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A variant upstream of HLA-DRB1 and multiple variants in MICA influence susceptibility to cervical cancer in a Swedish population

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Keywords
Cervical cancer, cis-eQTL, frameshift mutation, HLA-DRB1, MICA

Abstract
In a genome-wide association study, we have previously identified and performed the initial replication of three novel susceptibility loci for cervical cancer: rs9272143 upstream of HLA-DRB1, rs2516448 adjacent to MHC class I polypeptide-related sequence A gene (MICA), and rs3117027 at HLA-DPB2. The risk allele T of rs2516448 is in perfect linkage disequilibrium with a frameshift mutation (A5.1) in MICA exon 5, which results in a truncated protein. To validate these associations in an independent study and extend our prior work to MICA exon 5, we genotyped the single-nucleotide polymorphisms at rs9272143, rs2516448, rs3117027 and the MICA exon 5 microsatellite in a nested case-control study of 961 cervical cancer patients (827 carcinoma in situ and 134 invasive carcinoma) and 1725 controls from northern Sweden. The C allele of rs9272143 conferred protection against cervical cancer (odds ratio [OR] = 0.73, 95% confidence interval [CI] = 0.65–0.82; P = 1.6 × 10⁻⁷), which is associated with higher expression level of HLA-DRB1, whereas the T allele of rs2516448 increased the susceptibility to cervical cancer (OR = 1.33, 95% CI = 1.19–1.49; P = 5.8 × 10⁻⁷), with the same association shown with MICA-A5.1. The direction and the magnitude of these associations were consistent with our previous findings. We also identified protective effects of the MICA-A4 (OR = 0.80, 95% CI = 0.68–0.94; P = 6.7 × 10⁻⁵) and MICA-A5 (OR = 0.60, 95% CI = 0.50–0.72; P = 3.0 × 10⁻⁵) alleles. The associations with these variants are unlikely to be driven by the nearby human leukocyte antigen (HLA) alleles. No association was observed between rs3117027 and risk of cervical cancer. Our results support the role of HLA-DRB1 and MICA in the pathogenesis of cervical cancer.

Introduction
Worldwide, cervical cancer is the third most common cancer and the second most frequent cause of cancer deaths among women, and resulted in an estimated 530,000 new cancer cases and 275,000 deaths in 2008 [1]. In many low-income countries, cervical cancer is the most common cancer and the leading cause of cancer-related death among women [1]. Cervical cancer and its precursor lesions, cervical intraepithelial neoplasia (CIN) are caused by persistent infection with high-risk human papillomavirus (HPV), where CIN III is considered the same as carci-
noma in situ (CIS) [2]. During their lifetime, many women will become infected with HPV, but only a minority will develop CIN or cervical cancer. Consequently, other factors, for example, host genetic factors, play an important role in both the persistence of infection and progression to cancer [3, 4].

We have recently performed the first genome-wide association study (GWAS) of cervical cancer and identified three independent novel loci within the major histocompatibility complex (MHC) region at 6p21.3 that influence susceptibility to cervical cancer in a Swedish population. The first is located between HLA-DRB1 and HLA-DQA1 (rs9272143; odds ratio [OR] = 0.67, 95% confidence interval [CI] = 0.62–0.72 for C allele; \( P = 9.3 \times 10^{-24} \)); the second is adjacent to the MHC class I polypeptide-related sequence A gene (MICA) (rs2516448; OR = 1.42, 95% CI = 1.31–1.54 for T allele; \( P = 1.6 \times 10^{-18} \)); and the third at HLA-DPB2 (rs3117027; OR = 1.25, 95% CI = 1.15–1.35 for A allele; \( P = 4.9 \times 10^{-10} \)) [5]. The associations observed for these three new loci were found to be statistically independent of previously known associations with the human leukocyte antigen (HLA) alleles/haplotypes [5]. The transmembrane domain (TMD) of MICA encoded with the human leukocyte antigen (HLA) alleles/haplotypes [5]. The transmembrane domain (TMD) of MICA encoded 4, 5, 6, or 9 alanine (Ala) residues (alleles designated by exon 5 harbors a variable number of GCT repeats, which encode 4, 5, 6, or 9 alanine (Ala) residues (alleles designated A4, A5, A6 or A9, respectively). Additionally, the A5.1 allele (rs67841474) contains an extra guanine (G) insertion after two GCT triplets, which causes a frameshift mutation resulting in a premature stop codon that, in turn, truncates 10 amino acids of the TMD as well as the hydrophobic cytoplasmic tail [6]. The risk allele T of rs2516448 was found to be in perfect linkage disequilibrium (LD) (\( D' = 1, r^2 = 1 \)) with A5.1 and cervical neoplasia patients carrying the A5.1 allele have less membrane-bound MICA in their lesions [5].

In our initial GWAS, we were able to replicate the effect of the three susceptibility loci in a second cohort from southern and middle Sweden. However, validation of GWAS findings in multiple cohorts is necessary in order to report genotype–phenotype associations. The new susceptibility loci for cervical cancer require further investigation in a large sample size. It is also important to extend our prior work to MICA exon 5 microsatellite polymorphism and evaluate effect modification by age of onset and tumor stage. Therefore, we investigated the association between single-nucleotide polymorphisms (SNPs) of rs9272143, rs2516448, and rs3117027 as well as MICA exon 5 microsatellite polymorphism and risk of cervical cancer, in a large nested case–control study of 961 incident cervical cancer patients (827 CIS and 134 invasive carcinoma) and 1725 cancer-free controls from the Västerbotten County in northern Sweden.

### Material and Methods

#### Study population

Eligible women for the study were defined as Västerbotten County resident in northern Sweden who had at least one cytologically normal cervical smear and who had no prior operative treatment of the cervix. Linkage between the cytology registry and the Swedish Cancer Registry from 1961 identified 832 patients with CIS and 134 patients with invasive cervical cancer diagnosed after the sampling date of a normal smear. Controls were women in the study base who did not develop cervical cancer before the time point of diagnosis of a corresponding case. For each CIS case, two population-based controls were selected, matched for age of subject (±5 years) when the sample was collected. For each invasive cervical cancer case, one population-based control was selected, matched for age of subject (±5 years) when the sample was collected. A written informed consent was obtained from each participant and this study was approved by the Institutional Review Board (IRB) of the Umeå University. Genomic DNA was extracted from the buffy coat using standard phenol–chloroform extraction protocol. In total, DNA samples from 827 women with CIS and 1591 matched healthy controls, and 134 women with invasive cervical cancer and 134 matched healthy controls qualified for genotyping. The study population was not included in the previous GWAS study.

#### Genotyping assay

Single-nucleotide polymorphisms of rs9272143 and rs3117027 were genotyped with template-directed dye-terminator incorporation with fluorescence polarization detection (FP-TDI) (Tecan, Männedorf, Switzerland) and rs2516448 was genotyped using the TaqMan assay (Applied Biosystems, Foster City, CA). The information of the primers and probes is described in Supplementary Table S1. The polymerase chain reaction (PCR) amplification of the MICA microsatellite alleles of exon 5 was carried out using a 5’ end fluorescently (6-FAM)-labeled reverse primer and a forward unlabeled primer. The primer sequences for the MICA microsatellite were previously reported [7] and are described in Supplementary Table S1. The PCR products were mixed with Hi-Di Formamide and GeneScan 500 ROX size standard and separated on an ABI 3730xl DNA Analyzer (Applied Biosystems). Different alleles were annotated using GeneMapper 4.1 software (Applied Biosystems, Foster City, USA) based on the size of the PCR products. Eight percent of the samples were selected for repeat genotyping as duplicates, yielding a reproducibility of 100%. Genotype success rate was >98.21%.
Extension of Findings in Cervical GWAS

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Table 1. Selected demographic characteristics of study subjects.

<table>
<thead>
<tr>
<th></th>
<th>Cases</th>
<th>Controls</th>
<th>P²</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>N² (%)</td>
<td>N² (%)</td>
<td></td>
</tr>
<tr>
<td>Age (years)¹</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;36</td>
<td>478 (49.33)</td>
<td>851 (49.74)</td>
<td>0.22</td>
</tr>
<tr>
<td>≥36</td>
<td>483 (50.67)</td>
<td>874 (50.26)</td>
<td></td>
</tr>
<tr>
<td>Mean± SD</td>
<td>36.86 ± 9.05</td>
<td>36.43 ± 8.86</td>
<td></td>
</tr>
<tr>
<td>Study design</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Study 1</td>
<td>827⁴ (86.06)</td>
<td>1591 (92.23)</td>
<td></td>
</tr>
<tr>
<td>Study 2</td>
<td>134² (13.94)</td>
<td>134 (7.77)</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>961</td>
<td>1725</td>
<td></td>
</tr>
</tbody>
</table>

SD, Standard error.
¹The median age is 36 years for both cervical cancer patients and control subjects.
²Number of samples.
³Difference in age between cervical cancer patients and control subjects was evaluated by using t-test. P value is two-sided.
⁴Number of subjects with invasive carcinoma.

**Results**

The characteristics of the cervical cancer patients and cancer-free controls enrolled in the study are described in Table 1. Overall, there was no significant difference in age between the cervical cancer patients and the control subject (P = 0.22), suggesting that matching based on age was adequate. The median age was 36 years for both cases and controls. Of the 961 cervical cancer patients, 827 (86.06%) had a diagnosis of CIS and 134 (13.94%) of invasive carcinoma.

Table 2 summarizes the estimates of the main effects for each SNP. Genotype frequency distributions in the control subjects were consistent with those expected from the HWE model for all SNPs (all P > 0.05). The variant allele T of rs2516448 in the MHC class I region was significantly associated with increased risk of cervical cancer (OR = 1.33, 95% CI = 1.19–1.49; P = 5.8 × 10⁻⁷), whereas the variant allele C of rs9272143 in the MHC class II region was strongly associated with decreased risk of cervical cancer (OR = 0.73, 95% CI = 0.65–0.82; P = 1.6 × 10⁻⁷). Both the direction and magnitude of these associations were in accordance with our previous findings [5]. In contrast, there was no association between rs3117027 and risk of cervical cancer (OR = 0.99, 95% CI = 0.88–1.12 for variant allele A; P = 0.86). The LD between these three SNPs was very weak (r² = 0) (Supplementary Table S2), consistent with previous study [5].

The allele frequencies of the MICA exon 5 microsatellite in cervical cancer patients and control subjects are shown in Table 3. Analysis showed that MICA-A5.1 (G insertion of rs67841474) had the highest frequency in both patients (60%) and control subjects (52%). In accordance with our previous finding [5], this microsatellite allele was in perfect LD (D’ = 1, r² = 1) with the risk allele T of rs2516448 in both cases and controls, and showed a comparable association with susceptibility to cervical cancer (OR = 1.34, 95% CI = 1.20–1.50; P = 3.8 × 10⁻⁷) as the rs2516448 T allele. In the overlapping 943 cervical cancer patients and 1683 cancer-free control subjects, the OR (95% CI) was 1.34 (1.20–1.51) for both A5.1 and the T allele of rs2516448. In addition, significant protective effects were seen for MICA-A4 (OR = 0.80, 95% CI = 0.68–0.94; P = 6.7 × 10⁻³) and MICA-A5 (OR = 0.60, 95% CI = 0.50–0.72; P = 3.0 × 10⁻⁸). No correlation was found between rs9272143 and rs3117027 and alleles of MICA exon 5 microsatellite (r² = 0) (Supplementary Table S2).

An allelic dosage effect on cervical cancer risk was observed for variant at rs9272143 in the MHC class II region and the MICA-A4, A5 and A5.1 alleles, when comparing the heterozygous and homozygous carriers of the variant allele with the noncarriers (Fig. 1). In particu-
Table 2. Summary estimates of the main effects of the selected variants at 6p21.3 reported to independently associate with cervical cancer.

<table>
<thead>
<tr>
<th>Locus</th>
<th>SNP</th>
<th>Position</th>
<th>Genotyping Rate (%)</th>
<th>Allele</th>
<th>Nearby gene</th>
<th>Alleles</th>
<th>HWE3</th>
<th>Frequency</th>
<th>Cases</th>
<th>Controls</th>
<th>OR (95% CI)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>rs9272143</td>
<td>32600803</td>
<td>99.96</td>
<td>T &gt; C</td>
<td>0.54</td>
<td>T</td>
<td>960</td>
<td>0.38</td>
<td>1725</td>
<td>0.45</td>
<td>1.6 x 10^-7</td>
<td>1.6</td>
</tr>
<tr>
<td>2</td>
<td>rs2516448</td>
<td>31390410</td>
<td>99.55</td>
<td>C &gt; T</td>
<td>0.14</td>
<td>C</td>
<td>955</td>
<td>0.60</td>
<td>1719</td>
<td>0.52</td>
<td>3.0 x 10^-8</td>
<td>3.0</td>
</tr>
<tr>
<td>3</td>
<td>rs3117027</td>
<td>33089623</td>
<td>99.63</td>
<td>C &gt; A</td>
<td>0.29</td>
<td>A</td>
<td>960</td>
<td>0.30</td>
<td>1716</td>
<td>0.31</td>
<td>9.7 x 10^-9</td>
<td>9.7</td>
</tr>
</tbody>
</table>

HWE, Hardy-Weinberg equilibrium; MAF, minor allele frequency; OR, odds ratio; CI, confidence interval.

1 Genome build 37.3, (GRCh37/hg19) Assembly.
2 Wild-type allele.
3 Variant allele.
4 P-values for Hardy-Weinberg equilibrium in the controls.
5 Number of samples that were successfully genotyped for specified SNP in cervical cancer patients and control subjects, respectively.
6 Frequency of the variant alleles in the cases and controls, respectively.
7 Odds ratios and 95% confidence intervals for each allele in log-additive model were derived from unconditional logistic regression adjusting for age at recruitment and study design.

Discussion

We replicated the associations of cervical cancer with rs9272143 located in the MHC class II region as well as with rs2516448 and MICA-A5.1 in the class I region identified in our previous GWAS, with ORs of similar magnitude to that previously reported [5]. We also identified protective effects of both the MICA-A4 and MICA-A5 alleles against cervical cancer. None of these variants showed heterogeneity by age of onset. The association...
between HLA-DPB2 variant rs3117027 and risk of cervical cancer was not replicated in this study.

SNP rs9272143 is located 4.38 kb upstream of HLA-DQA1 and 43.19 kb upstream of HLA-DRB1. It has recently been identified as a cis-expression quantitative trait locus (cis-eQTL), with the T allele being associated with decreased expression of HLA-DRB1 as compared to the C allele [9]. HLA-DRB1 belongs to the HLA class II β-chain paralogs, which encodes the β-chain of the peptide-antigen receptor HLA-DR. It is expressed in Lanherans cells (LC), the antigen presenting cells of squamous epithelia in the cervix, and plays a central role in the cell-mediated immune response by presenting processed foreign antigens to CD4+ helper T-lymphocytes [10]. CD4+ T-cell activation results in the secretion of a variety of small proteins, or cytokines. Our study points to the importance of expression level of HLA-DRB1 in cervical carcinoma. Impaired class II gene expression [11–13] and a reduced number of LC have been reported in genital HPV infections [14, 15] and in lesions due to HPV [16]. The increased incidence and progression of HPV infections in immunosuppressed individuals illustrates the critical importance of the CD4+ T-cell-regulated cell-mediated immune response in the resolution and control of HPV infection [10, 17]. Regression of anogenital warts is accompanied histologically by a CD4+ T-cell-dominated Th1 response. Failure to develop effective cell-mediated immune response to clear or control infection results in a persistent infection and, in the case of the oncogenic HPVs, an increased probability of progression to CIS and invasive carcinoma [17]. Therefore, HLA-DRB1 may be involved in

<table>
<thead>
<tr>
<th>rs9272143</th>
<th>Ca</th>
<th>Co</th>
<th>OR</th>
<th>95%CI</th>
<th>P &lt; 0.0001</th>
<th>Overall</th>
<th>Heterozygotes</th>
<th>Homozygotes</th>
<th>Overall</th>
<th>Heterozygotes</th>
<th>Homozygotes</th>
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<tbody>
<tr>
<td>Overall</td>
<td>960</td>
<td>1725</td>
<td>0.73</td>
<td>0.65–0.82</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>TC versus TT</td>
<td>465</td>
<td>867</td>
<td>0.76</td>
<td>0.63–0.90</td>
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<td></td>
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<tr>
<td>CC versus TT</td>
<td>130</td>
<td>345</td>
<td>0.53</td>
<td>0.41–0.67</td>
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<tr>
<td>By tumor stage (Phet &lt; 1 × 10−3)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Carcinoma in situ</td>
<td>826</td>
<td>1591</td>
<td>0.67</td>
<td>0.60–0.76</td>
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</tr>
<tr>
<td>By age (Phet = 0.57)</td>
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<td></td>
<td></td>
<td></td>
<td>&lt;36</td>
<td>477</td>
<td>851</td>
<td>0.71</td>
<td>0.60–0.84</td>
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</table>

<table>
<thead>
<tr>
<th>MICA-A4</th>
<th>Ca</th>
<th>Co</th>
<th>OR</th>
<th>95%CI</th>
<th>P &lt; 0.0001</th>
<th>Overall</th>
<th>Heterozygotes</th>
<th>Homozygotes</th>
<th>Overall</th>
<th>Heterozygotes</th>
<th>Homozygotes</th>
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<tbody>
<tr>
<td>Overall</td>
<td>949</td>
<td>1689</td>
<td>0.80</td>
<td>0.68–0.94</td>
<td>P = 6.7 × 10−4</td>
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<tr>
<td>Heterozygotes</td>
<td>223</td>
<td>474</td>
<td>0.79</td>
<td>0.65–0.95</td>
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<tr>
<td>Homozygotes</td>
<td>19</td>
<td>46</td>
<td>0.70</td>
<td>0.41–1.21</td>
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<tr>
<td>By tumor stage (Phet = 0.40)</td>
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<td></td>
<td></td>
<td>Carcinoma in situ</td>
<td>817</td>
<td>1558</td>
<td>0.82</td>
<td>0.69–0.97</td>
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<tr>
<td>By age (Phet = 0.76)</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td>&lt;36</td>
<td>473</td>
<td>831</td>
<td>0.82</td>
<td>0.65–1.03</td>
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</table>

<table>
<thead>
<tr>
<th>MICA-A5</th>
<th>Ca</th>
<th>Co</th>
<th>OR</th>
<th>95%CI</th>
<th>P = 3.0 × 10−4</th>
<th>Overall</th>
<th>Heterozygotes</th>
<th>Homozygotes</th>
<th>Overall</th>
<th>Heterozygotes</th>
<th>Homozygotes</th>
</tr>
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<tbody>
<tr>
<td>Overall</td>
<td>949</td>
<td>1689</td>
<td>0.80</td>
<td>0.60–0.97</td>
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<tr>
<td>Heterozygotes</td>
<td>163</td>
<td>428</td>
<td>0.60</td>
<td>0.49–0.73</td>
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<tr>
<td>Homozygotes</td>
<td>8</td>
<td>36</td>
<td>0.34</td>
<td>0.16–0.75</td>
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<tr>
<td>By tumor stage (Phet = 0.47)</td>
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<td></td>
<td></td>
<td></td>
<td>Carcinoma in situ</td>
<td>817</td>
<td>1558</td>
<td>0.58</td>
<td>0.48–0.71</td>
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<tr>
<td>By age (Phet = 0.53)</td>
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<td></td>
<td></td>
<td>&lt;36</td>
<td>473</td>
<td>831</td>
<td>0.56</td>
<td>0.44–0.73</td>
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</table>

Figure 1. Stratified analysis of association between rs9272143, MICA-A5.1, -A4, and -A5 and risk of cervical cancer. Unless specified, the odds ratios (ORs) and 95% confidence intervals (CIs) of per variant allele (log-additive model) and per genotype were calculated using unconditional logistic regression with adjustment of age at recruitment and study design (carcinoma in situ vs. invasive carcinoma) when appropriate. P for heterogeneity (Phet) was derived from the Cochran Q test. Squares represent odds ratios; size of the square represents inverse of the variance of the log odds ratio; horizontal lines represent 95% confidence intervals; diamonds represent overall estimate; solid vertical lines represent an odds ratio of 1; dashed vertical lines represent the overall odds ratios. Ca, case subject; Co, control subject.
the key event of establishing a robust defense against HPV infection through antigen presentation to CD4+ helper T-lymphocytes. It is, hence, biologically plausible that carriers of the C allele of rs9272143, which have higher expression level of HLA-DRB1 are less susceptible to cervical cancer. However, it is unknown whether rs9272143 is the pathogenic variant or other functional variant(s) which affect(s) the expression of HLA-DRB1 could be responsible for this signal. Functional studies would help to provide insight into it.

MICA encodes a membrane-bound protein, which acts as a ligand to stimulate an activating receptor, NKG2D, expressed on the surface of essentially all human natural killer (NK), γδ T, and CD8+ αβ T cells [18–20]. Normally, MICA is constitutively expressed in low levels on epithelial cells in the gut and thymus, endothelial cells, fibroblasts, and monocytes [21–23]. But it is upregulated or expressed de novo in stressed conditions, such as during viral and bacterial infections [20, 24, 25], heat shock [22], DNA damage response [26], oncogenic transformation [18, 19], and in autoimmune conditions [27]. MICA serves as signal of cellular stress, and engagement of NKG2D by MICA triggers NK cells, and costimulates some γδ T cells and antigen-specific CD8+ αβ T cells, resulting in a range of immune effector functions, such as cytotoxicity and cytokine production [21, 28]. The recognition of the MICA molecule by the NKG2D receptor enables immune cells to identify and attack infected or transformed cells without the need of MHC class I expression or antigen recognition [29]. Thus, the MICA/NKG2D interaction is an effective mechanism for immunosurveillance. This strong selection pressure seems to have led tumor cells to evolve mechanisms to minimize or avoid the response mediated by NKG2D by shedding MICA from the cell surface [30, 31]. The shedding of MICA has been reported to be mediated by metalloproteinases through proteolytic cleavage of the extracellular parts and palmitoylation of two cysteine residues in the cytoplasmic tail of MICA was found to be necessary for efficient cleavage [31, 32]. The shedding of soluble MICA by human tumors not only hinders recognition of the MICA-expression tumor cells, but also results in systemic downregulation of NKG2D on NK and CD8+ T cells, and evasion of NKG2D-mediated immune recognition [30, 31].

The SNP rs2516448 is located 7.32 kb downstream of the MICA gene and its effect is independent of previously known associations with HLA alleles/haplotypes [5]. The T allele of rs2516448 that increased the susceptibility to cervical cancer is in perfect LD with the MICA-A5.1 allele, which encodes a truncated protein lacking part of the TMD and the whole cytoplasmic tail and is most commonly seen in the MICA*008 allele [6]. Suemizu et al. [33] found that the cytoplasmic tail-deleted MICA-A5.1 gene product was aberrantly transported to the apical surface of human intestinal epithelial cells instead of the basalolateral surface where the interaction with intraepithelial T and NK lymphocytes takes place. Thus, MICA-A5.1 carriers may have an aberrant immunological surveillance by NK and T cells. Meanwhile, in contrast to other MICA alleles that are shed as truncated soluble species after proteolysis by metalloproteinases, the protein translated from the MICA-A5.1 allele is released from cells as a membrane-anchored full-length molecule in exosomes due to the lack of the two cysteines required for proteolytic shedding. Incubation of NK cells with the MICA-A5.1 (MICA*008) containing supernatant triggers significantly more NKG2D downregulation than the MICA*019 culture supernatant. Strikingly, incubation with exosomes containing MICA-A5.1 (MICA*008) also impairs NK-cell cytotoxicity [34]. Taken together, the preceding evidence might explain the result in this study that individuals carrying the MICA-A5.1 allele have a predisposition for their infected or transformed cells to escape from attack by immune cells. The MICA-A5.1 allele has also been associated with different autoimmune diseases and other tumor forms [35–42], supporting its role in immune response and tumor development.

In contrast to MICA-A5.1, alleles encoding only four (MICA-A4) or five (MICA-A5) Ala residues in the TMD of MICA protein, respectively, were found to confer protection against cervical cancer. In particular, a very strong protective effect was observed for the A5/A5 genotype. Further studies with larger sample sizes are warranted to verify this result, given the limited number of MICA-A5 homozygotes in this study. Interestingly, in breast cancer, MICA-A4 and MICA-A5 have also shown a protective effect [41, 42]. The mechanism by which MICA-A4 and MICA-A5 protect against cervical cancer is yet unknown. The nearby HLA-B*0702 has been reported to be associated with cervical cancer risk [5, 43, 44]. However, in a recent study, we found that the association with HLA-B*0702 was actually driven by the joint effects of both rs9272143 and MICA-A5.1 (unpublished data), suggesting that HLA-B*0702 is unlikely to be the causal variant responsible for the association with MICA-A4 or MICA-A5. These short tandem repeats are not located in any of the extracellular domains and do not directly affect the putative binding site of MICA with NKG2D. As the amino acids encoded by the microsatellite are situated in the TMD of the molecule, it is possible that certain alleles provide a more stable anchoring of MICA to the cell surface and therefore permit better binding to NKG2D and, as a consequence, a more efficient NKG2D-mediated immunosurveillance [41, 45]. It is also worth noting that MICA-A4 is in high LD with the amino acid substitution
of Glycine (Gly) by Tryptophan (Trp) at position 14 in the z1 domain and MICA-A5 is in high LD with the amino acid substitution of Gly by Serine (Ser) at position 175 in the z2 domain of MICA in the IMGT/HLA database [46]. The top surface of the MICA z1-z2 platform has been found to interact directly with NKG2D [47, 48]. Further studies are warranted to determine whether these amino acid changes could affect the binding affinity of MICA to the NKG2D receptor and whether they are responsible for the associations with MICA-A4 and MICA-A5.

The SNP rs3117017 resides in the pseudogene HLA-DPB2, but close to the functional gene HLA-DPB1, which encodes the β-chain of the peptide-antigen receptor HLA-DP. In contrast to our previous GWAS of cervical cancer, we did not observe a significant association between this SNP and risk of cervical cancer. It is noteworthy that the effect size of rs3117027 variant was much smaller (OR = 1.25) than the other two hits and the P value was close to genome-wide significance threshold in the initial GWAS discovery cohort (P = 3.1 × 10⁻⁶). It is possible that this study lacks sufficient statistical power to detect its modest effect on susceptibility for cervical cancer. Further studies with larger sample sizes are needed to draw a firm conclusion. On the other hand, the subjects enrolled in this study are from northern Sweden only, while the subjects in the GWAS were a national collection. The lack of replication may indicate no direct association between rs3117027 and cervical cancer. One cannot dismiss the possibility, however, that the LD between rs3117027 and the putative causal variant varies between ethnically distinct populations.

This study has several limitations. First, the number of invasive cervical cancer cases (134) included in the study is modest. Although we have observed evidence for heterogeneity by tumor stage for rs9272143, the statistical power is insufficient to draw any firm conclusion. Future studies with larger numbers of invasive cancers are warranted to validate this finding. Second, except for age, information on other risk factors for cervical cancer such as HPV infection, parity, oral contraceptive use, and tobacco smoking [49], which might modify the effects of the susceptibility loci, was not available in our study. Possible interactions between the susceptibility loci and these risk factors should be thoroughly investigated in future studies.

In summary, associations identified in our previous GWAS with rs9272143 in the MHC class II region, as well as rs2516448 and the MICA-A5.1 allele in the class I region were replicated in a northern Swedish population, providing credible evidence that these genetic variants influence susceptibility to cervical cancer. We also identified a reduction in risk associated with the MICA-A4 and MICA-A5 alleles. Our results do not support previous suggestion that HLA-DPB2 variant rs3117027 is positively associated with cervical cancer. The association with rs2516448 seems to be driven by the functional allele MICA-A5.1. However, it is unknown whether other allele combinations not measured by this study could be responsible for the signals of rs9272143 as well as MICA-A4 and MICA-A5 alleles. Further functional studies are warranted to identify the causal variant (s) responsible for these signals and their functional effect (s).

Acknowledgments

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Conflict of Interest

None declared.

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Table S1. Genotyping information for SNPs and MICA microsatellite.
Table S2. Linkage disequilibrium (D’ and r²) between SNPs and alleles of MICA microsatellite in controls.