Methylation Analysis of the FAM19A4 Gene in Cervical Scrapes Is Highly Efficient in Detecting Cervical Carcinomas and Advanced CIN2/3 Lesions

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Abstract

Primary testing for human papillomavirus (HPV) in cervical screening requires triage to differentiate women with transient infection from those with persistent infection who require more intensive management given their risk for cervical (pre)cancer. In this study, the clinical performance of a novel methylation marker FAM19A4 for the triage of high-risk (hr)HPV-positive women was evaluated. Using a training-validation set approach, we analyzed a FAM19A4 quantitative methylation-specific PCR (qMSP). The training set comprised hrHPV-positive cervical scrapes of 43 women with cervical intraepithelial neoplasia grade 3 or worse (CIN3+) and 135 women with ≤CIN1. The validation set comprised hrHPV-positive cervical scrapes of 52 women with CIN2+, including 33 CIN3+, 19 CIN2, and 166 women with ≤CIN1. The methylation threshold of FAM19A4 qMSP that gave rise to CIN3+ specificity of 70% in the training set was applied in the validation set. This resulted in CIN3+ sensitivity of 75.8% [95% confidence interval (CI), 61.1–90.4] at 67.0% (95% CI, 60.3–73.8) specificity. Next, the validated qMSP was applied to an independent series of hrHPV-positive cervical scrapes of 22 women with cervical cancer, 29 with advanced CIN2/3 [i.e., women with a known preceding hrHPV infection (PHI) lasting ≥5 years as proxy of longer duration of lesion existence], and 19 with early CIN2/3 [i.e., PHI <5 years]. All carcinomas (22/22) and advanced CIN2/3 lesions (29/29) were FAM19A4 methylation–positive, compared with 42.1% (8/19; 95% CI, 19.9–64.3) of early CIN2/3 lesions. In conclusion, FAM19A4 is an attractive triage marker for hrHPV-positive women, with a high reassurance for the detection of cervical carcinoma and advanced CIN2/3 lesions. Cancer Prev Res; 7(12); 1251–7. ©2014 AACR.

Introduction

An infection with a high-risk type of human papillomavirus (hrHPV) is necessary; however, it is not sufficient for the development of cervical cancer (1). Following a persistent hrHPV infection, genetic and epigenetic changes in the host and/or viral genome are acknowledged to be involved in progression toward invasive cervical cancer (2, 3). Functional studies have shown that gene silencing by promoter hypermethylation of some tumor suppressor genes is a contributing factor to cervical carcinogenesis (4–8). Gene promoter hypermethylation can be easily assessed by sensitive, (quantitative) methylation-specific PCR (MSP)-based methods on cervical scrapes, and even self-collected cervico-vaginal samples. This has led to the idea that methylation analysis can provide an attractive early-detection biomarker, amongst others, to be used as triage method for hrHPV-positive women in cervical screening (3, 9). Indeed, promising results have been obtained (10–15) with sensitivities for CIN2+ [i.e., cervical intraepithelial neoplasia (CIN) grade 2 (CIN2), CIN3, and cervical cancer] and CIN3+ (i.e., CIN3 and cervical cancer) similar to those of cytology analysis on cervical scrapes (11, 12), the latter currently being the most widely suggested triage tool. Of interest, recent work has revealed that methylation levels of several genes are particularly high in cervical scrapes of women with cervical cancer and advanced high-grade CIN lesions, the latter characterized by a longer duration (≥5 years) of a preceding hrHPV infection (PHI; refs. 3, 16). As a consequence, methylation analysis could be particularly effective in detecting advanced precursor lesions (with likely a high short-term progression risk) and cervical cancers (3), and can serve as a complementary tool for cytology to gain a higher reassurance of not missing advanced lesions (17).

Most studies performed so far have used panels of methylation markers to reach sufficiently high sensitivities for high-grade CIN and cervical cancer (11, 13, 18, 19). In search for novel methylation markers, we recently have performed methylation-specific digital karyotyping of
different passages of HPV16E6E7-transduced primary human foreskin keratinocytes (20). This study resulted in the identification of novel DNA methylation events, including some directly following HPV16E6E7 expression, and others associated with the acquisition of an immortal phenotype (i.e., representing disease progression). The latter involved FAM19A4, LHX1, NXK2-8, PHACTR3, and PRDM14 genes. Pilot studies identified involved the identification of novel DNA methylation events, includ- 

ing human foreskin keratinocytes (20). This study resulted in different passages of HPV16E6E7-transduced primary 

cytology were directly referred for colposcopy, indepen-

dent or worse dyskaryosis (grade squamous intraepithelial lesions (ASC-H). Moderate 

atypical squamous cells of undetermined significance equals low-grade squamous intraepithelial lesions (LSIL), 

In this classification, borderline or mild dyskaryosis (BMD) equals high-grade squamous 

cytology classification, which is standard in the Netherlands 

using the CISOE-A (Composition, Inflammation, Squa-

Materials and Methods 

Study population 

Cervical scrapes for training and validation. Independent 

training and validation sets of hrHPV-positive cervical 

scrapes (n = 178 and n = 218, respectively) were used. For the training set, baseline cervical scrapes of hrHPV-positive 

women who participated in the intervention arm of a population-based cervical screening trial (POBASCAM; refs. 22, 23) were used. Scrapes in the validation set were from women who participated in population-based screening using the same screening and referral algorithm as in the intervention arm of the POBASCAM trial (11, 24). For all women, cotesting for hrHPV and cytology on the cervical 

scrapes at baseline was performed. Cytology was scored 

by qMSP in a large series of hrHPV-positive cervical 

scrapes derived from a screening population. The validated FAM19A4 qMSP assay was additionally evaluated in an independent series of hrHPV-positive cervical scrapes in relation to severity and duration of the underlying lesion. For this purpose, scrapes from women with cervical cancer, and women with CIN2/3 with a PHI of <5 years or ≥5 years, were used. PHI was used as proxy of lesion duration, and accordingly these CIN2/3 lesions were assigned as early and advanced disease stages (16), respectively.

The present study describes the verification and valida-

tion of the clinical performance of FAM19A4 methylation 

analysis by qMSP in a large series of hrHPV-positive cervical 

scrapes.

The training set comprised hrHPV-positive scrapes of 178 women. Of these, 43 were of women that were histologi-

cally diagnosed with a CIN3+ lesion within 36 months of follow-up [including 4 squamous cell carcinoma (SCC) and 1 adenocarcinoma (AdCa)]. These women had a median age of 31 years (range, 25–55), and 15 women had normal and 28 abnormal (i.e., BMD or worse) cytology at baseline. The remaining 135 scrapes were of women without evidence of CIN2+ further referred to as ≤CIN1 (including 27 CIN1 and 9 histologically confirmed absence of CIN) up to the next screening round (5 years later) and had a median age of 34 years (range, 17–61). Of these, 99 women had normal and 36 abnormal cytology at baseline. The training set did not include any CIN2 lesions as CIN3+ is a better endpoint for (pre)cancer (11, 27).

The validation set comprised a consecutive series of 250 hrHPV-positive scrapes. Of 218 samples, sufficient material was left for qMSP analysis, and valid qMSP results were obtained. This series comprised 52 women with a CIN2+ lesion within 36 months of follow-up [2 SCCs and 1 adenocarcinoma in situ (ACIS), 30 CIN3, 19 CIN2] with a median age of 34.5 years (range, 24–58). Of these, 19 women had normal and 33 abnormal cytology at baseline. The remaining 166 scrapes were of women who had no evidence of CIN2+ (including 11 CIN1 and 8 histologically confirmed absence of CIN) within the same follow-up time. Of these, 139 had normal and 27 had abnormal cytology at baseline. The median age of this group was 39 years (range, 19–62).

Cervical scrapes of women with cervical carcinoma or CIN2/3 with a known duration of preceding hrHPV infec-

tion. Separate series of hrHPV-positive cervical scrapes were used to quantitatively evaluate FAM19A4 methylation in relation to severity and duration of the underlying lesion. This series comprised (i) 22 hrHPV-positive cervical scrapes of women diagnosed with cervical cancer during population-based screening or while visiting a gynecologic outpatient clinic (19 SCC, 1 adenosquamous carcinoma and 2 AdCa). Of these scrapes, 19 had abnormal and 3 normal cytology. The median age of women was 38 years (range, 30–85); and (ii) 48 hrHPV-positive cervical scrapes of women diagnosed with a CIN2/3 in the second round of the control arm of the POBASCAM trial (blind HPV testing), and accordingly have a known 5-year history of hrHPV
infection. The scrapes evaluated preceded the CIN2/3 biopsy. The duration of prior hrHPV infection was considered a proxy for duration of CIN2/3 existence (16, 28). Women with same hrHPV-type in both screening rounds were considered to have a PHI of ≥5 years, and their CIN2/3 lesions were considered advanced CIN2/3 lesions (n = 29). Women who acquired the hrHPV infection after study entrance (PHI <5 years) were considered to have early CIN2/3 lesions (n = 19). Of the 29 hrHPV-positive scrapes of women with advanced CIN2/3, 5 had normal cytology and 24 had abnormal cytology. The median age of these women was 40 years (range, 34–56). Of the 19 hrHPV-positive scrapes of women with early CIN2/3, 7 had normal cytology and 12 had abnormal cytology. The median age of these women was 40 years (range, 39–50). This study followed the ethical guidelines of the Institutional Review Board of the Medical Center.

DNA isolation, bisulphite treatment, and qMSP methylation analysis

DNA from cervical scrapes was isolated using the Nucleospin 96 Tissue Kit (Macherey-Nagel) and a Microlab Star robotic system (Hamilton) according to the manufacturers’ protocol (11). Extracted DNA was subjected to bisulphite treatment using the EZ DNA Methylation Kit (Zymo Research) as described previously (7, 8). Bisulphite-converted DNA was used as template for DNA methylation analysis. DNA methylation analysis of FAM19A4 was performed by qMSP using housekeeping gene β-actin (ACTB) as a reference gene (20). A multiplex qMSP assay was developed according to criteria described by Snellenberg and colleagues (29). Specificity of each primer pair for bisulphite-converted methylated DNA was confirmed by the absence of amplification of unmodified DNA to ensure that no amplification would occur in case of incomplete bisulphite conversion. Quantification Cycle (Cq) values were measured at a fixed fluorescence threshold. Samples with a Cq > 40 for FAM19A4 were considered to represent a negative test result. All samples had a Cq value for ACTB <32 to assure good sample quality. All analyses were performed on an ABI 7500 real-time PCR-system (Applied Biosystems). The FAM19A4 result of a sample was expressed in Cq ratio, calculated by the following formula: 2^(-ΔCq(ACTB)-ΔCq(FAM19A4)) × 100.

Statistical analysis

Assessment of FAM19A4 methylation analysis was performed by a training-validation set approach using two independent series of cervical scrapes that were sufficiently large to ensure an unbiased assay analysis. In the training set, an ROC curve of the FAM19A4 qMSP assay was made for all ratio values, and the area under the curve (AUC) was determined. The threshold value that gave rise to a CIN3+ specificity of 70% in the training set was chosen to consider a specimen positive for FAM19A4 methylation. With this threshold, the biomarker test was converted into a categorical variable and subsequently evaluated in the independent validation set. Sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), and referral rate were determined together with 95% Wald confidence intervals (95% CI), for outcome of CIN2+ and CIN3+. The threshold value for scoring cytology positive was ASCUS (i.e., BMD). For quantitative evaluation of FAM19A4 methylation, fold changes over a reference category (i.e., hrHPV-positive women with ≤CIN1 in the validation set) were determined. Differences in methylation levels between the different groups were analyzed by the Mann–Whitney U test. P values below 0.05 were considered significant. All statistical analyses and computation of graphs were performed in IBM SPSS Statistics 20 and Excel.

Results

Clinical validation of FAM19A4 on physician-taken cervical scrapes of hrHPV-positive women

In the training set of 178 hrHPV-positive cervical scrapes, FAM19A4 methylation analysis revealed a significant discrimination of women with CIN3+ from those with ≤CIN1 (P = 0.004). ROC curve analysis showed an AUC of 0.775 (Fig. 1). The methylation threshold of FAM19A4 that in the training set gave rise to a CIN3+ specificity of 70% was chosen for validation set analysis. In the validation set (n = 218), application of this threshold resulted in a CIN3+ sensitivity of 75.8% (95% CI, 61.1–90.4) at a specificity of 67.0% (95% CI, 60.3–73.8), and a CIN2+ sensitivity of 69.2% (95% CI, 56.7–81.8) at 69.9% (95% CI, 62.9–76.9) specificity. In comparison, application of cytology (threshold ASCUS) in this set reached a CIN3+ sensitivity of 63.6% (95% CI, 47.2–80.0) at a specificity of 78.9% (95% CI, 73.0–84.4), and a CIN2+ sensitivity of 63.5% (95% CI, 50.4–76.5) at 83.7% (95% CI, 79.1–89.3) specificity.
Table 1. Sensitivity, specificity, PPV, NPV, and referral rates for colposcopy for endpoints CIN2+ and CIN3+ in the validation set of 218 hrHPV-positive cervical scrapes

<table>
<thead>
<tr>
<th>Triage Endpoint</th>
<th>Sensitivity [% (95% CI)]</th>
<th>Specificity [% (95% CI)]</th>
<th>PPV [% (95% CI)]</th>
<th>NPV [% (95% CI)]</th>
<th>Referral rate [% (95% CI)]</th>
</tr>
</thead>
<tbody>
<tr>
<td>FAM19A4a</td>
<td>CIN2+ 69.2 (56.7–81.8)</td>
<td>69.9 (62.9–76.9)</td>
<td>41.9 (31.4–52.3)</td>
<td>87.9 (82.3–93.4)</td>
<td>39.4 (33.0–45.9)</td>
</tr>
<tr>
<td></td>
<td>CIN3+ 75.8 (61.1–90.4)</td>
<td>67.0 (60.3–73.8)</td>
<td>29.1 (19.5–38.7)</td>
<td>93.9 (89.9–98.0)</td>
<td>39.4 (33.0–45.9)</td>
</tr>
<tr>
<td>Cytologyb</td>
<td>CIN2+ 63.5 (50.4–76.5)</td>
<td>83.7 (79.1–89.3)</td>
<td>55.0 (42.4–67.6)</td>
<td>88.0 (82.9–93.0)</td>
<td>27.5 (21.6–33.5)</td>
</tr>
<tr>
<td></td>
<td>CIN3+ 63.6 (47.2–80.0)</td>
<td>78.9 (73.0–84.4)</td>
<td>35.0 (22.9–47.1)</td>
<td>92.4 (88.3–96.5)</td>
<td>27.5 (21.6–33.5)</td>
</tr>
</tbody>
</table>

aAt the threshold that gave rise to a 70% CIN3+ specificity in the training set.

bThreshold ASCUS.

Discussion

FAM19A4 was previously identified by a genome-wide DNA methylation screen as a methylation event associated with the acquisition of an immortal phenotype of HPV16E6E7-transduced cells, and suggested as promising disease marker (20). In this study, we verified the value of FAM19A4 methylation analysis as triage marker to assess the presence of (pre)cancerous cervical lesions in hrHPV-positive women. We composed and validated the biomarker qMSP assay by a training-validation set approach, resulting in a triage marker for hrHPV-positive cervical scrapes that had an overall CIN3+ sensitivity of 75.8% (95% CI, 61.1–90.4) at 67.0% (95% CI, 60.3–73.8) specificity, and CIN2+ sensitivity of 69.2% (95% CI, 56.7–81.8) at 69.9% (95% CI, 62.9–76.9) specificity. Of note, the validated FAM19A4 methylation assay detected all cervical carcinomas (22/22) and advanced CIN2/3 lesions (29/29). Consequently, the FAM19A4 methylation marker can be a valuable tool to differentiate hrHPV-positive women who should be sent for colposcopy because of the presence of
Methylation Analysis of Cervical Scrapes

Table 2. FAM19A4 methylation levels per lesion category

<table>
<thead>
<tr>
<th>Category</th>
<th>Cq ratio FAM19A4</th>
<th>Fold changes over reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>≤CIN1</td>
<td>0.123</td>
<td>1 (reference)</td>
</tr>
<tr>
<td>Early CIN2/3</td>
<td>0.383</td>
<td>3.1</td>
</tr>
<tr>
<td>Advanced CIN2/3</td>
<td>8.357</td>
<td>67.9</td>
</tr>
<tr>
<td>Carcinoma</td>
<td>33.309</td>
<td>270.8</td>
</tr>
</tbody>
</table>

Note: Cq, cycle threshold.

Cancer or advanced CIN2/3 lesions with a high short-term progression risk for cancer, and therefore in need of treatment.

So far, methylation-based assays that have been put forward as triage tools for HPV-positive women make use of a panel of two to five markers to ensure sufficient detection of high-grade cervical lesions (11, 13, 18, 19). Here, we found that the FAM19A4 marker alone had a similar performance in terms of CIN2+, CIN3+, and cervical carcinoma detection as a panel of previously studied methylation markers (11). Recently, other single methylation markers, i.e., PAX1 and ZNF582, have been reported as a promising methylation markers for cervical screening and women with LSIL, respectively (30, 31). Yet, these markers have not been validated in population-based screening studies and require further investigation.

CIN2/3 reflects a heterogeneous disease. Early and advanced CIN2/3 lesions, displaying a low and high short-term progression risk for cancer, respectively, can be distinguished on the basis of molecular host cell alterations (3). Our study strengthens previous findings of DNA methylation analysis being more sensitive over cytology for the detection of the most advanced lesions and cervical cancers (3, 16, 17). As shown in Fig. 2, our findings are in line with a recent hypothesis that both tests do not detect exactly the same lesions, with DNA methylation analysis having a preference for detecting the more advanced CIN3+ lesions, and cytology tending to also detect early CIN2/3 lesions (3, 17). Our findings support that the FAM19A4 methylation marker can serve as an alternative or complementary tool for cytology (17) to gain a higher reassurance of not missing advanced lesions and cervical cancer (3). It should be noticed that our study was performed within the setting of well-organized screening in the Netherlands with a high-quality standard of cytology reading (32). In countries without less organized cytology infrastructure, objective molecular triage testing by the FAM19A4 methylation marker might even have higher additive value in terms of reassurance.

In line with Bierkens and colleagues (16) reporting on CADM1/MAI methylation, methylation levels of FAM19A4 increased with increasing disease severity, being particularly high in cervical scrapes of women with cervical cancer. These data reflect that hrHPV-positive women with a positive FAM19A4 methylation test should be sent for immediate colposcopy given high risk of advanced lesions in need of treatment. FAM19A4 methylation–negative women could be offered a repeat test after 12 to 18 months instead of direct colposcopy referral (3), which could markedly reduce over referral and overtreatment. The effect on patient outcome of such strategy, nonetheless, requires confirmation in a prospective trial with intervention based on methylation status. We acknowledge that in such scenario part of CIN2/3 lesions may remain undetected. These lesions are most likely early-onset lesions with few chromosomal abnormalities (28), and are supposed to have low risk to progress to invasive cancer within the screening interval. Yet, to fully support this hypothesis, additional proof is needed, for example, by demonstrating no or limited chromosomal aberrations in these lesions (28) or by active surveillance of women with FAM19A4 methylation–negative, colposcopically evaluable small CIN2. The high confidence of not having cervical cancer in case of absence of FAM19A4 methylation is supported by a recent analysis of an extra series of hrHPV-positive cervical scrapes of women with cervical SCC with unknown cytology (n = 35), all of which were FAM19A4 methylation–positive (data not shown).

Previous studies have shown that self-sampling can increase the participation rate in population-based screening and allows the efficient detection of CIN2/3 lesions (33–38). Because triage by methylation markers is possible on the same sample used for hrHPV testing, this would obviate the need of additional visits to the physician for cytology triage (12). Given recent studies on the application of methylation marker testing to self-collected specimens (10, 12, 15), further evaluation of FAM19A4 as a methylation triage test in hrHPV-positive self-samples is warranted.

In conclusion, FAM19A4 is an attractive methylation triage marker for hrHPV-positive women that reaches an overall CIN3+ sensitivity of 75.8% at a specificity of 67.0%, with particularly a high reassurance for the detection of cervical carcinoma and advanced CIN2/3 lesions.

Disclosure of Potential Conflicts of Interest

C.J.L.M. Meijer reports receiving other commercial research support and has ownership interest (including patents) in Self-screen B.V. He is
a consultant/advisory board member for Qiagen. He has also provided expert testimony for GSK and Merck. J. Berkhof is a consultant/advisory board member for Roche and Qiagen. P.J.F. Snijders, R.D.M. Steenbergen, and D.A.M. Heideman have ownership interest (including patents) in Self-screen BV. No potential conflicts of interest were disclosed by the other authors.

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