sky in the technically difficult region below 1 keV have produced interesting results on both the quasi-isotropic background radiation and on inherently cool or "soft" X-ray sources. An increasing number of intense soft X-ray sources, associated with old supernova remnants, including Cygnus Loop, Vela X and Pup A, contrast with the notable absence of any new supernova remnants in the Uhuru catalogue of 2-6 keV sources in a review of this topic by Dr K. Pounds (University of Leicester).

Perhaps the best evidence yet for line features (OVII and OVIII?) was reported in the Cygnus Loop spectrum between 0.5 and 0.7 keV from a Cal-Tech rocket experiment, making use of 'Teflon' and oxygen filters. The indicated mono-energetic features were of the expected strength for a thermal X-ray source at a temperature of 3-4 million degrees, in line with the current view that soft X-rays probably arise in the older supernova remnants from the interstellar gas, heated by the expanding "blast-wave". Dr H. Friedman (Naval Research Laboratory) reported some of the most impressive data yet on the X-ray background below 1 keV. Galactic latitude scans in two ~ 0.15 and 0.25 keV energy bands are best fitted by a two component source model, consisting of the extrapolated (extragalactic) background spectrum observed at higher energies and suitably attenuated by absorption in the galaxy, together with a population of low energy galactic sources which contribute most of the flux at low latitudes. From the observed latitude distribution the scale height of these (as yet unresolved) sources was deduced to be some five times the neutral H scale height or ~ 500 pc.

γ -Ray astronomy was relegated to the last hour of the final day, which was unfortunate because intriguing new balloon observations by several groups brought evidence—albeit somewhat conflicting—of the first galactic γ -ray sources in the 20-100 MeV energy range. If even a fraction of the exciting γ -ray results are confirmed there is little doubt that this infant branch of astronomy will be able to hold its own much better against its now well-established spectral neighbour at the next symposium in three years time.

FISHERIES

Salmon-Trout Hybrids

from our Marine Vertebrate Correspondent

HYBRIDIZATION between various members of the salmon family has been recorded in the scientific literature for a very long time, but it was not until the intense interest taken in improving salmonid fisheries during the past cen-

tury that anything more than casual observations were made. With the establishment of trout hatcheries, especially that at Howietown, Stirlingshire, in the 1870s hybrids were produced experimentally between salmon and trout, and other species, with a view to producing fish more suited to cultivation. Similar experimental crossings of these two species have been produced in recent work in Ireland. First generation hybrids between salmon and trout are thus well known from artificial crossings but have been rarely found in the wild.

A recent study (in *J. Fish Biol.*, 4, 233; 1972) by R. H. Payne, A. R. Child, and A. Forrest of the Salmon and Freshwater Fisheries Laboratory, Weymouth, has attempted to assess the degree of natural hybridization in British waters. The two species are closely related and externally similar in their migratory stages so that blood samples were used to distinguish the parent species and their hybrids. The fish were supplied by commercial salmon fishermen in estuaries and in coastal waters and were thus a sample of the migratory population of salmonids. The blood of salmon and trout and their hybrids contains single serum esterases, but that of the salmon has greater electrophoretic mobility when subjected to electrophoresis in gels of alkaline pH. It is thus possible to demonstrate by this method differences between the two species and also to detect any natural hybrids.

Payne *et al.* studied blood samples from more than four thousand fishes which on external examination were apparently salmon. Seventeen (nearly 0.4 per cent) proved to be natural hybrids between salmon and trout. It is thus apparent that hybrids are rather more common in nature than had been appreciated. During the summer of 1970 four such hybrids, obtained from the Amble, Northumberland, fishery, weighed 1.8, 2.2, 2.8 and 3.8 kg. The authors note that three of these fish would have been commercially acceptable as "grilse" and the heaviest as "salmon" (grilse being commercially defined as salmon of less than 3.6 kg), a situation of some interest in view of the United Kingdom regulations regarding correct labelling of food fish.

The figures produced by Payne *et al.* show, however, that the level of introgression is generally low in British waters, except for the north-east coast. Judged on the number of hybrids found in the Northumberland fishery, and that of the River Esk, Angus (0.9 per cent and 0.7 per cent of samples of 537 and 1,160 respectively), introgression in this area is relatively frequent. As Payne *et al.* point out, however, it is possible that elsewhere introgression may be as frequent but

the hybrids might have the general appearance of sea trout and would thus not have been sampled as putative salmon. On the other hand, the higher level of introgression in north-eastern areas might be explained by the generally shorter lengths of north-eastern rivers, with a reduced number of spawning areas and trout and salmon may thus be brought together on the redds.

Payne *et al.* conclude by suggesting that in rivers with large trout populations and a small salmon run the fertilization of salmon eggs by male trout may be an important contributory factor to the extinction of salmon. This interesting suggestion deserves further consideration and study, especially in areas where salmon appear to be becoming scarce.

RIBOSOMES

Binding Sites in Sight

from our Molecular Biology Correspondent

NOTWITHSTANDING the diverting conjuring tricks that have been performed with ribosomes — incomparably the most spectacular of which is to pull functioning ribosomes out of a hat containing the fifty-odd proteins and three RNAs—almost nothing is still known about the manner in which a protein recognizes its particular slot on the RNA and the nature of the interactions that anchor it there. The isolation and characterization of the primary protein binding sites on the ribosomal RNA are the most desirable objectives now on the horizon, and the indications are that they may fairly soon be achieved.

It seems to be established that among the twenty proteins of the 30S subunit of *Escherichia coli* there are six which bind specifically and strongly to the RNA in the first step of the assembly process. The most forthright approach to the isolation of protein-specific sites on the RNA is to digest the complexes formed by these proteins with a nuclease, and isolate such parts of the RNA as may be protected by the bound protein. A promising start was reported not long ago by Schaup *et al.* (*Mol. Gen. Genet.*, 114, 1; 1972), who digested the 1:1 complex of 16S RNA and the protein S4 with T_1 ribonuclease, and found that about 30 per cent of the RNA was preserved in an apparently essentially homogeneous ribonucleoprotein fragment. Digestion and fingerprinting of the RNA allowed only a tentative identification of some of the oligonucleotides with sequence tracts from near the 5' end of the 16S chain. An interesting feature, however, is that the protected RNA is not an unbroken chain: when analysed by gel electrophoresis it turned out to con-