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Special Article

Lessons Learned From Past Gene-Environment Interaction Successes

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Genetic and environmental factors are both known to contribute to susceptibility to complex diseases. Therefore, the study of gene-environment interaction (G×E) has been a focus of research for several years. In this article, select examples of G×E from the literature are described to highlight different approaches and underlying principles related to the success of these studies. These examples can be broadly categorized as studies of single metabolism genes, genes in complex metabolism pathways, ranges of exposure levels, functional approaches and model systems, and pharmacogenomics. Some studies illustrated the success of studying exposure metabolism for which candidate genes can be identified. Moreover, some G×E successes depended on the availability of high-quality exposure assessment and longitudinal measures, study populations with a wide range of exposure levels, and the inclusion of ethnically and geographically diverse populations. In several examples, large population sizes were required to detect G×Es. Other examples illustrated the impact of accurately defining scale of the interactions (i.e., additive or multiplicative). Last, model systems and functional approaches provided insights into G×E in several examples. Future studies may benefit from these lessons learned.

exposure; gene-environment; genome-wide association studies; interactions; metabolism genes; pathway genes; pharmacogenomics

Abbreviations: ALDH, aldehyde dehydrogenase; CYP, cytochrome P-450 family; FeNO, exhaled nitric oxide; *FTO*, fat mass– and obesity-associated gene; GWAS, genome-wide association study; G×E, gene-environment interaction; PD, Parkinson disease.

Genetic and environmental factors are both known to contribute to susceptibility to complex diseases. Studies of genetic variation range from hypothesis-driven studies examining a small number of candidate genes to more agnostic (i.e., hypothesis-free) surveys of variation across the entire genome, or genome-wide association studies (GWASs). GWASs leverage patterns of linkage disequilibrium with a high density of genetic markers to capture a large proportion of the common genetic variation in a population. Therefore, gene-environment interaction (G×E), defined broadly as the interplay between gene(s) and environmental factor(s) as they affect some trait (discussed in Gauderman et al. (1)), is a focus of studies addressing chronic diseases such as neurodegeneration, cancer, and asthma, and more recently also pharmacogenomics applications—the former to better understand biological pathways to disease or identify subpopulations susceptible to specific exposures in human studies and the latter to contribute to "precision medicine" and treatment plans tailored to the genetic makeup of patients (2). We selected G×E examples that we knew to have been successful in reaching these aims, illustrating different approaches and study designs that may have contributed to success.

The purpose of this paper is to describe a spectrum of approaches and underlying principles that have been successful for identifying G×E in order to inform future studies. These success stories may be broadly categorized as studies of single metabolism genes, complex metabolism pathways, broad ranges of exposures, functional approaches and model systems, and pharmacogenomics.

SINGLE METABOLISM GENES

Many of the genetic variants identified in G×E investigations are in metabolism genes and affect enzymatic function;

they may increase susceptibility to an environmental exposure and adversely affect health in exposed variant carriers. Recent efforts have focused on studying the genetics (or in some cases, epigenetics) of metabolism to identify single nucleotide polymorphisms that, by altering exposure metabolism, ultimately alter susceptibility to disease outcomes. Some of the oldest and best-characterized G×Es with well-established biologic relevance and human health consequences are classic Mendelian genetic diseases of single metabolism genes that depend on the presence of common environmental (dietary or pharmacological) agents to adversely affect health (Table 1, Lesson 1), such as phenylketonuria and glucose-6-phosphate dehydrogenase (G6PD) deficiency. Phenylketonuria is caused by a defect in the gene encoding the enzyme phenylalanine hydroxylase, which is needed to break down the amino acid phenylalanine. In children with phenylketonuria, the resulting amino acid accumulation is responsible for severe intellectual and developmental disabilities, and dietary restrictions that eliminate phenylalanine intake can minimize or prevent adverse outcomes entirely (3). Similarly, glucose-6-phosphate dehydrogenase deficiency is the

Table 1. Summary of Lessons Learned From G×E Research Activity.

Lessons	Interaction and Phenotype
1. G×E in metabolism genotypes/phenotypes are usually related to absorption, distribution, metabolism, and excretion (ADME) characteristics of targeted exposures. These are an obvious place to explore biological pathways and candidate genes.	Phenylketonuria and glucose-6-phosphate deficiency: single metabolism genes × diet/pharmacological agents
	CYP2D6/*PON1*/*ALDH2* with pesticide exposure for Parkinson disease
	NAT2 and smoking for bladder cancer
	*ALDH2*2* and alcohol intake for esophageal cancer
	AS3MT and arsenic for skin lesions
	Genes relevant to pharmacogenomics
2. G×E discoveries can lead to environmental interventions to prevent diseases (especially in cases where presence of both are required for outcome).	Phenylketonuria and glucose-6-phosphate deficiency: single metabolism genes × diet/pharmacological agents
	CYP2C9/*VKORC1* and warfarin for anticoagulation response
	Nicotine-metabolism genes and therapy for smoking cessation
	Aspirin/NSAIDs use and *MGST1*/*IL16* for colorectal cancer
3. Temporal considerations (birth cohorts, timing of exposure, etc.) may influence G×E findings and need to be considered.	*PON1* and pesticide exposure for Parkinson's disease
	FTO and physical activity for BMI
4. Quality of exposure assessment affects detection of G×E.	*PON1* and pesticide exposure for Parkinson disease
	FTO and physical activity for BMI
	NOS2 and traffic pollution for respiratory symptoms
5. Scale studied can affect the detection of interactions.	*NAT2* and smoking for bladder cancer
6. Large population sizes are typically needed for G×E discovery.	*NAT2* and smoking for bladder cancer
	FTO and physical activity for BMI (Caucasian populations)
	Aspirin/NSAIDs use and *MGST1*/*IL16* for colorectal cancer
7. Variability in exposure distribution increases the power to detect G×E and the importance of investigating ethnically and geographically diverse populations.	*ALDH2*2* and alcohol intake for esophageal cancer
	FTO and physical activity for BMI
	AS3MT and arsenic for skin lesions
	NOS2 and traffic pollution for respiratory symptoms
	Carbamazepine × *HLA-B**1502 for Stevens-Johnson syndrome
8. No single G×E method is universally the most powerful. The appropriate G×E method depends on underlying assumptions, correlations between risk factors, and the true G×E model.	*ALDH2*2* and alcohol for esophageal squamous-cell carcinoma
	See Gauderman et al. (1)
9. Studying highly exposed populations/cohorts can provide high-quality exposure assessment.	*FTO* and physical activity for BMI
	10q24.32 × arsenic and arsenical lesions
10. Model systems and functional approaches may provide G×E insights.	Genetics of lead susceptibility (*Drosophila* model)
	FTO and physical activity for BMI (human tissue samples/mouse models)
	ALDH2 and pesticides for Parkinson disease (ex vivo model system)
	NOS2 and traffic pollution for respiratory symptoms (biomarker study)

Abbreviations: *ALDH2*, aldehyde dehydrogenase 2 gene; *AS3MT*, arsenite methyltransferase gene; BMI, body mass index; CYP, cytochrome P-450 family; *FTO*, fat mass– and obesity-associated gene; G×E, gene-environment interaction; HLA-B, human leukocyte antigen-B; *IL16*, interleukin 16 gene; *MGST1*, microsomal glutathione s-transferase 1 gene; *NAT2*, N-acetyltransferase 2 gene; *NOS2*, nitric oxide synthase 2 gene; NSAID, nonsteroidal antiinflammatory drug; *PON1*, paraoxonase 1 gene; *VKORC1*, vitamin K epoxide reductase complex subunit 1 gene.

most common human enzyme defect, associated with neonatal jaundice and acute hemolytic anemia triggered by consumption of fava beans or treatment with antibiotic and antimalarial drugs (4). These disease phenotypes are entirely preventable and amenable to environmental interventions; the outcome occurs only if both the genetic and environmental factors are present (Table 1, Lesson 2).

GENES IN COMPLEX METABOLISM PATHWAYS

In contrast to the enzymes involved in phenylketonuria and glucose-6-phosphate dehydrogenase deficiency, many other metabolizing enzymes are biologically versatile and often redundant in their actions (5), which complicates relating any single genotype to a phenotype of interest. Nevertheless, early G×E studies focused on polymorphic variants in metabolism genes that affect enzymatic or metabolic function of proteins that activate or detoxify exogenous and endogenous toxins. Examples include members of the large microsomal oxidative cytochrome P-450 (CYP) superfamily of proteins (6), N-acetyltransferase 2 (NAT2) (7), and glutathione S-transferases (GSTs) (8) that are implicated in cancer (9), Parkinson disease (PD) (10), and Alzheimer disease (11). For example, long before the first familial PD gene was identified, the "poor metabolizer" enzymatic phenotype of the cytochrome P450 2D6 (*CYP2D6*) gene was the first PD candidate gene (12, 13) because the enzyme is active in the brain region linked to PD, metabolizes relevant endogenous neural compounds (14, 15), and inactivates neurotoxins known to cause Parkinsonism in animal models and humans (16). Many population studies have shown an increased risk of PD for *CYP2D6* poor metabolizers compared with all other metabolizer types (17), and some PD studies that include pesticide exposures also observed G×Es for poor-metabolizer variants of *CYP2D6* (18–21) (Table 1, Lesson 1).

Additionally, common variants of the paraoxonase 1 (*PON1*) gene act on the toxic oxon (metabolite) of organophosphate pesticides and are well characterized with regard to their influence on enzyme activity in human serum (22, 23). Thus, in populations with chronic organophosphate exposure, carriers of slow-metabolizer variants of the *PON1* gene have been shown to be at increased risk for PD (elderly) and developmental deficits (children) (Table 1, Lesson 1) (24). The PD studies were conducted among central California residents using records from the California Pesticide Use Reporting System to generate long-term organophosphate pesticide estimates with sophisticated geographic information system tools (25). The neurodevelopmental studies were able to rely on biomarkers of exposure collected during short but relevant periods in pregnancy (26, 27). In these studies, considering temporality of exposure was important due to the potential impact on early life (i.e., neurodevelopmental outcomes) and later-onset disease outcomes (i.e., PD) that needed to be examined to best characterize the interactions (Table 1, Lesson 3). Moreover, exposure-assessment approaches used in these studies were sophisticated and robust (Table 1, Lesson 4).

Another G×E example related to variation in metabolism genes is one of the best-established G×Es in cancer: the association of genetic variation in *NAT2*, smoking, and risk of bladder cancer (28) (Table 1, Lesson 1). NAT2 catalyzes metabolism of aromatic monamines, known bladder carcinogens found in cigarette smoke. Several common genetic variants in *NAT2* are related to reduced enzyme activity (29) and segregate populations into rapid-, intermediate-, and slow-acetylation phenotypes, which affect the ability to detoxify aromatic amines. Because tobacco smoking is a strong risk factor for bladder cancer, and aromatic amines found in tobacco smoke are known bladder carcinogens, reduced detoxification capacity was hypothesized to increase susceptibility. Indeed, studies in different populations consistently demonstrated that slow acetylation activity increases risk of bladder cancer among smokers but not among never smokers (7, 30–34). Many studies used candidate-gene approaches focusing on the hypothesis related to the role of *NAT2* in metabolism (7, 32–34). A genome-wide interaction analysis of smoking and bladder cancer, however, observed interactions with different single nucleotide polymorphisms depending on whether the interaction was evaluated on an additive or multiplicative scale (30), highlighting the importance of defining the scale of measurement discussed by Gauderman et al. (1) and by others previously (28, 35, 36) (Table 1, Lesson 5). Interestingly, the multiplicative interaction between *NAT2* and smoking, even though it is supported by strong prior knowledge, did not reach a genome-wide significance threshold. The authors estimated it would require over 15,000 cases with a 1:2 ratio of cases:controls to reach the statistical significance threshold (i.e., large sample sizes are required to discover G×Es without strong priors due in part to stringent significance thresholds required for agnostic studies) (30). Meanwhile, this interaction was observed in previous candidate-gene studies with 1,100–3,000 cases, illustrating the power of hypothesis-driven studies compared with GWAS approaches when prior knowledge exists (Table 1, Lesson 5, 6).

The well-established interaction between a variant in the aldehyde dehydrogenase (ALDH) 2 gene (*ALDH2*) and alcohol on risk of esophageal squamous-cell carcinoma (37–41) highlights several other considerations. Alcohol is oxidized to form acetaldehyde, a carcinogen. ALDH2 detoxifies acetaldehyde to acetate. The *ALDH2*2* allele slows this detoxification process (Table 1, Lesson 1). The obvious hypothesis—that an increase in risk due to alcohol consumption will be larger among individuals who carry the *ALDH2*2* allele—has been borne out in observational studies (38–41). Originally studied as a candidate gene, the *ALDH2*2* allele has also been "rediscovered" via GWAS, using both a marginal approach (testing for association without considering effect modification by alcohol intake) and using a G×E approach (41). There are 2 particularities to the *ALDH2* example worth noting. First, the *ALDH2*2* allele is common in East Asian populations but quite rare in European-ancestry populations. This underscores the importance of conducting studies in ethnically diverse populations—not only can this increase diversity of environmental exposures, it can increase diversity of genetic exposures (Table 1, Lesson 7). Second, *ALDH2*2* is associated with exposure. Individuals who carry an *ALDH2*2* allele experience an unpleasant flushing reaction to alcohol and are less likely to drink regularly or heavily (37). This gene-environment correlation has implications for downstream analysis. Tests that assume that genotype and environmental exposure are independent—such as the case-only test, a method to test association between genetic

and environmental factors within exposed and unexposed cases only—can be more powerful than tests that do not make this assumption when the assumption holds (42). Although this assumption may be reasonable for many (or most) tested variants (42), when it is violated, tests assuming gene-environment independence can have inflated type I error rates or decreased power. In the case of *ALDH2*2*, because the gene-environment correlation and G×E act in opposite directions, the case-only test failed to detect the *ALDH2*2*-alcohol interaction at a nominal level of association in a study where the standard logistic regression test of interaction including controls was highly significant (43). As this example illustrates, the most appropriate method or approach for analyzing G×E can be highly dependent on an understanding of underlying assumptions and correlations between risk factors. As discussed in more detail in Gauderman et al. (1) and McAllister et al. (44), no single G×E method is universally the most powerful approach, and efficiency depends on the hypothesis tested and underlying true G×E model (Table 1, Lesson 8).

VARIATION OF EXPOSURE LEVELS

Low exposure variability may be one key factor for not being able to identify G×E (45). A wide range of exposure levels among study participants provides greater statistical power for identifying G×E (1) and an opportunity to contrast different models (e.g., linear, threshold, age-specific) to understand how exposure affects the gene-trait relationship.

A compelling example of the benefits of targeting a population with both high- and low-exposure scenarios comes from a study of interaction between physical activity and the fat mass– and obesity-associated gene (*FTO*) on waist circumference conducted in a multicenter study in India (46). The study included 2 sites, one in northern India (New Delhi) and the other in southern India (Trivandrum), each including close to 500 individuals. The population in Delhi had low levels of physical activity, similar to what is typically observed in Caucasian populations. In contrast, the population in Trivandrum had a wide range of physical activity levels and included individuals with high or low activity. The original association between *FTO* genetic variation and obesity, generated primarily in Caucasian populations (47–49), was replicated in the Delhi population but not the Trivandrum population. However, in Trivandrum, an interaction was detected between physical activity and *FTO*—the association between *FTO* variant and obesity was strongest in individuals with low physical activity and diminished gradually with increasing levels of physical activity. This pattern of interaction has been replicated in studies conducted in Caucasian populations (50). However, due to a narrower range of physical activity, a much larger sample size ($n > 200{,}000$) was required for this interaction to achieve statistical significance (Table 1, Lesson 6). This example demonstrates the advantages of having robust measures of environmental factors and a wide range of exposure levels for identifying G×E, with strong variation in exposure increasing the power to detect G×E. Studying geographically, culturally, or sociologically diverse populations may make it more likely to observe variations in exposure (Table 1, Lessons 4, 7, 9). Another study showed that the influence of a common *FTO* variant on body mass index varies across birth cohorts, calendar time periods, and life cycles (51), illustrating the importance that temporal considerations may have for G×E studies and demonstrating that global or local environmental changes over time can modify the observed allelic penetrance of genetic risk factors for complex traits (Table 1, Lesson 3).

Another approach to achieving an adequate range of exposures is to examine a highly exposed population. Long-term exposure assessment on a study population highly exposed to a specific agent from the environment may provide unique insights for characterizing G×E if the population is well-characterized longitudinally. Inorganic arsenic is a known human carcinogen (52), and natural or man-made contamination of ground water used as drinking water in several regions across the globe makes this exposure a serious global health issue (53, 54), particularly in Bangladesh where >57 million people are exposed at levels exceeding the limit recommended by the World Health Organization (55, 56). A GWAS approach was used to identify genetic polymorphisms associated with an "arsenic-metabolism efficiency" phenotype, and these variants were found to affect risk of arsenical skin lesions (57). Arsenic-metabolism efficiency can be measured in urine as ratios of arsenic metabolites to total arsenic. Dimethylarsinic acid, the end metabolite, is most readily excreted in urine, and individuals with high concentrations of dimethylarsinic acid are viewed as more efficient metabolizers, at lower risk of arsenic toxicity (58–62). The recent GWAS (57) identified 2 independent association signals for dimethylarsinic acid concentrations in a *10q24.32* region containing *AS3MT*, a gene involved in arsenic methylation, consistent with several candidate-gene studies (reviewed in Agusa et al. (63)). The low-efficiency alleles at these 2 single nucleotide polymorphisms were independently associated with increased risk for arsenical skin lesions. Furthermore, the association between arsenic exposure and skin-lesion risk was weaker among individuals with high-efficiency *10q24.32* genotypes than among those with low-efficiency genotypes (64). This example illustrates the strength of using a highly exposed population with sufficient variation in exposure (Table 1, Lesson 7) and using high-quality exposure measures to identify G×E (Table 1, Lesson 9). This example further illustrates the strength of studying metabolism pathways of an exposure to identify genetic variants that influence disease (Table 1, Lesson 1).

MODEL SYSTEMS AND FUNCTIONAL APPROACHES

Replication has been a cornerstone of genetic association studies, and the requirement for independent replication contributed to the success of GWAS (65, 66). In examples described above, particularly *NAT2* × smoking with bladder cancer, *FTO* × physical activity with body mass index, and *ALDH2* × alcohol with esophageal cancer, interactions were replicated multiple times in different populations. However, as discussed in the other articles in this group (1, 44, 67) and previously, there are many challenges to replication in the G×E context, and what constitutes appropriate replication in the G×E context is currently being debated (28, 68, 69). Functional approaches can complement and support population-based epidemiologic studies by providing potential mechanistic insights to observed findings

(Table 1, Lesson 10) (70) and are described in Ritchie et al. (67). These approaches include model systems, in vitro experiments, and biomarker measurements. They may also provide additional evidence for an interaction in situations where replication in another independent population is not possible due to lack of availability of an appropriate replication population, such as in studies of a rare disease or environmental exposure (28, 68).

Chronic lead exposure and genetic polymorphisms affecting lead processing and excretion functions provide an example in which functional approaches helped to validate genetic associations that were difficult to resolve with human data (71–73). Although genetically driven variations in human susceptibility to adverse health effects from lead toxicity is a well-appreciated phenomenon (74, 75), studies trying to establish the genetics of human susceptibility have been challenging due to the variety of clinical symptoms elicited by lead toxicity. Moreover, studies with chronic low levels of lead exposures require long-term exposure assessments that account for life-cycle susceptibility, such as during pregnancy and early childhood, which are difficult in human populations. Using *Drosophila melanogaster*, researchers used mutants to assess functional causality of candidate genes and were able to identify a genetic network related to lead susceptibility, building upon known genes previously identified in human GWAS (76) (Table 1, Lesson 10).

Insights into the underlying mechanisms related to the *FTO* gene and interaction with physical activity for obesity phenotypes was provided in a series of mechanistic studies. Energy balance is known to be modulated by both food consumption and physical activity as well as by the dissipation of energy as heat through constitutive heat generation (thermogenesis) in mitochondria-rich brown adipocytes in brown fat and through inducible thermogenesis in beige adipocytes in white fat. Thermogenesis is triggered in part by response to exercise and partially controlled by mitochondria. Functional studies have recently shown that one of the common *FTO* alleles associated with obesity phenotypes can repress mitochondrial thermogenesis in adipocyte precursor cells (77, 78). This leads to a developmental shift from energy-dissipating beige adipocytes to energy-storing white adipocytes with repression of basal mitochondrial respiration and increased lipid storage. These functional studies provide some biological evidence for the interaction of *FTO* and physical activity in generating obesity. These predictions were further functionally validated with knockdown and overexpression of *FTO* and other regulators in human patient tissue samples and mice models (77, 78) (Table 1, Lesson 10).

Furthermore, functional studies of PD have helped to elucidate findings from human genetic association studies. Pesticide exposure was suggested as an environmental risk factor for PD, although the mechanism was unknown. ALDH plays a key role in neuronal protection by metabolizing biogenic amine-related aldehydes (e.g., 3,4-dihydroxyphenylacetaldehyde) and by protecting neurons against aldehyde- and oxidative stress–related neurotoxicity (79) (Table 1, Lesson 1). Therefore, researchers used an ex vivo model system to identify several pesticides that inhibited enzyme activity of ALDH (Table 1, Lesson 10). These same pesticides were associated with an increased risk of PD in a population-based study, and genetic variation in *ALDH2* appeared to modulate PD risk due to these pesticide exposures (80).

Identifying a plausible biological mechanism using biomarkers can also help validate human-population study findings, as illustrated by G×E in asthma. Exhaled nitric oxide (FeNO) levels are known biomarkers of airway inflammation that are predictive of childhood asthma (81). Researchers found that common, inducible nitric oxide synthase 2 (*NOS2*) promoter haplotypes combined with residential traffic-related exposure appeared to interact to affect exhaled FeNO levels in children, presumably because *NOS2* is induced by environmental exposures (82). Previously, common genetic variants and promoter haplotypes of *NOS2* were associated with childhood exhaled FeNO values (81). Moreover, exposure to residential traffic and allergens were independently associated with elevated FeNO levels (82). The discovery of this G×E (*NOS2* promoter haplotypes × traffic exposure) benefited from a large, well-characterized population with substantial variation in exposure levels (Table 1, Lessons 4 and 7). In addition, higher FeNO levels were associated with elevated *NOS2* mRNA in the bronchial epithelium of asthmatics after allergen exposure (83). Although this G×E finding needs replication, the biomarker study correlating higher FeNO levels with higher *NOS2* expression suggests a plausible biological mechanism of how ubiquitous air pollutants and genetic variation might drive a biological pathway relevant to inflammation that could contribute to asthma (Table 1, Lesson 10).

PHARMACOGENOMICS

There are several lessons to be learned from pharmacogenomic G×E studies that may be applied more broadly to G×E studies of complex diseases. Pharmacogenomics, which specifically examines the role of genetic variation in various drug-response phenotypes (84–86), can use either targeted or untargeted G×E approaches, with the drug as the environmental exposure and drug-response phenotype as the outcome (87). Variations in drug response may cause some individuals to require a higher dose while others require a lower dose because of increased sensitivity or adverse side effects. For example, common genetic variants in cytochrome P450 2C9 (*CYP2C9*) and vitamin K epoxide reductase complex subunit 1 (*VKORC1*) genes contribute to variability in patients' responses to treatment with the anticoagulant warfarin, explaining as much as 18%–30% of the response variability observed in European populations (88) (Table 1, Lesson 2). Notably, many successes in pharmacogenomics have been observed, despite challenges of small population sizes and rarity of adverse events (85, 86, 89), due to the fact that the environmental agent (i.e., drug) is known, easy to measure, and is often associated with a well-defined outcome phenotype, such as lowering blood pressure (85). In addition, for many pharmaceuticals, the mechanism of action and metabolic pathways are well understood, making targeted studies with a prior hypothesis more successful than agnostic GWAS studies, particularly given the usual small population sizes of these studies, and making findings from such studies easy to interpret (Table 1, Lesson 1).

An important lesson from pharmacogenomics studies relates to the importance of studying diverse populations, because

considerable variation in drug response across ethnicities has been observed. In many cases, this variation is due to frequencies of genetic variants depending on population ancestry (85). For example, in East and Southeast Asian populations, a strong association of carbamazepine-induced Stevens-Johnsons syndrome was reported for the human leukocyte antigen-B (HLA-B)*1502 allele (OR = 84.75; 95% CI: 42.53, 168.91; $P = 8.96 \times 10^{-5}$), while no associations were observed in Japanese or Caucasian patients (90). To date, a majority of GWAS and pharmacogenomics studies have been conducted in populations of European descent. Performing genetic studies on populations of diverse ancestry will likely provide further insights into disease mechanisms and ensure that all populations derive benefits from pharmacogenomics research (91) (Table 1, Lesson 7).

G×E findings in pharmacogenomics may also be applied to disease prevention, such as smoking cessation. Evidence suggests that both nicotinic receptor α5 subunit (*CHRNA5*) and cytochrome P450 2A6 (*CYP2A6*) genotypes influence smoking cessation success and response to pharmacotherapy. In a large smoking-cessation trial, the effectiveness of smoking-cessation pharmacotherapy and medication efficacy was dependent on *CHRNA5* haplotype (92). Similar pharmacogenomic interactions were observed in patient responses to nicotine replacement therapy with *CHRNA5* (93) and *CYP2A6* genetic variants (94). An additional study reported that the prescription medication varenicline was more efficacious than nicotine patches and depended on the *CYP2A6* genotypes for slow metabolizers, while the effect of the common drug bupropion on smoking relapse did not seem to be affected by *CYP2A6* genotype–driven nicotine metabolism (94, 95). These studies support the notion that personalized smoking-cessation intervention based on genotype may increase the effectiveness of such treatments (Table 1, Lesson 2).

In another example of G×E in pharmacogenomics, related to disease prevention, researchers performed an agnostic genome-wide G×E gene-discovery study in colorectal cancer patients who regularly used either aspirin, nonsteroidal antiinflammatory drugs, or both. Use of aspirin and/or nonsteroidal antiinflammatory drugs was associated with reduced risk of colorectal cancer in individuals with TT genotypes of *MGST1* (for microsomal glutathione s-transferase 1) and higher risk among those with the TA or AA genotypes (90). Meanwhile, regular use of aspirin and/or nonsteroidal antiinflammatory drugs was associated with lower risk of colorectal cancer among individuals with interleukin 16 (*IL16*) AA genotypes but not with the less-common genotypes. These results may have implications for targeting populations at risk of colorectal cancer for specific intervention efforts, such as treatment with nonsteroidal antiinflammatory drugs and/or aspirin, based on genetic information (Table 1, Lesson 2). To detect these interactions, the investigators combined data from 10 observational studies for a total of 8,634 cases and 8,533 controls. Even with this large sample size, only a few interactions were observed (Table 1, Lesson 6).

CONCLUSIONS

The characteristics of the above examples illustrate several important lessons for G×E research. First, studying variants that are known to disrupt exposure metabolism is a promising strategy for identifying disease-related variants that interact with exposure. Other pathways where mechanisms of exposure action are well understood (e.g., pharmacogenomics) may also be successful approaches. Second, studying G×E in human studies designed to characterize a specific exposure (such as arsenic or specific pesticides) over an extended period and in a large population will provide opportunities to use high-quality exposure measures, to study a wide range of exposure levels, and to examine longitudinal measures of exposure. Importantly, using carefully collected and comprehensive exposure data with a wide variation among study participants increases statistical power for G×E detection. Yet even with high-quality exposure assessment, many of these studies required large population sizes for the G×E discovery. In addition, G×E research should include diverse populations representing many geographic areas, cultures, and ethnicities. Finally, functional studies—including model systems, laboratory studies, or biomarkers measured in human tissues—may lend valuable insights to G×E findings, complementing large-scale, population-based epidemiologic findings.

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