Cool Gas in the Virgo Cluster?

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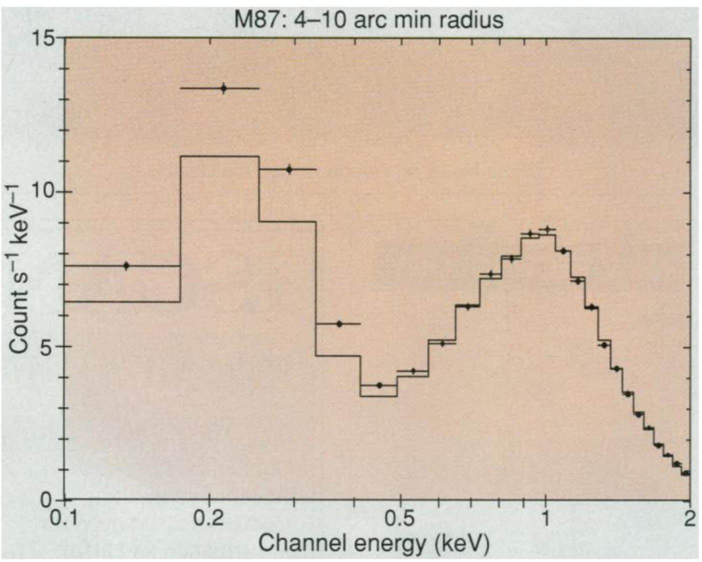
A vew of Virgo with the galaxy M87 at its center. [Photograph: Royal Observatory, Edinburgh/ Photo Researchers, Inc.]

Clusters of galaxies, such as the well-studied Virgo cluster, are marked by characteristic x-ray emission attributable to hot intergalactic gas, which is known to be at a temperature of about 20 million kelvin. As reported in a recent issue of *Astrophysical Journal*, Lieu and colleagues have made an interesting discovery (*1*) using data on the Virgo cluster taken with the Extreme Ultraviolet Explorer (EUVE). They found that the very soft x-ray emission from this region exceeds that expected from the hot intracluster gas, which might indicate the existence of a region of cooler condensed gas with a temperature as low as 500,000 K and a total mass of around 10^{11} solar masses. The relative soft x-ray excess is only about 10 to 20% after correction of the data for photoelectric absorption by gas in our own galaxy, but it could imply that they are seeing the tip of an iceberg, so to speak, if such a metaphor can ever be used for gas at 500,000 K. Most of the radiation from such gas would be absorbed along our line of sight by the interstellar medium (ISM).

The effect is observed not only with EUVE but also in data taken earlier with the x-ray astronomy satellite ROSAT. Lieu *et al.* used joint EUVE-ROSAT spectral fits to determine the best parameters for the soft excess. Because the raw data are now in public archives, it is possible to extract and examine the spectra oneself (see <http://heasarc.gsfc.nasa.gov/docs/rosat/archive.html> on the Internet). The figure shows the ROSAT spectrum obtained from an area 4 to 10 arc min around M87 with a model single-temperature spectrum that best fits the data above 0.5 keV. It is clear that there is a discrepancy between model and data at lower energies in the sense that the data show a soft excess.



A background-subtracted, ROSAT spectrum of the region within 4 to 10 arc min of M87 in the Virgo cluster. The model (solid line) is the best fitting single-temperature model to the data above ~0.5 keV. Galactic absorption corresponding to a column density of 1.8×10^{20} cm^{-2} (*1*) has been included. Note the marked discrepancy between the model and data around 0.2 to 0.3 keV. [Courtesy of S. W. Allen, Institute of Astronomy, Cambridge University]

To assess the possible significance of the result, consider first what is known of clusters of galaxies and their x-ray emission. Clusters are the most massive bound objects known in the universe that are relaxed and have stopped collapsing. About one-twentieth of the total mass of a typical cluster is in stars and galaxies, two-thirds is in dark matter of unknown composition, and the remaining one-quarter or so is in a hot intergalactic gas known as the intracluster medium (ICM). The gas is at the virial temperature and emits principally in the x-ray band. The nearby Virgo cluster has been particularly well studied in the x-ray spectrum and has been mapped both spectrally and spatially. The emission peaks around the central giant galaxy M87, where the radiative cooling time of the ICM drops to below a billion years and cooler components have been detected (*2*). These components have temperatures down to about 5×10^6 K and are presumed to be the result of the gas around M87 cooling and flowing inwardly very slowly (that is, a cooling flow). As the gas cools, its density rises in order to maintain the pressure required to support the weight of the overlying gas, and the cooling itself, which is essentially a two-body process owing to the interaction of the electrons and ions, occurs more rapidly. Because of the rapid cooling, very little gas is expected to be observable at temperatures below about 5×10^6 K.

The previous x-ray data (*3*) indicate a cooling flow around M87 of about 10 solar masses per year. Lieu *et al.* found that the soft excess would imply a rate of about 340 solar masses per year, which is enormous for a cluster with such a low x-ray luminosity. The level is more appropriate for a cluster 30 times more luminous and is indeed typical of some luminous clusters (*4*) that show very strongly peaked x-ray emission. In these clusters, the cooling takes place from the hotter gas, whereas for M87, the large rate is only inferred for the 500,000 K gas. If it is cooling at that rate, it will only last about a 10^8 years or so, and then its soft x-ray emission will vanish from detectability. A note added in the paper by Lieu *et al.* claims that there are similar soft excesses in several other clusters, including the well-known Coma cluster; the existence of such excesses would strongly argue against this excess being a transient, rare event.

I find it difficult to accept that a gaseous component of the ICM is kept at a temperature of 500,000 K by some unknown heat source, because the radiative cooling rate is then so high. The process is liable to be unstable so that either cooling wins and the gas cools out of detectability or heating wins and the gas heats up to join the bulk of the ICM. Overall, the interpretation of the soft excess as attributable to 500,000 K gas leads to puzzling consequences.

The soft excess can be made to disappear if the galactic absorption were slightly less than predicted. As it is, Lieu *et al.* report, from radio observations of the column density of galactic neutral hydrogen in this direction, a precise measurement that is less than that of earlier surveys. The reduction needed to eliminate the soft excess is

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slightly greater than that allowed by the uncertainties placed on this column density. It is not the hydrogen, however, that is the dominant soft x-ray absorber but helium and, to a lesser extent, the L shells of heavier elements. If for some reason, such as perhaps the way the gas is ionized, the abundance of neutral helium is different from the expected value (which is attributable mainly to the Big Bang), then agreement can be obtained with no soft excess. Indeed, the best fit to the spectrum (see figure) that I obtained with a single-temperature model is with (i) helium at 70% of the measured value and (ii) the other elements, including the absorbing hydrogen at 100% of the measured value.

It is not possible to measure the column density of neutral helium directly. The neutral-helium absorption model (5) used in most x-ray spectral models has been recently revised and is unlikely to be at fault. If some small absorption correction, attributable say to ionization, were generally applicable to the ISM, then its effect would not have been found with the spectra of active galaxies and quasars because they are often expected to show a soft excess. It is only with clusters that the predicted spectrum in the soft x-ray band should be reliable. An absorption interpretation accounts for the occurrence of the effect in other clusters and for the fact that, as a fraction, the soft excess appears to be constant with radius. This last point would require a rather peculiar emission model.

A further possibility is that the excess is the result of some calibration uncertainty. Such an uncertainty seems unlikely because the result was observed in at least two different detectors, but it would explain why the excess has not been reported before. Some of us who have worked on the ROSAT spectra of clusters have seen a similar effect earlier and dismissed it as either a calibration problem or an error in the galactic column density or have reported it without emphasizing it (6). Lieu *et al.* have done us all a service by highlighting the issue, which represents the discovery of either a new component of the ICM (or at least of clusters), a small correction to the x-ray absorption properties of the ISM, or a problem with the detector calibrations.

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The Whole Lactose Repressor

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When Monod and Jacob and their colleagues began studies of enzymatic adaptation and bacterial genetics in *Escherichia coli* at mid-century, they could not have known that deciphering the intricacies of these processes would open an entirely new field that is only today reaching its zenith. Regulation of genetic expression is central to survival in all living organisms, providing the ability to respond to chemical communication from intra- and extraorganismal sources. Our first glimpse into the elegance of genetic regulatory systems was provided by elucidation of the mechanism by which bacteria regulate expression of the enzymes for lactose metabolism.

Once the *lacI* gene product was identified as the agent that regulates expression of the lactose operon enzymes (*1*), purification of the lactose repressor protein (*2*) and in vitro demonstration of its DNA- and sugar-binding properties followed rapidly (*3*). However, solution of the crystallographic structure of this prototypic genetic regulatory protein, pursued by many research groups, eluded investigators for almost three decades. Attempts to coax diffraction-grade crystals from myriad solutions of this protein, even in the zero gravity of space shuttle missions, were uniformly unsuccessful. Even after yielding to crystallization (*4*), this protein has provided multiple challenges to solving the phase problem. The structures of the dimeric purine repressor and the core domains of *lac* and purine repressors produced by proteolytic removal of the NH_2-terminal DNA-binding domain (*5*) were solved only recently. In this issue, Lewis, Lu, and their colleagues report structures of the intact tetrameric lactose repressor protein and its complexes (*6*)—our first view of the repressor-operator and the conformational changes in this protein that result in its complex and fascinating behavior.

In the years since its initial purification, the lactose repressor has been a target of intense study. Extensive genetic information, equilibrium and kinetic analyses of ligand binding, as well as chemical and physical characterization of wild-type and mutant proteins have been compiled (*7*, *8*). This tapestry of data defines many of the characteristics of this molecule and enriches the insights provided by these structures. The assignment of binding capacities to core and NH_2-terminal domains, as well as a significant portion of phenotypic data on mutant proteins, can be rationalized effectively by the structures (*7*, *8*). The mobility of the NH_2-terminal DNA-binding domains is reflected in the absence of electron density for this region in the free and inducer-bound forms of the protein (*6*). Although contacts between the helix-turn-helix binding motif and operator DNA are not well resolved in the structure of the complex, the arrangement nonetheless indicates clearly the binding orientation and the involvement of the hinge helix in high-affinity binding. The rotation of two subdomains within the repressor core monomer in response to inducer binding reflects additional structural flexibility that may account for the difficulties in crystallizing this protein. The results of crystallographic analysis also confirm the utility of homology modeling methods to establish general folding patterns for crystallization-resistant proteins. The essential fold of the core domain monomer was predicted successfully for the lactose repressor on the basis of the crystallographic structures of bacterial periplasmic sugar-binding proteins (*9*).

Given homomeric assembly of this protein and knowledge of other tetramer structures, the V shape of the repressor tetramer and the consequent absence of 2:2:2 symmetry are surprising (see figure). Only a small buried surface (and hence small free energy) contributes to this quaternary arrangement. The separation of monomer-monomer and dimer-dimer subunit interfaces evident in the tetrameric structure was demonstrated initially by chemical and physical methods (*10*–*13*). Monomers associate to dimer through a surface of the bilobate core domain formed by residues distributed widely in the primary sequence (*6*); this interface transmits the allosteric communication between monomers (cooperativity) that accompanies inducer binding (*12*). In contrast, dimer-dimer assembly occurs by way of a compact four-helical bundle formed by only 18 COOH-terminal residues from each subunit, an arrangement predicted from genetic studies (*13*) and reminiscent of a similar motif in the eukaryotic regulatory protein p53 (*14*). No allosteric communication appears to occur through this interface. One of the key unanswered questions (not

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