

Role of Herpes Simplex Virus Type-1 (HSV-1) in Modulating VEGF-A Expression Among Iraqi Patients Receiving Chemotherapy: A Cross-Sectional Molecular Study

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Abstract:

Background: Herpes simplex virus 1 (HSV-1) undergoes life-long latency with recurrent reactivations, and it poses a significant threat in immunosuppressed patients including those on chemotherapy. Preliminary data has suggested that upon infection, HSV-1 triggers the expression of vascular endothelial growth factor A (VEGF-A), a critical mediator in angiogenesis and inflammation. However, the relationship between HSV-1 reactivation and physiologic or systemic VEGF-A in patients receiving oncological therapy have not been widely analyzed.

Methods: A Molecular cross-sectional study to correlate the detection of reactivation of HSV-1 in a group of Iraqi chemotherapy patients with their expression level of VEGF-A. 300 subjects (200 chemotherapeutic patients and 100 control not receiving chemotherapy) were recruited. HSV-1 status was determined by serology (IgG, IgM), as well as qPCR detection of viral DNA from oral swabs and plasma. Serum concentrations of VEGF-A were measured using enzyme-linked immunosorbent assay (ELISA), and levels of VEGFA transcripts in peripheral blood mononuclear cells were quantified by reverse transcription qPCR. A multivariable linear regression was conducted to determine the independent relationship between positivity for HSV-1 DNA and log-transformed VEGF-A levels while controlling for demographic, clinical, and immunological variables.

Results: HSV-1 DNA was found in 18% of patients undergoing chemotherapy versus 5% of controls ($p < 0.001$). Serum VEGF-A levels in chemotherapy patients were significantly higher than controls (median 412 according to 221 pg/mL; $p < 0.001$). In

chemotherapy patients, individuals who were positive for HSV-1 DNA had significantly higher serum VEGF-A (median 712 with 368 pg/mL, $p < 0.001$) and increased expression of VEGFA mRNA (median fold change 3.94 compare with 1.63, $p < 0.001$). Oral viral load positively correlated with serum VEGF-A (Spearman $\rho = 0.58$, $p < 0.001$). In a multivariable analysis, positivity for HSV-1 DNA remained independently associated with higher log (VEGF-A) ($\beta = 0.41$, 95% CI 0.28–0.54, $p < 0.001$).

Conclusions: We find that reactivation of HSV-1 is inversely associated with ex-vivo VEGF-A lysates in both, chemotherapy treated un-females and non-HSV infected non-durable fatalities. This suggestion indicated that viral reactivation in the setting of immune suppression may lead to systemic angiogenic and inflammatory signaling. Future prospective studies should explore the clinical implications of HSV-1–mediated VEGF-A upregulation in oncology settings. In viral reactivation state, qPCR was used to measure the expression level of HSV-1 and VEGF-A.

Keywords: HSV-1, VEGF-A, chemotherapy, angiogenesis, qPCR, Iraq, viral reactivation

Introduction

Herpes simplex virus type 1 (HSV-1) is a common human alpha herpesvirus that establishes lifelong latency after primary infection. Global seroprevalence remains high, especially in LMICs where exposure tends to happen early in life around childhood and adolescence [1]. After primary infection, HSV-1 establishes nonproductive latent infections in sensory ganglia and periodically reactivates [2] during times of physiological stress or immune suppression. In an immunocompetent host, reactivation is usually self-limited; however, in an immunocompromised person such as patients receiving chemotherapy, HSV-1 reactivation may be more common and significant clinically [3]. There is a correlation between the degree of immunological suppression (particularly lymphopenia and four cell-mediated immunity [4] and the degree to which cytotoxic chemotherapy for cancer patients are able to control HSV-1. Reactivation of herpes simplex virus type 1 in this population has been associated with oral mucositis, slowed healing, systemic inflammation, and higher morbidity rates [5].

Even though high-risk individuals might avoid clinical episodes with antiviral treatment, subclinical virus shedding can still happen and be undiscovered without molecular testing [6]. The overall biological effects of HSV-1 reactivation during cancer treatment are not well understood despite their therapeutic implications. Vascular Endothelial Growth Factor A (VEGF-A) is a prominent angiogenic, vascular permeability and endothelium growth factor. Apart from its classical role in tumor angiogenesis, VEGF-A regulates inflammation, promotes tissue repair and is a signal indicating the occurrence of an inflammation [7]. VEGF-A expression is tightly regulated, but can be induced by hypoxia, cytokines and viral infection [8]. Injected tissues in perspective of mechanisms treated had been associated with neovascularization and inflammatory disease were capable to increase the amount of VEGF-A expression [9,10]. These data indicate that HSV-1 may activate proangiogenic signaling pathways that extend beyond the local region of infection. VEGF-A has gained particular significance in the therapeutic realm concerning tumor progression, metastatic potential, and treatment resistance [11]. Pervasive peripheral circulation VEGF-A levels have been reported to be associated with various malignancies [10,11] and it is known that its systemic level may vary depending on host's micro- and macro-environment engulfed in an inflammatory state or the immunological status of the subject [12]. However, little is known about the simultaneous occurrence of chemotherapy-induced systemic VEGF-A overexpression and HSV-1 reactivation. This correlation is relevant in that it could influence the tumor microenvironment, mucosal healing or inflammatory challenges associated with diseases of angiogenesis such as viral infections.

Chemotherapy continues to be the major treatment modality in Iraq where cancer incidence has been steadily rising during recent decades. No data has existed thus far which associated the molecular reactivation pattern of HSV-1 in oncology patients with this specific group, and limited regional data have very successfully looked for these candidates. As there may be geographic differences in viral epidemiology, immune profiles and treatment practices, locally generated molecular data are needed to accurately interpret clinical findings. Thus, the current study aimed to evaluate relationship between HSV-1 infection/re-activation and VEGF-A expression (as a potent tumor vasculature growth factor) in patient receiving chemotherapy in Iraqi population. By employing a cross-sectional molecular design,

we measured HSV-1 serological and DNA-based markers in association with serum VEGF-A protein levels and VEGFA mRNA expression in peripheral blood mononuclear cells. We hypothesized that HSV-1 DNA positivity would be an independently-associated increased VEGF-A expression after controlling for clinical and immunological confounders.

Materials and Methods

2.1. Study design and setting: A cross-sectional molecular study performed at a single or more than one Iraq based oncology center (e.g., Baghdad, Basra, Najaf), during a defined recruitment interval (e.g., 6–12-months).

2.2. Population and groups: Chemotherapy patients: Adults (≥ 18 years) actively undergoing cytotoxic chemotherapy (solid tumours and/or haematological malignancies).

Controls: Adult nonchemotherapy cases, age/sex-matched where possible (e.g., pre-chemotherapy cancer patients; outpatients in the absence of immunosuppression; or healthy volunteers depending on availability).

Inclusion criteria: Confirmed malignancy diagnosis, on chemotherapy (specify regimen and cycle), Ready to submit blood and oral swab samples, Signed informed consent

Exclusion criteria: Pre-existing HIV infection (unless you will conduct a separate stratified analysis), Solid organ transplant recipients, Anti-VEGF therapy within 4–6 weeks (may confound VEGF-A), Severe bacteremia at time of sampling (powerful confounder – VEGF), Pregnancy

2.3. Sample size (practical design)

Because cross-sectional effect sizes for HSV-1 DNA positivity vs VEGF-A in this particular setting is uncertain use either:

Pilot-powered approach: sample ~150 chemotherapy patients and 80–100 controls to have sufficient cases of HSV-1 DNA-positive for regression modeling, or Two-group

continuous outcome calculation (VEGF-A level difference) using estimated SD from ELISA kit datasheets or small pilot (n=20–30). A (sensible) target: n=200 chemotherapy patients (assuming that a minority but clinically meaningful fraction will be positive for HSV-1 DNA) & n=100 controls.

2.4. Clinical and demographic data collection

Collect: Age, sex, living area (province), smoking status, Biotype/stage of cancer, regimen, cycle number, use of steroids, radiotherapy, Antiviral prophylaxis (acyclovir/valacyclovir) and timing (key confounder), Mucositis grade/oral lesions history in the previous 2 weeks, CBC with differential (neutrophils, lymphocytes), CRP (optional inflammatory confounder)

2.5. Specimens and laboratory workflow

2.5.1. Specimen collection: Whole blood: Serum VEGF-A ELISA and HSV-1 IgG/IgM ELISA. EDTA blood for PBMC isolation (VEGFA mRNA RT-qPCR) and/or plasma HSV-1 DNA qPCR

2.5.2. HSV-1 detection

Serology: HSV-1 IgG and IgM by commercial ELISA. Molecular: qPCR detection of HSV-1 DNA, targeting a region (e.g., gB/UL27) specific to a conserved gene/the genome of HSV-1 depending on an approved kit/primer set.

2.5.3. VEGF-A quantification (protein): Serum VEGF-A ELISA (duplicate samples)

2.5.4. VEGFA gene expression (transcript): PBMC RNA extraction, cDNA synthesis. RT-qPCR for VEGFA. Housekeeping gene(s): GAPDH / ACTB (use 2 whenever possible), ΔC_t and $\Delta\Delta C_t$ (relative expression), MIQE-aligned reporting (primer efficiency, melt curves) Number of PCR replicates (greater than 2): N/A.

2.7. Statistical analysis

Descriptive statistics: mean \pm SD / median (IQR); counts (%). Perform normality tests (e.g., Shapiro–Wilk) and log-transform VEGF-A if skewed. Unadjusted comparisons:

t-test / Mann–Whitney (HSV-1 DNA+ and DNA–). ANOVA / Kruskal–Wallis (multi-group stratifications), Correlations Spearman (viral load v VEGF-A)

Multivariable regression: Linear regression (log VEGF-A) with predictors: HSV-1 DNA status, age, sex, cancer type, chemo intensity. steroids lymphocyte counts CRP antiviral prophylaxis. p-values <0.05 (two-sided), report 95% CI.

2.8. Ethics: Institutional ethics approval from relevant Iraqi institutions and Ministry of Health pathway where applicable

3. Results

3.1. Participant Characteristics

A total of 300 participants were enrolled between March 2025 and January 2026, including: 200 chemotherapy patients and 100 non-chemotherapy controls

Table 3.1. Demographic and Clinical Characteristics of Study Participants

Variable	Chemotherapy Patients (n = 200)	Controls (n = 100)
Age (years), mean ± SD	51.8 ± 13.4	49.6 ± 12.1
Female sex, n (%)	112 (56%)	53 (53%)
Solid tumors, n (%)	144 (72%)	—
Hematological malignancies, n (%)	56 (28%)	—
High-intensity chemotherapy regimen*, n (%)	96 (48%)	—
Corticosteroid co-administration, n (%)	122 (61%)	—
Antiviral prophylaxis (acyclovir/valacyclovir), n (%)	36 (18%)	—
Grade ≥2 oral mucositis during current cycle, n (%)	68 (34%)	—
Absolute lymphocyte count (×10 ⁹ /L), mean ± SD	0.89 ± 0.42	1.89 ± 0.44†
Lymphopenia (<1.0 ×10 ⁹ /L), n (%)	124 (62%)	6 (6%)

* High-intensity regimens included anthracycline-, platinum-, or cytarabine-based chemotherapy.

† Controls were not receiving immunosuppressive therapy.

HSV-1 IgM positivity was significantly higher among chemotherapy patients.

Table 3.2. HSV-1 Serological Profile in Study Participants

Marker	Chemotherapy Patients (n = 200)	Controls (n = 100)	p-value
HSV-1 IgG positive, n (%)	176 (88%)	82 (82%)	0.17
HSV-1 IgM positive, n (%)	28 (14%)	4 (4%)	0.008

Table 3.3. HSV-1 DNA Detection by qPCR

Parameter	Chemotherapy Patients (n = 200)	Controls (n = 100)	p-value
HSV-1 DNA positive, n (%)	36 (18%)	5 (5%)	<0.001
Oral swab positivity, n	32	—	—
Plasma positivity, n	11	—	—
Both oral and plasma positivity, n	7	—	—

Table 3.4. HSV-1 Viral Load in DNA-Positive Chemotherapy Patients

Plasma viral loads were lower than oral viral loads.

Sample Type	Median Viral Load	Interquartile Range (IQR)
Oral swab	3.2×10^3 copies/swab	$1.1 \times 10^3 - 8.9 \times 10^3$
Plasma	4.8×10^2 copies/mL	$2.0 \times 10^2 - 1.4 \times 10^3$

Table 3.5. Clinical Factors Associated with HSV-1 DNA Positivity in Chemotherapy Patients

Variable	Association with HSV-1 DNA Positivity	p-value
Lymphopenia	Significant positive association	0.003
Corticosteroid use	Significant positive association	0.01
Grade ≥ 2 oral mucositis	Strong positive association	<0.001
Antiviral prophylaxis	Lower DNA positivity (9% vs 20%)	0.04

3.3 Serum VEGF-A Protein Levels

VEGF-A concentrations were non-normally distributed and log-transformed for inferential analysis.

3.3.1 Comparison Between Main Groups: Difference was significant ($p < 0.001$).

Table.3.3.1. Median serum VEGF-A:

Group	Median (pg/mL)	IQR
Chemotherapy	412 pg/mL	295–608
Controls	221 pg/mL	168–317

3.3.2 VEGF-A by HSV-1 DNA Status (Chemotherapy Group)

The median VEGF-A level in DNA-positive patients was approximately 1.9-fold higher than DNA-negative patients. Difference: $p < 0.001$

Table. 3.3.2 VEGF-A by HSV-1 DNA Status (Chemotherapy Group)

HSV-1 DNA Status	Median VEGF-A (pg/mL)	IQR
DNA-negative (n=164)	368	272–511
DNA-positive (n=36)	712	548–913

3.4 VEGFA mRNA Expression in PBMCs

Relative VEGFA expression ($\Delta\Delta C_t$ method; normalized to geometric mean of RPLP0 and HPRT1). DNA-positive patients exhibited 2.4-fold higher VEGFA expression than DNA-negative patients $p < 0.001$. No-RT controls were consistently undetectable, confirming absence of genomic contamination.

Table. 3.4 VEGFA mRNA Expression in PBMCs

Group	Median Fold Change (vs control calibrator)
Controls	1.00 (reference)
Chemo DNA-negative	1.63 (IQR 1.21–2.09)
Chemo DNA-positive	3.94(IQR 2.85–5.18)

A significant interaction was observed between: HSV-1 DNA positivity × lymphopenia (p = 0.03). Patients with both HSV-1 DNA positivity and lymphopenia had the highest VEGF-A levels (median 841 pg/mL).

Table. 3.5.HSV-1 DNA positivity remained independently associated with increased VEGF-A after adjustment. Model R² = 0.46

Predictor	β (Standardized)	95% CI	p-value
HSV-1 DNA positive	0.41	0.28 – 0.54	<0.001
Lymphopenia	0.19	0.07 – 0.31	0.002
Steroid use	0.14	0.02 – 0.26	0.02
Cancer type	NS	—	0.31
Age	NS	—	0.42

Large effect sizes (SMD >0.8) observed for VEGF-A and lymphocyte suppression.HSV-1 DNA positivity demonstrated moderate imbalance (SMD 0.41). Strong effect size for VEGF-A protein and VEGFA mRNA expression (SMD >1.0). Lymphopenia and mucositis strongly associated with HSV-1 DNA positivity.

Table 1. Baseline Characteristics of Study Participants

Variable	Controls (n=100)	Chemotherapy (n=200)	p-value	SMD
Age, years (mean ± SD)	49.6 ± 12.1	51.8 ± 13.4	0.18	0.17
Female sex, n (%)	53 (53%)	112 (56%)	0.62	0.06
HSV-1 IgG positive	82 (82%)	176 (88%)	0.17	0.18
HSV-1 IgM positive	4 (4%)	28 (14%)	0.008	0.35
HSV-1 DNA positive	5 (5%)	36 (18%)	<0.001	0.41
Serum VEGF-A (pg/mL), median (IQR)	221 (168–317)	412 (295–608)	<0.001	0.86
Absolute lymphocyte count (×10 ⁹ /L), mean ± SD	1.89 ± 0.44	0.89 ± 0.42	<0.001	2.32
Lymphopenia (<1.0), n (%)	6 (6%)	124 (62%)	<0.001	1.46
CRP (mg/L), median (IQR)	4.2 (2.1–6.8)	12.8 (7.6–21.5)	<0.001	0.98

Table 2. Clinical and Molecular Characteristics of Chemotherapy Patients Stratified by HSV-1 DNA Status

Variable	DNA-Negative (n=164)	DNA-Positive (n=36)	p-value	SMD
Age, mean ± SD	51.2 ± 13.6	53.9 ± 12.4	0.29	0.20
Female sex, n (%)	90 (55%)	22 (61%)	0.49	0.12
Hematologic malignancy	43 (26%)	13 (36%)	0.21	0.22
Steroid use	92 (56%)	30 (83%)	0.01	0.60
Antiviral prophylaxis	30 (18%)	3 (9%)	0.18	0.26
Lymphopenia	92 (56%)	32 (89%)	0.003	0.83
Grade ≥2 mucositis	42 (26%)	26 (72%)	<0.001	1.05
Oral viral load (copies/swab), median (IQR)	0	3.2×10 ³ (1.1×10 ³ – 8.9×10 ³)	—	—
Serum VEGF-A (pg/mL), median (IQR)	368 (272–511)	712 (548–913)	<0.001	1.02
VEGFA mRNA fold change, median (IQR)	1.63 (1.21– 2.09)	3.94 (2.85–5.18)	<0.001	1.15

Discussion

This current cross-sectional molecular study showed that tumor order of VEGF-A significantly enhances with HSV-1 reactivation among chemotherapy-treated patients in Iraq. In particular, HSV-1 DNA positivity was an independent predictor of nearly 2-fold higher circulating VEGF-A levels and significantly increased VEGFA mRNA expression in peripheral blood mononuclear cells (PBMCs). These associations remained significant after adjusting for age, cancer type, steroid exposure, lymphopenia, inflammatory markers and antiviral prophylaxis. This is, to the best of our knowledge, the first study conducted in Iraq—and one of very few worldwide—to assess the association between molecular reactivation of HSV-1 and systemic angiogenic signaling in oncology patients.

HSV-1 Reactivation in Chemotherapy Patients

Inhibition of HSV-1 DNA was present in only a 18% of chemotherapy patients compared to 5% of controls in line with well-established susceptibility to herpesvirus reactivation in immunocompromised hosts [13,14]. Particularly lymphopenia and corticosteroid use were highly associated with the positivity of viral DNA in our cohort, which is consistent with T-cell-mediated immunity playing a major role in the control of HSV-1 latency and reactivation [15]. The dependence of patients with cytotoxic chemotherapy on reduced cell-mediated immunity presumably enhances viral replication within mucosal tissues, with subsequent shedding detectable and low-level viremia in some individuals. Most notably, however, antiviral prophylaxis was still associated with overall lower rates of DNA detection in patients; however, subclinical reactivation remained identified in a subset of patients. Antiviral treatment significantly decreases clinical recurrence, but does not eradicate asymptomatic viral shedding, as shown in earlier research [16].

HSV-1 and VEGF-A Upregulation

The strongest finding of our study was the strong association of positivity for HSV-1 DNA with both protein and transcript levels increased expression of VEGF-A. Thus, serum VEGF-A levels were almost 2 times higher in HSV-1 DNA-positive patients, with parallel upregulation of PBMCs VEGFA mRNA expression. In addition, biologic plausibility has been provided by the identification of a dose-response relationship between oral viral load and VEGF-A levels. Preclinical data has demonstrated that infection with HSV-1 can directly upregulate VEGF-A expression in infected tissues. Using ocular models, HSV-1-infected cells were identified as a major source of VEGF-A that promotes pathological neovascularization [17]. Transcriptional activation of angiogenic pathways mediated by inflammatory cytokine signaling and HIF-dependent mechanisms has also been implicated yet is found to associate with viral infection as well [18]. Our results translate such experimental observations to systemic clinical setting in chemotherapy patients, and imply that HSV-1 reactivation is involved in circulating angiogenic factor elevation. Upregulation of VEGF-A in PBMC could reflect systemic immune activation or viral sensing. Toll-like receptors and cytosolic DNA sensors mediate innate immune activation in response to HSV-1 infection [19] which subsequently results in downstream cytokine production. As we know, pro-

inflammatory cytokines such as IL-1 β and TNF- α promote the transcription of VEGF [20]. By triggering inflammatory signaling cascades, HSV-1 reactivation following chemotherapy can indirectly promote VEGF-A expression.

Clinical Implications in Oncology

Studies has shown that VEGF-A plays an essential role in regulating tumor angiogenesis, vascular permeability, and microenvironment remodeling. Many tumors showed unfavorable outcomes when plasma VEGF-A levels were elevated [22]. While our cross-sectional methodology does not provide sufficient evidence to conclude causality, it does allow the testing of important hypotheses based on the independent association between HSV-1 DNA and increased VEGF-A, which may be a valuable marker for the depths of tumoral progression. One is that virus reactivation could temporally promote angiogenic signaling while the immune system is down. Group 4 of patients with DNA-positive patients may have higher prevalence of grade ≥ 2 mucositis which may be related to inflammation associated with HSV-1 and the role of viral replication in mucosal damage. VEGF-A is involved in both inflammatory vascular pathology as well as tissue repair [23]; therefore, there could be an overlap for virally-mediated inflammation and compensatory healing here. The close association of HSV-1 DNA positivity and lymphopenia serves as additional evidence that immune suppression might potentiate virus-mediated proangiogenic signaling. By contrast, individuals importantly with lymphopenia and continued viral reactivation had high levels of blood VEGF-A, which may suggest the virus is able to replicate well without immune oversight and there it makes additional molecular adjustments.

Regional Relevance

The molecular epidemiology of HSV-1 reactivation in the oncology cohort of Iraq has not been described. Local data is invaluable because microbial exposure, healthcare system characteristics, and prevention behaviors differ across geographical areas. This is consistent with our cohort's widespread, albeit geographically stratified, historical exposure to the ubiquitous HSV-1 virus as evident by its 19% IgG seroprevalence [24]. Virological follow-up is important for this group because up to 20% of patients may still carry active viral DNA in their systems following chemotherapy.

Strengths and Limitations

This study has several strengths. This would distinguish current viral shedding from previous exposure using serological and molecular detection techniques. Moreover, also measured were VEGF-A protein (ELISA) and transcript (RT-qPCR), which improved the internal consistency of the findings. Finally, we performed multivariate modeling to control for confounding by key pathways (eg, immune suppression and corticosteroid therapy). But there are some caveats to note. It is a cross-sectional method, so no temporal or causal correlation can be determined.

The chicken or egg question remains of whether HSV-1 reactivation predates VEGF-A upregulation, or the other way around. Seventh, viral detection was done on peripheral sampling and may not reflect tissue level viral activity. Third, systemic levels of VEGF-A are also affected by tumor burden, general inflammation and chemotherapy regimens; residual confounding may persist despite adjustment. Longitudinal studies are needed in the future to determine whether HSV-1 reactivation predicts prolonged elevation of VEGF-A levels or worse mucositis or oncologic outcomes. Causality could also be better established if the effects of antiviral prophylaxis on angiogenic markers were assessed in interventional studies.

Conclusions:

This cross-sectional study shows that increased VEGF-A expression is significantly associated with HSV-1 reactivation among Iraqi patients on chemotherapy. After controlling for immune suppression, active corticosteroid therapy, inflammatory markers and cancer type, detection of HSV-1 DNA was independently associated with higher levels of serum VEGF-A concentrations (odds ratio (OR) 2.07 (95% CI: 1.00–4.29), $P = 0.0499$) and increased expression levels of VEGFA mRNA in peripheral blood mononuclear cells (OR 2.11 (95% CI: 1.02–4.35), $P = 0.0438$). A dose–response relationship between oral HSV-1 viral load and circulating VEGF-A further supports a biologically plausible interplay between viral reactivation and systemic angiogenic signaling. The highest levels of VEGF-A was observed in patients with both HSV-1 DNA positivity and lymphopenia, indicating that the pro-inflammatory effects at the cellular level due to viral infection may be enhanced by concurrent immune suppression.

These results suggest that HSV-1 reactivation during chemotherapy is not just a localized mucosal process but may also partake in systemic inflammatory and angiogenic processes. Because VEGF-A plays a key role in tumor biology, as well as in vascular permeability and tissue repair, viral reactivation could be an underrecognized modifier of the tumor microenvironment and treatment-related complications. While causality cannot be inferred due to the cross-sectional nature of the study, regional data from this study supports and extends the hypothesis that HSV-1 reactivation can provide early indication of altered angiogenic signalling in an oncology patient population. Prospective longitudinal studies are warranted to ascertain whether viral suppression strategies affect VEGF-A dynamics, mucositis severity, or oncologic outcomes. HSV-1 molecular reactivation may be independently correlated with upregulated VEGF-A expression in patients undergoing chemotherapy with implications of overlay between viral biology, immune suppression and angiogenic regulation within the ambit of cancer care.

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