

# HSV -1 & HSV-2 DETECTION BY OPTIMIZED REAL TIME TRIPLEX PCR ASSAY WITH INBUILT **HUMAN SAMPLE QUALITY CHECK**

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ABSTRACT SUMMARY Multiplex real-time (RT)-PCR assays have been widely used tools for detection of human herpesvirus (HSV) pathogens. Due to genome similarity among herpes group especially HSV-1 & HSV-2, most of the assay are cross-reactive or less sensitive. While the other assay available for detection of HSV-1 and HSV-2 virus doesn't provide any check over the quality of the sample. The present study was designed to develop a single-step triplex real-time polymerase chain reaction (PCR) assay for detection of HSV-1, HSV-2 separately along with sample quality check, using human  $\beta$ -actin as a housekeeping gene. The primers and probes for the target genes of HSV-1, HSV-2, and  $\beta$ -actin were designed and an RT triplex PCR assay was standardized modulating variables including annealing temperature, extension temperature, primers, probes, and other reagent concentrations. The assay was validated and sensitivity, a specificity of the assay was determined by various experiments. This novel assay was found to be sensitive, specific, and reproducible for the detection of HSV-1 and HSV-2 in patients sample. The technology was able to detect and quantify all genotypes of HSV-1 and HSV-2. The detection limit for different HSV viral genomes was found to be 100% for viral copies ≥100 copies/mL in a single-tube assay system. The present diagnostic assay can be routinely used in the diagnostic and prognostic assay of HSV-1 and HSV-2 in clinical samples; which is a major advantage in managing seriously/critically ill patients.

## **KEYWORDS**

HSV-1, HSV-2, Real time PCR.

\*Corresponding Author Amita Jain MD-P.H.DVirology research and diagnostic laboratory, Department of Microbiology, King George's Medical University, Lucknow, Uttar Pradesh, India. Pin code: 226003. INTRODUCTION:

Herpes simplex virus (HSV) 1 and 2 are DNA viruses of family Herpesviridae, the viral genome is a linear, double stranded DNA molecule of ~152261 to ~154746 nucleotides. Both the herpes viruses are major public health problem.HSV-1 has been associated with oro-labial disease, with most infections occurring during childhood, and HSV-2 with genital disease with infection following sexual debut. Consequences of HSV infection can range from inconsequential (cold sores in otherwise healthy patients) to highly morbid and fatal (in neonates).2

Early detection of circulating HSV-1 and HSV-2 play an important role in managing such infections as well as assessing response to therapy. The current diagnostic assay available for HSV like ELISA, viral culture and PCR are ridden with various disadvantages viz. cross reactivity, expensive, time consuming, technically challenging and low sensitivity.3Detection of serum markers such as IgM and IgG specific to HSV1&2 takes a week or more to become detectable in body fluids. Crude antigen tests could detect antibody to herpes simplex in general but were poor at differentiating accurately between types 1 and 2.4 Viral culture is expensive, time consuming, technically challenging and less sensitive. HSV PCR, with its consistently and substantially higher rate of HSV detection, has replaced other tests for diagnosis. There are few assays for HSV-1 & HSV-2 detection in uniplex reaction. There are few multiplex real time(RT) PCR assays available to detect these viruses simultaneously.<sup>6</sup> However, development process of these assays has to face few challenges like cross reactivity and lower reproducibility. Clinically HSV DNA titers vary greatly, from levels as high as 10<sup>10</sup> copies/ml during acute HSV infection, to very low levels in patients undergoing antiviral therapy. Assays should have sufficient amount of reagents to detect both low & high viral counts. Variable viral load at different phases of infection is a big hurdle. Genome variability also poses a technical challenge for developing an assay for HSV-1 and HSV-2 detection. HSV structure has wide range of HSV-1 and HSV-2 genome variability. Due to genetic diversity many of the assays have limitations in picking up all the existing genotypes.8 Available HSV-1&2 PCR assays show cross reactivity among HSV-1 & HSV-2 due to genome similarity among HSV-1 & HSV-2. 7.8 Another challenge to the assay in developing countries is to maintain quality of samples as it deteriorates during transportation from the collection centre to central laboratory for

testing due to unavailability to maintain cold chain.

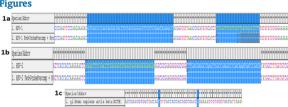
The objective of this study was to develop a triplex assay for differential diagnosis of HSV-1 and HSV-2 alongside an exogenous internal control (Human  $\beta$ -actin). The incorporation of an exogenous internal control increases the reliability of the RT-PCR results by permitting discrimination of true negative results from false negatives which may occur due to poor quality of samples/improper nucleic acid extraction/the presence of PCR inhibitors in the sample. Human  $\beta$ actin gene is expressed at relatively constant levels in all individuals.

All the primer and probes sequences were optimally designed for respective viruses i.e. HSV-1 and HSV-2. Sequences from various genotypes were downloaded from the GenBank nucleotide database and aligned using the program MEGA 5 Details of sequences and primer and probes are mentioned in table 1 and fig 1a-c.

Table 1: List of primers and probes design used for HSV-1 & 2 detection.

Sequence ID	Oligonucleotide	Lengt	Target	Prod	Fluorescent
	sequence 5'-3'	h	gene	uct size	tagging of Probe
HSV-1 Fwd	CCCAAGTTCCCAAC AAAGAC	20	Ul26	143- 151b	FAM
HSV-1 Rvs	CTTTCTTCCCACACA CACA	19		P	
HSV-1 Probe	/5FAM/AGATGCACA TGCGGTTTAACA CCCGT/3 IABkFQ /	26			
HSV-2 Fwd	GCTCACCACCAAGG AACTC	19	UL27	141b P	Cy5
HSV-2 Rvs	GCCGACACCAAAGC CATA	18			
HSV-2 Probe	5'Cy5/CCCGCCCCC TCCGCGCCT/3IAbR QSp /-3'	19			

β-actin Fwd	ACCGAGCGCGGCTA CAG	17	β-actin	60	HEX
β-actin Rvs	CTTAATGTCACGCAC GATTTCC	22			
β-actin Probe	5'/5HEX/TTCACCAC C/ZEN/ACGGCCGAG C/3IABkFQ/-3'	19			
Condition:	designed to prevent formation which ma unwanted fluoresce	& HSV- tide da 5 rimers a primer ay have nce. heracies ding c The cr ruled o gned pr PLC pur	2 were of tabase a and prolonged from the control of table t	downloand aligness we or cross sulted the as the ly to a trivity with the latest trivity with the latest	paded from gned using are optimally as dimer in the primers mplify all with the best were
Figures					



**Fig. 1.**(a): Alignment of HSV-1 primers and probe with UL-26 region (b) Alignment of HSV-2 primers and probe with UL27& (c) Alignment of internal control primers and probe with Human  $\beta$ -actin gene.

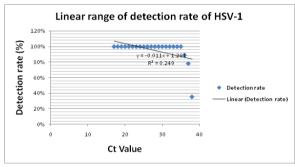


Fig.2. (a): Linear range of HSV-1 detection

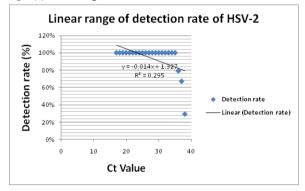


Fig 2 (b) Linear range of HSV-2 detection.

A testing panel of 20 clinical samples from clinical bank store(-80°C) were subjected to real time PCR. The testing panel includes positives for HSV-1(5), HSV-2(5), co-positives (5) and negatives (5) for both HSV-1 and HSV-2. PureLink Viral RNA/DNA Mini Kit (Invitrogen, USA) according to the manufacturer's guidelines, while FastStart Essential DNA Probe Master (Roche, Germany) mastermix were used for real time PCR. Details of real time PCR is mentioned in table 2.

The PCR reaction was optimized keeping in mind the concept of 'limiting concentration' to combat the challenge of variable viral load. A series of dilution of primers and probes were made using a dilution matrix for optimizing the concentration of both. Amplification reactions were performed with a RTthermocycler (light cycler 480, Roche) program consisting of a denaturation step of 10 minutes at 95°C followed by 45 cycles of denaturation at 95°C for 15 seconds, annealing for 20 seconds at 55°C and extension at 72°C for 15 seconds. The fluorescence was acquired at the time of annealing. All the primers and probes were designed in such a way that there was no primer dimer or cross dimer formation which later results in unwanted fluorescence. After optimization of the multiplex reaction, all the above tested 20 samples were retested using the triplex format (table 2).

Table 2: Comparative results of 20 known samples tested with our primers & probes insingleplex& multiplex format

primers & prob				1	
S.No. Sir	Singleplex Reaction		Multiplex /Triplex		
110			Reaction		
		HSV-2 (Copy	HSV-1 (Copy	HSV-2 (Copy	
No	<u>.                                    </u>	No.)	No.)	No.)	
	(10 <sup>8</sup> )	-	+ (10 <sup>8</sup> )	-	
	(10³)	-	+ (10 <sup>3</sup> )	-	
	(10 <sup>7</sup> )	-	+ (10 <sup>7</sup> )	-	
	(10 <sup>5</sup> )	-	+ (10 <sup>5</sup> )	-	
5. +	(10⁵)	-	+ (10 <sup>5</sup> )	-	
6		+ (10 <sup>2</sup> )	-	+ (10 <sup>2</sup> )	
7		+ (10 <sup>4</sup> )	-	+ (10 <sup>4</sup> )	
8		+ (10 <sup>7</sup> )	-	+ (10 <sup>7</sup> )	
9		+ (10 <sup>4</sup> )	-	+ (10 <sup>4</sup> )	
10.		+ (10 <sup>5</sup> )	-	+ (10 <sup>5</sup> )	
11. +	(10°)	+ (10³)	+ (10°)	+ (10 <sup>3</sup> )	
12. +	(10³)	+ (10 <sup>6</sup> )	+ (10 <sup>3</sup> )	+ (10°)	
13. +	(10 <sup>5</sup> )	+ (10 <sup>7</sup> )	+ (10 <sup>5</sup> )	+ (10 <sup>7</sup> )	
14. +(	(10 <sup>8</sup> )	+ (10 <sup>5</sup> )	+(10 <sup>8</sup> )	+ (10 <sup>5</sup> )	
15. +	(10⁴)	+ (10 <sup>3</sup> )	+ (10 <sup>4</sup> )	+ (10 <sup>3</sup> )	
16		-	-	-	
17		-	-	-	
18		-	-	-	
19		-	-	-	
20		-	-	-	
Primer 1	ıl of forwa	rd and reverse	·0.35µl of forward and		
	primer (10pm)		reverse primer (10pm)		
	·0.5µl probe(5pm)		·0.175µl probe		
	·Finally diluted to		·2.3 µl of primer & probe		
10	10picomole/microlitre		cocktail		
		·Finally diluted to 10picomole/microlitre			
			β actin: 0.2μl primer/		
			0.15µl probe		
Extraction TN	A by Invit	rogen	TNA by Invitrogen		
	2.5µlReal Ti		·12.5µlReal Time		
	Mastermix (2x)		Mastermix (2x)		
	·2.5µl of primer & probe of		·2.3 µl of primer & probe		
lead	each target in separate		cocktail		
		rocparace			
rea	action	-	·5.2μl H₂O (DN	Ase and	
rea ∙5µ	action ıl H <sub>2</sub> O (DN <i>I</i>	Ase and RNAse	·5.2µl H₂O (DN RNAse free)		
rea ·5µ fre	action ıl H₂O (DNÆ e)	Ase and RNAse	·5.2µl H₂O (DN RNAse free) ·5µl extracted	total nucleic	
rea ∙5µ fre •5µ	nction ıl H <sub>2</sub> O (DNA e) ıl extracted	Ase and RNAse I total nucleic	·5.2µl H₂O (DN RNAse free) ·5µl extracted acid was adde	total nucleic	
rea •5µ fre •5µ aci	action al H <sub>2</sub> O (DNA e) al extracted id was add	Ase and RNAse I total nucleic ed to 20 µl of	·5.2µl H₂O (DN RNAse free) ·5µl extracted	total nucleic	
rea -5µ fre -5µ aci pre	nction al H <sub>2</sub> O (DNA e) al extracted ad was add epared mas	Ase and RNAse I total nucleic ed to 20 µl of	·5.2µl H₂O (DN RNAse free) ·5µl extracted acid was adde prepared mas	total nucleic	
real time	nction al H <sub>2</sub> O (DNA e) al extracted d was add epared mass itial Denat	Ase and RNAse I total nucleic ed to 20 μl of stermix uration: 10 mi	·5.2µl H₂O (DN RNAse free) ·5µl extracted acid was adde prepared mas	total nucleic	
rea   rea	action  Il H <sub>2</sub> O (DNA e)  Il extracted id was add epared mas itial Denat enaturation nnealing: 2	Ase and RNAse I total nucleic ed to 20 µl of stermix uration: 10 mi n: 45 cycles at 0sec at 55°C	·5.2µl H <sub>2</sub> O (DN RNAse free) ·5µl extracted acid was adde prepared mass	total nucleic	
Real time In PCR condition Ar by Ex	action ul H <sub>2</sub> O (DNA e) ul extracted id was adde epared mas itial Denat enaturation nnealing: 2 ctension: 1!	Ase and RNAse of total nucleic ed to 20 µl of stermix uration: 10 mi n: 45 cycles at 0sec at 55°C 5sec at 72°C	·5.2µl H <sub>2</sub> O (DN RNAse free) ·5µl extracted acid was adde prepared mass	total nucleic	
rea   ·5µ   fre   ·5µ   fre   ·5µ   aci   pre   Real time   ·In   PCR   ·De   condition   ·AI	action ul H <sub>2</sub> O (DNA e) ul extracted id was adde epared mas itial Denat enaturation nnealing: 2 ctension: 1!	Ase and RNAse of total nucleic ed to 20 µl of stermix uration: 10 mi n: 45 cycles at 0sec at 55°C 5sec at 72°C	·5.2µl H <sub>2</sub> O (DN RNAse free) ·5µl extracted acid was adde prepared mass	total nucleic	
Real time In PCR Ondition by LightCycler 480 II system	action ul H <sub>2</sub> O (DNA e) ul extracted id was adde epared mas itial Denat enaturation nnealing: 2 ctension: 1!	Ase and RNAse of total nucleic ed to 20 µl of stermix uration: 10 mi n: 45 cycles at 0sec at 55°C 5sec at 72°C	·5.2µl H <sub>2</sub> O (DN RNAse free) ·5µl extracted acid was adde prepared mass	total nucleic	
Real time In PCR condition by Example 1480 II	action ul H <sub>2</sub> O (DNA e) ul extracted id was adde epared mas itial Denat enaturation nnealing: 2 ctension: 1!	Ase and RNAse of total nucleic ed to 20 µl of stermix uration: 10 mi n: 45 cycles at 0sec at 55°C 5sec at 72°C	·5.2µl H <sub>2</sub> O (DN RNAse free) ·5µl extracted acid was adde prepared mass	total nucleic	

To determine the analytical sensitivity: the plasmids were used. A log-10 serial dilution of each standard plasmid from 10<sup>8</sup>-10copies/ml was

prepared. Serial dilutions were then assayed in triplicate using the optimised singleplex and triplex RT-PCRs. For analysis CT values were compared. Each test was performed on three occasions to verify repeatability and regression analysis and one-way ANOVA was performed on the CT values (the limit of detection [LOD] of the assay) (GraphPad Prism 6).

Table 3: Comparative results of real time PCR with claimed primers and probes, in singleplex and multiplex format with published primers & probes (n=300)

	Singleplex PCR with our newly designed Probes and Primers	our newly designed
HSV-1(positives/ number tested)	9/300	9/300
HSV-2(positives/ number tested)	2/300	2/300
·Human β-actin(positives/ number tested)	294/300	294/300

For analytical specificity determination: To determine specificity, a testing panel of 28 samples were prepared for two groups of viruses; first Herpes groups which includes Cytomegalovirus, Epstein Bar virus, Varicella Zoster virus and another non herpes group like Human parvovirus B19, Japanese encephalitis virus, Dengue, hepatitis B virus, hepatitis C virus, Human Immunodeficiency Virus, Enterovirus, Influenza virus, Respiratory Syncytial virus, Metapneumovirus, Mumps virus and Measles virus. The panel was tested with designed primers and probes by RT PCR to check cross reactivity with other viruses.

Designed primer and probes were evaluated diagnostic specificity and sensitivity for respective viruses i.e. HSV-1 and HSV-2 on routine clinical samples like CSF, serum, skin vesicles and genital swabs. A total of 300 routinely received clinical samples were tested for HSV-1 and HSV-2 by designed real time PCR reaction in both singleplex and triplex formats. The primer-probe set was also evaluated for viral load sensitivity. The experiment was conducted to see the high viral load of one virus over the amplification of low copy number of the other virus in multiplex reaction. Sample with high viral load of HSV-1 (10°copies/ml) was mixed with 10 fold dilution of HSV-2 sample starting with viral load (10°copies/ml) and vice versa.

#### RESULTS:

The self designed primers and probes sequences (table 1 and fig 1a-c) targeting HSV-1 and HSV-2 were bioinformatically checked, with all the genome submitted to NCBI. They were suitable to amplify all the types and subtypes of their respective viruses and did not show any complementarity with human genome or any other viruses genome.

The self designed primer and probes had high sensitivity as standard curves (CT or Crossing Points versus log10 DNA or RNA copies) demonstrated linear amplification for both HSV-1 and HSV-2 DNA. The detection limits of primer-probes set were 100% for copies ≥100 copies/ml viral genome copies, respectively, in singleplex and triplex reactions. CT values obtained with singleplex and triplex assays for detection of HSV-1 and HSV-2 targets was significantly indifferent. Regression analysis of standard curves confirmed linearity. Singleplex RT-PCR for HSV-1 had correlation co-efficient (R2) of 0.989 and 101.91% amplification efficiency(E), whereas the singleplex RT-PCR for HSV-2 had R2 = 0.991 with 101.32% E. Internal control yielded CT values between 18 and 35. The lower limit of the test is 100 copies/ml for both HSV-1 & HSV-2, respectively with 100% sensitivity. For copies≤100 copies/mL sensitivity was 80% and 72% respectively. Real time assay was negative for copies < 100 copies/ml.Real time PCR was performed in triplex format in triplicate on each standard and on two different days to graph the limit of detection (LOD) of the assay. The linear range of detection of HSV-1 and HSV-2 both were from 10<sup>8</sup> to 100 copies/mL (Figure 2a and 2b).

The primer-probe set did not show any cross reactivity against other non-Herpes genomes that may co-exist in clinical samples. All the 20 samples with known HSV-1 and HSV-2 results tested in singleplex as well as multiplex reactions showed similar results with no significant difference in the viral load of the samples (table 2). No cross reactivity was observed with herpes and non herper group of viruses. The 28 samples panel which were tested for specificity, were found to be negative for HSV-1 or HSV-2; however human  $\beta$ -actin was positive in

all the samples. Thus specificity of the assay was considered 100%. For diagnostic sensitivity and specificity, a batch of 300 clinical samples was tested for HSV-1 and HSV-2 by self designed primer-probe set in both singleplex and multiples reaction (table 3). HSV-1 DNA was detected in 9 samples and HSV-2 DNA was detected in 2 samples. Human  $\beta$ -actin gene had mean CT value of 28.17 in 294 samples. Human  $\beta$ -actin gene was not amplified in six samples. All the 6 patients were asked to provide a repeat/fresh sample or repeat for extraction of viral DNA. On repeat testing of 6 samples, one tested positive for HSV-1.

#### DISCUSSION:

HSV-1&2 viruses are becoming major public health issues due to their widespread transmission leading to significant morbidity and mortality. Human herpesviruses infection may involve central nervous system during primary infection or following reactivation from a latent state. The infection could be life threatening in immunecompromised patients also. Rapid and reliable detection of these viruses is the key to take preventive measures timely and stop their transmission, thus infective complications in patients.<sup>2,3</sup> designed primers and probes sequences targeting HSV-1 and HSV-2 were bioinformatically checked, with all the genome submitted to NCBI. They were suitable to amplify all the types and subtypes of their respective viruses and did not show any complementarity with human genome or any other viruses genome. Our designed primer-probe set also identifies large range of conserved genome segment and reliably quantify and predict the viral load which may be modified during the treatment.

We have designed primers-probes set which can simultaneously and rapidly detect and quantify load of HSV type 1 and type 2 DNA. The triplex assay was sensitive enough to detect and quantify a very low copy number without mutual interference and cross reactivity with other viruses, thus our primers-probes set had 100% specificity and sensitivity. Our HSV DNA viral load results indicate that the triplex system described here would be a reliable tool in clinical settings as were able to detect viral copies upto 100 copies/ml with human sample quality check. Though many commercial kits are available in the market which can detect and quantify both the HSV types, but they donot have wide range of viral copies detection. 10-14 The clinical samples evaluated by available multiplex system need to be diluted and repeatedly tested in order to exceeding the upper limit of viral load quantification. Our triplex assay has inbuilt human sample quality check (by  $\beta$  actin detection), which none of the available kits offer.  $^{10\text{-}14}$ Clinical sample quality check made this designed assay more reliable by reducing the chances of any false negative reporting. False negative reports were major concern in developing countries, where sample transport and storage is not appropriate.

The increased sensitivity and turnaround times of PCR based assays have the potential to significantly affect patient management; particularly if such assays are designed to include viruses for which antiviral drug therapy is available. When throughput is high, as is the case in our laboratory, multiplexed PCR assays are also cost-effective and provide a wider differential diagnosis than do individual assays.

Out of total 300 samples tested, 6 (2%) had poor quality. Of 6 samples, one tested positive for HSV-1 which would have been reported false negative, reflecting the advantage of present assay over other assays available.

We have established and evaluated a sensitive and cost effective inhouse adaptable real-time PCR based assay for effective simultaneous detection of HSV-1 and HSV-2 in all types of samples. The lower limit of detection was less than 100 copies/ml for both HSV-1&2. Our designed assay was sensitive, specific and reproducible and could amplify various genotypes of HSV. Our assay can efficiently amplify HSV in both singleplex and triplex format.

## CONCLUSION:

Present study has resulted into the development of highly specific and sensitive diagnostic assay for HSV-1 and HSV-2 detection in clinical samples. The designed primer probes set will rapidly and simultaneously detect HSV-1 and HSV-2 in triplex real time PCR format, which is a major advantage in managing seriously/critically ill patients.

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Conflict of Interest: The authors have declared that no conflict of interest exists.

#### REFERENCES

- McGeoch D J, Dalrymple M A, Davison A J, Dolan A, Frame M C, McNab D, Perry L J, Scott J E, Taylor P. The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1. J Gen Virol. 1988;69:1531–1574.
- R. J. Whitley and B. Roizman, "Herpes simplex virus infections," The Lancet, vol. 357, no. 9267, pp. 1513–1518, 2001.
- Ashley RL. Laboratory techniques in the diagnosis of herpes simplex infection. Genitourin Med. 1993;69:174-83.
- Coyle PV, Desai A, Wyatt D, McCaughey C, O'Neill HJ. A comparison
  of virus isolation, indirect immunofluorescence and nested
  multiplex polymerase chain reaction for the diagnosis of primary
  and recurrent herpes simplex type 1 and type 2 infections. J Virol
  Methods 1999;83:75-82.
- Elfath M. Elnifro, Ahmed M. Ashshi, Robert J. Cooper, Paul E. Klapper. Multiplex PCR: Optimization and Application in Diagnostic Virology. Clin Microbiol Rev. 2000 Oct; 13(4): 559–570.
- Weidmann M, Armbruster K, Hufert FT. Challenges in designing a Taqman based multiplex assay for the simultaneous detection of Herpes simplex virus types 1 and 2 and varicella-zoster virus. J Clin Virol 2008; 42:326-334
- Aryee, EA; Bailey, RL; Natividad-Sancho, A; Kaye, S; Holland, MJ; (2005) Detection, quantification and genotyping of Herpes Simplex Virus in cervicovaginal secretions by real-time PCR: a cross sectional survey. Virol J, 2 (1). p. 61.
- Szpara ML, Gatherer D, Ochoa A, et al. Evolution and Diversity in Human Herpes Simplex Virus Genomes. J of Virol. 2014;88(2):1209-1227. doi:10.1128/JVI.01987-13.
- K. Tamura, D. Peterson, N. Peterson, G. Stecher, M. Nei, S. Kumar. MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol. Biol. Evol., 28 (2011), pp. 2731-2739.
- J. Druce, M. Catton, D. Chibo et al., "Utility of a multiplex PCR assay for detecting herpesvirus DNA in clinical samples," J of Clin Microbiol, vol. 40, no. 5, pp. 1728–1732, 2002.
- Espy MJ, Rys PN, Wold AD, et al. Detection of herpes simplex virus DNA in genital and dermal specimens by LightCycler PCR after extraction using the IsoQuick, MagNA Pure, and BioRobot 9604 methods. J Clin Microbiol. 2001;39:2233–6.
- Burrows J, Nitsche A, Bayly B, et al. Detection and subtyping of herpes simplex virus in clinical samples by LightCycler PCR, enzyme immunoassay, and cell culture. BMC Microbiol 2002:2:2–12.
- Adelson M.E., Feola M., Trama J., Tilton R.C., Mordechai E. Simultaneous detection of herpes simplex virus types 1 and 2 by real-time PCR and Pyrosequencing. J Clin Virol. 2005 May;33(1):25-34
- Prakash S, Jain A, Jain B. Development of novel triplex single-step real-time PCR assay for detection of Hepatitis Virus B and C simultaneously. Virol. 2016 May;492:101-7.