information contained in a single subunit would be sufficient to code only for about 300,000 daltons of protein, which compares with the total weight of known viral proteins of about 3,650,000 daltons.

The presence of two types of subunit in 30–40S preparations of Rous sarcoma virus (RSV) RNA was first reported by Duesberg and Vogt (*Proc. natn. Acad. Sci. U.S.A.*, **67**, 1673–1680; 1970) when they electrophoresed the RNA on gels; these are the more slowly migrating (larger) *a* subunit and the smaller *b* subunit. The size of the class *a* subunits is in the range $2.4-3.4\times10^6$ daltons and that of the *b* subunits is about $2.2-2.9\times10^6$ daltons (Duesberg and Vogt; *J. Virol.*, **12**, 595–599; 1973). But Martin and Duesberg (*Virology*, **47**, 494–497; 1972) then showed that the 60–70S RNA extracted from cloned RSV particles derived from clonal populations of infected cells carry only the *a* subunit. In a further report, Duesberg and Vogt (*Virology*, **54**, 207–219; 1973) showed that the *a* subunit of cloned Schmidt–Ruppin strain of RSV is slightly larger than the *a* subunit of the cloned Prague RSV strain.

Different (noncloned) strains of avian sarcoma virus have different ratios of *a*/*b* subunits. Avian leukaemia virus particles, however, contain only *b* subunits. Since the sarcoma virus can transform chick fibroblasts whereas the leukaemia virus is unable to do so, this observation led to the concept that the *a* subunit may carry information necessary to accomplish transformation and that this sequence is missing from the leukaemia virus genome. Consistent with this idea was the observation of Duesberg and Vogt that transformation-defective variants of avian sarcoma virus all possess only the class *b* size of subunit. The derivation of *b* subunits from *a* subunits might therefore be explained by the occurrence of a deletion in the *a* subunit which removes information essential for transformation. If all the subunits in either size class are identical, then a single event would be sufficient to generate the defective viruses; but if the subunits represent different sequences, presumably a deletion would have to take place in each type of molecule in order to generate the size change between sarcoma and leukaemia virus.

Two approaches have been taken to determine the complexity of the RNA genomes and these have yielded contradictory results. Chemical analysis suggests a polyploid structure for the avian RNA virus genome. After digesting the RNA of the Schmidt–Ruppin strain of Rous sarcoma virus with T1 ribonuclease and separating the oligonucleotides on two-dimensional gels, Billeter, Parsons and Coffin (*Proc. natn. Acad. Sci. U.S.A.*, **71**, 3560–3564; 1974) obtained roughly twice the number of spots generated by 28S rRNA. By determining the molar yield of 11 of these spots, they were able to suggest a complexity for the viral genome of about $3.4\pm0.9\times10^6$ daltons. A similar estimate was made by Quade, Smith and Nichols (*Virology*, **61**, 287–291; 1974) for the RNA of the Prague strain of RSV (3.3×10^6 daltons). These estimates would suggest that the genome is polyploid, since the sequence complexity of the viral RNA is about the length of a single 30–40S subunit molecule.

That *b* subunits are derived by a deletion of *a* subunits is suggested by the chemical and hybridisation analyses reported by Lai, Duesberg, Horst and Vogt (*Proc. natn. Acad. Sci. U.S.A.*, **70**, 2266–2270; 1973). Comparing the T1 ribonuclease digests of the RNAs of avian sarcoma viruses and transformation-defective derivatives showed that all the large spots of the *b* subunit are found in the digest of the *a* subunit; but the *a* molecules contain one or two additional spots not found in the *b* digest. The labelled cDNA prepared from the *a* subunit hybridises with about 70% of the *a* RNA when saturation is reached; it hybridises with 60–65% of the *b* RNA, a result which would be consistent with the omission from the *b* RNA of a sequence present in the *a* RNA. Neiman *et al.* (*J. Virol.*, **13**, 837–846; 1974) have compared the RNA genome of the Prague strain of RSV with a spontaneous transformation-defective mutant derived from it by hybridising these viral RNAs with excess chicken DNA of normal embryos and sarcomas. The transformation-defective strain seems to lack a sequence present in the parent sarcoma virus.

Hybridisation experiments have been used also to measure the complexity of the 60–70S RNA of RSV. When labelled cDNA prepared from the viral genome is annealed with an excess of RNA, the reaction rate depends upon the complexity of the RNA. Taylor *et al.* (*J. molec. Biol.*, **84**, 217–221; 1974) reported a sequence complexity of 9.3×10^6 daltons, which corresponds to about three different subunits if each subunit is about 3×10^6 daltons. This clearly suggests a haploid genome. No reconciliation between the chemical and hybridisation analyses is at present apparent.

What is responsible for maintaining the association of subunits in the 60–70S complex? The denaturation maps recently constructed by Mangel, Delius and Duesberg (*Proc. natn. Acad. Sci. U.S.A.*, **71**, 4541–4545; 1974) suggest that hydrogen bonding at several locations may be implicated. The T4 gene 32-protein binds cooperatively to single stranded nucleic acid and (mildly) denatures both 60–70S and 30–40S preparations. The molecules treated with 32-protein can then be visualised by electron microscopy. In the presence of 32-protein, 30–40S RNA is linear, appears fully coated with protein (thus losing the extensive secondary structure seen in the absence of 32-protein), and has a maximum length (some molecules are shorter, presumably due to degradation) of 2.75×10^6 daltons. The complex of 32-protein with 60–70S RNA consists of several linear molecules held together at different sites, with four to eight free ends per complex. Most of the RNA is coated with protein. The average length is 6×10^6 daltons, which would suggest that the complex includes only two subunits.

A hundred years ago

THE ZODIACAL LIGHT.—On the evening of Sunday last, the 24th inst., a surprisingly bright display of this as yet problematical phenomenon was exhibited. There was a repetition on the following evening, but in a less favourable sky. The light had the usual yellowish or pale lemon tinge of the more notable exhibitions in these latitudes. The axis of the light appeared to pass λ Piscium, and the vaguely-defined apex was situate somewhere about 19 Arietis, but it was not possible to locate it with anything like precision. The light was broad and of a deeper, perhaps, ruddy tint near the horizon. The display to which we have adverted, excelled in brightness any that has been witnessed in the neighbourhood of London for many years. It appears very probable that opportunities for favourable application of the spectroscope may be afforded in the dark evenings of the present and following months.

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Manganese can grow rapidly

from Peter J. Smith

FERROMANGANESE nodules and crusts typically grow on the ocean floor at rates of 0.1–1.0 cm per million years and have Fe/Mn ratios of 0.5–2.0. But Scott *et al.* (*Geophys. Res. Lett.*, **1**, 355; 1974) now report that they have found a manganese oxide (MnO_2) crust with a much higher growth rate, an abnormally low iron concentration and unusual trace element characteristics. The newly discovered crust is thus