In focus in HCB

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Gastric gland mucin O-linked N-acetylglucosamine as a cancer biomarker

Mucins secreted throughout the gastrointestinal tract serve to protect the epithelial lining mucosa from local environmental insults (Corfield 2015). These mucins are heavily glycosylated with varieties of O-linked glycoconjugates, often containing unique terminal α -1,4-linked N-acetylglucosamine (α GlcNAc) residues, preferentially linked to the mucin core protein MUC6 (Zhang et al. 2001; see also; Corfield 2017 for review). Interestingly, these α GlcNAc moieties present in mucin have been shown to act as a natural antibiotic against the microbe *Helicobacter pylori*, an organism linked to gastric cancers (Kawakubo et al. 2004). In their review, Yamanoi and Nakayama (2018) discuss some clinical conditions in which the expression of α GlcNAc residues on gastric mucins are reduced relative to that of the MUC6 backbone itself. Specifically, they discuss results demonstrating that diminished expression of α GlcNAc on gastric MUC6 protein is related to the malignant potential of several pre-cancerous conditions of the gastrointestinal tract including pyloric gland adenoma of the stomach, chronic atrophic gastritis, Barrett's esophagus, and pancreatic epithelial neoplasias. The authors posit that immunohistochemical evaluation of α GlcNAc and MUC6 could be used as biomarkers for early detection of the malignant potential of several gastrointestinal lesions.

Seeking to crack the “sugar code”

Kaltner et al. (2018) provide an in-depth historical overview and discussion of lectins present in a variety of plant and animal organisms, including the endogenous galectins found in mammalian species (note: see also the special February 2017 issue of *Histochemistry and Cell Biology*, devoted to “The Sugar Code” for other topics in this area). Given the presence of anomeric orientations of carbohydrate linkages among glycoconjugates, the potential structural variety and diversity of the formed sugars is enormous. Thus, unlike the linear nucleotide and amino acid codes, the “sugar code” (Gabijs and Roth 2017) has to date proven refractory to solving. The review presents a detailed history of the discovery of “lectins”, including their crucial role in the categorization of blood group antigens. Sprinkled throughout the review are interesting and relevant quoted passages from some of the early pioneers in “lectinology”, providing an intimate link with the historical progress in this field. The review also includes discussions of lectin–glycan binding and provides multiple examples of the relevance and physiological significance of the complex carbohydrate moieties present on cellular and extracellular proteins and lipids. Ongoing and future investigations will seek to unravel the “sugar code” and decipher the complex glycome.

Hematopoietic potential of the proepicardium

The hemogenic endothelium (HE), a specific subpopulation of endothelial cells of embryonic blood vessels, is the source of hematopoietic cells (Dzierzak and Speck 2008; Jaffredo et al. 1998). The existence of HE has been demonstrated in various embryonic tissues including the endocardium (Nakano et al. 2013). The mouse proepicardium provides the progenitor cells for heart development, but it also has its own endothelium-lined capillary system (Niderla-Bielińska et al. 2015). Based on this finding,

The following two review articles, both highlighting aspects of glycoconjugates, appear in this issue as part of the 60th anniversary of *Histochemistry and Cell Biology*.

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Jankowska-Steifer and colleagues (2018) now show that cultured proepicardial cell populations, in particular the CD31⁺/CD45[−]/CD71[−] cell population, have hematopoietic potential. They produced colonies of different types containing either granulocytes, erythrocytes, monocytes/macrophages and megakaryocytes, or granulocytes and macrophages, or erythrocytes as shown by immunohistochemical detection of CD31, CD41, CD71, c-kit, Mpl, Fli1, Gata-2, and Zeb1. Among others, colocalization of the proepicardium-specific marker WT1 and the HE-specific Runx1 was observed. The hematopoietic potential of the proepicardium was also verified by in situ mRNA detection of genes specific for the HE such as Runx1, Notch1, Gata2, and Sox17.

SGBS pre-adipocytes: phenotypic changes and browning

The Simpson–Golabi–Behmel syndrome (SGBS) is characterized by pre- and postnatal gigantism, developmental delay, macrocephaly, abnormal facial appearance with prominent eyes, polydactyly, and additional malformations (DeBaun et al. 2001). The SGBS cell line, isolated from the subcutaneous adipose tissue of an infant with SGBS, represents an in vitro model for pre-adipocytes (Wabitsch et al. 2001). Montanari and Colitti (2018) have investigated in detail the phenotypic changes of SGBS cells occurring during their differentiation by quantifying lipid droplets, mitochondrial morphology, and a panel of genes involved in adipocyte differentiation and browning. For this, differentiation-related changes were analyzed at day 0 and during differentiation at days 7, 14, and 21. Lipid droplets increased in size up to day 21, but their number per cell remained unchanged. Likewise, the expression of peroxisome proliferator-activated receptor γ , leptin, and lipase E continuously increased up to day 21. In contrast, adiponectin reached a peak at day 14, decreasing afterward. Another behavior was observed for genes involved in the browning process, decreasing from day 0 to day 7, increasing afterward, and peaking at day 21. Mitochondria exhibited a significant shift from a networked profile at day 7 to a fragmented and swollen one at days 14 and 21. Together, this study demonstrated striking phenotypic changes during the differentiation of SGBS cells.

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