Short Communication

The Gc2 Allele of the Vitamin D Binding Protein Is Associated with a Decreased Postmenopausal Breast Cancer Risk, Independent of the Vitamin D Status

Sascha Abbas,1 Jakob Linseisen,1 Tracy Slanger,1 Silke Kropp,1 Elke Jonny Mutschelknauss,2 Dieter Flesch-Janys,2 and Jenny Chang-Claude1

1Division of Cancer Epidemiology, German Cancer Research Center, Heidelberg, Germany and 2Institute for Medical Biometrics and Epidemiology, University Clinic Hamburg-Eppendorf, Hamburg, Germany

Abstract

Vitamin D pathway gene polymorphisms may influence breast cancer risk by altering potential anticarcinogenic effects of vitamin D. The association between polymorphisms in the vitamin D binding protein (Gc) and postmenopausal breast cancer risk, with additional focus on the influence of serum 25-hydroxyvitamin D [25(OH)D], the biomarker for vitamin D status in humans, has not been examined thus far. We assessed the combined effects of two known functional polymorphisms in the Gc gene (rs4588 and rs7041), composing the phenotypic alleles Gc1s, Gc1f (combined: Gc1), and Gc2, on postmenopausal breast cancer risk and potential effect modification by 25(OH)D status in a population-based case-control study including 1,402 cases and 2,608 matched controls. Odds ratios (OR) for breast cancer risk adjusted for potential confounders were calculated for Gc genotypes. ANOVA was used to compare geometric means of serum 25(OH)D across Gc genotypes. Serum 25(OH)D concentrations in the control group significantly differed by Gc genotype, being lowest in Gc2 allele carriers. The geometric means of 25(OH)D were 53.0, 47.8, and 40.4 nmol/L for Gc1-1, Gc2-1, and Gc2-2 genotypes, respectively (P trend < 0.0001). Gc2-2 genotype was associated with a significantly decreased risk of postmenopausal breast cancer with an odds ratio (95% confidence interval) of 0.72 (0.54-0.96), compared with homozygote Gc1s allele carriers. No interaction between 25(OH)D status and Gc genotype was observed, nor did the association change considerably after adjustment for 25(OH)D status. Our results provide evidence for a serum 25(OH)D-independent effect of Gc2 allele carrier status in postmenopausal breast cancer. (Cancer Epidemiol Biomarkers Prev 2008;17(6):1339–43)

Introduction

Antiproliferative effects of vitamin D in various cell types including normal and malignant breast cells, by influencing cell differentiation, cell growth, and apoptosis, are well established (1-3). In addition, both vitamin D status, as measured by serum 25-hydroxyvitamin D [25(OH)D] or 1,25-dihydroxyvitamin D [1,25(OH)2D], the biologically active form of vitamin D, and polymorphisms in vitamin D pathway genes have been associated with breast cancer risk (4-6). A key protein in influencing cell differentiation, cell growth, and apoptotic effects of vitamin D, and polymorphisms in the vitamin D binding protein (Gc) gene (rs4588 and rs7041), composing the phenotypic alleles Gc1s, Gc1f (combined: Gc1), and Gc2, on postmenopausal breast cancer risk and potential effect modification by 25(OH)D status in a population-based case-control study including 1,402 cases and 2,608 matched controls. Odds ratios (OR) for breast cancer risk adjusted for potential confounders were calculated for Gc genotypes. ANOVA was used to compare geometric means of serum 25(OH)D across Gc genotypes. Serum 25(OH)D concentrations in the control group significantly differed by Gc genotype, being lowest in Gc2 allele carriers. The geometric means of 25(OH)D were 53.0, 47.8, and 40.4 nmol/L for Gc1-1, Gc2-1, and Gc2-2 genotypes, respectively (P trend < 0.0001). Gc2-2 genotype was associated with a significantly decreased risk of postmenopausal breast cancer with an odds ratio (95% confidence interval) of 0.72 (0.54-0.96), compared with homozygote Gc1s allele carriers. No interaction between 25(OH)D status and Gc genotype was observed, nor did the association change considerably after adjustment for 25(OH)D status. Our results provide evidence for a serum 25(OH)D-independent effect of Gc2 allele carrier status in postmenopausal breast cancer. (Cancer Epidemiol Biomarkers Prev 2008;17(6):1339–43)
Materials and Methods

We used a large population-based case-control study (MARIE study) carried out in the city of Hamburg and the Rhein-Neckar-Karlsruhe region, Germany. The study was approved by the ethics committees of the University of Heidelberg and the University of Hamburg. Cases were eligible if they had a histologically confirmed primary invasive or in situ breast cancer diagnosed between 01/01/2001 and 30/09/2005 in Hamburg and between 01/08/2002 and 31/07/2005 in the Rhein-Neckar-Karlsruhe region, were of ages 50 to 74 years, and a resident of one of the study regions. Of the 5,970 eligible patients who could be contacted, 3,919 (65.6%) participated. Controls were recruited from population registries matched by year of birth and study region to the cases. Of the 17,093 controls selected from population registries matched by age at menopause (<47, 47-51, 52-55, ≥56 y, unknown), body mass index (<22.5, 22.5-<25, 25-<30, ≥30 kg/m²), education level (low, middle, high), first-degree family history of breast cancer (yes, no, unknown), history of benign breast disease (yes, no), number of pregnancies (≥28th week; 0, 1, 2, ≥3), age at menarche (<12, 12-14, ≥15), breast-feeding history (ever, never), total number of mammograms (0, 1-4, 5-9, ≥10, unknown), smoking status (never, past, current), and use of menopausal hormone therapy (never, past, current).

Statistical interaction was evaluated with the likelihood ratio test by including an interaction term of the dichotomous genotype variable (Gc2 carriers versus noncarriers) and potential interaction variables (continuous variable for 25(OH)D) in the model.

In an ANOVA, mean values of the log-transformed serum 25(OH)D concentrations differed significantly by genotype (Fig. 1). When combining Gc1s, Gc1f, Gc2, their by their respective single-nucleotide polymorphism in rs7041 (Asp416Glu, T/G) and rs4588 (Thr420Lys, C/A) as follows: Gc1f, T and C; Gc1s, G and C; and Gc2, T and A, at single-nucleotide polymorphism rs7041 and rs4588, respectively (Supplementary Table S1). The corresponding combined genotypes were Gc1s-1s, Gc1s-1f, Gc1f-1f, Gc2-1s, Gc2-1f, and Gc2-2 (Supplementary Table S2). When combining Gc1s and Gc1f allele carriers, the combined genotypes were Gc1-1, Gc2-1, and Gc2-2.

We assessed the association of Gc combined genotype with postmenopausal breast cancer risk, taking the most frequent genotype as the reference category, by means of logistic regression with stratification by year of birth and additional stratification by time of blood collection (quarters of the year) in models assessing interaction with 25(OH)D. Odds ratios (OR) and corresponding 95% confidence intervals (95% CI) are presented. The following variables were included in the multivariate model: age at menopause (<47, 47-51, 52-55, ≥56 y, unknown), body mass index (<22.5, 22.5-<25, 25-<30, ≥30 kg/m²), education level (low, middle, high), first-degree family history of breast cancer (yes, no, unknown), history of benign breast disease (yes, no), number of pregnancies (≥28th week; 0, 1, 2, ≥3), age at menarche (<12, 12-14, ≥15), breast-feeding history (ever, never), total number of mammograms (0, 1-4, 5-9, ≥10, unknown), smoking status (never, past, current), and use of menopausal hormone therapy (never, past, current).

We measured serum 25(OH)D in a subset of 1,391 postmenopausal cases and 1,365 randomly selected postmenopausal controls matched on year of birth and time of blood collection using the OCTEIA vitamin D enzyme immunoassay (IDS) as previously described in more detail (4).

Genotyping was done in collaboration with the molecular laboratory BioGlobe GmbH using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry based on Sequenom’s hME and iPLEX technology. Women were allocated to three common Gc alleles (haplotypes), Gc1s, Gc1f, Gc2, by their respective single-nucleotide polymorphism in rs7041 (Asp416Glu, T/G) and rs4588 (Thr420Lys, C/A) as follows: Gc1f, T and C; Gc1s, G and C; and Gc2, T and A, at single-nucleotide polymorphism rs7041 and rs4588, respectively (Supplementary Table S1). The corresponding combined genotypes were Gc1s-1s, Gc1s-1f, Gc1f-1f, Gc2-1s, Gc2-1f, and Gc2-2 (Supplementary Table S2). When combining Gc1s and Gc1f allele carriers, the combined genotypes were Gc1-1, Gc2-1, and Gc2-2.

Results

Descriptive characteristics of the study population have previously been described (4). Median 25(OH)D concentration was 44.9 nmol/L for cases and 51.5 nmol/L for controls. No deviation from Hardy-Weinberg equilibrium was observed for rs4588 and rs7041 (P = 0.60 and P = 0.56 in the controls, respectively). The observed allele frequencies in the controls were comparable to those reported in the dbSNP database for Caucasians. Serum 25(OH)D concentrations differed significantly by genotype in the control group, being lowest in homozygote Gc2 carriers (Fig. 1). When combining Gc1s and Gc1f allele carriers, geometric mean 25(OH)D concentrations were 53.1 and 59.4 nmol/L for Gc1s-1s and 2-1f and 2-1s and 2-2, and 47.4 and 57.4 nmol/L for Gc1f-1f and Gc2-1s, 1s-1f and 2-2, 1s-1f and 2-2, and 2-1f and 2-2 (ANOVA, Scheffe test).
were 53.0, 47.8, and 40.4 nmol/L for Gc1-1, Gc2-1, and Gc2-2 genotypes, respectively, with a significant linear trend by increasing number of Gc2 alleles ($P_{\text{trend}} < 0.0001$; data not shown). Adjustment on time of blood collection and body mass index did not change the mean 25(OH)D estimates.

We observed a significant inverse association between the Gc genotype and postmenopausal breast cancer risk comparing homozygote carriers of the Gc2 allele with the most frequent genotype, Gc1s-1s [OR, 0.72; 95% CI, 0.54-0.96; $P_{\text{trend}} = 0.04$] (Table 1). When compared with noncarriers, Gc2 carriers had an OR of 0.88 (95% CI, 0.77-1.01). Adjustment for serum 25(OH)D status did not change the risk estimates substantially (Table 1). We did not observe a significant interaction between serum 25(OH)D and Gc genotype ($P_{\text{interaction}} = 0.22$).

Because vitamin D possibly exerts its anticarcinogenic activities via the estrogen pathway, we assessed possible differential effects by receptor status of the tumor. We did not observe a significant interaction between Gc genotype and estrogen receptor (ER) status of the tumor ($P_{\text{interaction}} = 0.56$ in a case-only model). However, a significant inverse association for postmenopausal breast cancer comparing Gc2 carriers with noncarriers was observed only for progesterone receptor (PR)–positive tumors [OR, 0.81 (95% CI, 0.69-0.96) and 1.03 (95% CI, 0.84-1.27), for PR+ and PR−/C0 tumors, respectively; $P_{\text{interaction}} = 0.006$; Table 2]. The effect modification was independent of the ER status, with an inverse association in both ER+/PR+ and ER−/PR−/C0 tumors and no association in ER+/PR− and ER−/PR−/C0 tumors (data not shown).

### Discussion

In this population-based case-control study, we observed a significantly reduced risk of postmenopausal breast cancer.

### Table 1. ORs for postmenopausal breast cancer by Gc genotype in the vitamin D binding protein

<table>
<thead>
<tr>
<th>Gc genotype</th>
<th>Cases</th>
<th>Controls</th>
<th>Crude model*</th>
<th>Adjusted model 1 †</th>
<th>Adjusted model 2 †</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n (%)</td>
<td>n (%)</td>
<td>OR (95% CI)</td>
<td>OR (95% CI)</td>
<td>OR (95% CI)</td>
</tr>
<tr>
<td>Gc1s-1s</td>
<td>472 (33.7)</td>
<td>837 (32.1)</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Gc1s-1f</td>
<td>255 (18.2)</td>
<td>450 (17.2)</td>
<td>1.00 (0.83-1.21)</td>
<td>1.00 (0.82-1.22)</td>
<td>1.05 (0.83-1.32)</td>
</tr>
<tr>
<td>Gc1f-1f</td>
<td>39 (2.8)</td>
<td>65 (2.5)</td>
<td>1.07 (0.71-1.61)</td>
<td>1.00 (0.65-1.52)</td>
<td>1.03 (0.62-1.70)</td>
</tr>
<tr>
<td>Gc2-1s</td>
<td>433 (30.9)</td>
<td>844 (32.4)</td>
<td>0.92 (0.78-1.08)</td>
<td>0.90 (0.76-1.07)</td>
<td>0.86 (0.71-1.05)</td>
</tr>
<tr>
<td>Gc2-1f</td>
<td>117 (8.3)</td>
<td>216 (8.3)</td>
<td>0.96 (0.75-1.24)</td>
<td>0.96 (0.74-1.25)</td>
<td>0.85 (0.63-1.15)</td>
</tr>
<tr>
<td>Gc2-2</td>
<td>86 (6.1)</td>
<td>196 (7.5)</td>
<td>0.79 (0.60-1.04)</td>
<td>0.72 ($p_{\text{trend}} = 0.04$)</td>
<td>0.76 (0.54-1.07)</td>
</tr>
<tr>
<td>Gc1-1</td>
<td>766 (54.7)</td>
<td>1,352 (51.8)</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Gc2-1</td>
<td>550 (39.2)</td>
<td>1,060 (40.7)</td>
<td>0.93 (0.81-1.06)</td>
<td>0.91 (0.79-1.05)</td>
<td>0.85 (0.72-1.00)</td>
</tr>
<tr>
<td>Gc2-2</td>
<td>86 (6.1)</td>
<td>196 (7.5)</td>
<td>0.79 (0.60-1.03)</td>
<td>0.72 ($p_{\text{trend}} = 0.02$)</td>
<td>0.75 (0.54-1.04)</td>
</tr>
<tr>
<td>Gc2-1/2-2</td>
<td>0.91 (0.79-1.03)</td>
<td>0.88 (0.77-1.01)</td>
<td>0.84 ($p_{\text{trend}} &lt; 0.05$)</td>
<td>0.84 (0.72-0.98)</td>
<td>0.84 ($p_{\text{trend}} &lt; 0.05$)</td>
</tr>
</tbody>
</table>

* Conditional logistic regression stratified by year of birth.
† Conditional logistic regression stratified by year of birth adjusted for age at menopause, first-degree family history of breast cancer, history of benign breast disease, number of pregnancies (≥28th wk), age at menarche, breast-feeding history, total number of mammograms, use of hormone therapy, body mass index, education level, and smoking status.
‡ Adjustment as in model 1 with additional stratification by time of blood collection and additional adjustment on 25(OH)D status as continuous variable; 25(OH)D status was available only for 1,391 cases and 1,365 controls.
* $P_{\text{trend}} < 0.05$.

### Table 2. ORs for postmenopausal breast cancer by Gc genotypes in the vitamin D binding protein gene according to ER and PR status of the tumor

<table>
<thead>
<tr>
<th>Gc genotype</th>
<th>ER+ tumors</th>
<th>PR+ tumors</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n (Ca/Co)</td>
<td>OR (95% CI)</td>
</tr>
<tr>
<td></td>
<td>540/1,352</td>
<td>0.88 (0.76-1.03)</td>
</tr>
<tr>
<td>Gc1-1</td>
<td>387/1,060</td>
<td>0.72 (0.52-0.98)</td>
</tr>
<tr>
<td>Gc2-1</td>
<td>1</td>
<td>0.92 (0.78-1.08)</td>
</tr>
<tr>
<td>Gc2-2</td>
<td>1</td>
<td>0.92 (0.78-1.08)</td>
</tr>
<tr>
<td>Gc2-1/2-2</td>
<td>1</td>
<td>0.92 (0.78-1.08)</td>
</tr>
<tr>
<td>ER−/C0 tumors</td>
<td>n (Ca/Co)</td>
<td>OR (95% CI)</td>
</tr>
<tr>
<td></td>
<td>168/1,352</td>
<td>0.89 (0.69-1.13)</td>
</tr>
<tr>
<td>Gc1-1</td>
<td>120/1,060</td>
<td>0.75 (0.45-1.26)</td>
</tr>
<tr>
<td>Gc2-1</td>
<td>1</td>
<td>0.91 (0.71-1.18)</td>
</tr>
<tr>
<td>Gc2-2</td>
<td>1</td>
<td>0.91 (0.71-1.18)</td>
</tr>
<tr>
<td>Gc2-1/2-2</td>
<td>1</td>
<td>0.91 (0.71-1.18)</td>
</tr>
<tr>
<td>PR−/C0 tumors</td>
<td>n (Ca/Co)</td>
<td>OR (95% CI)</td>
</tr>
<tr>
<td></td>
<td>477/1,352</td>
<td>0.81 (0.69-0.96)</td>
</tr>
<tr>
<td>Gc1-1</td>
<td>324/1,060</td>
<td>0.57 (0.40-0.81)</td>
</tr>
<tr>
<td>Gc2-1</td>
<td>1</td>
<td>0.86 (0.73-1.02)</td>
</tr>
<tr>
<td>Gc2-2</td>
<td>1</td>
<td>0.86 (0.73-1.02)</td>
</tr>
<tr>
<td>Gc2-1/2-2</td>
<td>1</td>
<td>0.86 (0.73-1.02)</td>
</tr>
</tbody>
</table>

NOTE: Conditional logistic regression stratified by year of birth adjusted for age at menopause, first-degree family history of breast cancer, history of benign breast disease, number of pregnancies (≥28th wk), age at menarche, breast-feeding history, total number of mammograms, use of hormone therapy, body mass index, education level, and smoking status.

Data on ER and PR status were available for 1,296 and 1,295 cases, respectively. $P_{\text{interaction}} = 0.56$ and 0.006 for ER and PR status in a case-only model, respectively.

Abbreviations: Ca, cases; Co, control.
In postmenopausal breast cancer that is independent of serum 25(OH)D status. A possible anticarcinogenic mechanism lies in the activation of the vitamin D receptor pathway, which in turn leads to anticarcinogenic action of vitamin D (17). It is possible that potential of Gc to convert to GcMAF, a potent activator of macrophages (7). GcMAF has been shown to be effective as an antitumorogenic drug in metastatic breast cancer patients (9) and to inhibit tumor growth and increase apoptotic activity in pancreatic cell lines (8). The conversion of Gc to GcMAF requires a deglycosylation process mediated by β-galactosidase and sialidase (i.e., the removal of galactose and sialic acid residues; ref. 18). It is therefore of interest that, compared with Gc1s and Gc1f, the conversion of Gc2 protein (containing galactose only) to GcMAF requires solely β-galactosidase activity (19). We observed a decreased breast cancer risk only in Gc2 allele carriers but no differences in risk estimates between Gc1s and Gc1f carriers with the same glycosylation pattern. Thus, we hypothesize that different glycosylation patterns in the Gc alleles may explain the observed 25(OH)D-dependent decrease in breast cancer risk. Both qualitative and quantitative differences between Gc2MAF and Gc1MAF are possible.

One previous study assessed the two polymorphisms composing the Gc alleles and found no association with postmenopausal breast cancer risk (15). However, the study did not have adequate power to assess the effects of the different Gc alleles and did not take the vitamin D status into account.

We also looked at the differential effects of the Gc genotype on breast cancer by receptor status of the tumor. The anticarcinogenic effects of vitamin D could be mediated via the estrogen pathway by down-regulation of the ER and, thus, attenuating estrogenic bioresponses like cell growth (20, 21). No interaction was observed between the ER of the tumor and Gc genotypes.

However, the observed inverse association in progesterone-positive, but not progesterone-negative, tumors deserves further investigation.

Strengths of our study are the large sample size, the adjustment for all potential breast cancer risk factors, and the consideration of serum 25(OH)D status. Limitations due to the retrospective case-control design are negligible because genotype distribution is not prone to selection or recall bias. If the probability of being carriers of the risk alleles was associated with stage of diagnosis, the lower participation among cases with later stage at diagnosis would have biased our results. However, the genotype distribution of the two analyzed polymorphisms did not differ significantly by stage of the tumor. The 25(OH)D concentrations could be affected by diagnosis or treatment. The median difference (25th-75th percentile) between time of diagnosis and time of blood collection in the cases was 80 (14-260) days. However, in a sensitivity analysis excluding patients with blood samples taken within 6 months of diagnosis, we observed negligible changes in the risk estimates of the association between 25(OH)D levels and breast cancer risk (4). A notable change in 25(OH)D concentration after chemotherapeutic treatment has also not been observed previously (22, 23).

We selected known functional variants with potential effect on vitamin D metabolism; however, our findings on breast cancer risk need verification in further studies.

In summary, we observed a significant inverse association between genotypes in the vitamin D binding protein and postmenopausal breast cancer, comparing homozygote Gc2 with homozygote Gc1s allele carriers. Additionally, the Gc2 allele was associated with a decreased serum 25(OH)D concentration. Our data suggest a protective effect for Gc2 allele carrier status in postmenopausal breast cancer that is independent of serum 25(OH)D status. A possible anticarcinogenic mechanism of the Gc protein is provided by its potential conversion to GcMAF, a macrophage-activating factor known to display anticarcinogenic activities. However, further research on the influence of Gc genotypes on Gc protein and GcMAF activity is necessary.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Acknowledgments

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