REVIEW

Nutrigenomics: a case for the common soil between cardiovascular disease and cancer

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Abstract The border between health and disease is often set by a complex equilibrium between two elements, genetics on one hand, lifestyle on the other, To know it better, means to give new weapons, often crucial, in the hands of the doctors and their patients. It also means to adjust therapies, to find out which drug is good for a patient and which prevention strategy will work better for him/her. Nutrigenomics is an approach to individualize or personalize food and nutrition, and ultimately health, by tailoring the food to the individual genotype. In this review, we present the interaction between certain genetic polymorphisms and diet and increased cardiovascular or cancer risk. It is, indeed, now clear that a large number of bioactive food components may provide risk or protection at several stages of both atherosclerosis and cancer formation processes. We are giving here few examples of gene-food interactions relevant for both the risk of cardiovascular disease and cancer, since a common soil could exist in the genesis of cardiovascular disease and of some types of cancer (mainly gastrointestinal tract and hormonedependent).

Keywords Nutrigenomics · Cardiovascular disease · Cancer · Polyunsaturated fatty acids

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Introduction

The border between health and disease is often set by a complex equilibrium between two elements, genetics on one hand, lifestyle on the other, To know it better means to place new weapons, often crucial, in the hands of medical doctors and of their patients. It also means to adjust therapies, to find out which drug is good for a patient and which prevention strategy will work better for him/her.

Nutrigenomics is an approach to nutrition and human health that studies the effect of genetic differences in human response to food and how food has an impact on gene expression, biochemistry, metabolism and promotion of health [6, 54]. It is based on two main observations: (1) the nutritional environment modifies the expression of genes, and (2) depending on the genotype of an individual, the metabolism of nutrients may vary and ultimately result in a different health status [3]. Thus, nutrigenomics treats food as a major environmental factor in the gene-environment interaction, with the final aim to individualize or personalize food and nutrition, and ultimately individual strategies to preserve health, by tailoring the food to the individual genotype, similarly to the way pharmacogenetics would personalise therapeutic approaches by tailoring drugs to the individuals' genetic background [12].

A common soil presumably exists in the genesis of cardiovascular disease and some cancers, in particular gastro-intestinal cancers and those hormone-dependent, such as breast, prostate or ovarian cancers [4].

It is now clear that a large number of bioactive food components may provide risk or protection at several stages of both atherosclerosis or cancer formation processes.

We are giving here few examples of gene-food interactions relevant for both the risk of cardiovascular disease and cancer.



Nutrigenomics and cardiovascular disease

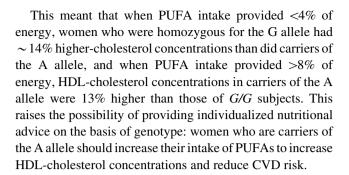
Nutrition has been largely recognized as an important risk protection factor for cardiovascular disease. Among dietary factors total fat and specific fatty acids have been mostly studied. Fatty acids food composition has been strongly related to lipid metabolism and consequently to metabolic risk factors and the risk of cardiovascular disease. However, such relation could be modulated by variations in genes that play a function in FA metabolism [42].

Apolipoprotein A1

Apolipoprotein (apo) A-1 is primarily found in high density lipoprotein particles (HDL). HDLs are produced by the liver and intestine and are responsible for the transport of cholesterol from peripheral tissues back to the liver for metabolism through a series of complex interactions with other lipoproteins, enzymes, transfer proteins, and receptors [62]. Both Apo A-I and HDL-associated cholesterol have been identified as protective factors for CVD [26, 59].

The gene coding for apo A-1, APOA1, which is found on the long arm of chromosome 11, is highly polymorphic and a specific single-nucleotide polymorphism (SNP) in its promoter region, known as APOA1–75G>A, [21, 36] has been extensively studied in relation to apo A-1 and HDL-cholesterol concentrations. A meta-analysis concluded that the rarer A allele may be associated with mildly increased apo A-1 concentrations [21].

One way in which diet may influence APOA1 gene expression is the intake of n-3 and n-6 polyunsaturated fatty acids (PUFAs). PUFAs can modulate the gene expression of several enzymes involved in lipid and carbohydrate metabolism [48, 50]. In a study involving 50 men and women fed diets rich in PUFA, reductions in LDL cholesterol associated with the PUFA diet compared with the saturated fat diet were more marked in women who were carriers of the rarer A allele than in women who were homozygous for the G allele, but no such effect was evident in men [35]. In another study, a significant interaction in terms of HDL-cholesterol concentration was observed between APOA1 genotype and PUFA intake [41]. In the latter study, subjects were divided into low (<4% of energy), medium (4-8% of energy) and high (>8% of energy) PUFA intake groups. In women who were carriers of the A allele, HDL-cholesterol concentrations increased significantly with increasing PUFA intake. The opposite effect was seen in women who were homozygous for the G allele (HDL-cholesterol decreased as PUFA intake increased). In men, PUFA intake had no significant effect on either HDL cholesterol or apo A-1 concentrations.



Apolipoprotein A5

The apolipoprotein A5 gene is another good example of recently reported gene-diet interactions. APOA5 gene is an important regulator of triglyceride (TG)-rich lipoprotein (TRL) metabolism [46] with two roles, (1) by assembling VLDLs [51, 58]; (2) as activator of intravascular TG hydrolysis by lipoprotein lipase (LPL) [16, 37].

Several common APOA5 SNPs have been associated with increased plasma total TG, RLP, and VLDL concentrations [27, 28, 43]. However, the association between APOA5 gene and postprandial lipid levels was suggested to be modulated by the type of fat consumed with the diet [20, 34].

In particular, the hypothesis that FA intake may modulate the effect of APOA5 variants on lipid metabolism was assessed in the Framingham population by Lai et al. [27], who examined the interaction between the APOA5-1131T>C and 56C>G polymorphisms and FA intake in their relation to the body mass index (BMI) and obesity risk in men and women. They found a consistent and statistically significant interaction between the -1131T>C SNP (but not the 56C>G) and total fat intake for BMI. In subjects homozygous for the -1131T major allele, BMI increased as total fat intake increased. Conversely, this increase was not present in carriers of the -1131C minor allele. The same authors found also significant interactions in determining obesity and overweight risks. APOA5-1131C minor allele carriers had a lower obesity and overweight risk compared with TT subjects in the high fat intake groups, but not when fat intake was low. When specific fatty acid group were analyzed, monounsaturated fatty acids showed the highest statistical significance for these interactions [27].

Endothelial nitric oxide synthase

NO is synthesized from the amino acid L-arginine by a family of enzymes, referred to as NO synthase (NOS). Three distinct isoforms of NOS have been identified to date [38]. The inducible NOO is expressed in vessel walls and



macrophages by certain cytokines and endotoxin lipopolysaccharides in pathological conditions [39]. The constitutive neuronal NOS is expressed in the central and peripheral nervous system as well as in the macula densa of kidneys. It plays important roles in physiological [52] and pathophysiological [23] conditions. The constitutive endothelial NO synthase (eNOS) is expressed in the endothelium, where it produces NO from L-arginine. NO diffuses from the endothelium to vascular smooth muscle cells, where it increases the concentration of cGMP by stimulating soluble guanylate cyclase, leading to vascular relaxation.

Several studies suggest that the basal release of NO from the endothelium contributes to basal vascular tone [44, 57] and regulates blood flow and blood pressure. Recent reports have suggested a possible role of NO in the pathogenesis of coronary spasm [25]; moreover, it inhibits the proliferation of smooth muscle cells [11], protects against platelet aggregation in vitro [9] and in vivo [60] and inhibits platelet adhesion to endothelium [45]. All these processes are important events during atherogenesis. A Glu298Asp polymorphism in the eNOS gene has recently been associated with development of ischemic heart disease and myocardial infarction [18, 19]. Preliminary data also indicated that Glu-Asp298 polymorphism is associated with coronary spasm [18, 19, 31, 61].

Dietary supplementation with n-3 fatty acids has been shown to improve microvascular endothelial function, in vitro, in those at risk for cardiovascular disease [40], and this may be a mechanism for the inverse association between fish consumption, the major dietary source of n-3 fatty acids, and cardiovascular disease mortality [15]. However, the impact on endothelial function of n-3 FA depends on eNOS genotype, a greater influence being observed in Asp298 carriers of Glu298Asp eNOS. Flowmediated arterial dilation (FMD), a nitric oxide-dependent endothelial response that can be measured non-invasively in vivo using high-resolution ultrasound is, indeed, influenced by such a SNP. Leeson et al. [31] found a positive association between plasma n-3 FA and FMD in Asp298 carriers, while in Glu298 homozygotes no association was found. The difference by genotype in the association between FMD and plasma n-3 FA levels was significant in an interaction model. Similar patterns were seen with red blood cell membrane n-FA.

Arachidonate 5-lipoxygenase (Alox 5 or 5-LO)

Another gene the activity of which can be modulated by PUFA is the arachidonate 5-lipoxigenase (5-LOX) gene. It is a key enzyme in the biosynthesis of leukotrienes, important mediators of inflammation [8]. In particular, the

dihydroxy leukotriene B₄ is a potent leukocyte chemoattractant, whereas the cysteinyl leukotrienes increase vascular permeability and promote contraction of vascular smooth muscle [49]. The 5-lipoxygenase pathway has been linked to atherosclerosis, a chronic inflammatory process involving the recruitment and accumulation of monocytes, macrophages, and dendritic cells in arterial walls, through ecicosanoid activation. [32, 47].

PUFA, n-6 or n-3 derived, can differently affect eicosanoid synthesis. Indeed, intake of omega 6 fatty acids increases while intake of omega 3 fatty acids decreases the production of leukotriens [7, 22].

Variation in the 5-lipoxygenase promoter have been demonstrated to alter eicosanoid-mediated inflammatory circuits in the arterial wall and promote atherogenesis. Carriers of the variant alleles of the tandem Sp1 binding motifs in the promoter of 5-LOX gene showed increased mean intima-media thickness (IMT) as compared with carriers of the wild-type allele.

Dwyer et al. [5] observed that dietary arachidonate and linoleic acid (n-6 FA) intake was associated with increased IMT in carriers of the variant 5-LOX genotypes, but not in wild type carriers. Conversely, dietary EPA and DHA (n-3 FA) intake was associated with a decrease in IMT in carriers of two variant alleles. Probably, dietary arachidonic acid and its metabolic precursor (linoleic acid) amplified the atherogenic effect of the variant genotypes by increasing the levels of eidcosanoids. In contrast, increased intake of eicosapentaenoic and docosahiexaenoic acids would reduce the production of inflammatory leukotrienes and inhibit their pro-atherosclerotic effect.

Nutrigenomics and cancer

Several pieces of evidence have repeatedly implicated dietary components and genetic susceptibilities as important determinants of cancer risk and tumor behaviour. Variation in cancer incidence among and within populations with similar dietary patterns suggests that an individual's response may reflect interactions with genetic factors, which may modify gene, protein and metabolite expression patterns. Diet composition in fatty acids has strong implications in the risk of cancer development and such effect may be mediated through gene-environment interactions as it has been described for cardiovascular disease risk.

Cyclooxygenase-2

Dietary intake of marine fatty acids from fish may protect against prostate cancer development. This association is



modified by genetic variations in cyclooxygenase-2 (COX-2), a key enzyme in fatty acid metabolism and inflammation [17].

Increasing evidence from animal and *in vitro* studies shows that omega-3 (ω -3) fatty acids, especially long chain eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), protect against prostate cancer [29, 53]. EPA and DHA are mainly found in fatty fish, and recent epidemiological studies showed that frequent consumption of fish is associated with reduced risk of prostate cancer [1, 55, 56].

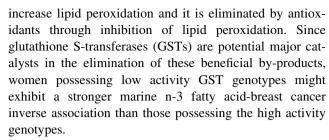
Polyunsaturated fatty acids, both n-3 and n-6, are converted in the body to eicosanoids, such as prostaglandins and thromboxanes. These compounds have several biological effects, including modulation of inflammatory and immune responses, cell differentiation and cellular growth. One of the mechanisms by which n-3 fatty acids may affect carcinogenesis is through their suppressive effect on the byosinthesis of eicosanoids derived from arachidonic acid (AA). In general, AA-derived eicosanoids have proinflammatory effects and may promote carcinogenesis, whereas EPA-derived eicosanoids have anti-inflammatory effects and may inhibit prostate cancer growth. A diet with a high ratio of n-3 to n-6 fatty acids results in a shift toward production of EPA-derived eicosanoids rather than AAderived eicosanoids and, as a result, may inhibit the development of prostate cancer.

Cyclooxygenase-2 (COX-2), a key enzyme in eicosanoid synthesis, is overexpressed in prostate cancer tissue when compared to benign tissue from the same patients [24, 30]. Also, use of nonsteroidal anti-inflammatory drugs (NSALDs), which inhibit the activity of COX enzymes, is associated with a decreased risk of prostate cancer [33].

In a case control study on 1,378 patients with prostate cancer and 782 controls in Sweeden, Hedelin and coworkers [17] observed a significant interaction between intake of salmon-type fish, rich in n-3 fatty acids and a genetic variant of COX-2 in determining the risk of prostate cancer. Among homozygotes or heterozygotes of the variant allele of +6365 T/C SNP of COX-2 gene, high intake of salmon-type fish was associated with a significant decrease in the risk of prostate cancer, while there was no association between fish intake and cancer risk in carriers of the wild-type allele.

Glutathione s-transferases

Marine n-3 fatty acids have been also associated with a protective effect against breast cancer in experimental studies and in post-menopausal women [10, 13, 14]. This inhibition is correlated with the extent of lipid peroxidation generated in tumor tissues or cells [2, 13]. The suppression of cancer growth by n-3 FA is enhanced by drugs that



In the Singapore Chinese Health Study, there were no associations between GSTM1 and GSTP1 genotype and breast cancer risk. However, the GSTT1 null genotype was associated with a 30% reduced risk of breast cancer. Moreover, the association between marine n-3 fatty acid and breast cancer was analysed after stratification by GSTM1, GSTT1 and GSTP1 genotypes. They found that women with genetic polymorphisms encoding lower or no enzymatic activity of GSTT1 experienced more breast cancer protection from marine n-3 fatty acids than those with high activity genotypes, consistent with the hypothesis that the peroxidation products of n-3 fatty acids are directly involved in breast anticarcinogenesis.

Conclusion and perspectives

The Nutrigenomic approach may offer some clues to the proposed "common soil" between cardiovascular disease and cancer. Nutritional factors, indeed, are important mechanisms for development of both ischemic cardiovascular disease and highly prevalent types of cancer. However, the mechanisms linking diet to these diseases are still not completely understood. The area of nutrigenomics is expanding and gaining momentum. Although the evidence base is growing, consistent data are lacking, which hampers the ability to make specific recommendations. This can be addressed with population studies of appropriate experimental design, clinical trials of adequate size and quality, and product-specific trials in subjects selected for specific genetic variants.

As progress continues to be made in developing the scientific evidence base for nutrigenomics, attention must also be paid to addressing some of the other issues surrounding the field, such as acceptance by the public and establishing appropriate, credible sources to disseminate information.

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