of the thin metallic film, through the resonant absorption of electromagnetic radiation at particular frequencies depending, in this case, on the temperature and on the magnitude of the applied magnetic field. The cell was placed in a compressional cooling apparatus in which the temperature of the liquid was lowered by reducing its volume and thus solidifying some of it, which was able to reach the so-called superfluid B phase which is stable below its transition temperature at about 2 mK.

In the event, a series of striking absorption peaks was indeed found approximately at the frequencies predicted by theory. Although the peaks were broader than ordinary NMR resonances in ^{3}He, they were quite well defined, thus eliminating the lurking possibility that spin waves in ^{3}He might be modes which are overdamped and therefore unobservable. As the authors point out, it is quite possible that the observed width of the resonance maxima is merely an experimental effect arising from small variations in the spacing of the quartz plates. The change with temperature of the resonant frequencies turned out qualitatively to be very much in line with theoretical expectations.

The experimental results are not, however, in close quantitative agreement with theory. However, although the authors' tentative explanation of the discrepancies (typically about 20%) may or may not be correct, there seems little doubt that they were indeed observing spin waves. Further experimental and theoretical work is clearly required, but it seems that spin wave resonance has now been added to the rapidly growing battery of techniques available for elucidating the dauntingly complicated properties of superfluid ^{3}He. □

Complementary genetics

from M. J. Hobart

An EMBO Workshop on Complement Genetics was held in Cambridge, UK on 18–22 March, 1977. It was organised by Dr P. Lachmann, MRC Group on Mechanisms in Tumour Immunity, Cambridge.

THE genetics of the complement system were put on the map, both chromosomally and as a topic of general scientific interest, by the discoveries in 1974 by F. H. Allen, S. M. Fu and their colleagues that the genes coding for Factor B and C2 are linked to *HLA*. This had been foreshadowed in 1973 by the work of P. Demant and colleagues showing that the Ss protein, coded within the *H-2* region of mice, was a complement component, subsequently shown by several groups of workers to be C4.

The complement system consists of at least 18 proteins, including proenzymes and inhibitors, whose activity is usually triggered by the binding of antibody to antigen. It is the major humoral effector system for the elimination of bacteria and viruses in vertebrates and is characterised by complex reaction pathways reminiscent of the clotting, fibrinolysis and kinin systems.

There is now good evidence that three complement components are coded by genes located within the *HLA* region: C2, Factor B and C4. The electrophoretic variants of C4 described by P. Teisberg (Ulleval Hospital, Oslo) show clear *HLA* linkage and both G. Mauff (Hygiene Institute, Cologne) and G. Hauptmann (Institut d'hematologie et de transfusion sanguine, Strasbourg) reported their methods which show the same phenomenon with rather improved resolution. These results confirm the earlier evidence for C4 linkage from studies of a deficient patient's family (C. Rittner, Institute of Forensic Medicine, Bonn). *HLA* linkage is now firmly established for C2 polymorphism (C. Alper, Center for Blood Research, Boston). The less common allele of *C2* (*2C²* in the nomenclature proposed) was reported by T. Meo (Basel Institute for Immunology) to be in strong linkage disequilibrium with *HLA* BW15 and *HLA* CW3.

Alper also demonstrated polymorphism of C8 detected by isoelectric focusing and specific functional detection by haemolytic assay. There are at least three structural variants of C8, two of them common. The locus is not closely linked to *HLA*. Two new families with C8 deficient members were described by N. K. Day (Sloan Kettering Institute, New York) and F. Tedesco (Transplantation, Immunology and Blood Transfusion Service, Milan). In both families, there were totally C8 deficient individuals with different *HLA* types, showing that the deficiency genes also cannot be close to *HLA*. Furthermore it was apparent that there is difficulty in ascertaining the heterozygous deficiency states, since in both families, both parents of the propositi had C8 levels within the normal range. Furthermore Alper reported that members of a deficient family heterozygous for the structural variant could nevertheless have low C8 levels. This may explain the discrepancy between these reports and that of Merritt *et al.* (*Third International Workshop on Human Gene Mapping. Birth Defects* **XII** (7) 331, The National Foundation, New York, 1976) which claimed *HLA* linkage for C8 deficiency.

D. Glass (Robert B. Brigham Hospital, Boston) presented a large series of carefully measured cases of heterozygous C2 deficiency. There seems to be a significant association with juvenile rheumatoid arthritis and systemic lupus erythematosus in these patients. J. Soothill (Institute for Child Health, London) and J. Mowbray (St. Mary's Hospital, London) have evidence that there is an increased incidence of heterozygous C2 deficiency in infantile asthma and eczma. However, it was pointed out in discussion that apparently high recombination frequency between C2 and *HLA* observed by Glass is probably due to ascertainment errors inherent in measuring complement levels.

C3, C4, C5 and C8 are known to be composed of more than one polypeptide chain, but in no case is there any evidence that more than one locus is involved in coding for the observed polymorphisms. A possible explanation for this phenomenon is given by preliminary experiments of H. Colten (Children's Hospital Boston) and his colleagues (reported by Alper). They have shown that both C4 and C3 obtained from cell-free synthesis by immunoprecipitation occur as larger than expected chains. Their suggested interpretation of this result is that C3 and C4 (and, by analogy, perhaps C5 and C8) are synthesised as single polypeptide chains which are cleaved before secretion, rather like insulin. Only one cistron will then be involved in coding for the whole molecule and all markers will be alleles, irrespective of the chain on which they are found. Since there are now some 20 variants of C3, all of them apparently alleles, this view has its attractions. Some similar complement components seem to be the products of tandem duplicated genes. This is the case with C2 and Factor B. Both are linked to *HLA* in the same subregion and with no crossovers indentified between them. Both are single polypeptide chains, heat labile and form part of a complex C3 splitting enzyme. C6 and C7 are consecutively acting components and are both single polypeptide chains. They show close linkage to each other as demonstrated by allotyping (M. J. Hobart, MRC Group on Mechanisms in Tumour Immunity, Cambridge). Although C3, C4 and C5 are similar, C4 is linked to *HLA* but the other two components are not. If these molecules are the products of related genes, then they have been duplicated by processes other than (or additional to) tandem duplication.

A remarkable case of combined

subtotal deficiency of C6 and C7 was reported by P. J. Lachmann (MRC Group on Mechanisms in Tumour Immunity, Cambridge). The proband is in good health. The deficiencies of both components segregate together in the grandchildren, which is to be expected if the structural genes for both proteins are involved, since they are closely linked. Trace C6 and C7 activity appear in the proband's serum in the same pattern of bands, different from either normal C6 or C7 when separated by isoelectric focusing. An interesting speculation is that this may be the result of a 'Lepore' fusion of C6 and C7 genes.

At times the Workshop veered from the strict limits of complement genetics, Alper and F. S. Rosen (Children's Hospital, Boston) presented evidence that C3 nephritic factor is an IgG, on the basis of functional detection of clonal electrophoretic variants and on the transmission of such a clone across the placenta. A. Ferreira (New York University) described a new C4-binding protein in mice, the molecular association giving the appearance of *H-2* linkage. Since more than half of the known complement components now have genetic markers, new components are needed if healthy growth of the topic is to be maintained! □

Progress in coronaviruses

from David J. Garves

A symposium on Human and Animal Coronaviruses was held at the Agricultural Research Council Institute for Research on Animal Diseases, Compton UK on 24–25 March, 1977, and was organised by Professor A. P. Waterson, Royal Postgraduate Medical School, London, and Dr D. J. Garves, Compton.

THE Coronaviridae comprise a family of morphologically similar viruses that cause a wide variety of diseases in man and other animals. Following the recognition of coronaviruses as a distinct taxonomic group in 1968 (see *Nature* **220**, 650), with virus particles having a peripheral halo in negatively stained preparations, the number of viruses classified in the group and our knowledge of their characteristics has greatly increased. There are still large gaps in our understanding of the diagnosis, pathogenesis, structure and serology of this economically and, potentially, medically important group and attempts were made to fill these gaps at the symposium.

Recent reports of coronavirus-like particles in samples from human and equine enteritis, human nephropathy and feline infectious peritonitis have raised the problem of which criteria should be used to identify a coronavirus. It has been found that coronaviruses are difficult to establish in cell culture and for this reason morphology of the virus particle provides the major distinguishing feature. J. Almeida (Wellcome Research Laboratories) and R. Bingham (Royal (Dick) School of Veterinary Studies, Edinburgh) reported new evidence for the morphology and structure of the internal component of avian infectious bronchitis virus. They showed electron micrographs of virus particles within which flask-shaped structures could be seen, the mouth of the 'flask' appearing to open at the outer membrane of the virus. Whether these structures are present in other coronaviruses and what relation they have to the organisation of the genetic material has yet to be determined.

Recent studies on the polypeptide structures of human and animal coronaviruses have shown that, while the number and size of the structural proteins vary between members of the family, some similar features can be seen. The polypeptide profiles may provide a method to distinguish relationships within the coronaviruses and in this context the apparent similarity between the polyacrylamide gel patterns for avian infectious bronchitis virus (M. R. Macnaughton, Clinical Research Centre, London) and calf diarrhoea coronaviruses (J. Laporte, Thiverval-Grignon, France) was of interest.

The genome of avian and porcine coronaviruses has been shown to comprise single-stranded RNA but whether this has a messenger role, as in oncornaviruses and enteroviruses, or is a complementary strand, as in paramyxoviruses, has not been determined. Our understanding of the strategy of the coronavirus genome is greater, however, following the reports of Macnaughton and D. H. Pocock (ARC, Compton) that avian and porcine coronavirus RNA contains polyadenylic acid tracts. This evidence strongly suggests that the RNA has a messenger function and is yet another feature, together with virion morphology and the genome size, that coronaviruses have in common with the RNA tumour viruses. Bingham reported, however, that attempts to detect a reverse transcriptase in avian infectious bronchitis virus have proved unsuccessful, in line with the evidence from inhibitor studies suggesting that coronavirus replication does not proceed by way of DNA.

D. J. Alexander (Central Veterinary Laboratory, Weybridge) reported on the finding of long term infection of chickens with infectious bronchitis virus and these results, together with the evidence of chronic infection of mice with hepatitis virus and the carrier status of pigs with transmissible gastroenteritis, prompted K. McIntosh (University of Colorado, Denver) to suggest that future work on the human respiratory coronaviruses should consider implications of inapparent, chronic infections. It is possible that Balkan endemic nephropathy may result from such an infection, as K. Apostolov (Royal Postgraduate Medical School, London) reported a possible serological relationship between this disease and a human respiratory coronavirus.

Coronavirus serology is confused at the moment, with cross reactions being detected between human, bovine, murine and porcine viruses. The serological relationship between porcine transmissible gastroenteritis virus and a canine enteric virus is strong and D. J. Reynolds, (Compton) also presented evidence of antibodies to transmissible gastroenteritis in cats. It is possible that the agent in the cat responsible for the very high antibody levels may be associated with feline infectious peritonitis, a possible coronavirus whose morphology and physicochemical properties were presented by A. Osterhaus (Utrecht, Netherlands). The morphology of the purified particles was not characteristic of other coronaviruses and whether this was due to degradation or a different surface projection structure is not known. The agent of feline infectious peritonitis demonstrated the problem caused by the fact that coronavirus identification rests principally on the shape of the surface projection. It was generally agreed that other features including virus structure, the characteristics of the genome and the mode of replication within the cell needed to be determined before any virus could be assigned to the Coronaviridae, although this information is not known for some well accepted coronaviruses. Similarly, more data would be required before any meaningful subdivisions, such as separating the avian from the mammalian members, could be made within the Family.

In the field of coronavirus disease control there seemed to be doubtful correlation between antibody levels in serum and secretions and resistance to infection. It was recommended that more effort should go into investigating cellular and humoral aspects of immunity to diseases caused by coronaviruses. □