P. Crocker

Mammalian Carbohydrate Recognition Systems

Results and Problems in Cell Differentiation

Springer

Paul R. Crocker (Ed.)

Mammalian Carbohydrate Recognition Systems

With 52 Figures and 10 Tables

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33

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Preface

Over the last decade, the number of known mammalian carbohydrate binding proteins (CBPs) has increased considerably. With the recent completion of the human genome, this number is likely to increase further still. Fortunately, most of the known CBPs can be placed into a small number of distinct families based on the primary amino acid sequence. Currently, there are five recognised categories, namely C-type lectins, Galectins, I-type lectins, P-type lectins and legume-related lectins. In addition, there are 'stand-alone' CBPs such as the hyaluronic acid-binding protein, CD44, although here, too, recent evidence suggests that this CBP may be part of a larger gene family. Each class of CBP has a characteristic protein fold required for carbohydrate recognition and, in most cases, the three-dimensional structure of at least one member has been determined in the presence of a bound oligosaccharide ligand. Given the enormous complexity of carbohydrates themselves and the huge array of glycoproteins and glycolipids that present them, it is not surprising that CBPs are involved in remarkably diverse functions. This is exemplified by the Galectins which mediate specific functions in the nucleus, cytoplasm, cell surface and in the extracellular milieu. Other CBPs are found in discrete cellular and extracellular compartments in a way that is intrinsically linked to their known functions. The 12 chapters of this book are focused on structure-function relationships of these CBP families, including CD44, and are written by leading experts in the field. The order of chapters is based on the cellular localisation of CBPs, beginning with a review on the endoplasmic reticulum chaperones, calreticulin and calnexin, and ending with the Collectins, a group of remarkable molecules that function in host defence to pathogens. The intervening chapters cover Galectins and a range of membrane proteins (ERGIC-53, mannose-6-phosphate receptors, CD44, the mannose/GalNAc-SO4 receptor, Siglecs and Selectins). Collectively, they discuss the molecular basis for carbohydrate recognition and how this triggers various biological responses, ranging from control of glycoprotein folding to initiation of leukocyte recruitment in inflammation. The new millennium offers exciting opportunities not only to identify and molecularly characterise new CBPs but also to deepen our understanding of how carbohydrate recognition by this diverse group of proteins leads to 'glycosignalling' and control of cellular behaviour. I would like to take this opportunity to thank all the authors for their excellent contributions.

Paul R. Crocker, Dundee July 2000

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Contents

Lectins of the ER Quality Control Machinery

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Abbreviations. CNX: calnexin CRT: calreticulin CPY: carboxypeptidase Y CK2: casein kinase 2 ER: endoplasmic reticulum UGGT:UDP-glucose glycoprotein glucosyltransferase

1 Introduction

Calnexin was first identified as a type I transmembrane phosphoprotein located in the endoplasmic reticulum (ER; Wada et al. 1991). In subsequent work, this protein has been shown to belong to a new family of chaperones or proteins with lectin-like properties with orthologs present in all eukaryotes so far studied (Wada et al. 1991; Hebert et al. 1995). Calnexin and calreticulin, an ER luminal homologue, share extensive sequence similarity and both bind calcium.

Calreticulin was originally isolated as a calcium storage protein from the sarcoplasmic reticulum and the ER. Only later was it discovered that calreticulin also binds oligosaccharides and hence belongs to the calnexin-like lectins. Two calnexin homologues, calmegin (Watanabe et al. 1994) and/or calnexin-t (Ohsako et al. 1994), have also been described in testis and display the same 'lectin' properties as calnexin in their luminal domains and also cytoplasmic C-terminal regions. Regions of these proteins share amino acid sequence identity ranging from 42–78% (Wada et al. 1991).

2 Structural Aspects

Common features in the luminal domain of all calnexin and calreticulin-like proteins are the high affinity $Ca2^{+}$-binding site and the proline-rich repeat motifs 1 (I-DPD/EA-KPEDWDD/E) and 2 (G-W–P-I-NP-Y; Fig. 1A). The proline-rich motif is also known as the P-domain in calreticulin (Trombetta and Helenius 1998). Calnexin, calreticulin and calmegin all contain multiple

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