reveal differences for ERα. Ponceau protein staining and detection of the 62 kDa nucleoporin (NUP62) were used as loading controls.

Additional file 8: Figure S5. Expression analysis with exposure to YC-1. **(A)** High expression of the Ribosome pathway (false discover rate <5%) is shown in the parental MCF7. **(B)** Top panels, the Ribosome pathway is significantly altered (that is, underexpressed) in MCF7 cells, but not in MCF7-LTED cells, exposed to YC-1. Bottom panels, both MCF7 and MCF7-LTED cells show underexpression of the cell cycle pathway with exposure to YC-1. **(C)** Western blot analysis results of phospho-serine 235/236 S6 ribosomal protein, E2F1 and control TUBA in MCF7 and MCF7-LTED cells in basal or YC-1-exposed conditions.

Additional file 9: Table S4. Pathways differentially expressed (false discovery rate <5%) in MCF7 and/or MCF7-LTED cells, in basal and/or YC-1 conditions.

Additional file 10: Table S5. Differential expression analysis of predicted E2F1 target sets (false discovery rate <1%) in MCF7 and MCF7-LTED cells exposed to YC-1.

Additional file 11: Figure S6. Results from RAC1 activity assays with depletion and/or reconstitution of MYC-Vav3. Left panel, graph depicting RAC1 activity from triplicate assays in the conditions depicted across the *x*-axis. The asterisks correspond to significant differences ($P < 0.05$). Right panels, Western blot analysis results of total VAV3, MYC (for MYC-Vav3) and control TUBA in MCF7 and MCF7-LTED cells transduced with shRNA control (pLKO.1) or shRNA-*VAV3* plus MYC-Vav3 constructs.

Additional file 12: Table S6. Results of the GWAS and the replication study for SNPs in *VAV3*.

Abbreviations

ChIP: Chromatin immunoprecipitation; EGFR: Epidermal growth factor receptor; ERα: Estrogen receptor α; GSEA: Gene set expression analysis; GWAS: Genome-wide association study; IC_{50}: Half-maximal inhibitory concentration; LTED: Long-term estrogen-deprived; MTT: Methylthiazol tetrazolium; PDB: Protein Data Bank; sGC: Soluble guanylyl cyclase; shRNA: Short hairpin RNA; SNP: Single-nucleotide polymorphism.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

HA, AU and MAP conceived the project and coordinated the experiments and data analyses. HA, PH and RLB performed the compound screen. JSM, NB and MAP carried out the microarray data analyses. XB performed the protein structure analyses. AI, EN and WZ performed the ChIP data analysis. LC, HA, MAP and LDC performed the targeted ChIP assays. HA, NG, GM and LGB performed the cellular and molecular studies. HA and LC performed the *ESR1* shRNA-based assays. KK, TM, YN and HZ performed the genetic association study. NG, FC, MTS, ARV, MG, AIE, ABRP and XRB performed the tumor and immunohistochemical studies. JBo, EK, GPT, TF, DCS and OS performed the analyses of the Swedish breast cancer study. HA, JSM, MV, ME and MAP contributed the cell lines and performed the erlotinib analysis. RGM, MPHMJ, JBr, AF, JBa, RC, KLB, KEC, JAK and AV contributed the reagents and to the experimental design. MAP drafted the manuscript. All authors read and approved the final manuscript.

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Polygenic Inheritance of Paclitaxel-Induced Sensory Peripheral Neuropathy Driven by Axon Outgrowth Gene Sets in CALGB 40101 (Alliance)

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Conflict of Interest
The authors declare no conflict of interest.

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Abstract

Peripheral neuropathy is a common dose-limiting toxicity for patients treated with paclitaxel. For most individuals there are no known risk factors that predispose patients to the adverse event, and pathogenesis for paclitaxel-induced peripheral neuropathy is unknown. Determining whether there is a heritable component to paclitaxel induced peripheral neuropathy would be valuable in guiding clinical decisions and may provide insight into treatment of and mechanisms for the toxicity. Using genotype and patient information from the paclitaxel arm of CALGB 40101 (Alliance), a phase III clinical trial evaluating adjuvant therapies for breast cancer in women, we estimated the variance in maximum grade and dose at first instance of sensory peripheral neuropathy. Our results suggest that paclitaxel-induced neuropathy has a heritable component, driven in part by genes involved in axon outgrowth. Disruption of axon outgrowth may be one of the mechanisms by which paclitaxel treatment results in sensory peripheral neuropathy in susceptible patients.

Keywords

paclitaxel; neuropathy; polygenic; heritability; pathway

Introduction

Peripheral neuropathy is a common and often dose-limiting toxicity associated with cancer chemotherapy treatment. Paclitaxel is a chemotherapeutic agent in the taxane family, and functions by inhibiting microtubule assembly and inducing apoptosis. It is commonly prescribed in the treatment of carcinomas of the breast, ovary, lung, and head and neck[1]. Sensory peripheral neuropathy induced by paclitaxel is dose-dependent and is the most common toxicity associated with this microtubule inhibitor. Severe toxicity (Grade 3 or higher) generally occurs in 5–10% of patients although rates as high as 30% have been reported for certain dosage regimens[2]. Known risk factors for paclitaxel induced neuropathy include prior exposure to a neurotoxic agent or medical conditions associated with peripheral neuropathy, such as diabetes[2–6], though most patients who suffer from paclitaxel-induced neuropathy do not have an identifiable predisposition. The pathogenesis of paclitaxel induced peripheral neuropathy is unclear. Paclitaxel treatment may target axons, myelinating Schwann cells, or the dorsal root ganglion and neuron cell bodies of peripheral nerves[7]. At any of these sites, damage may be mediated by microtubule stabilization or mitochondrial disruption[8]. At very high single or cumulative doses almost all patients will experience some degree of peripheral neuropathy, but in certain susceptible patients neuropathy will occur at lower cumulative doses or with greater severity. Interindividual susceptibility to paclitaxel induced peripheral neuropathy may be driven by an overall increase in exposure to paclitaxel, or an increased sensitivity to damage or decreased capacity for repair at any of the putative targets of paclitaxel in the peripheral neuron.

Given the wide interindividual variability in incidence and severity of the toxicity independent of any known risk factors, it is likely that there is an underlying genetic basis

for susceptibility to paclitaxel-induced neuropathy. Small candidate gene studies focusing on genes involved in paclitaxel pharmacokinetics and pharmacodynamics (*e.g.*, *ABCB1, CYP2C8*) or paclitaxel targets (*e.g.*, β-tubulin) have had mixed results, with some identifying variants associated with neuropathy[9–11], and others failing to replicate previous results[12, 13]. Recently, a genome-wide association study from this group[14] identified several SNPs with moderate effect size in *FZD3, FGD4*, and *EPHA5* associated with severity or dose at onset of paclitaxel-induced sensory peripheral neuropathy. An independent genome-wide study identified SNPs in *RWDD3* and *TECTA* associated with onset of paclitaxel-induced neuropathy[15], but these findings were not replicated by others[16]. The large number of putative causative variants identified, many with small effect size, and the discrepancies from study to study suggest a complex polygenic etiology for susceptibility to paclitaxel-induced neuropathy.

Pharmacogenomic studies, especially those involved in the study of drug toxicities, come with their own particular set of challenges. Sample sizes are often limited, and phenotype definitions can be imprecise[17]. This is compounded in cases where the toxicity does not appear to be driven by one or a few polymorphisms with large effect size, such as *CYP2D6* polymorphisms and morphine toxicity[18], but rather by a number of variants each with small potential contribution to disease, as we propose is the case for paclitaxel-induced peripheral neuropathy. For these phenotypes, determining the extent to which genetic variability contributes to a particular toxicity can be challenging. Traditional heritability studies require large numbers of siblings or family structures that are not practicable, especially when studying potentially toxic drugs. Even when evidence for a heritable component to toxicity is available, candidate gene/candidate variant studies or traditional genome-wide association studies will likely be unable to identify variants with small effects that together explain a large portion of the expected heritability.

Recently, a method has been developed to estimate additive genetic variation or narrow-sense heritability driven by common SNPs (i.e. those typically captured on genotyping platforms) in unrelated individuals using linear mixed models[19, 20]. This approach was applied to genome-wide SNP data in breast cancer patients treated with paclitaxel to determine the extent to which paclitaxel-induced sensory peripheral neuropathy is heritable and to identify causal SNPs driving this heritability.

Materials and Methods

Patient Data and Study Design

The patient cohort for this study was taken from the paclitaxel arm of CALGB 40101 (Alliance), a Phase III trial studying adjuvant therapy for patients with breast cancer; all patients in the current study were also enrolled in CALGB 60202 (Alliance), the pharmacogenomic companion study, and signed an IRB-approved, protocol-specific informed consent for use of their specimens. Paclitaxel was administered every two weeks over three hours at 175 mg/m^2 for four or six cycles. A total of 1,040 paclitaxel-treated individuals were included in the cohort; after quality control, including principal component analysis, call rate (>98%), and clustering performance, 859 Caucasian patients were retained for further analysis. Germline DNA was genotyped on the HumanHap610-Quad Genotyping

BeadChip (Illumina) platform. SNP quality control measures for minor allele frequency (≥ 0.01), genotyping call rate (≥99%), and Hardy-Weinberg equilibrium in controls (exact test $p \geq 0.001$) were applied using PLINK (v1.07). Genotyped data was imputed to call genotypes of un-typed SNPs using MACH[21, 22] (1.0) and the 1000 Genomes[23] Pilot I (June 2010) data from unrelated Caucasian (CEU) individuals as a reference; imputed data was filtered for $r^2 > 0.9$. Recent publications describe further details regarding the pharmacogenomic[14] and clinical[24] studies. Details regarding patient selection, SNP quality control and imputation are outlined in Supplemental Figure 1.

Phenotype

Two phenotypes are of interest in studying paclitaxel-induced neuropathy – severity of the neuropathy and cumulative dose at onset of neuropathy. These outcomes may be driven by distinct or overlapping sets of genes. Peripheral neuropathy was graded on a scale of 0 to 5 according to the National Cancer Institute Common Toxicity Criteria for Adverse Events (NCI-CTCAE) version 2.0. The distribution of neuropathy grades in our cohort (Figure 1) matches expected numbers from prior clinical trials[25, 26]. Because the linear mixed modeling approach requires a continuous quantitative or binary phenotype, both severity of neuropathy and dose at onset of neuropathy were treated as continuous variables. Severity of neuropathy was modeled using the highest grade of neuropathy over the course of treatment with log-transformed cumulative dose administered at highest grade of neuropathy (mg/m^2) as a covariate. For patients who did not experience the toxicity, cumulative dose administered over the course of the study was used as the covariate. Onset of neuropathy was modeled using deviance residuals from a time-to-event analysis as a continuous phenotype. The deviance residuals are a normalized transform of the martingale residuals, which estimate the difference at a particular cumulative dose t between observed (incidence of grade 2 or peripheral higher neuropathy, 0 or 1) and expected events (predicted hazard for neuropathy at dose t) for a given patient. Residuals from survival models have been previously used to model time to onset of various phenotypes as a quantitative trait when it is not possible to apply a survival model directly[27–29]. The time-to-event analysis was conducted using a null Cox proportional hazards model without predictors, with time defined as cumulative paclitaxel dose and event defined as first instance of grade 2 or higher peripheral neuropathy[14]. For patients who did not experience grade 2 or higher neuropathy, cumulative dose administered over the course of the study was used, producing right–censored dosage date. Deviance residuals from the Cox score test were calculated using the survival package in R[30, 31].

Pathway Definitions

Pathways evaluated were selected based on putative pathology for paclitaxel-induced neuropathy. Five Gene Ontology[32] (GO Release 2012-09-15) Biological Process terms were included: Axonogenesis (GO: 0007409), Myelination (GO: 0042552), Transmission of Nerve Impulse (GO: 0019226), Microtubule-Related Processes (GO: 0007017), and Mitochondrial Organization and Transport (GO: 0006839 and 0007005), along with a manually curated set of genes associated with congenital peripheral neuropathy[33] and a set of genes in the paclitaxel pharmacokinetic/pharmacodynamic pathway[34]. For GO terms, all possible genes (regardless of evidence code) were included. For each pathway, gene

boundaries for the largest isoform of each gene were extracted from the UCSC Table Browser using UCSC gene annotations from human genome build 37 (hg19). These gene boundaries (plus an additional 10 kb upstream and downstream) were used to extract all dbSNP135[35] SNPs in the gene regions. Pathway SNP lists were used to extract the pathway-specific portion of the genome in PLINK (v1.07)[36].

For SNP sets grouped by position in the genome (genic vs. intergenic), gene and SNP annotations were extracted from the UCSC Table Browser using CCDS[37] gene annotations from human genome build 37 (hg19), and SNP annotations from dbSNP135. Genic regions were defined as 10 kb upstream and downstream of transcription start and stop sites. For genes with multiple CCDS isoforms, the longest isoform was used. The Biofilter[38] software (v2.0.0) was used to extract SNPs by genomic position.

Linear Mixed Modeling Heritability Analysis

Heritability estimates for the whole genome and for pathways were generated using the GCTA (v1.01) software tool[39]. We estimated the genetic relatedness matrix (GRM) for 859 Caucasians using all post-QC genotyped SNPs. Principal components analysis was conducted using GCTA, and the first 20 eigenvectors for each individual were used as covariates in all subsequent analyses to control for any remaining population stratification. To ensure that all subjects in the study were unrelated, we excluded one of each of a pair of individuals with genetic relationship greater than 0.03, roughly corresponding to second cousins or closer familial relationships; ten individuals were excluded in this step. An additional four individuals were excluded due to incomplete phenotype information for a final population of 845 unrelated Caucasians (Supplemental Figure 1). All analyses were restricted to autosomes, and were conducted with the assumption that causal SNPs will have the same allele frequency distribution as genotyped SNPs.

For pathway specific heritability analyses, a separate GRM was constructed for each pathway and for its complement (whole genome GRM excluding SNPs in the pathway) using the set of 845 unrelated Caucasians. Total genetic variance for severity and onset of neuropathy was partitioned simultaneously onto pathway and "non-pathway" SNPs. Likewise, for genomic position based heritability analyses, total genetic variance for both phenotypes was partitioned onto genic and intergenic regions. To correct for the simultaneous evaluation of multiple pathways, GCTA p-values were Bonferroni corrected by multiplying each p-value by the number of pathways tested together (seven in the first round and ten in the second round). Empirical distributions representing the null hypothesis that the trait is not heritable were generated as follows for each pathway specific heritability estimate: for severity of neuropathy, residuals and expected values were extracted from linear regression of grade of neuropathy with log cumulative dose of paclitaxel and the first 20 principal components. For each of 1000 permutations, residuals were permuted, summed with expected values for each individual, and used to estimate pathway-specific heritability in GCTA. For onset of neuropathy, deviance residuals were calculated as described, then input as an independent variable in a linear regression including 20 principal components from which residuals and expected values were extracted. As with severity of neuropathy, for each of 1000 permutations, residuals were permuted, summed with expected values for

each individual, and used to estimate pathway-specific heritability in GCTA. Empirical p-values were generated by calculating the probability of obtaining a heritability estimate greater than that estimated from observed data.

PLINK Set Test

Briefly, the PLINK Set test as implemented in this study calculates the mean of all significant ($p < 0.05$) per-SNP p-values after filtering for SNPs in linkage disequilibrium ($r^2 \geq 0.5$). An empirical p-value is applied to each set test by permuting phenotype labels across individuals. SNP p-values for severity and onset of neuropathy were calculated in PLINK by linear regression of residuals from regression of grade of neuropathy on number of minor alleles, with log cumulative dose of paclitaxel and principal components as covariates in both initial regression and PLINK set test.

Results

The variance explained by common (MAF > 1%) SNPs for paclitaxel-induced neuropathy was estimated in a cohort of 845 unrelated Caucasian breast cancer patients treated with single agent paclitaxel. Two outcomes were of interest – severity of neuropathy (measured on a grade of 0 to 5) and cumulative dose administered at onset of neuropathy (≥ grade 2), both treated as continuous quantitative variables. The variance explained by all genotyped SNPs across the genome was estimated as 41% for severity of neuropathy and 55% for onset of neuropathy, but with high standard errors (44% and 47%, respectively) due to the small sample size. To narrow in on the causative SNPs driving heritability and reduce noise from non-causative SNPs, two methods were applied: (1) a genomic position based SNP selection, extracting SNPs in genic regions, and (2) a biological pathway based selection that extracted SNPs that fall in biological pathways that are associated with putative mechanisms for susceptibility to paclitaxel-induced neuropathy.

When partitioning the genome in SNP sets by genomic location (Figure 2), a trend toward higher heritability was found in genic regions for severity ($h^2 = 49\% \pm 37\%$, $p = 0.07$) and onset of peripheral neuropathy ($h^2 = 48\% \pm 35\%$, $p=0.08$). For severity of peripheral neuropathy, pathway specific results show highest heritability estimates for the Axonogenesis gene set ($h^2 = 21\% \pm 12\%$, $p = 0.040$; Table 1). A complementary pathway analysis approach, the PLINK set test, was used to further extend our pathway based heritability results. Consistent with the GCTA analysis, only the Axonogenesis set is significant ($p = 0.012$) for severity of neuropathy using the set test (Supplemental Table 1). For onset of peripheral neuropathy, no significant signal of heritability was detected in any of the pathways tested (Supplemental Table 2).

"Children" of the GO Axonogenesis term, defined as terms with a "is_a" or "part_of" relationship with the Axonogenesis term, were subsequently tested for the severity of neuropathy phenotype (Table 2). Of the ten terms tested, GO Regulation of Axonogenesis (GO: 0050770), GO Axon Extension (GO: 0048675), and GO CNS Neuron Axonogenesis (GO: 0021955) showed strong heritability signals ($h^2 = 13\% \pm 6\%$ ($p = 0.009$), $10\% \pm 5\%$ ($p = 0.020$) and $5\% \pm 3\%$ ($p = 0.020$), respectively). To determine whether the signal from these three terms comes from independent genes in each set or overlapping genes in the

three sets, heritability estimates were calculated using the pair-wise and three-way union or intersection of the GO Regulation of Axonogenesis, GO Axon Extension, and GO CNS Neuron Axonogenesis sets. The union or intersection of the GO CNS Neuron Axonogenesis set with GO Axon Extension or GO Regulation of Axonogenesis sets resulted in lower heritability estimates than either independent set with high standard error (data not shown). For the GO Axon Extension and GO Regulation of Axonogenesis sets, the heritability signal from each independent set and the union and intersection sets are very similar (Figure 3), suggesting that a large portion of the SNPs driving the heritability in the Regulation and Extension sets come from the 44 genes found in both gene sets.

Heritability estimates were also calculated using imputed data; as with the genotyped SNPs, whole genome estimates of heritability with imputed SNPs had very high standard errors. For genomic position and pathway analyses, results from imputed data were similar to those described above for genotyped data, with a trend to higher heritability estimates in genic versus intergenic regions for the severity of peripheral neuropathy (Supplemental Table 3) and in the GO Axonogenesis set for severity of peripheral neuropathy (Supplemental Tables 4 – 6).

Discussion

These results suggest that a portion of variation in severity and onset of paclitaxel-induced sensory peripheral neuropathy is captured by additive effects of common SNPs in this clinical trial population. Previous studies have indicated that heritability is driven primarily by SNPs in genic regions[40], and a similar trend is found in our study. Within genic regions, we also noted a higher proportion of variance in severity and onset of peripheral neuropathy captured by SNPs in intronic regions (data not shown), but it is unclear whether this is due to a bias in the design of the genotyping chip or true bias in the genomic location of SNPs associated with paclitaxel induced neuropathy. If real, the enrichment of heritability signal in introns suggests that the majority of causal SNPs have subtle biological effects – for example, small changes in expression or stability that may be regulated by intronic SNPs, rather than overt changes in protein structure or function caused by variation in exons. This is consistent with a polygenic model in which many small, additive effects together contribute to the phenotype.

Further, a set of genes was identified that drive a substantial portion of the heritability of severity of paclitaxel-induced peripheral neuropathy, implicating axonogenesis, and more specifically the regulation of axon outgrowth, in the pathophysiology of this adverse event. These results are supported by evidence from human biopsies, electrophysiological studies, and animal and cell-based models that paclitaxel causes a distal axonopathy, in which the degeneration of axons occurs first at axon ends. This pattern of neuronal damage is consistent with a length-dependent neuropathy, targeting the long axons that extend into the hands and feet first, as typically occurs with paclitaxel induced neuropathy[41–44]. Further, there is evidence that demyelination and ganglionopathy, if they do occur, are secondary to axon damage[41, 44, 45]. The current results suggest that susceptibility to paclitaxel-induced neuropathy is caused in part by heightened sensitivity to or reduced capacity to repair this distal axon damage.

Of the 44 genes in the GO Axon Extension and GO Regulation of Axonogenesis overlap set (Supplemental Table 7), a number have been implicated in neuropathy, including hereditary neuropathy genes (*MAP1B*[46], *NGF*[47],*FXN*[48]), *genes with variants or expression signatures associated with diabetic or HIV-induced peripheral neuropathy (APOE*[49, 50], *MAPT*[51], *CDH4*[51]), *genes involved in neurological pain pathways (MT3*[52], *TRPV2*[53], *CCR5*[54], *CXCL12*[55]), *and genes involved in response to or repair/prevention of peripheral nerve damage (RYK*[56], *SLIT1*[57], *NTRK3*[58], *NGF*[59, 60], *TRPV2*[53], *NTN1*[61], *NDEL1*[62]). The majority (38) of these 44 genes fall in the GO term Regulation of Axon Extension (GO 0030516), which is a subset of both GO Regulation of Axonogenesis and GO Axon Extension.

The pathway results are also consistent with gene expression analyses in mouse and human studies of diabetic neuropathy. In a study examining the pathophysiology of diabetes-induced neuropathy the GO Axonogenesis term was identified as an overrepresented pathway in a differential expression analysis in the *db/db* vs *db/+* mouse sciatic nerve[51]. Similarly, the GO Regulation of Axonogenesis term was identified as an overrepresented set in genes up-regulated in sural nerve biopsies from patients with advanced progression of diabetic neuropathy[63]. Although neuron damage is caused by different mechanisms in diabetes and following paclitaxel treatment, these results suggest that susceptibility to sensory peripheral neuropathy is driven by the same sets of genes.

Despite success in estimating heritability for paclitaxel-induced neuropathy and identifying a subset of the genome driving this heritability, some limitations in available methods and data are noted. One of the primary limitations of any pathway or gene set based analysis is the gene set definitions available. All available set definitions are limited by current knowledge about the pathway in question, and well curated sets are restricted to those pathways of interest to researchers. Further, the number of SNPs captured per gene varies, either because of true differences between number of variants or haplotype structure between genes, or because of differences in coverage between genes on the genotyping platform that was used. Such variability in local coverage is known to be a limitation in all commercial genotyping platforms[64]. While imputation of missing SNPs did increase SNP density in each set, heritability estimates with imputed data were close to those with just genotyped data; because of the high imputation quality threshold used ($r^2 > 0.9$), it is likely that additional SNPs are in high LD with genotyped SNPs, adding little additional information. For onset of peripheral neuropathy, no significant signal of heritability was detected in any of the pathways tested, either because genes driving heritability of onset of neuropathy are in a pathway we did not select, or because the use of deviance residuals from the Cox proportional hazards regression rather than a direct proportional hazards regression did not adequately model the data. It is also possible that one or more of the selected pathways is incompletely annotated. Gene Ontology terms are annotated using a combination of experimental evidence and computational analyses, and can be both manually and electronically annotated[32, 65]. The extensive set of sources for term annotation makes Gene Ontology the most comprehensive source of annotated terms available, but also contributes to significant noise (incorrectly assigned genes) being built into the terms. Unfortunately, highly accurate manually annotated gene sets are currently limited, and those that exist reflect the current body of knowledge regarding a given pathway. The Gene

Ontology was the only database that included gene sets for each of the peripheral neuropathy mechanisms of interest. For the GO set Axonogenesis, more restrictive set definitions were investigated, including limiting pathway genes to those annotated to Axonogenesis by experimental evidence and those that were direct associations. The GO Axonogenesis experimental set gave an estimate of heritability significantly lower than that derived from the complete gene set (8% vs 22% for the complete set), suggesting that using a more conservative gene annotation would result in loss of power (Supplemental Table 8).

The standard errors for the whole-genome heritability analyses are high due to the limited sample size. Large sample sizes are difficult to obtain in genomic studies of drug toxicities, since recruitment into these studies is often limited to existing clinical trials. However, by narrowing in on the "causative" SNPs, signals of heritability were obtained even with relatively small sample sizes. In this study, constraints were also imposed by the linear mixed modeling method applied, which requires a continuous or dichotomous phenotype. Although severity of neuropathy is best modeled as an ordinal variable, it is treated as a continuous quantitative variable for the purpose of this study. Likewise, onset of neuropathy is best fit in a survival model but deviance residuals from a survival model were used as a continuous trait in the current analysis. Despite these limitations, the results from the modified phenotype definitions are likely close to those that would be estimated from the application of non-linear phenotype definitions. For example, effect estimates for SNPs in biological pathways from severity of neuropathy modeled as a linear or ordinal variable (Supplemental Figure 3) or onset of neuropathy modeled as a linear phenotype or time-to-event analysis (Supplemental Figure 4) are highly correlated ($r^2 = 0.91$ and 0.97, respectively). However it is important to note that, because of the constraints on the phenotype definition, we treat heritability estimates obtained from our analyses simply as an indication of association between a certain sets of SNPs and our phenotypes of interest, rather than absolute measures of percent of variance explained by a particular SNP set. Finally, a gene boundary cutoff of 10 kb was selected to ensure that the SNPs are associated with the genes in our pathway (as opposed to a neighboring gene), though at the cost of losing potential causative SNPs in upstream and downstream regulatory regions of a gene. Because most genetic variability appears to be explained by SNPs in or near genes[40] our approach likely captures a significant fraction of the variability explained by the genes in a given set.

In summary, these results suggest that there is a heritable component to the severity and dose to onset of paclitaxel-induced sensory peripheral neuropathy. Further, genes involved in axon outgrowth may modulate the severity of paclitaxel-induced neuropathy. Understanding the mechanisms and pathways involved in susceptibility to paclitaxel-induced sensory peripheral neuropathy will help identify therapies that can mitigate the toxicity and guide future drug development.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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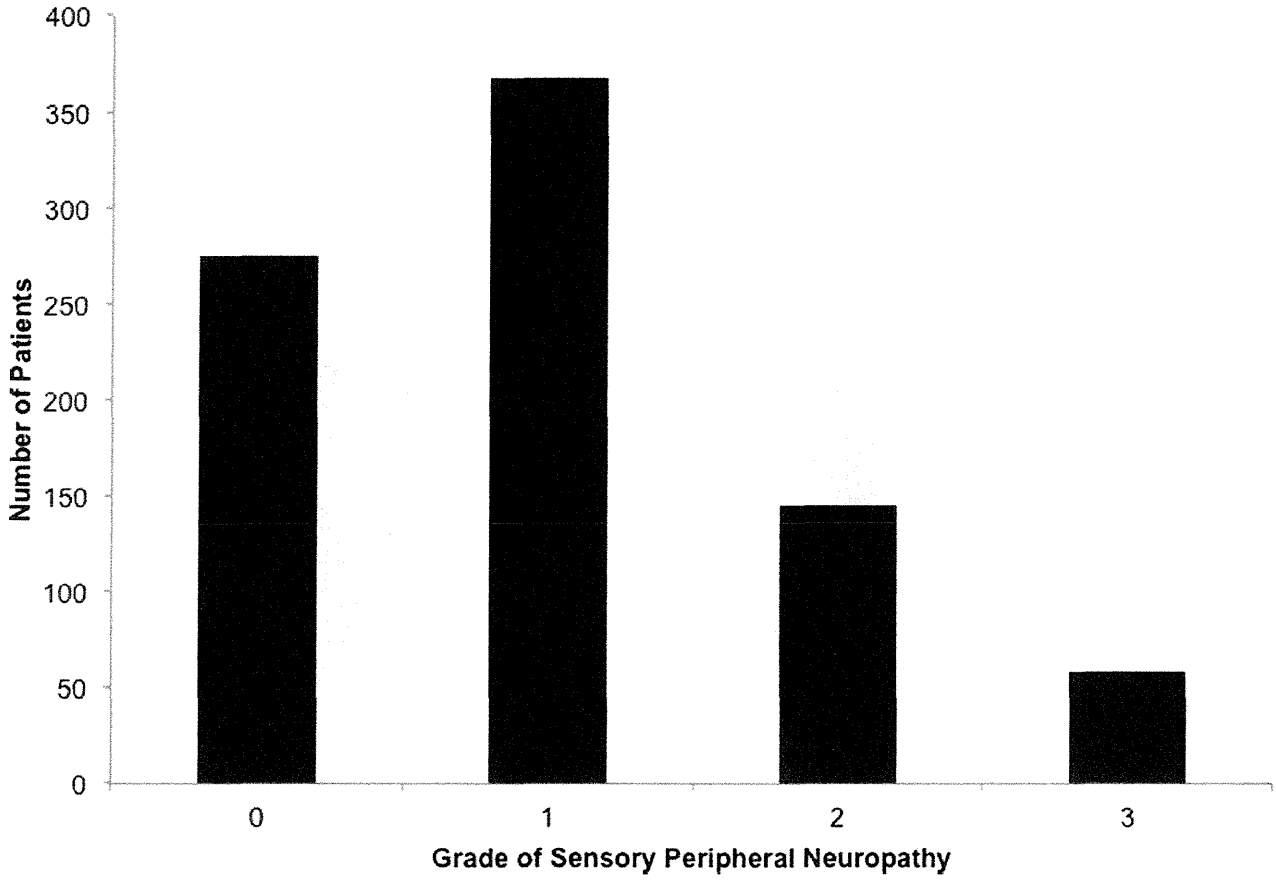

Figure 1. Distribution of sensory peripheral neuropathy in the study population

The distribution of the highest reported grade of sensory peripheral neuropathy is shown for 849 unrelated genetic Europeans from the paclitaxel arm of CALGB 40101. Toxicity is measured using the NCI-CTCAE Scale v2.

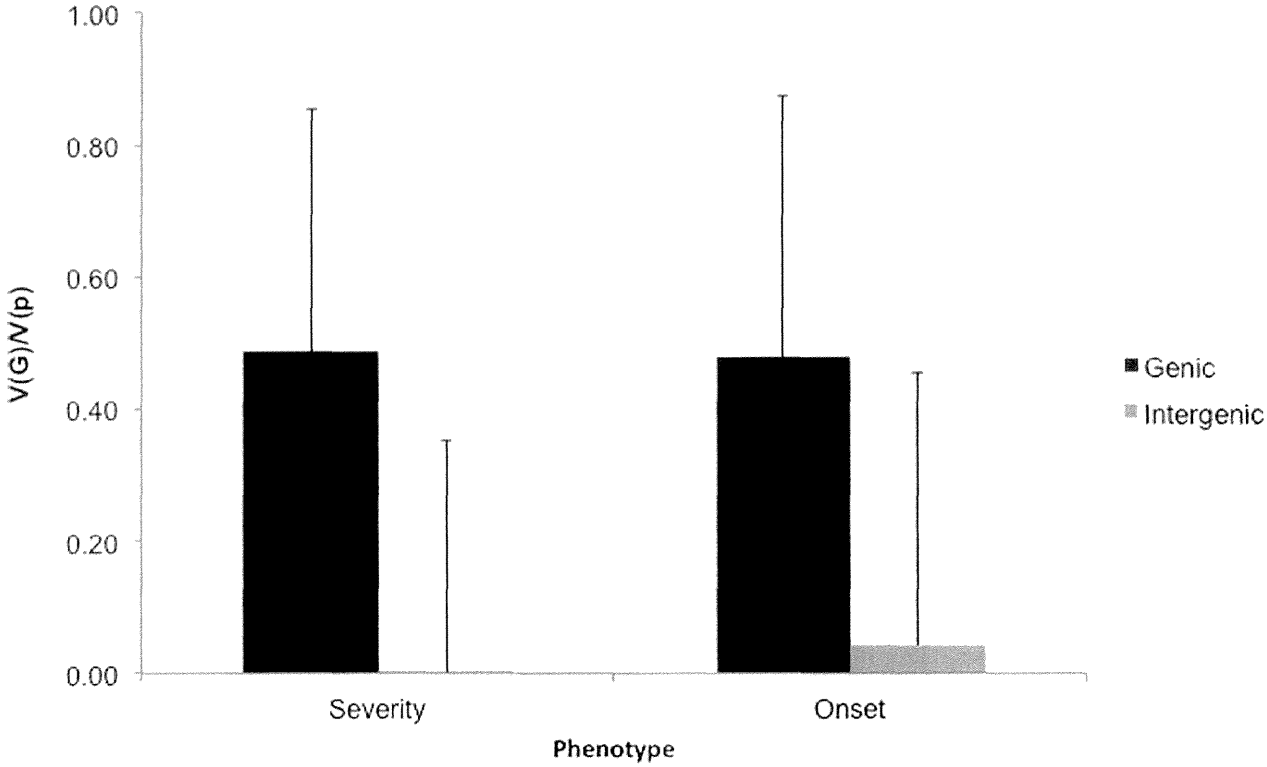

Figure 2. Heritability estimates for severity and onset of paclitaxel-induced sensory peripheral neuropathy for SNPs in genic and intergenic regions

Total genomic variance for both severity and onset of neuropathy was partitioned onto genic and intergenic regions. The error bars denote the SE for the heritability estimates.

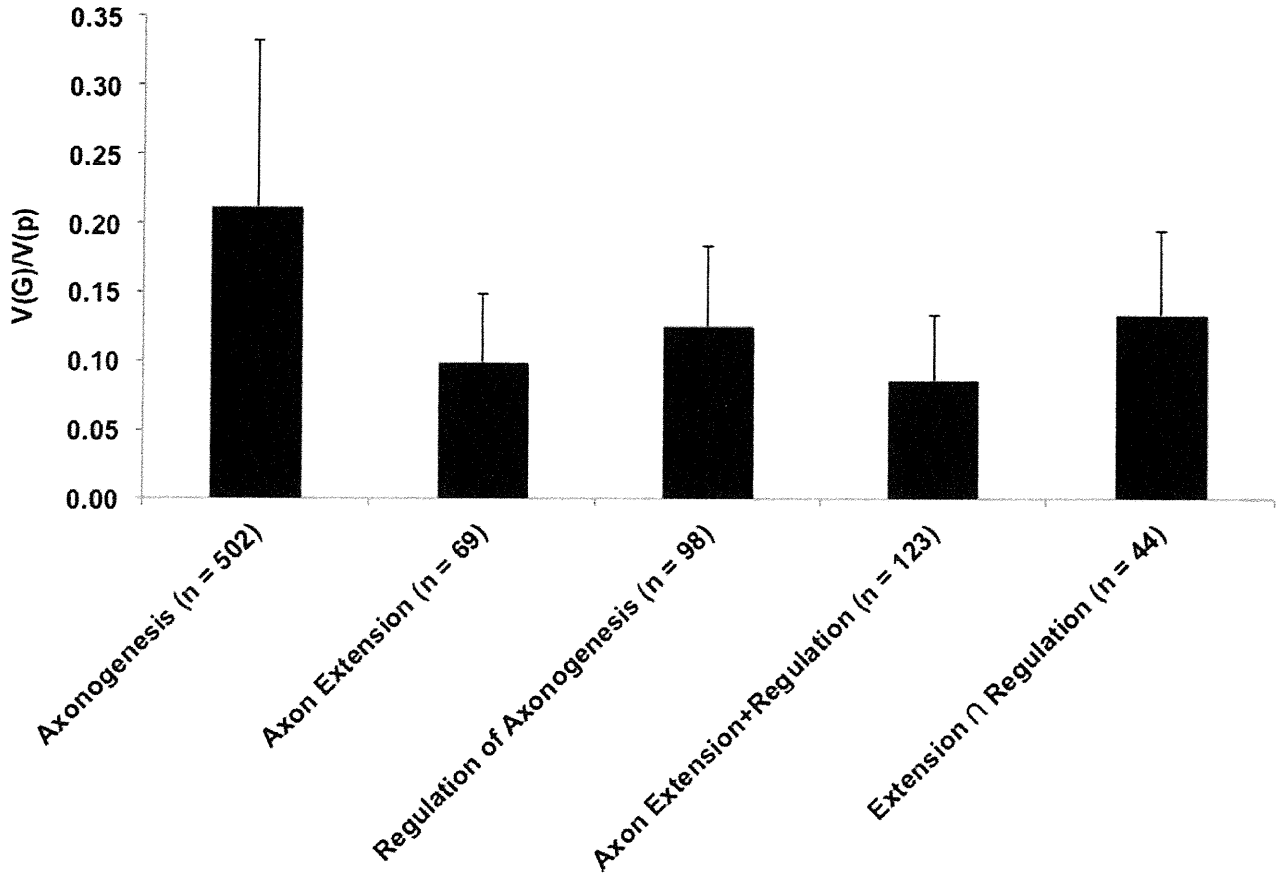

Figure 3. Heritability estimates for severity of paclitaxel-induced sensory peripheral neuropathy for SNPs in selected GO biological pathways

Heritability was estimated for sets of SNPs within all pathways contained within the GO Axonogenesis pathway. Results are shown (heritability ± SE) for those pathways with significant ($P < 0.05$) heritability signals. The heritability estimates for the intersection between and union of the Axon Extension and Regulation of Axonogenesis are also shown.

Table 1

Heritability estimates for severity of paclitaxel-induced sensory neuropathy using SNPs in biological pathways implicated in the toxicity

Pathway	Heritability Estimates					Pathway Characteristics		
	V(G)/V(p)[1]	SE	P[2]	Padj[3]	Empirical P[4]	# Genes	Size (Mb)	#SNPs
GO Axonogenesis	0.213	0.120	0.040	0.28	0.011	502	78.0	17,581
GO Impulse Transmission	0.000	0.122	0.500	1	0.999	746	106	22,886
GO Myelination	0.029	0.035	0.200	1	0.255	75	6.86	1,336
Congenital Peripheral Neuropathy	0.000	0.030	0.500	1	0.999	40	4.03	947
Paclitaxel Pharmacokinetics/ Pharmacodynamics	0.011	0.017	0.300	1	0.221	10	1.20	402
GO Mitochondrial Transport and Organization	0.012	0.055	0.400	1	0.545	274	19.7	3,668
GO Microtubule Related Processes	0.000	0.072	0.500	1	0.999	34	3.55	5,775

[1] Heritability was estimated for sets of SNPs within ±10 kb of genes in biological pathways implicated in the pathophysiology of paclitaxel-induced sensory peripheral neuropathy. The congenital neuropathy and paclitaxel pharmacokinetics/pharmacodynamics pathways were manually constructed from the literature.

[2] P-value from GCTA. Software upper limit for p-value is 0.5; maximal values are noted as 1.

[3] P-value corrected for seven observations.

[4] P-value from permutation analysis.