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Two separate lines of investigation have pointed to an important role(s) for Ian proteins in the development of T lymphocytes. First, a differential display study revealed that the expression of Ian1 is strongly induced at or after T cell-positive selection in the thymus; a wave of expression was also detected after the earlier b-selection stage (1). Second, positional cloning of lymphopenia (lyp), which is a major susceptibility locus for type I diabetes mellitus (iddm1) in the diabetes-prone BioBreeding (BB-DP) rat model of this disease (14, 15), has identified a frameshift (probably null) mutation in the Ian5 gene as the basis of this trait. In its homozygous state, the lyp mutation is associated with severe peripheral T cell lymphopenia (16, 17) and it has been demonstrated that both peripheral T lymphocytes and mature CD4⁺ and CD8⁺ single-positive (SP) thymocytes from lyp/lyp animals are much more susceptible to spontaneous apoptosis than their wild-type (w.t.) counterparts (18, 19).

Given these two independent indications of the importance of Ian genes in T cell development, one in mouse and the other in the rat, we undertook a study of gene expression of the entire Ian gene cluster in lymphomyeloid cells in order to assess expression levels of all Ian family members. We have commenced the study of Ian function by examining the susceptibility to c-irradiation-induced apoptosis of thymocytes and B cells isolated from lymphopenic rats which are homozygous for an Ian5 null mutation. We have developed polyclonal antisera against Ian1 and Ian9, and have used these reagents first to prove that the Ian9 gene, which is predicted to have an unusual triplicated structure comprising domains encoded by Ian11, Ian10 and Ian9, does indeed produce a corresponding protein product. Second, we determined levels of Ian1 and Ian9 proteins in various lymphoid populations.

Materials

Animals

Rats of the congenic strains PVG-RT1^uRT7^b, PVG-RT1^ulyp/lyp (18) and PVG (the latter used exclusively as a source of

macrophages) and C57BL/6 mice were maintained in specific pathogen-free conditions in The Babraham Institute Small Animal Barrier Unit. Animals (males and females) were used between 8 and 12 weeks of age. In unpublished analyses we have confirmed that the PVG-RT1^ulyp/lyp strain, which derives its mutant lyp gene from the Edinburgh subline of BB-DP rats (20), carries the frameshift mutation in the Ian5 gene described by Hornum et al. (11) and MacMurray et al. (2).

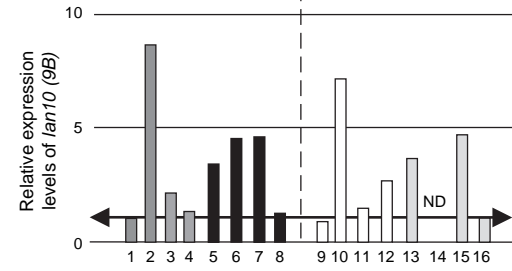
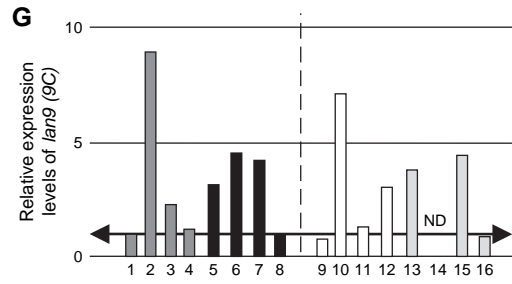
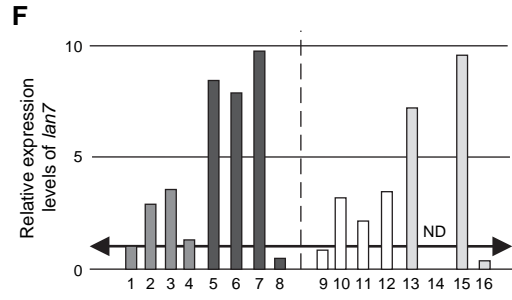
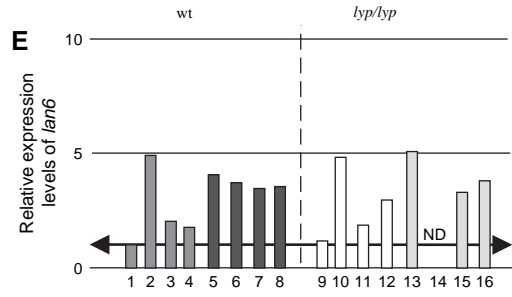
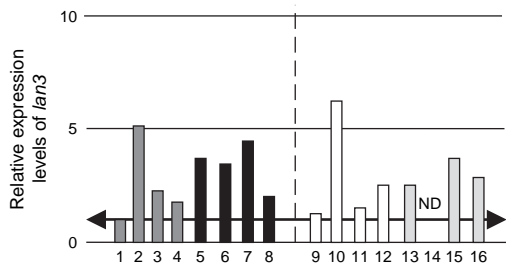
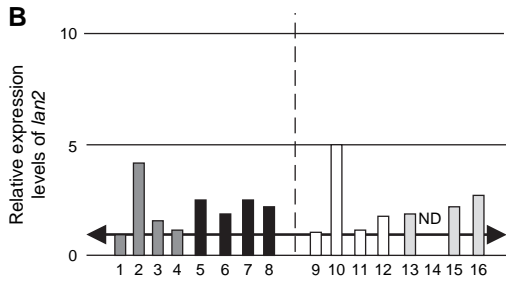
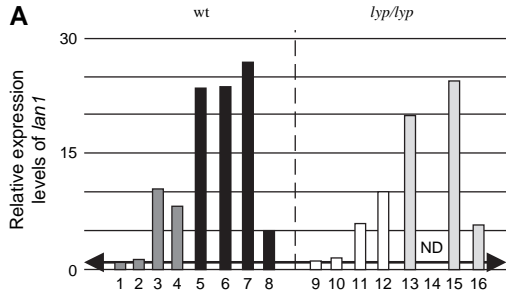
Sample preparation

Various rat primary cell sub-populations were isolated using combinations of mAbs with magnetic bead separations (DJTJ 0-1.6u1thy cell sub-0(L347 Tcway.428 P6e740(D)j)-356(5ra-352CS

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Real-time PCR set up

The two HKGs (6PFKc and cirhin) were selected for their stable expression in the cell populations isolated and studied (Supplementary Data, Figure S1 and Table S1, available at International Immunology Online): the M value, which is a measure of this stability (41), was 0.56 for rat, 0.64 for



It should be noted that where any expression was seen in cell lines this was generally of the order of expression seen in

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N-terminal third of the lan9 triple (formerly lan11); lan9B, corresponding to the central third of the lan9 triple (formerly lan10), and lan9C, corresponding to the C-terminal third of the lan9 triple (formerly lan9). Using trace data from the National Center for Biotechnology Information, we have also been able to assemble a dog lan9 sequence that lacks probably only a few residues at its amino-terminus. Predicted lan9 amino acid sequences for human, rat and dog are aligned in Fig. 5(A) where they are compared with an lan consensus. This alignment compares the three internal 'repeats' within lan9 (lan9A, lan9B and lan9C) and highlights the conserved elements of the GTPase motif (3, 51). A schematic represen-

It has yet to be determined whether any of the three potential GTP-binding regions of lan9 is active. Proteins containing multiple sets of guanosine nucleotide-binding domains are highly unusual but a precedent does exist in EngA (and its orthologues), present in all bacterial genomes and Arabidopsis. EngA contains two tandem GTP/GDP-binding domains. The crystal structure of the *Thermotoga maritima* EngA family member TM-Der has been solved (55). This study is particularly interesting in the context of the lan9 'triple' because it presents evidence that the two guanosine nucleotide-binding sites of TM-Der are not equivalent. Thus, while both sites have GTPase activity, the more C-terminal site, GD2, has an exceptionally slow intrinsic rate of release of the product GDP. This suggests that the two GTPase domains make different contributions to the regulation of the protein, presumably through different interactions with extrinsic regulators. We are obviously far from knowing the function of lan9 but the conserved sequence differences that we have pointed out between the three parts of the molecule suggest that similar subtle biochemical mechanisms may be at work as in TM-Der. We noted that in LN T cells, levels of lan9 protein are reduced when the cells originate from an lan5-deficient (*lyp/lyp*) animal. It is noteworthy that the decreases in protein levels of lan1 and lan9 observed in *lyp/lyp* as compared with *w.t.* LN T cells are discordant with the results obtained on mRNA levels by real-time PCR. This raises the possibility of post-transcriptional regulation of lan1 and lan9 expression: previously this has been suggested for hlan1 (3).

On a more general note, it will be important to find out whether all the lan family of polypeptides are engaged in the same cellular activity (e.g. apoptosis) or have diverse roles. The field of known GTPases offers a broad selection of possible functions ranging from the intracellular signaling 'switch', for which *ras* is a paradigm (51), to involvement in cytokinesis and vesicle trafficking, of which the dynamins and the septins (both carrying coiled-coil domains) are good examples (56, 57).

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We are grateful to Anne Cooke and Jenny Minson for providing antibodies. We thank Bethan Hughes, Michael Mimmack, Paul Evans, Steven Madison, Zoe Norgate and Jo Vandesompele for valuable advice on the real-time PCR. We thank Len Stephens for reading the manuscript. We thank Trevor Smith and Maureen Hamon for help with protein purification. This study was supported by the Biotechnology and Biological Sciences Research Council (BBSRC) initiative grant no. 202/GAN13085 to G.W.B. and J.R.M. and BBSRC Competitive Strategic Grant funding to the Laboratory of Functional Immunogenetics.

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Our attention has been drawn to the publication by Krückken et al. 2004. *Gene* 341:291., who showed bioinformatic and northern blot evidence for the existence of the lan9 'triple'.

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7-AAD 7-amino-actinomycin D
 BB-DP diabetes-prone BioBreeding
 DN double negative
 DP double positive

ER endoplasmic reticulum
 GAPDH glyceraldehyde-3-phosphate dehydrogenase
 GST glutathione-S-transferase
 h human
 HKG housekeeping gene
 lan immune-associated nucleotide
 ISH in situ hybridization
 LN lymph node
lyp lymphopenia
 m mouse
 ORF open reading frame
 6PFKc 6-phosphofructokinase C
 r rat
 SIRP signal regulatory program
 SP single positive
w.t. wild type

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