woolly leukaemia viral RNA. As shown in Table 1, the cDNA prepared from the woolly leukaemia virus RNA hybridises to both the woolly leukaemia virus and woolly sarcoma viral RNA; at saturation (Crt of 1.0 mol l⁻¹) approximately 50% of the sequences contained in the woolly leukaemia cDNA are protected by the woolly sarcoma virus RNA. The results indicate, as previously suggested, that the woolly sarcoma virus contains only a portion of the woolly leukaemia genome[11].

The crude cDNA probe prepared from the woolly sarcoma viral RNA, which contains mostly woolly leukaemia virus sequences, was also hybridised to the same viral RNAs and showed slightly greater hybridisation to the woolly sarcoma vrus RNA than to the woolly leukaemia virus RNA. After purification of the woolly sarcoma virus probe to remove woolly leukaemia virus sequences (see legend to Table 1), the wooly 'src' probe was re-tested for its specificity and the results are also shown in Table 1. The woolly src probe hybridised well to the woolly sarcoma virus RNA and not at all to the viral RNA from the woolly leukaemia virus, or viral RNA from RD114 virus, RT21c rat virus, or amphotropic mouse leukaemia virus. In addition, the woolly viral src sequences were detected in cellular RNA in non-producer rat cells tranformed by the woolly sarcoma virus but not in rat cells transformed by the Schmidt–Ruppin strain of Rous sarcoma virus. These src sequences were also detected in horse cells producing both the woolly leukaemia and woolly sarcoma viruses but not in horse cells producing the woolly leukaemia virus alone. The results show that woolly sarcoma virus contains two sets of nucleic acid sequences. One set of the sequences is contained in the woolly leukaemia virus, and another set is specific for the woolly sarcoma virus. These results are consistent with finding on other avian and mammalian sarcoma viruses which showed their genomes to contain both leukaemia virus sequences and distinctive sequences specific to the sarcoma viruses[2,12,13]. In order to quantitate the relative percentage of the two sets of sequences in the woolly sarcoma virus genome, ³²P radio-labelled RNA was prepared from the woolly sarcoma virus, by labelling the viruses

released from WB334 cells with inorganic ³²P and separating the high molecular weight RNAs as shown in Fig. 1b. The ³²P-labelled woolly sarcoma virus RNA was then hybridised to a two-fold molar excess of ³H-cDNA from the woolly leukaemia virus, or to a two-fold excess of cDNA purified to represent the novel sequences in the woolly sarcoma virus. At these ratios of DNA to RNA, the src probe protected 52% of the ³²P-labelled RNA and the Wo-lv cDNA protected 52% of the ³²P-labelled RNA.

Thus we have analysed the RNA subunits contained in the virus complex containing an amphotropic mouse type-C virus pseudotype of the woolly virus. The data indicate that the high molecular weight forms of the two viral RNAs in this virus complex are essentially completely separable by velocity sedimentation in sucrose gradients and that no detectable heterodimers occur between the mouse type-C viral RNA and the woolly sarcoma viral RNA. The woolly sarcoma viral RNA is smaller than the accompanying helper viral RNA, and contains only a portion of the Wo-lv genome. In the woolly sarcoma viral RNA a set of sequences has been detected which comprise approximately 15% of the woolly sarcoma genome; the sarcoma virus specific sequences are not detected in the woolly leukaemia virus. Thus, the genome of the naturally occurring Wo-sv seems to be similar to the genomes of rodent sarcoma viruses formed in laboratory experiments[14,15]; that is the sarcoma virus genome represents a set of new sequences plus a portion of the genome of the helper virus contained in the original virus stock. The ability to obtain large quantities of purified RNA and cDNA specific for the woolly sarcoma virus should allow an identification both of the origin of the sarcoma-specific sequences of the woolly sarcoma virus and possibly by in vitro translation, identification of any possible gene product(s) of these sequences.

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Table 1 Hybridisation with woolly leukaemia and woolly sarcoma virus cDNAs

RNA Source Viral	c.p.m. hybridised with ³H-cDNA from Wo-lv	Wo-sv Crude	Purified
Wo-lv	2,116	965	18
Wo-sv	1,158	1,150	33
RD-114	41	98	10
Amphitrope	186	156	25
RT21C	38	108	13
None	43	93	10
Cellular			
Non-producer cells			
Wo-sv NRK	—	—	333
SR NRK	—	—	22
Producer cells			
Wo-lv NRK	2,230	—	12
Wo-lv horse	2,165	—	12
Wo-lv/Wo-sv horse	2,177	—	308

Each hybridisation with woolly leukaemia virus ³H-cDNA contained 2,500 TCA c.p.m. The hybridisations with the crude woolly sarcoma virus cDNA contained 1,800 TCA c.p.m. and with the purified woolly sarcoma virus cDNA 630 TCA c.p.m. The sarcoma-specific cDNA was obtained by hybridising the crude cDNA to woolly leukaemia virus RNA and subsequent chromatogtaphy on hydroxylapatite[14,15]. The hybridisations with viral RNA were carried out to Crt values of 1.0 mol s l⁻¹ and with cellular RNA to Crt values of 5×10^3 mol s l⁻¹. Analytical hybridisation conditions and analysis with the use of sl nuclease have also been fully detailed in earlier publications[11]. The source of the cells has been described[14] except for the horse cell which was obtained from the American Type Cell Collection.

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Errata

In the letter "Stab initiation of explosions" by M. M. Chaudhri (Nature, 263, 121; 1976) the expression giving q_1 in equation (2) should be

$$q_1 = \left[1 + \sqrt{\left(\frac{\pi}{2} \frac{v(1 - \sin^2 15°)R\rho C}{4\lambda} \right)} \right]^{-1}$$