**MDM2 SNP309 G allele increases risk but the T allele is associated with earlier onset age of sporadic breast cancers in the Chinese population**

San San Lum1, Hui Wan Chua1, Huihua Li2, Wen-Feng Li3,4, Nanyan Rao3, Jin Wei3, Zhiming Shao5 and Kanaga Sabapathy1,4,*

1Laboratory of Molecular Carcinogenesis, Division of Cellular and Molecular Research and 2Division of Clinical Trials and Epidemiological Sciences, Humphrey Oei Institute of Cancer Research, National Cancer Centre, 11 Hospital Drive, Singapore 169610, Singapore, 3Department of Breast Surgery, Cancer Hospital/Cancer Institute, Fudan University, Shanghai 200032, People’s Republic of China and 4Department of Biochemistry, National University of Singapore, 8 Medical Drive, Singapore 117597, Singapore

*To whom correspondence should be addressed. Tel: +65 6436 8349; Fax: +65 6226 5694; Email: cmrksb@nccs.com.sg

Sporadic breast cancer in women <40 years is uncommon in Caucasians, in contrast to a much earlier onset in Chinese Asians. However, the molecular determinants for this earlier onset are unclear. It has been reported that SNP309 in the promoter of MDM2, the negative regulator of p53, affects the onset age of cancers in females. Essentially, the G allele, rather than the T allele, has been suggested to accelerate the age of cancer onset. Hence, we examined if MDM2 and p53 polymorphisms would be determinants of the early onset phenomenon in Chinese women. Our results indicate that the MDM2 SNP309 G allele is more prevalent in the Chinese population compared with reported frequencies in Caucasians, and increases breast cancer risk of both sporadic cases and those with family history. However, it was the T/T genotype that was associated with earlier onset age of sporadic breast cancers in contrast to the G allele that was associated with the familial cases. Though p53 codon 72 single-nucleotide polymorphism (SNP) did not affect general cancer risk or age of onset, arginine homology, in contrast to proline homology, was found to decrease breast cancer risk in the later onset sporadic cases. Both SNP309 and codon 72 polymorphisms did not affect the stage of cancer. Together, the data suggest that the MDM2 SNP309 G allele is a risk factor for breast cancer, it does not accelerate, but delays the onset of the sporadic disease in Chinese women, highlighting that differences in ethnicity and family history may influence the role of MDM2 SNP309 in cancer susceptibility.

**Introduction**

Breast cancer is one of the major cancers affecting morbidity and mortality of females worldwide (1). It is often associated with postmenopausal stage, surfacing generally around or after 50 years of age. The median age in the Caucasian population is ~61 years, where >75% of the cases occur in women >50 years of age (2,3). Breast cancer incidence <40 years of age is uncommon in most western Caucasian populations, besides those that are associated with hereditary familial cases (2,4). However, though breast cancers still occur in postmenopausal women, with >50% of the cases occurring in women >50 years of age (5), there is an emerging trend in the Asian Chinese populations where there is an increase in the number of women succumbing to the disease at a much earlier age (6,7). This earlier onset of the disease, which is non-familial, is seen in women starting from 20 years of age, leading to a large number of cases occurring in women under the age of 40 years (5). Thus, there appears to be a shift in the onset age, leading to the suggestion that the distribution in the Asian Chinese population follows a bimodal pattern (Figure 1) (6). Hitherto, the causes or the genetic basis for the earlier onset of breast cancers in Asians are not understood.

$p53$ is a critical tumor suppressor gene that is commonly mutated in many human cancers (8). In breast cancers, it is mutated in around 30–35% of the cases and mutations often lead to poorer prognosis (9,10). Moreover, Li–Fraumeni patients with germ line $p53$ mutations often develop breast cancers (11,12), highlighting an important role for this protein in regulating cancer predisposition. Besides mutations, a common single-nucleotide polymorphism (SNP) in codon 72 of $p53$, resulting in either an arginine (Arg) or proline (Pro) residue, has been demonstrated to affect p53 function. The Arg polymorphic variant has been shown to induce apoptosis better than the Pro form, and conversely, the Pro form was shown to have a higher capacity for DNA repair and induction of cell cycle arrest than the Arg form (13–15). Consistent with its functional relevance, this polymorphism has been implicated in cancer predisposition, though literature is divided over the role of either variant in affecting cancer risk. An initial report suggested a positive correlation between the Arg allele and susceptibility to cancer (16). However, subsequent reports have both supported the initial findings or found no such correlation (17–25), which could perhaps be due to ethnic variations of the frequency of these alleles in different healthy populations (26). Recently, we have demonstrated that although there were no significant differences of the genotypic frequency between healthy controls and breast cancer cases among the Asian Chinese population, the expression of the Arg allele was elevated in Arg/Pro heterozygote breast cancers, suggesting a positive role for this allele in cancer predisposition (27).

Similar to $SNP$s affecting the function of $p53$, polymorphic variants with functional relevance have been identified in many upstream and downstream genes of the $p53$ pathway. For example, polymorphisms in $MDM2$ and $MDM4$ have been recently found to affect cellular response (28,29). Of note, the SNP in the promoter of $MDM2$, the negative regulator of $p53$, has been intensely studied (28,30,31). This SNP309, resulting in either a T or G allele, was shown to affect SP-1 binding, thereby modulating MDM2 transcription, and hence, its levels (28). The effect on MDM2 levels have a snow-balling effect on p53 amounts in the cell, and consistently, the G allele which leads to higher MDM2 transcription was shown to attenuate the p53 response (28). Because the SP-1-binding site is found in the estrogen receptor (ER)-binding motif on the MDM2 promoter, it was suggested that the G allele would be more sensitive to estrogen response compared with the T allele. Consistently, Bond et al. (30) searched for and found a correlation between the G allele and earlier onset of three different cancers in younger females, who would generally have higher estrogen levels than their older postmenopausal counterparts.

One could therefore envisage that the earlier onset of non-familial breast cancers in the Asian population could be associated with the $MDM2$ and/or $p53$ polymorphisms that would weaken the p53 pathway. In an attempt to find a genetic basis to this phenomenon, we have investigated the status of the common $p53$ and $MDM2$ polymorphic alleles in non-familial breast cancer cases occurring from 20 to 86 years of age (both earlier and later onset cases), comparing it with healthy controls from the Asian Chinese population. Our data suggest that whereas the $p53$ codon 72 SNP does not affect the age of onset, the $MDM2$ SNP309 G allele, which is highly prevalent in the healthy Chinese controls compared with the reported frequencies in Caucasians, is associated with higher cancer risk, regardless of the age of onset of the disease. However, contrary to earlier reports, the G allele was not associated with the earlier onset of sporadic cancers. In contrast, it was the T allele of $MDM2$ SNP309 that was associated with...
MDM2 SNP affects early onset breast cancer

MDM2 promoter SNP309 was determined by sequencing reactions. Briefly, a part of the MDM2 promoter (320 bases) was amplified using the following PCR primers—external primers: sense, 5'-CGGGGTCCTGCAGGTAAAGGT-3' and antisense, 5'-AGCGAATGCGTGCTTACCCT-3'. PCR amplification was performed in 25 μl reactions using 0.5 μl of Q buffer (Qiagen), 2.5 μl of 10x PCR buffer (Qiagen, Hilden, Germany), 0.4 μM of each primer, 0.4 μM of deoxy-nucleotide triphosphates, 1.5 U of Taq polymerase (Qiagen) and genomic DNA, using the following PCR conditions: 94°C (80 s), 30 cycles of 94°C (25 s), 51°C (60 s), 72°C (60 s) and 72°C (8 min). PCR product was purified via a purification kit (Qiagen) and DNA was eluted with water. Part of the purified DNA was used to perform a prosequencing PCR with the antisense primer to detect the SNP309 and to obtain a sequencing product, with 3 μl of big dye terminator V3.1 cycle Sequencing kit (ABI, California, USA), 0.5 μl of di-methyl sulfoxide (Sigma, Missouri, USA), 0.2 μM of antisense primer and the eluted DNA under the following PCR conditions: 94°C (3 min), 32 cycles of 94°C (30 s), 51°C (60 s) and 60°C (3 min). Sequencing run was performed with the ABI Prism 377 DNA Sequencer machine. Sequences were aligned and checked for SNP309 via a DNA sequencing program. DNA SeqMan, Genotyping was performed in batches of about 18–36 samples each time. Healthy and cancer samples were processed separately. Singaporean healthy samples were analyzed at the Singapore laboratory and the Shanghai samples (both cancer and healthy) were analyzed by the same investigator at the Shanghai laboratory. Cancer samples were analyzed in a blinded manner randomly, with no knowledge of the relevant information (i.e. onset age, status of the other genes such as p53, MDM2, etc.). All samples were numbered such as H1, H2 for healthy samples and C1, C2, etc. for cancer samples. To verify results, randomly selected samples (~10% of total) were reanalyzed by sequencing different individuals at both the laboratories, which gave consistent results throughout.

Statistical analysis

Fisher’s exact test was used to evaluate Hardy–Weinberg equilibrium for the control healthy group. Odds ratio (OR) together with 95% confidence interval were estimated to investigate the role of SNPs in female breast cancer risk by means of unconditional logistic regression adjusted for age. The role of individual SNP in breast cancer was assessed appropriately based on the relationship—OR1 (p53, Arg/Arg versus Pro/Pro; MDM2, G/G versus T/T); OR2 (p53, Arg/Pro versus Pro/Pro; MDM2, G/T versus T/T) and OR3 (p53, Arg/Arg versus Arg/Pro; MDM2, G/G versus G/T) to reflect a biological model of gene effect (33), as follows:

- Recessive model: OR1 = OR3 ≠ 1 and OR1 = 1;
- Dominant model: OR2 = OR3 ≠ 1 and OR1 = 1;
- Over-dominant model: OR3 = OR1 ≠ 1 and OR1 = 1;
- Codominant model: OR1 > OR1 > 1 and OR3 > OR3 > 1 (or OR1 < OR1 < 1 and OR3 < OR3 < 1). Kruskal–Wallis method was carried out to investigate the effects of SNPs on age of onset of disease, whereas Fisher’s exact test was performed to evaluate the effects of SNPs on cancer stage and the comparison of the genotype distribution between healthy subjects and cases. All statistical analyses were performed using STATA version 9 (Stata Corporation, College Station, TX).

Results

Status of MDM2 SNP309 in healthy Chinese population

The G/G genotype of MDM2 SNP309 was found to be less frequently represented in healthy Caucasian populations, ranging from 1.7 to 16.3% compared with the T/T genotype (30,34–36). However, the G/G genotypic frequency was more abundant—up to 24%—in the healthy Azhkenazi Jewish population (30), who are generally thought to have a higher lifetime cancer risk (37). Consistently, some reports have noted an increase in the frequency of this genotype with acceleration age of onset in Caucasian populations, suggesting that this genotype could be associated with cancer risk (28,30). We therefore determined the prevalence of this SNP in the healthy Chinese population from two distinct geographical locations: Shanghai (China) and in Singapore (Singapore). The analysis indicated that the frequency of those with the G/G genotype was 21.4% (n = 18 of 84) in the Shanghai female population and much higher in the Singapore females (34.1% in females alone) (n = 15 of 44) (Table I). However, the difference between the two populations was not statistically significant (P = 0.139). Fisher’s exact test showed that MDM2 SNP309 polymorphism is in HWE among Shanghai healthy subjects (P = 0.376) and Singapore healthy subjects (P = 1.000). This higher
incidence of the G/G genotypic frequency in the Chinese population correlated with that found in the Japanese population of which 33% was of this genotype (39) and another study on Chinese population from the Nanjing area in the Jiangsu province, which is on the southeast of China next to Shanghai (25.1%) (38). Comparison of the MDM2 SNP309 frequencies between the Chinese population from Shanghai (this study) and the adjoining Jiangsu area (38) revealed no significant differences ($P = 0.130$) (Table I). It is also interesting to note that both the Japanese and Chinese populations have been reported to have a higher incidence of early onset non-familial breast cancers in contrast to the Caucasian population (6).

Comparison of the p53 codon 72 genotype revealed that the Arg/Arg homozygotes were more prevalent compared with the Pro/Pro homozygotes in the Shanghai Chinese population (36.3–16.3%) ($n = 298/80–1380$) (Table I).

Breast cancer risk is associated with MDM2 SNP309 regardless of family history and the p53 Arg allele tended to be associated with reduced cancer risk in later onset cases

Peripheral blood samples from breast cancer patients of various ages were used to determine the role of the SNP309 and codon 72 polymorphism on cancer risk. All comparisons were made between healthy and cancer cases from Shanghai. We divided all the sporadic breast cancer patients into two groups, those <40 years of age and those >40 years of age and have termed them the early onset group (20–40 years of age) and later onset group (age of 41 and above). We have chosen this cutoff age as the earlier onset of the disease, which is non-familial, is seen in Asian Chinese women starting from 20 years of age and 40 years of age, respectively (Figure 2B). No significant effect of p53 on sporadic breast cancer risk was detected, with ORs of Arg/Arg versus Pro/Pro, Arg/Pro versus Pro/Pro and Arg/Arg versus Arg/Arg being 0.54 (0.25, 1.16), 0.71 (0.34, 1.46) and 0.76 (0.43, 1.36), respectively (Table III). Together, these results indicate that although the p53 codon 72 SNP does not affect general breast cancer risk in the Chinese population, the Arg variant might decrease sporadic breast cancer risk via a codominant mode in the later onset group.

<table>
<thead>
<tr>
<th>Population</th>
<th>Genotype</th>
<th>Pro/Pro (%)</th>
<th>Pro/Arg (%)</th>
<th>Arg/Arg (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shanghai females</td>
<td>80</td>
<td>16.3</td>
<td>47.5</td>
<td>36.3</td>
</tr>
<tr>
<td>Jiangsu province females</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Singapore females</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>MDM2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$n$</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>G/G (%)</td>
<td>84</td>
<td>21.4</td>
<td>44.0</td>
<td>34.5</td>
</tr>
<tr>
<td>G/T (%)</td>
<td>605</td>
<td>25.1</td>
<td>50.9</td>
<td>24.0</td>
</tr>
<tr>
<td>T/T (%)</td>
<td>44</td>
<td>34.1</td>
<td>47.7</td>
<td>18.2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Age group (years)</th>
<th>Family history of breast cancer</th>
<th>Tumour grade</th>
</tr>
</thead>
<tbody>
<tr>
<td>$&lt; 40$,$n = 241$</td>
<td>32/241</td>
<td>IV 4 1</td>
</tr>
<tr>
<td>$≥ 41$,$n = 208$</td>
<td>9/208</td>
<td>III 31 12</td>
</tr>
</tbody>
</table>

*Defined as with at least one first- or second-degree relative with breast and/or ovarian cancer, regardless of age.

**Six had mutations in Brca1 and one had mutation in Brca2.***

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Fig. 2. *MDM2* SNP309, but not codon 72 polymorphism of *p53*, affects breast cancer risk (A–C). Genotypic analysis of *p53* codon 72 polymorphism (left panel) and SNP309 of *MDM2* (right panel) comparing the frequency of various genotypes in healthy controls and breast cancer cases, analyzed as all cases (A), sporadic cases only (B) and familial cases only (C). n = 84 (*Mdm2*) and n = 80 (*p53*) for healthy samples from this study, designated as healthy controls (1), and n = 605, for healthy samples from a related study by Ma et al. (38), designated as healthy controls (2). n = 393 (*p53*) and n = 402 (*Mdm2*) for all breast cancer cases, and n = 35 for both *p53* and *MDM2* for familial breast cancer cases.

Table III. The effects of *p53* codon 72 SNP on female breast cancer risk

<table>
<thead>
<tr>
<th></th>
<th>OR (95% confidence interval) a</th>
<th>Arg/Arg versus Pro/Pro</th>
<th>Arg/Arg versus Arg/Pro</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sporadic later onset (&gt;40)</td>
<td>0.52 (0.16, 1.75)</td>
<td>0.26 (0.07, 0.90)</td>
<td>0.49 (0.19, 1.23)</td>
</tr>
<tr>
<td>Sporadic early onset b (≤40)</td>
<td>0.80 (0.27, 2.38)</td>
<td>0.80 (0.24, 2.69)</td>
<td>1.00 (0.39, 2.53)</td>
</tr>
<tr>
<td>Sporadic later onset (&gt;50)</td>
<td>0.55 (0.17, 1.77)</td>
<td>0.27 (0.08, 0.93)</td>
<td>0.50 (0.20, 1.24)</td>
</tr>
<tr>
<td>Sporadic early onset b (≤50)</td>
<td>0.84 (0.28, 2.49)</td>
<td>0.82 (0.24, 2.77)</td>
<td>0.98 (0.38, 2.50)</td>
</tr>
<tr>
<td>All sporadic cases (non-familial)</td>
<td>0.71 (0.34, 1.46)</td>
<td>0.54 (0.25, 1.16)</td>
<td>0.76 (0.43, 1.36)</td>
</tr>
<tr>
<td>Familial cases (non-sporadic)</td>
<td>0.64 (0.20, 2.02)</td>
<td>0.55 (0.15, 1.96)</td>
<td>0.87 (0.30, 2.48)</td>
</tr>
<tr>
<td>All cases (sporadic + familial)</td>
<td>0.71 (0.34, 1.47)</td>
<td>0.54 (0.25, 1.16)</td>
<td>0.76 (0.43, 1.36)</td>
</tr>
</tbody>
</table>

*a*OR and corresponding confidence interval were adjusted for age.

bSporadic early onset patients who do not have familial history of cancer.

cDefined as with at least one first- or second-degree relative with breast and/or ovarian cancer, regardless of age.
A similar trend to the total cases was also noted when only the sporadic breast cancer cases were compared with our matched healthy controls (percent of G/G versus T/T versus G/T: healthy control/cases → 21.4/30.5 versus 34.5/19.9 versus 44.1/49.6) (n = 84 for healthy and 367 for cases: 18/112 versus 29/73 versus 37/182) (P = 0.015) (Figure 2B), with the ORs of G/G versus T/T, G/T versus T/T and G/G versus G/T being 2.81 (1.40, 5.63), 2.33 (1.28, 4.24) and 1.21 (0.64, 2.28), respectively, which suggested that the variant G allele is associated with increased breast cancer risk in a dominant mode [G/G + G/G versus T/T: 2.49 (1.43, 4.35)] (Table IV). Interestingly, the variant G allele increased breast cancer risk in a dominant mode, especially among females >40 years of age [G/G + G/G versus T/T: 3.52 (1.38, 8.99)] (Table IV). Comparison with the Jiangsu controls also revealed that the sporadic breast cancer risk (non-familial) was increased among subjects with G/G [G/G versus T/T: 1.46 (1.01, 2.12)].

Of the 35 cases with family history and genotyped, 11 were of the G/G (31.4%), 22 were of G/T (62.9%) and only 2 (5.7%) were of the T/T genotype, which was significantly different from the genotype distribution of controls (P = 0.002) (Figure 2B). The ORs of G/G versus T/T, G/T versus T/T and G/G versus G/T were 6.78 (1.25, 36.81), 11.46 (2.26, 58.14) and 0.59 (0.21, 1.70), respectively, implying a dominant effect of variant G [G/G + G/G versus T/T: 9.32 (1.96, 44.45)] (Table IV). Comparison of the familial cancer frequencies with the healthy control frequencies obtained from the larger study from the Jiangsu area also revealed a similar trend (percent of G/G versus T/T versus G/T: healthy control/cases → 34.9/45.1 versus 49.9/35.2 versus 34.3/19.8) (n = 170 for healthy and 804 for cases: 37/113 versus 45/128 versus 31/33) (P = 0.009) (Table IV). Further analysis of sporadic cases only also showed a similar trend (percent of G/G versus T/T versus G/T: healthy control/cases → 25.1/31.4 versus 24.0/5.7 versus 50.9/62.9) (n = 111) (P = 0.027) (Figure 2C), with a dominant effect of variant G [G/G + G/G versus T/T: 5.20 (0.23, 21.90)]. Together, these results indicate a positive correlation between the G allele of MDM2 SNP309 with breast cancer risk, both among females >40 years of age with sporadic cancers and those with family history of cancer.

Altering the cutoff age to <50 or >50 did not change the conclusions for both p53 and MDM2 status, as the ORs were similar to that obtained using 40 years as a cutoff age (Tables III and IV).

### Table IV. The effects of MDM2 SNP309 on female breast cancer risk

<table>
<thead>
<tr>
<th></th>
<th>OR (95% confidence interval)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>G/T versus T/T</td>
</tr>
<tr>
<td>Sporadic later onset (&gt;40)</td>
<td>3.02 (1.12, 8.11)</td>
</tr>
<tr>
<td>Sporadic early onset&lt; (≤40)</td>
<td>1.68 (0.68, 4.17)</td>
</tr>
<tr>
<td>Sporadic later onset (&gt;50)</td>
<td>2.88 (1.07, 7.74)</td>
</tr>
<tr>
<td>Sporadic early onset&lt; (≤50)</td>
<td>1.72 (0.69, 4.29)</td>
</tr>
<tr>
<td>All sporadic cases (non-familial)</td>
<td>2.33 (1.28, 4.24)</td>
</tr>
<tr>
<td>Familial cases (non-sporadic)</td>
<td>11.46 (2.26, 58.14)</td>
</tr>
<tr>
<td>All cases (sporadic + familial)</td>
<td>2.56 (1.41, 4.66)</td>
</tr>
</tbody>
</table>

<sup>a</sup>OR and corresponding confidence interval were adjusted for age.
<sup>b</sup>Sporadic early onset patients who do not have familial history of cancer.
<sup>c</sup>Defined as with at least one first- or second-degree relative with breast and/or ovarian cancer, regardless of age.

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p53 codon 72 polymorphism has no effect on age of onset or stage of breast cancer

We next evaluated if p53 polymorphism at codon 72 affected the age of disease onset. Kruskal–Wallis analysis indicated no association of any of the p53 alleles with age of onset (P = 0.806) (Table V and Figure 3A). The mean age of onset for the Arg/Arg, Arg/Pro and Pro/Pro groups were found to be 43.14 ± 13.28, 42.04 ± 12.56 and 43.02 ± 13.28, respectively. Moreover, there was no effect of the various genotypes on the age of onset either among sporadic cases (P = 0.721) (Figure 3B) or familial cases (P = 0.942) (Figure 3C).

Similarly, Fisher’s exact test indicated no association of any of the p53 alleles with the stage of breast cancers (P = 0.652) (Table V and supplementary Figure 1A, available at Carcinogenesis Online). All genotypes were equally represented in all stages of the disease (supplementary Figure 1A, available at Carcinogenesis Online).

### Table V. P values of the effects of p53 codon 72 and/or MDM2 SNP309 on the age onset and cancer stage of female breast cancer

<table>
<thead>
<tr>
<th></th>
<th>p53</th>
<th>MDM2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age onset</td>
<td>0.806</td>
<td>0.033</td>
</tr>
<tr>
<td>Cancer stage</td>
<td>0.652</td>
<td>0.610</td>
</tr>
</tbody>
</table>

MDM2 SNP309 G allele delays onset of breast cancer but does not affect stage of cancer

As the MDM2 SNP309 G allele was suggested in some studies to be associated with earlier onset of age of cancers in females (30), we analyzed if this phenomenon is applicable to our study population where early onset of the disease is a common feature. Kruskal–Wallis analysis revealed that SNP309 indeed affected the onset age of breast cancer patients (sporadic + familial) (P = 0.033) (Table V). The mean age of onset for the G/G, G/T and T/T groups were found to be 44.11 ± 13.70, 44.46 ± 13.65 and 39.99 ± 12.26, respectively. Pair-wise test of SNP309 showed that patients with G/T genotype tend to develop cancer significantly later than patients with T/T genotype (P = 0.011) (Figure 3A). Moreover, patients with G/G genotype also developed cancers slightly later in life compared with those with the T/T genotype (P = 0.03). Whereas ~61% of those with the T/T genotype had developed breast cancer by 40 years of age, only 47% of G/T and 50% of G/G genotypes had the disease by this age (Figure 3A). The difference between those with the G/T and G/G genotypes was not significant (P = 0.841) (Figure 3A). Similarly, when the rate of cancer onset was analyzed based on 50% of the population for each genotype, the average age was 34 years for those with the T/T genotype, whereas it was 42 and 39 years for those with the G/T and G/G genotypes, respectively (Figure 3A). Further analysis of sporadic cases only also showed a similar trend (Figure 3B). The mean age of onset for the G/G, G/T and T/T groups were found to be 45.33 ± 13.73, 44.76 ± 13.94 and 40.23 ± 12.32, respectively. Pair-wise test of SNP309 also showed that patients with G/T genotype tend to develop cancer significantly later than patients with T/T genotype (P = 0.020) (Figure 3B). Moreover, patients with G/G genotype also developed cancers later in life compared with those with the T/T genotype (P = 0.009). Whereas ~61% of those with the T/T genotype had developed breast cancer by 40 years of age, only 45% of both G/T and G/G genotypes had the disease by this age (Figure 3B). The difference between those with the G/T and G/G genotypes was not significant (P = 0.595) (Figure 3B). Similarly, when the rate of cancer onset was analyzed based on 50% of the population for each genotype, the average age was 34 years for those with the T/T genotype, whereas it was ~46.5 years for those with the G/T and G/G genotypes (Figure 3B). In contrast, analysis of familial cancers only revealed that those with G/T genotypes were found to develop cancer later than those
with G/G genotype (42.32 ± 11.32 versus 31.73 ± 3.74) \((P < 0.001)\) (Figure 3C), a finding that is consistent with previous studies highlighting that the presence of the T allele can delay the onset of familial cancers in females.

Analysis of the effects of SNP309 on stage of disease did not reveal any significant differences among the different genotypes and the stages of breast cancer \((P = 0.610)\) (Table V and supplementary Figure 1B, available at Carcinogenesis Online). All genotypes were equally represented in all stages of the disease (supplementary Figure 1B, available at Carcinogenesis Online).

Together, the results suggest that although SNP309 did not affect the stage of cancer, those with the T/T genotype tended to be more prone to earlier onset of sporadic breast cancer in the Chinese population.

**Discussion**

The data presented here suggest that the G allele of **MDM2** SNP309 increases both sporadic and familial breast cancer risk. However, unexpectedly, the T allele in contrast to the G allele was associated with a tendency to decrease sporadic breast cancer risk in older women.

We undertook this study to evaluate if the relatively higher incidence of early onset non-familial breast cancers that is uniquely observed in the Asian Chinese population could be due to the effects of the SNPs in the MDM2/p53 axis. Interestingly, this population contains a higher frequency of the G allele of **MDM2** SNP309 (this report and ref. 38), which has been suggested to lead to higher transcription and hence, higher levels of MDM2 (28). However, though the SNP309 G allele seemed to increase breast cancer risk in the Asian Chinese population, it was not associated with early onset of the disease in sporadic cases. In fact, the G allele delayed the onset age, whereas the T allele was associated with earlier onset of the disease. These data are unexpected based on the earlier studies, as well as our findings with familial cases (Figure 3C) that suggest a positive correlation between the G allele and an earlier age of female breast cancer onset.

With the initial identification of the SNP in **MDM2** promoter, there has been a series of investigations aimed at validating the role of SNP309 G allele with early onset age of cancers. Since the SNP was noted in the SP-1-binding motif in the **MDM2** promoter where ER was shown to bind (40,41), it has been suggested to affect estrogen signaling, and hence, affected by estrogen levels (30). Consistently,
the distinct effects of this SNP were noted in females in contrast to males (30).

Closely analysis of the published data, however, reveals that there may not be a straight correlation between the SNP309 G allele and age of breast cancer onset. Bond et al. (28,30) in their first two reports found a correlation between this G allele and earlier onset of female breast cancers, particularly in familial Li–Fraumeni cases. Supporting these data, a recent report also suggested that the G allele was associated with accelerated onset of familial breast cancers, but concluded that this had no association with estrogen signaling (42). In contrast, several other studies investigating breast cancers did not observe any association between the G allele and age of cancer onset (34,35,38,43). The major difference between the limited studies that support a positive correlation between the G allele and breast cancer onset age and those that did not find any correlation is that the earlier studies analyzed familial cancer cases, whereas the latter studies evaluated sporadic cancers. Thus, it appears that the G allele is probably associated with early age of onset in familial cancer cases, an observation that we could confirm, as those with G/G genotype tended to develop cancer earlier than those with G/T genotype (Figure 3C). This could be taken to mean that there may be other factors that would prime these familial cases to cancer predisposition, perhaps in an estrogen-dependent manner. On the contrary, sporadic cases without any form of underlying familial genetic risk may not have this priming factor that would enable the manifestation of the effects of the G allele (which increases MDM2 levels). Thus, one could envisage that in familial cases where the p53 pathway is already often affected and weakened, increasing the MDM2 levels (by the presence of the G allele) would enhance cancer susceptibility probably through the alteration of other gene products that suppress tumorigenesis. In sporadic cases, however, where the p53 pathway may not be affected yet, presence of the G allele alone would not be sufficient to accelerate the age of cancer onset as MDM2 could be a limiting factor in inhibiting p53 and other potential tumor suppressors. Further investigations are required to test this hypothesis and to identify other molecular targets of MDM2 that may be responsible for the early onset of cancers in familial cases. The most important finding presented here is that instead of the initially expected association of the G allele with early age of cancer onset noted in familial cancer cases, we observed a significant association between the T/T genotype and younger age at sporadic cancer onset. It is also interesting to note that when Bond et al. (30) segregated familial breast cancer patients based on ER positivity, the ER patients with the T/T genotype had an earlier age of cancer onset compared with those who were of the G/G genotype. Though we do not have ER data to correlate with the MDM2 genotypes, it is evident that T/T genotype can also be associated with promotion of the early onset of female cancers, though the molecular details are not known. These findings cannot be explained merely based on the elevated estrogen signaling in younger women. Moreover, it is also unconceivable that the T allele, with the expected lowered MDM2 production, could promote the early onset of cancers through modulating the p53 pathway. Hence, it is possible that the T allele could affect the recruitment of different factors onto the MDM2 promoter, thereby influencing its transcription, therefore suggesting that MDM2 may have a p53-dependent and -independent effect with respect to familial and sporadic breast cancer cases, respectively. Altogether, these data suggest that the G allele need not always be associated with earlier onset of cancers, as was shown in familial cases, but the opposite could be true in sporadic cases.

Besides this difference, our study also revealed that there is an association of the G allele with breast cancer risk in Asian Chinese females. It is noteworthy that the Chinese (and Japanese) population contains a higher frequency of people with the G genotype (this report and refs 37,38), which correlates with a higher percentage of them being predisposed to early onset of sporadic breast cancers (6). However, there have been no reports associating the G allele with general breast cancer risk in other populations (34,35,38,43). Moreover, the age-adjusted ratio of general cancer risk is generally lower in the Chinese (Asians) than in the western Caucasian populations (1), arguing against a general mechanism for the MDM2 SNP309 G allele to be associated with pan-cancer risk. Therefore, it is possible that the G allele can affect breast cancer risk in the Chinese population, perhaps in combination with estrogen levels and with other ethnicity-associated genetic factors that have yet to be identified.

Finally, although the status of MDM2 SNP309 is correlated with cancer risk and age of onset, the p53 codon 72 polymorphism, that has functional significance, did not seem to affect age of cancer onset. This suggests that MDM2 may be targeting other substrates besides p53 in influencing cancer predisposition. Nonetheless, consistent with the notion that the p53 pathway is often affected in cancers, this p53 polymorphism was indeed found to decrease the risk of sporadic breast cancers. The Arg variant was found to decrease the risk compared with the Pro form, especially in older women. This indicates that the functional significance of the p53 polymorphism may be relevant in influencing cancer predisposition, besides its effects on survival and prognosis when the gene is mutated (10,12).

Taken together, the data presented here suggest that there is a positive correlation between the G allele of MDM2 SNP309 and breast cancer risk in the Asian Chinese population. Moreover, the T/T genotype, which is thought to lead to lowered production of MDM2, is associated with the earlier onset of non-familial breast cancer cases. This is in contrast to the positive correlation of the SNP309 G allele with accelerated age of onset of familial breast cancer cases and other cancers such as gastric and nasopharyngeal carcinoma (44,45). These findings therefore demonstrate that MDM2 SNP309 indeed affects cancer risk and age of onset, but in different ways in the Asian Chinese population, highlighting that other ethnicity-associated factors may also have essential roles in determining cancer susceptibility.

### Supplementary material

Supplementary Figure 1A and B can be found at [http://carcin.oxfordjournals.org/](http://carcin.oxfordjournals.org/)

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### References

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