US Department of the Interior

PART of North America's largest herd of caribou which migrates yearly between forest and tundra in northwestern Alaska. They regularly cross the basin of the Noatak river, one of the proposed National Wildlife Refuges which will be created as a result of the Alaska Native Claims Settlement Act of 1971.

The Noatak region lies in a transition zone between northern boreal forest and arctic tundra. With 500 species of vascular plants the flora of the proposed 7.5 million acre refuge is as great as that of the whole of Greenland or Iceland. The Department of the Interior intends to establish a 20-year moratorium on any developmental activities in the region to allow a comprehensive analysis of this intact slice of arctic ecosystem to be conducted. At a time when immense pressures are being applied to arctic ecosystems, in the form of roads, pipeline corridors and oil and gas extraction fields, the decision is as wise as it is opportune. What is learned from the analyses will benefit not only the future of the Noatak region but perhaps the future of all arctic lands.

be *cis*-dominant and *trans*-recessive and may be either 'up' (increasing transcription) or 'down' (decreasing transcription) in phenotype.

Clustering under common genetic control of the structural genes for enzymes of the same metabolic pathway is seen in prokaryotes but not eukaryotes, and represents an apparent distinction between these major phylogenetic groups. Taken together with their greater genomic complexity, the presence of large amounts of redundant DNA sequence and their intricate patterns of development and differentiation one might expect the gene control processes of eukaryotes to involve something more than those seen in prokaryotes. But the genetic analysis of gene control in eukaryotes has hardly begun and it is too early to say whether this expectation will be fulfilled. Two articles (Arst and MacDonald; page 26; Arst and Scazzochio, page 31) in this issue of *Nature* identify regulator sites involved in the control of two enzyme systems in the ascomycete fungus *Aspergillus nidulans*.

Proline catabolism in *Aspergillus* involves three enzyme activities: a permease, an oxidase and a dehydrogenase, which are under three distinct forms of control—induction by proline, nitrogen metabolite repression, and carbon catabolite repression. A probable structural gene for the permease (*prn*B) is tightly linked to a probable structural gene for a component common to both the oxidase and dehydrogenase (*prn*A). *prn*A$^-$ mutants lack oxidase and dehydrogenase and *prn*B$^-$ mutants lack the permease. All three activities are inducible, permease and oxidase are carbon catabolite repressible (dehydrogenase was not investigated), but only oxidase and dehydrogenase are nitrogen metabolite repressible—the permease is not. The two repression systems seem to act independently of each other. A gene *are*A is probably a regulator gene producing a positive control element which allows the synthesis of a large number of enzymes and permeases involved in nitrogen metabolism. One class of mutants (*are*A^r) leads to inability to use a variety of nitrogen sources including proline and presumably lacks a functional *are*A product. Second site mutations, called *prn*^{d}, restore the ability of *are*A^r mutants to utilise proline as a nitrogen source. *prn*^{d} mutations are *cis*-dominant, *trans*-recessive mapping betwen but not suppressing or allelic to *prn*A$^-$ or *prn*B$^-$ mutations, which are themselves tightly linked. *prn*^{d} mutations do not significantly affect the induced levels of enzymes and are probably best interpreted as carbon catabolite derepressed since uninduced levels of the products of both *prn*B (which is not ammonium repressible) and *prn*A are higher in *prn*^{d} mutants than in wild type in the presence of partial glucose repression.

The model favoured by Arst and MacDonald to explain their results of a regulator site (*prn*^{d}) located between two structural genes (*prn*A and *prn*B) is reminiscent of the divergent arginine operon in *E. coli*. They suggest that *prn*^{d} may be the binding site for a negative control element produced by a gene, such as *cre*A, identified by mutations which are commonly recessive and lead to carbon catabolite derepression.

In a second paper Arst and Scazzochio describe the isolation of a second site revertant (*uap*-100) of a mutant *are*-102 which has reduced levels of, among other enzymes, uric acid/xanthine permease. *uap*-100 is tightly linked to the probable structural gene (*uap*A) for uric acid permease. It is *cis*-dominant, *trans*-recessive and after maximal induction has a permease activity 2.5 times that of fully induced wild type. They interpret these results as identifying a regulator site with promoter-like properties.

Although the description of these two control systems is at an early stage it seems likely that Arst and his colleagues have identified an operon-type structure involved in proline catabolism and a promoter-like regulator site adjacent to the putative structural gene for uric acid permease in the eukaryote *Aspergillus nidulans*. The recent results of Hynes (*Nature*, **253**, 211; 1975) suggest that a similar regulatory mechanism affects the structural gene for acetamidase in *Aspergillus nidulans*.

Are mantle plumes jets or blobs?

from Peter J. Smith

IN a series of reports appearing over the past two years or so, Schilling and his colleagues (see, for example, Schilling, *Nature*, **242**, 565; 1973 and Hart *et al.*, *Nature phys. Sci.*, **246**, 104; 1973) have presented geochemical evidence which they claim is consistent with, and thus appears to support, the existence of a rising mantle plume beneath Iceland. In particular, they have interpreted the chemistry of basalt lavas from Iceland and surrounding areas in terms of two distinct magma sources—the conventional asthenosphere and a plume of hot primordial material derived from a much greater depth in the mantle. O'Hara (*Nature*, **243**, 507;

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