Pathway Analysis of Integrin Alpha X/Beta 2 (CD11c/CD18) in the Murine Mononuclear Phagocyte Lineage

Citation for published version:

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Peer reviewed version

General rights
Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy
The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.
Pathway Analysis of Integrin Alpha X/Beta 2 (CD11c/CD18) in the Murine Mononuclear Phagocyte Lineage

Barry M. Bradford, Andreas Lengeling, David P. Sester, David A. Hume, Tom C. Freeman & Neil A. Mabbott.

The Roslin Institute and R(D)SVS, the University of Edinburgh, Edinburgh, UK.

Introduction:
Integrin alpha X (CD11c) is commonly used to discriminate dendritic cells from macrophages within the murine mononuclear phagocyte lineage. ITGAL (CD11a), ITGAM (CD11b), ITGAX and ITGAD (CD11d) all dimerise with the integrin beta2 subunit (CD18) and act as pattern recognition receptors. As a group these integrins mediate cellular adhesion, phagocytosis and co-stimulatory functions within MNPs; however specific functions following ITGAX binding have yet to be defined. In order to rationalise the available data and information on ITGAX and its potential functional role, we have attempted to construct a pathway diagram of integrin alpha/beta2-mediated signalling utilising the modified Edinburgh Pathway Notation (mEPN) scheme.

Methods:
Following the meta-analysis of lineage-specific gene expression signatures in mouse leukocyte populations, the profile of ITGAX mRNA was observed to co-cluster with a restricted set of genes (highlighted in purple), the products of which suggest novel functions involved in the regulation of the actin cytoskeleton. Extensive mining of the literature guided by protein interaction data available in the STRING (functional protein interaction networks) and REACTOME (a curated knowledgebase of biological pathways) databases was performed until specific interactions with cluster gene products were identified.

Results:
Presented here is the current working pathway which operates as a detailed and extendable visual aid to understanding the functional context of ITGAX and this will be used to generate hypotheses and make in silico predictions of function.

References: