A bittersweet symphony

Adrian F Daly and Albert Beckers
Department of Endocrinology, Centre Hospitalier Universitaire de Liège, University of Liège, Domaine Universitaire du Sart-Tilman, 4000 Liège, Belgium

Abstract

This issue analyzes new work expanding the range of how genetic dysregulation of succinate dehydrogenase subunit (SDHx) genes can cause cancer syndromes with a prominent endocrine component, in this case Carney triad, which is characterized by gastrointestinal stromal tumors, paraganglioma, and pulmonary chondromas.

Introduction

Carney triad was originally recognized following the painstaking clinicopathological work of Dr J Aidan Carney at the Mayo Clinic between 1975 and 1977 (Carney et al. 1977). The initial triad consisted of gastric gastrointestinal stromal tumor (GIST; at the time gastric ‘leiomyosarcoma’), paraganglioma, and pulmonary chondroma. While it is traditional to use the term GIST in describing the gastric lesions in Carney triad, they are probably better described as ‘gastric stromal sarcoma’. Subsequently, other features – some of which were present in the early cases – have been added to the original triad, including adrenal cortical adenoma and esophageal leiomyoma; as noted by Dr Carney himself, what started as a triad may actually be a pentad (Carney 2009). Carney triad has long been a puzzling entity, having all of the features of a genetic disease, including multiple rare tumor types occurring metachronously or synchronously in different organs and having particularly aggressive features, including young age at onset. This profile in Carney triad is accompanied by a remarkably strong female predisposition. However, unlike the overlapping autosomal dominant Carney–Stratakis syndrome (CSS) of paraganglioma and GIST (Carney & Stratakis 2002, McWhinney et al. 2007, Pasini et al. 2008), Carney triad is not a familial condition. This has led to the question being raised on more than one occasion: is Carney triad a genetic disorder? (Matyakhina et al. 2007, Stratakis & Carney 2009).

Succinate dehydrogenase gene dysregulation is instrumental in orchestrating various endocrine cancer syndromes

The past few decades have observed remarkable successes in determining the causes of paragangliomas and GIST, two of the component tumors of the Carney triad (Neumann & Eng 2009, Barnett et al. 2013, Vicha et al. 2014). The number of mutated genes associated with sporadic and familial types of paraganglioma/pheochromocytoma has grown rapidly, involving processes that generally cluster as hypoxic/oxidative and kinase-dependent pathways (Gimenez-Roqueplo et al. 2012, Vicha et al. 2014). Core to our understanding of the pathogenesis of many of these tumors is the role of dysregulation of succinate dehydrogenase (SDH) subunit genes, SDHA through SDHD (collectively SDHx). Mutations of these genes occurring at the germline and somatic levels interfere with mRNA expression and protein function and have profound effects on tumoral biochemical pathways, thereby enhancing neoplastic growth. However, genetic modulation of SDHx function is not limited to a paraganglioma–pheochromocytoma phenotype alone. CSS is also caused by SDHx mutations, while mutations in these genes are also an important cause of sporadic GIST (McWhinney et al. 2007, Pasini et al. 2008, Janeway et al. 2011). Given that SDHx mutation syndromes also encompass a group of mitochondrial/neuromuscular
disorders (Alston et al. 2012), it is clear that the clinical phenotypes associated with SDHx mutations are remarkably varied.

Mutation, however, is only one of a number of mechanisms by which alteration in gene function may occur in cancers. For instance, epigenetic alterations are well established as playing an important role in both syndromic and sporadic endocrine cancers (Rodriguez-Rodero et al. 2014). This issue of Endocrine-Related Cancer reports results of a new study that demonstrates that specific and preferential hypermethylation of one SDH subunit gene (SDHC) is a crucial pathophysiological event in Carney triad (Haller et al. 2014). This study led by groups at the Eunice Kennedy Shriver National Institute of Child Health and Human Development and the Friedrich-Alexander University Erlangen-Nuremberg, Germany, demonstrates that hypermethylation of the SDHC promoter region is an abnormality that is specific to Carney triad tumors when compared with similar tumors that occurred outside of the setting of Carney triad. This epigenetic mechanism of SDHC silencing as a tumorigenic mechanism was further underlined by the demonstration of a marked reduction in SDHC mRNA in Carney triad tumors, decreased SDHC protein on Western blots of tumors, and a reduced functional activity of complex II that was attributable to SDHC deficiency. Crucially, this molecular genetic signature of a specific SDHC abnormality in Carney triad tumors differentiated them markedly from similar tumors such as sporadic GIST due to KIT mutations or familial paraganglioma syndrome type 1. This finding answers a long-standing conundrum about the etiology of Carney triad (yes, it is an (epi)genetic disorder!). It also expands significantly the variety of mechanisms by which SDHx gene dysregulation can orchestrate various distinct and overlapping neoplasia syndromes.

While the findings described herein by Haller et al. (2014) are the first to definitively link SDHC genetic dysregulation to tumorigenesis in Carney triad, earlier work from the Stratakis group had suggested that SDHC might have a role to play. Matyakhina et al. (2007) demonstrated that among 41 tumors in 37 cases of Carney triad, the most frequent recurrent genetic abnormality was a large-scale copy number loss that included the locus for SDHC (chromosome 1q21–q23.3). In addition to the epigenetic mechanism for the etiology of Carney triad through hypermethylation and silencing of SDHC, Haller et al. (2014) noted a definite – albeit less clear-cut – hypermethylation signal at the SDHB promoter. This epigenetic silencing profile of SDHB, along with SDHB copy number changes and loss of SDHB staining in Carney triad tumors implies that SDHx-related abnormalities might be somewhat more generalized than SDHC alone (Matyakhina et al. 2007, Gaal et al. 2011, Hallet et al. 2014). Study of more Carney triad tumors will help to define the relative variability or specificity of hypermethylation patterns in SDHC and SDHB. The etiology of this seemingly specific SDHC-focused epigenetic profile in Carney triad remains to be explained. This finding stands in sharp contrast to the more general hypermethylation profile in tumors from patients with germline SDHx gene mutations (Killian et al. 2013, Letouze et al. 2013).

The finding of a specific SDHC hypermethylation profile of tumors in Carney triad raises the possibility of using this epigenetic signature to study the nature of Carney triad itself. Carney triad is a disease characterized by incomplete disease penetrance. Patients usually present with only one of the component tumors, and a further third have two of the three tumors; presentation with all three together is very rare (Carney 2009). As only a quarter of patients will eventually develop all three tumors during their lifetimes, 75% of cases will have a gastric stromal sarcoma plus a pulmonary chondroma or a paraganglioma (Carney 2009). The presence of a specific SDHC hypermethylation signature in affected tumors could add a new method for firming up a suspected diagnosis of Carney triad in patients who have undergone surgical biopsy or resection. This molecular genetic signature could also assist in determining whether apparently sporadic GIST or paragangliomas might represent emerging Carney triad or CSS cases. This type of information could be useful clinically where family medical history is not known or is incomplete. Collection of clinical, pathological, and genetic information regarding patients and their tumors has already shown itself to be of help in studying the role of SDHx mutations in the etiology of paraganglioma syndromes, and differentiating among various etiologies of GISTs (van Nederveen et al. 2009, Gaal et al. 2011); we may need to incorporate tumoral epigenetic signatures into the pathology repertoire.

Using hypermethylation signatures, it could also be possible to explore the other potential disease associations with Carney triad. For example, the so-called fourth component of Carney triad, adrenal cortical adenomas, occurs in 19% of cases; most of them are unilateral and asymptomatic, with about half of them being detected by imaging (Carney et al. 2013). These tumors can be managed conservatively, but it would be intriguing to study existing excised adrenal tumors from Carney triad cases to examine if they too do demonstrate hypermethylation of SDHC. The potential involvement of other rare associations such as esophageal leiomyoma and esophageal carcinoid in the Carney triad could be similarly explored. Finally, the
reason for the remarkable female predominance of Carney triad will need to be assessed against the light of this new epigenetic disease mechanism.

Summary

Taken together, the range of syndromic conditions and sporadic tumors associated with abnormal SDHx gene regulation is increasingly varied. It is instructive, perhaps, to recognize that the mechanism by which a specific gene, such as SDHC, is dysregulated can lead to very important differences in disease characteristics at presentation and through the lifetime of the patient. The current study on Carney triad underlines the need to examine all of the different possible mechanisms of gene regulation when pursuing the etiology of unsolved endocrine tumor syndromes.

Declaration of interest

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

Funding

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

References


Received in final form 17 June 2014
Accepted 25 June 2014
Made available online as an Accepted Preprint 25 June 2014