences of three type I Bence Jones proteins. They discuss the origin of the many differences between the three Bence Jones proteins, which with one exception are all located in the  $\text{NH}_2$ -terminal half of the molecule. In an apparent attempt to explain the multiple differences as arising from a single event, they express the opinion that "The multiple structural differences . . . are incompatible with the concept of single point mutations now accepted for the abnormal hemoglobins." Instead they favor some sort of larger chromosomal

rearrangement such as that postulated by Smithies (3).

It seemed desirable to check this conclusion by analyzing the amino acid interchanges in the light of recent information concerning the triplet code (4). The point mutations found in hemoglobin have all been explainable as substitutions of single nucleotide base pairs. If the variability in Bence Jones proteins is the result of larger chromosomal rearrangements, then the preference for single nucleotide shifts should not be present.

Of 12 probable interchanges indicated by Titani *et al.* in the  $\text{NH}_2$ -terminal half of the Bence Jones proteins, eight were based on definite sequence information. These were Asp and Glu at position 1, Ile and Leu at 46, Glu and Ala at 55, Thr and Lys at 72, Leu and Val at 102, Glu and Asp at 103, Ile and Phe at 104, and Lys and Arg at 105. All eight of these amino acid interchanges can be explained as single nucleotide substitutions. For example, according to Nirenberg's table the codons for aspartic acid are GAU and GAC, which can change in one step to the codons for glutamic acid, GAA and GAG. From the data in Nirenberg's table, slightly less than 40 percent of all possible amino acid interchanges can be explained as being due to a single nucleotide substitution. The probability that eight interchanges would be so explicable is thus  $0.4^8$  or 0.0006.

It thus appears that the best explanation of the amino acid interchanges in Bence Jones protein, like those in hemoglobin, is that they are point mutations due to the substitution of a single nucleotide base pair. If this is the case, then the multiple changes must represent an accumulation of point mutations.

A similar analysis with the triplet code makes possible a prediction of the probable order of the amino acid residues in one of the proteins (Roy) at positions 75 and 76, where it appears there is a dipeptide interchange. The report of Titani *et al.* indicates that in the protein Cu the sequence of this dipeptide is Arg-Val. Available information indicates that in Roy these positions are occupied by Asp and Leu without any indication of order. Since the interchange of Asp and Arg requires a two-step mutation, and the other possible interchanges are one-step, the dipep-