Energy and metabolic alterations in predisposition to pheochromocytomas and paragangliomas: the so-called Warburg (and more) effect, 15 years on

Hartmut P H Neumann and Wouter de Herder

Unit for Preventive Medicine, University Medical Center, Albert-Ludwigs-University, Hugstetter Straße 55, D-79106 Freiburg, Germany

1Department of Internal Medicine, Sector of Endocrinology, Erasmus Medical Center, Rotterdam, The Netherlands

It happened in Pittsburgh, Pennsylvania, USA, in the year 2000. Bora Baysal, MD, PhD, a Turkish molecular biologist and trained pathologist, collaborated with physicians from Leiden, The Netherlands, who took care of the famous and etiologically puzzling Dutch paraganglioma family. He and his collaborators mapped the susceptibility gene locus to 11q23 and linked it to a gene encoding one of the four subunits of succinate dehydrogenase (mitochondrial complex II, SDHD), an enzyme that lies at the all-important crossroads of energy production, the Krebs tricarboxylic acid cycle and the glycolytic chain. The bombshell was dropped in the journal Science 15 years ago (Baysal et al. 2000). Paraganglioma syndrome ‘type 1’ (PGL1) finally had a genetic etiology: germline mutations of the SDHD gene. Within months, the SDH components B and C (together with SDHD umbrellaed under SDHx) were shown to predispose to similar tumors, if the respective genes (SDHB and SDHC) were mutated (Niemann & Müller 2000, Astuti et al. 2001). Soon there was evidence that not only head and neck paragangliomas but also pheochromocytomas and paragangliomas of the retroperitoneum and chest were caused by germline mutations of these genes (Gimm et al. 2000, Eng et al. 2003). These paradigm-shifting discoveries led to an onslaught, which continues today, of multiple studies both in paraganglioma and pheochromocytoma but more broadly into energy production and metabolism in carcinogenesis.

Lest we be caught up in this marathon sprint, let us pause to loudly celebrate the 15th anniversary of this discovery. Let us linger for a moment to enjoy and acknowledge all the achievements and progress in this field, highlighted by this special issue of Endocrine-Related Cancer. Baysal & Maher (2015), aptly, kick off this special issue with an overview of the genetics of the first two genes, SDHB and SDHD, in paraganglioma and pheochromocytoma.

SDHD became the first enzyme demonstrating that damage of the mitochondria is really a key feature in tumor cells opening a new chapter on the Warburg effect, the aerobic glycolysis by tumor cells. The paraganglionic tumors are, meanwhile, closely linked to mitochondrial insufficiency after the identification of structural abnormalities in three key enzymes, SDH, fumarate hydratase (FH) and malate dehydrogenase (MDH). Mannelli et al. (2015) present an erudite review on metabolism and pheochromocytoma/paraganglioma.

As appears typical of translational genetics, rapid scientific progress precedes clinical practice. For the latter, the neoplasia risk spectra had to be defined regarding age of manifestation, tumor location, tumor number, malignant tumors and tumor growth as well as longer-term outcome (Neumann et al. 2002, 2004, Gimenez-Roqueplo et al. 2003, Schiavi et al. 2005, Benn et al. 2006). In parallel, judicious effective clinical management had to be adjudicated, including adequate treatment for symptomatic and also for pre-symptomatically detected tumors. Organ sparing and endoscopic operation techniques were developed. With in-depth investigation and longitudinal follow-up, genetic counselors became equipped with risk estimates, incomplete penetrance (e.g., SDHB) and maternal imprinting (e.g., SDHD). With the diverse
locations of the paraganglial tumors and the subsequent identification of extra-paraganglial tumors such as epithelial thyroid cancers, renal cell carcinomas and, more recently, pituitary tumors (Lopez-Jimenez et al. 2008, Xekouki et al. 2012, Varsavsky et al. 2013, Denes et al. 2015), it became obvious that a multidisciplinary care (and research) strategy would optimally serve patients and families. As such, Benn et al. (2015) review the state-of-the-art knowledge on clinical manifestations of paraganglioma syndromes type 1–5. O’Toole et al. (2015) review the recent association of pituitary adenomas, and Tischler & deKrijger (2015), our reference pathologists, touch a problem that has been widely forgotten: the key role of the pathologist in the diagnosis and management of pheochromocytoma and paraganglioma and the identification of occult heritable cases.

When a major strategy of risk management is based on early diagnosis and surveillance, imaging technologies should continually improve and use energy and metabolic alterations in predisposition to pheochromocytomas and paragangliomas. Castinetti et al. (2015) redefine the position of nuclear medicine imaging of paraganglial tumors, especially those with still normal catecholamines/methanephrines or those with malignant spread detected by computerized tomography (CT) scanning and magnetic resonance imaging (MRI) from the viewpoint of the underlying germline mutations or a given malignant spread. New and old tracers had to be checked for their relevance for the diagnosis.

After the initial flurry of SDHx, it appeared that there remained many clinical high-risk individuals and families who were unaccounted for. It took a decade to characterize additional susceptibility genes, and again energy and metabolic alterations were shown to be affected: SDHA germine mutations for pheochromocytoma (Burnichon et al. 2009), SDHAF2 for familial head and neck paragangliomas (Bayley et al. 2010), FH (Castro-Vega et al. 2014), and most recently MDH2 in malignant pheochromocytoma (Cascón et al. 2015).

Exiting are cross-phenomenons of oxygen-sensing enzymes involved in the pathogenesis of extra-paraganglionic tumors. Structural alterations of the discussed key enzymes, in addition to the von Hippel Lindau (VHL) protein, by germline mutations followed by somatic mutation, e.g., biallelic inactivation, are involved in the pathogenesis of renal cancer. This was shown for the VHL gene (Neumann & Zbar 1997, Ebele et al. 2004), the SDHB gene (Vanharanta et al. 2004, Ricketts et al. 2008, Gill et al. 2011a,b), the SDHC gene (Malinoc et al. 2012) and the SDHD gene (Ricketts et al. 2012) in clear cell renal cancer and is likely to occur also for the FH gene in papillary renal cell cancer type 2 (Tomlinson et al. 2002).

Finally, as is the case for many cancer predisposition genes, these uncommon paraganglioma and pheochromocytoma susceptibility genes and their metabolic pathways have been shown with time to a play major role in both sporadic paraganglial and extra-paraganglial neoplasias.

‘If you want to find the secrets of the universe, think in terms of energy, frequency and vibration’

— Nikola Tesla

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of this editorial.

Funding
This editorial did not receive any specific grant from any funding agency in the public, commercial or not-for-profit sector.

Author contribution statement
The contribution of each co-author is 50%.

References


Received in final form 8 July 2015
Accepted 13 July 2015
Made available online as an Accepted Preprint 17 July 2015