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Alterations of T-cell surface markers in older women with persistent human papillomavirus infection

Ana Cecilia Rodríguez1,2,* , **Alfonso J García-Piñeres**3,4,* , **Allan Hildesheim**1, **Rolando Herrero**2, **Matthew Trivett**3, **Marcus Williams**3, **Ivannia Atmella**4, **Margarita Ramírez**4, **Maricela Villegas**2, **Mark Schiffman**1, **Robert Burk**5, **Enrique Freer**4, **José Bonilla**4, **Concepción Bratti**2, and **Ligia A Pinto**³

¹Division of Cancer Epidemiology and Genetics, National Cancer Institute, National Institutes of Health, Bethesda, MD, USA

²Proyecto Epidemiológico Guanacaste, INCIENSA Foundation, San José, Costa Rica

³HPV Immunology Laboratory, SAIC-Frederick, Inc./NCI-Frederick MD, USA

⁴Escuela de Química, Centro de Investigación en Estructuras Microscópicas and Centro de Investigación en Biología Celular y Molecular, University of Costa Rica, San José, Costa Rica

⁵Albert Einstein College of Medicine, Yeshiva University, Bronx, NY, USA

Abstract

We previously reported decreased lymphocyte proliferative responses among older women with persistent human papillomavirus (HPV) infection. To characterize the phenotype of peripheral lymphocytes associated with persistent HPV infection, we evaluated the expression of different cell surface markers in peripheral blood mononuclear cells (PBMCs) from a case-control study within a 10,049-woman population-based cohort study in Guanacaste, Costa Rica. Women in the cohort aged 46 to 74 and with HPV results at their 5th year anniversary visit were considered, and all women (n=87) with persistent HPV infections, all women (n=196) with transient HPV infections and a random sample of HPV DNA-negative women (n=261) frequency-matched to cases on age were selected for this study. A median of 3 years after the case-control matching visit, cervical cells were collected for liquid-based cytology and repeat HPV DNA genotyping. Blood was obtained from which PBMCs were extracted and cryopreserved for immunological phenotyping via flow cytometry. Significant increases in risk of HPV persistence were observed for three marker subsets indicative of immune cell activation/differentiation. Relative risk estimates were 5.4 (95%CI=2.2–13.3) for CD69+CD4+, 2.6 (95%CI=1.2–5.9) for HLADR⁺CD3⁺CD4⁺ and 2.3 (95%CI=1.1–4.7) for CD45RO⁺CD27[−]CD8⁺. A significant decrease in HPV persistence was observed for a subset marker indicative of an immature, undifferentiated memory state $CD45RO^+CD27^+CD4^+$ (OR=0.36; 95%CI = 0.17–0.76). Adjustment for these markers only partially explained the previously reported association between decreased lymphoproliferative responses and persistent HPV infection. Whether phenotypic alterations observed predispose to HPV persistence or result from it should be the focus of future studies.

Correspondence: Ana Cecilia Rodríguez, MD, Proyecto Epidemiológico Guanacaste, INCIENSA Foundation, Torre La Sabana, 7mo piso, Sabana Norte, San José, Costa Rica, acrodriguez@racsa.co.cr, Fax number (506) 2291 0832, Tel number (506) 2220 3039. *These authors contributed equally to this work

Current affiliations of authors:

Ana Cecilia Rodríguez is currently at: Proyecto Epidemiológico Guanacaste, INCIENSA Foundation, San José, Costa Rica Alfonso García-Piñeres is currently at: Escuela de Química, Centro de Investigación en Estructuras Microscópicas and Centro de Investigación en Biología Celular y Molecular, University of Costa Rica, San José, Costa Rica

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Keywords

HPV persistent infection; T-cell distribution; T-cell activation and differentiation; older women

Introduction

Infection of the cervix with one or more of approximately 10–15 carcinogenic human papillomavirus (HPV) genotypes is very common and a necessary cause for cervical cancer $1-5$. Most cervical HPV infections clear (become undetectable by HPV DNA tests) without sequelae; cervical pre-cancer and cancer arise from the small subset of infections that persist, typically for more than $1-2$ years $6-9$.

The host immune response is believed to be an important determinant of the fate of incident HPV infections. Certain HLA alleles have been associated with cervical cancer 10. Studies in HIV positive women have shown increased persistence and progression of HPV infection, with the most pronounced risk observed among women with reduced CD4 counts. This suggests that immune perturbations associated with HIV infection predispose to HPV persistence and its associated abnormalities 11. Additional immune function alterations have been described in HPV infection, including impairment of CD4+ T cell-mediated immunity and cytokine dysregulation in peripheral blood in women with cervical cancer or precancerous lesions 12–17. At the tissue level, a lack of dendritic cells 18, 19, and decrease in Th1 immune infiltrates have been described in the presence of HPV associated lesions $20, 21$.

Age-specific prevalence curves of HPV vary in different parts of the world, and in some countries a second peak of HPV infection has been described above age 50^{22-24} . The reasons for this second peak are not clear, but may include re-exposure through new partners of the woman or of her partner, reactivation of previous infections to detectable levels (reemergence of latent HPV infections) due to previously-described senescence of the immune system or a cohort effect $11, 25-27$.

We previously reported an association between HPV persistence and decreased responsiveness of peripheral blood mononuclear cells (PBMCs) to antigenic and mitogenic stimuli in women 46 – 74 years old who participated in a 10,049 women population-based cohort study in Guanacaste, Costa Rica 28. Herein, to better characterize the peripheral immune phenotypes associated with persistent HPV infection in this same group of women, we have evaluated various T-cell subsets within CD4⁺ and CD8⁺ lymphocyte populations with a particular emphasis on markers of immune activation in T-cells and differentiation within naïve and memory T-cells.

Methods

Study design and population

A population-based cohort of women 18 years and older was established in Guanacaste, Costa Rica to study the natural history of human papillomavirus infection and cervical neoplasia. Between June 1993 and December 1994, 10049 women were recruited into the study. Participation rate was 93%. Sexually active women underwent a pelvic examination where exfoliated cells for conventional and liquid-based cytology and HPV DNA tests were collected. Women who had evidence of cervical abnormality were referred to colposcopy and treatment if needed. After exclusion of hysterectomized women and those with prevalent precancer (cervical intraepithelial neoplasia (CIN) grade 2 or worse) or cancer, remaining participants were eligible for the follow-up phase of the study (N=9100). During follow-up, women who presented evidence of precancer or cancer were colposcopically

evaluated, treated or referred for treatment as needed and censored. Details have been described elsewhere ^{29, 30}.

Details of the methods employed for our case-control study among older women nested within the cohort described above have also been previously published 28 . In brief, individuals for the nested study were selected from the 7008 women enrolled in our prospective cohort and for whom PCR-based HPV DNA results from their $5th - 6th$ year of follow-up were available at the time this study was designed. All women who were between 45 and 75 years of age and positive for HPV DNA at the last visit during that period (N=324) were selected. A subset of women with negative HPV DNA result during this same period was also selected $(N=310)$. The HPV-negative group was frequency matched to the HPV-positive group on age and time since enrollment. All women selected were invited to participate in an additional study visit that occurred on average 36.2 months (range: 12.0 – 53.4 months) after the time of the HPV DNA test that led to their selection into the nested study. At the time of the additional visit, a pelvic examination was performed, exfoliated cells were collected for liquid-based cytology and repeat PCR-based HPV DNA testing, and 40 ml of blood were collected in heparinized tubes from which PBMCs were isolated and cryopreserved.

The participation rate for the nested study was over 92% (591 of 634 women). Among participants, we excluded 7 women whose blood sample was not available for testing (5 cases and 2 controls), 3 women with missing HPV DNA results (1 case and 2 controls) and 9 women (all cases) whose cytology result at the time of the additional visit was high grade squamous intraepithelial lesion (HSIL). An additional 28 women initially in the HPV negative control group were excluded due to evidence of incident HPV infection at the time of the additional study visit. After these exclusions were applied, 283 HPV-positive cases (some persistent, some not as discussed below) and 261 HPV-negative controls remained.

The study protocol was reviewed by the National Cancer Institute and the Costa Rican INCIENSA Institutional Review Boards. All participants provided informed consent.

HPV determination by PCR

Type-specific HPV DNA testing was performed by L1 MY09/11 degenerate-primer PCR with AmpliTaq Gold polymerase, as detailed elsewhere $^{23, 31}$. In brief, after amplification, PCR products were analyzed by electrophoresis and hybridized with radiolabeled generic probes for HPV. Samples positive for HPV DNA were typed by dot-blot hybridization with biotinylated type-specific oligonucleotide probes (2, 6, 11, 13, 16, 18, 26, 31–35, 39, 40, 42– 45, 51–59, AE9 (54v), 61, 62, 64, 66–74, AE10 (74v), 81, AE2 (82v), w13b (82), 83–85, and 89).

Flow cytometry analysis

PBMCs isolated by Ficoll-Paque (Amershan Pharmacia Biotech, Piscataway, NJ) gradient centrifugation were used in this study. Detailed methods have been described elsewhere 28 . In brief, blood samples were transported to the cryopreservation laboratory in coolers at \sim 20 \degree C. PBMCs were isolated and cryopreserved a median of 25.5 hours (interquartile range 1.45 hours) after specimen collection. PBMCs were cryopreserved in 20% fetal calf serum (FCS, BioWittaker) and 7.5% dimethylsulphoxide (DMSO, Sigma, St. Louis, MO) supplemented RPMI 1640 media (BioWhittaker) using a controlled rate freezer (Kryosave, Rockville, MD). Cryopreserved PBMCs were transported and stored in the vapor phase of liquid nitrogen. Cells were thawed as previously described 28, 32 and stained for a variety of cell surface markers. Although there is still some controversy regarding models of differentiation and functional activities characteristic of each subset within $CD4^+$ and $CD8^+$

T-cells 33, 34, in general T-cells can be divided into early or late activated cells, memory or naïve cells, and as differentiated or undifferentiated cells. We defined our T-cell subpopulations based on the presence/absence of the different cell surface markers as follows: 1) $CD4^+CD69^+$ and $CD8^+CD69^+$ were defined as early activated T-cells; 2) $CD4^+CD25^+$, $CD8+CD25^+$, $CD4^+HLA-DR^+$, $CD8^+HLA-DR^+$, $CD4^+CD38^+$ and $CD8^+CD38^+$ cells were defined as late activated T-cells; 3) CD45RO+CD45RA− cells were defined as memory Tcells; 4) CD45RO[−]CD45RA⁺ cells were defined as naïve T-cells; 5) CD27⁺CD45RO⁺ and $CD27^+CD45RA^+$ cells were defined as resting memory cells and differentiated naïve cells, respectively; 6) CD57+CD45RO+ and CD57+CD45RA+ cells were defined as differentiated memory cells and undifferentiated naïve cells, respectively; and 7) CCR7⁺CD45RO⁺ and CCR7+CD45RA+ cells were defined as central-memory and -naïve cells, respectively; and 8) CCR7−CD45RO+ and CCR7−CD45RA+ cells were defined as effector-memory and naïve cells, respectively.

PBMC $(2 \times 10^5 \text{ cells/ml})$ were stained per manufacturer's recommendations for 15 minutes at room temperature in the dark. 1 mL of lysing solution (154 mM Ammonium chloride; 10 mM potassium bicarbonate; 0.12 mM EDTA; pH 7.4) was then added. After 5 minutes, cells were washed two times in fluorescence-activated cell sorting (FACS) buffer (0.7% bovine serum albumin and 0.01% sodium azide in PBS) and analyzed within 6 hours in a five-color flow cytometry on a FC-500 flow cytometer (Beckman Coulter). CD69 and CD25 markers in $CD4^+$ and $CD8^+$ T-cells are reported as percentages of the total number of lymphocytes, with the lymphocyte population selected based on the forward scatter/side scatter pattern. The CD45RO, CD45RA, CD27, CCR7 and CD57 markers are reported as percentages of CD3+CD4+ or CD3+CD8+ lymphocytes. HLA-DR and CD38 marker populations were estimated as percentage of the CD3+CD4+ or CD3+CD8+ lymphocytes. The CD57 subpopulation was estimated as a percentage of CD3+CD4+ or CD3+CD8+ lymphocytes that were CD27⁺CD45RA⁺ or CD27⁺CD45RO⁺.

During flow cytometric analysis, we excluded results from consideration if the observed number of events (cell count) was below 5,000. Data were pre-checked before statistical analysis to assess tube-to-tube reproducibility. Repeated measurements among tubes for the same subject were compared, and these values needed to be within 5% of each other to be accepted. Additionally, the lymphosum was calculated by adding the percentage of T-cells, B-cells and NK-cells. This value needed to be 100±5%. If variation was higher for any of these checks, all data from this sample were excluded from analysis. Also, samples in a particular batch were excluded if an anomalous cell population was observed in some of the batch tubes. For most markers, observations from ≤ 25 women were excluded due to these technical reasons.

Lymphoproliferation assays

Lymphoproliferation responses were assessed as previously published 28. Briefly, PBMCs were cultured in triplicate in the presence of AIM-V media as a negative control; HPV-16 L1 VLP (Novavax, Malvern, PA) or influenza A virus (Flu) (Infectious virus, H3N2, A/ Hong Kong/8/68, 1:100, ATCC) as recall antigens; or phytohemagglutinin (PHA) (1:100, Sigma) as mitogen for a total of 5 and 3 days, respectively. 1 μ Ci of [³H]-thymidine (Amersham Biosciences, Piscataway, NJ) was added for 18 hours before harvesting and counted in an automated scintillation counter (Microbeta, Perkin-Elmer, Boston, MA).

Statistical analysis

For this analysis, the initial group of participants who were HPV DNA positive at the time of their follow-up visit was subdivided into two case groups. Those who had at least one type-specific HPV infection still present at the time of their additional visit for the present

study (HPV Persistence Group; $n = 87$, median persistence time $= 42$ months) and those who cleared all of their type-specific HPV infections by the time of their additional visit (HPV Clearance Group; $n = 196$).

These groups were compared against the HPV negative group (HPV Negative Group; $n =$ 261) for the main analysis. The HPV negative group included those women with negative HPV results at selection and the additional visit. This group was selected as the control/ comparison group since it is representative of women $46 - 74$ years old from our populationbased study. Given how common HPV infection is among sexually active individuals, we postulate that the majority of these women have been exposed to HPV and thus had the opportunity to develop persistent HPV infection (but did not). We also compared the HPV Persistence Group against the HPV Clearance Group as an ancillary analysis.

For some analyses, the HPV persistence group was further restricted to women with evidence of long term persistence. We considered women to be long-term HPV-DNA persistent if the same HPV type was detected since enrollment into the cohort in 1993–4 (n $= 32$; median persistence time of 107.4 months). Of note, only 13 women had more than one type-specific HPV-DNA persistent infection; of these 4 had long-term infections.

For the specific T-cell subsets evaluated (Tables 1–2), the percentage of cells expressing each subset of markers was computed for each woman. Categorical quartile variables were derived based on the frequency distribution observed among the study population with valid results for the specific subset. The Kruskal-Wallis test, commonly used to determine whether the mean rank distribution within ordered groups differ between population samples, was used to test whether for each T-cell subset there were differences in the distribution of the categorical quartile variables between the study groups (e.g., HPV negative and persistent HPV positive groups). When correlation between markers was evaluated, the non-parametric Spearman's coefficient was used.

Logistic regression was used to estimate the odds ratios (OR) and 95% confidence intervals (95% CI) for the quartile variables while adjusting for age and other parameters as specified in the individual tables. To test for trend, categorical variables were considered as continuous in the models. In addition to the overall analyses presented in the tables, analyses were performed stratified by age at the time of the additional visit (<55, 55–64 and 65–74 years) and restricting the case group to women with carcinogenic HPV types (HPV types 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68). When evaluating the impact of adjustment for immunophenotype subsets on the previously described association between proliferative potential and HPV persistence 28 , we created a joint variable that combined across the four immunophenotype subsets found to be significantly associated with HPV persistence in our study. This joint variable was defined as the sum of the individual quartile levels for each of the four phenotypic markers of interest (e.g., women in the lowest quartile for all four markers had a combined score of four). Quartile order was reversed for CD45RO+CD27+CD4+ to match risk for HPV persistence with the other markers. Based on the score, women were categorized into tertile groups $(4 - 8, 9 - 10)$ and $11 - 16$.

Results

As previously reported ²⁸, the distribution of $CD3^+$ T-cells and $CD4^+$ and $CD8^+$ T-cell subsets within $CD3^+$ T-cells was similar across the three study groups: HPV negative, HPV persistence, and HPV clearance groups (Tables 1–2 and data not shown). When immunophenotypic subsets of CD3+CD4+ cells were evaluated and the frequency distributions compared between the HPV persistence group and the HPV negative controls (Table 1), statistically significant differences in the distributions of the respective marker

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were observed with increases in the median levels among the persistence group for the following activation CD3+CD4+ T-cell subsets: CD69+CD4+, HLADR+CD3+CD4+, CD38+HLADR+CD3+CD4+ and CD38−HLADR+CD3+CD4+. In addition, a statistically significant difference in the distribution was observed for the $CD45RO^+CD27^+CD4^+$ subset, a marker of undifferentiated memory cells with a decrease in the median level among the persistence group. Significant differences were also observed when the HPV persistence group was compared to the HPV clearance group for the same markers with median levels similarly increased or decreased as when compared to the HPV negative group (data not shown). No significant differences for any of the markers analyzed were observed when the HPV clearance group was compared to HPV negative controls (data not shown).

Next, we compared immunophenotypic subsets of $CD3+CDB^+$ cells (Table 2). The only statistically significant difference noted between the HPV persistence and HPV negative group was for the mean rank distribution of the CD45RO+CD27−CD8+ cell population, a marker of differentiated memory cells with an increase in the median level for the persistent HPV positive group. A higher median value of CD45RO+CD27−CD8+ was also observed for the persistent HPV positive group when compared with the HPV clearance group with a significantly different quartile distribution (data not shown). No significant differences were observed when the HPV clearance group was compared to HPV negative controls (data not shown).

Associations between risk of HPV persistence and increasing percentages of specific subsets within $CD3+CD4+$ and $CD3+CD8+$ are presented in Tables 3 and 4, respectively. These analyses were restricted to the subsets whose population's mean rank distribution differed significantly between the HPV persistence and the HPV negative control groups. Although the distribution difference was significant for CD38+HLADR+CD3+CD4+ and CD38−HLADR+CD3+CD4+, these two subsets were not evaluated further since their observed effects were driven by the main effect seen for HLADR+CD3+CD4+ (correlation between these two subsets and $HLADR^+CD3^+CD4^+$ was 0.53 and 0.96, respectively).

Consistent with findings based on the T-cell markers population distributions, a statistically significant trend in risk for HPV persistence was observed among women with increasing quartile categories when compared with women in the lowest quartile for the following markers of immune activation and/or differentiation after adjusting for age CD4+CD69+ (ptrend < 0.001; 4th quartile OR = 5.4, 95% CI 2.2 – 13.3), HLADR⁺CD3⁺CD4⁺ (p-trend = 0.04; $4th$ quartile OR = 2.6, 95% CI = 1.2 – 5.9), and CD45RO⁺CD27⁻CD8⁺ (p-trend = 0.01; $4th$ quartile OR = 2.3, 95% CI 1.1 – 4.7;). Conversely, a decreased risk for HPV persistence was observed among women in the highest quartiles for the following marker of undifferentiated memory cells $CD45RO^+CD27^+CD4^+$ (p-trend = 0.006; 4th quartile OR = 0.36, 95% CI $0.17 - 0.76$. Effects of stronger magnitude were observed in analyses that restricted the case group to long term persistors (Tables 3 and 4). Similar effects were observed in analyses that evaluated persistence with carcinogenic HPV types (data not shown). We observed no evidence that the effects differed by age (45–54, 55–64, 65–74) (data not shown).

Next, we evaluated whether our previously reported association between proliferative responses and risk of HPV persistence could be explained by differences in the activation/ differentiation state of CD3+CD4+ or CD3+CD8+ subsets (Table 5). Adjustment of the effects seen for proliferative responses against PHA and HPV-16 VLP for levels of the Tcell markers found to be associated with persistence $(CD69^+CD4^+$, HLADR⁺CD3⁺CD4⁺, CD45RO+CD27+CD4+, and CD45RO+CD27−CD8+) only slightly attenuated effects (data not shown). A modest attenuation in the odds ratios was observed when we adjusted proliferative responses for the joint marker variable that combined across the four subsets

significantly associated with risk of persistence (Table 5. A). The age-adjusted OR comparing low to high responders to PHA was reduced from 2.7 (95% CI = $1.4 - 5.1$) to 1.9 (95% CI = $0.94 - 3.7$). Similarly, the age-adjusted OR comparing low to high responders to HPV-16 VLP was reduced from 2.7 (95% CI = $1.4 - 5.3$) to 1.9 (95% CI = 0.90 – 3.8). Adjustment of the immunophenotype effects for proliferative responses to PHA or HPV-16 VLP had a minor effect on the magnitude of the immunophenotype associatiosn with HPV persistence (Table 5. B). Finally, although limited by study size, we observed no evidence that the proliferation effects differed by levels of specific immunophenotypic markers or vice versa (i.e., no evidence for effect modification) (data not shown).

Discussion

Here we demonstrate that HPV persistence in older women is associated with peripheral phenotypic alterations of T-cells, in particular an increase in activated CD4 T-cells expressing CD69 or HLADR and an enrichment in differentiated memory CD45RO+CD27−CD8+ T-cells. We observed differences in the distribution of peripheral Tcell subsets among older women with persistent HPV infections when compared to women of the same age who were not HPV infected. The three subsets found to be positively associated with persistence (CD4+CD69+, HLADR+CD3+CD4+ and CD45RO+CD27−CD8+) were indicators of cellular activation and/or differentiation, whereas the single subset found to be negatively associated with persistence $(CD45RO⁺CD27⁺CD4⁺)$ was an indicator of an undifferentiated state of memory CD4 Tcells. This suggests the possibility that chronic HPV infection is associated with an activation of lymphocyte subsets at the periphery that appears to be unsuccessful at eliminating the virus, as previously suggested by findings of increased IL-2 production among a small number of women with persistent HPV infection and normal cytology ^{35, 36}. Alterations in peripheral subsets of T-cell activation and/or memory differentiation have been reported in the context of other infections such as HIV, dengue and CMV 33, 34, 37–39 as well as other chronic inflammatory conditions $40, 41$. The magnitude of overall changes of the medians were modest and typically within the expected normal range, suggesting that subtle changes in the distribution of immune cells may have important effects on the ability of the host to handle HPV infections. The underlying mechanisms for activation are unknown and deserve further study.

In a previous report from this same population, we observed an association of decreased PBMCs responses to mitogenic and antigenic stimuli and HPV persistence ²⁸. Together with the present observation of an association between markers of lymphocyte activation/ differentiation and HPV persistence, we hypothesize that chronic HPV infections, although local, are associated with activation and differentiation of peripheral subsets of T-cells, which is concomitant with an inability to respond *in vitro* to mitogenic or antigenic stimulation. Because the biological specimens used for immune assessment in the present study were collected at the end of the study (i.e., after persistence was established), it was not possible to determine whether immunological dysregulation leads to a predisposition to HPV persistence or whether HPV persistence induces the observed immunological changes. Future follow-up studies will be required to address whether HPV persistence is cause or a consequence of immune dysregulation.

Association between reduced proliferation and HPV persistence was only slightly attenuated after control for the distribution of T-cell immunophenotypes, suggesting that the T-cell phenotype changes cannot completely explain the previously observed proliferative effect. Similarly, the associations of phenotype changes with HPV persistence reported herein could not be completely explained by the changes in proliferative responses observed with persistent HPV infection. These data suggest the need for further studies to understand

underlying mechanisms of immune dysregulation associated with HPV persistence, such as role of immunoregulatory mechanisms involving regulatory T-cells 42 and of alterations at the level of antigen-presenting cells.

To the best of our knowledge this is the largest study to evaluate the distribution in peripheral blood of immunophenotypic lymphocyte subpopulations among women with different states of HPV infection without precancerous lesions and to show a dose response relationship between immunophenotypic T-cell distribution and risk of HPV persistence. Despite being the largest study of its kind to date, caution should be observed when interpreting our results given the multiple comparisons that were made and the possibility of false positive findings. There is a need for replication of our findings before they can be considered definitive. However, it is reassuring to note that all of the significant associations we observed pointed to a similar biological mechanism (an increase in the proportion of cells that were activated/differentiated), increasing the likelihood that the findings are real rather than false positive findings.

The small number of co-infections with other HPV types or other documented sexually transmitted diseases did not allow us to study co-infection as an effect modifier or confounder. As mentioned above, another limitation of the study is the collection of PBMCs after women had persisting HPV infections; therefore we are not able to disentangle the temporal relationship between immunological responses and HPV persistence. Finally, it should be noted that the present study could not evaluate the potential role of immune phenotype alterations on risk of progression to disease; additional studies that address this question would be of interest in the future.

In summary, markers of activation and/or differentiation of T-cells, mostly within the CD4 T-cells, are associated with HPV persistence. Our study suggests that a localized cervical infection is associated with peripheral T-cell phenotypic alterations. Future studies are needed to define the timing of these immune alterations and their role in disease progression.

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Abbreviations

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Table 1

 †† Markers expressed as percentage of total CD3 positive CD4 positive lymphocytes. *††*Markers expressed as percentage of total CD3 positive CD4 positive lymphocytes.

 $^{t\,\!/\!\gamma\prime}$ Markers expressed as percentage of total CD27 positive, CD45RO positive within CD4 positive lymphocytes. *†††*Markers expressed as percentage of total CD27 positive, CD45RO positive within CD4 positive lymphocytes.

 t ⁺⁺⁺⁺Markers expressed as percentage of total CD27 positive, CD45RA positive within CD4 positive lymphocytes. The rest of the markers are expressed as percentage of the CD4 positive lymphocytes *††††*Markers expressed as percentage of total CD27 positive, CD45RA positive within CD4 positive lymphocytes. The rest of the markers are expressed as percentage of the CD4 positive lymphocytes

 \vec{r} HPV group as defined in the methods section *‡* HPV group as defined in the methods section

*** Kruskal-Wallis test for equality of populations NIH-PA Author Manuscript

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CD8 Tcell immunophenotypic subgroups distribution by study group

 $\stackrel{\scriptstyle \ast}{\scriptstyle \ast}$ Markers expressed as percentage of total lymphocytes. *†*Markers expressed as percentage of total lymphocytes.

 $^t\!{}^+\!\!$ Markers expressed as percentage of total CD3 positive CD8 positive lymphocytes. *††*Markers expressed as percentage of total CD3 positive CD8 positive lymphocytes.

 $^\dagger\!f^\dagger\!M$ Markers expressed as percentage of total CD27 positive, CD45RO positive within CD8 positive lymphocytes. *†††*Markers expressed as percentage of total CD27 positive, CD45RO positive within CD8 positive lymphocytes.

 $^{t\uparrow\uparrow\uparrow}$ Markers expressed as percentage of total CD27 positive, CD45RA positive within CD8 positive lymphocytes. The rest of the markers are expressed as percentage of the CD8 positive lymphocytes *††††*Markers expressed as percentage of total CD27 positive, CD45RA positive within CD8 positive lymphocytes. The rest of the markers are expressed as percentage of the CD8 positive lymphocytes

 $^{\not\uparrow}$ HPV group as defined in the methods section *‡*HPV group as defined in the methods section

*** Kruskal-Wallis test for equality of populations NIH-PA Author Manuscript

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 $\rm\,^{*}$ For HPV Negative and HPV positive groups For HPV Negative and HPV positive groups $^{\not\prime}$ HPV group as defined in the methods section *‡*HPV group as defined in the methods section

 † Odds ratios for the HPV positive and long term HPV positive groups compared to the HPV negative group, adjusted for age. *†*Odds ratios for the HPV positive and long term HPV positive groups compared to the HPV negative group, adjusted for age.

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*** For HPV Negative and HPV positive groups $^{\not\!{t}}\text{HPV}$ group as defined in the methods section *‡*HPV group as defined in the methods section

 † Odds ratios for the HPV positive and long term HPV positive groups compared to the HPV negative group, adjusted for age. *†*Odds ratios for the HPV positive and long term HPV positive groups compared to the HPV negative group, adjusted for age.

Table 5

Odds ratios and confidence intervals for persistent HPV positive group by PHA and VLP proliferation assays Odds ratios and confidence intervals for persistent HPV positive group by PHA and VLP proliferation assays

95% CI

 $1.8 - 11.3$ $1.8 - 11.4$

 $1.2 - 7.5$

 $3.0\,$

 \overline{a}

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 $0.72 - 3.9$ $0.83 - 4.6$

 1.9

 $0.84 - 4.5$

 1.9 $\overline{17}$

 \overline{a}

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B. T-Cell Immunophenotypes

J

B. T-Cell Immunophenotypes

 $1.2 - 5.8$

For HPV Negative and HPV positive groups

 $\ensuremath{^\dagger}\xspace$ Odds ratios adjusted for age *†*Odds ratios adjusted for age

 \hbar^+ Odds ratios adjusted for age and the combined T-cell subset marker variable defined in Methods. *††*Odds ratios adjusted for age and the combined T-cell subset marker variable defined in Methods.

 $\sqrt[t]{\rm odds}$ ratios adjusted for age and the proliferative response to PHA \hbar^2 Odds ratios adjusted for age and the proliferative response to PHA

 \mathcal{I}^{\sharp}_{t} Odds ratios adjusted for age and the proliferative response to HPV-16 VLP *‡‡*Odds ratios adjusted for age and the proliferative response to HPV-16 VLP