

## MOLECULAR EPIDEMIOLOGY OF HUMAN PAPILLOMAVIRUS

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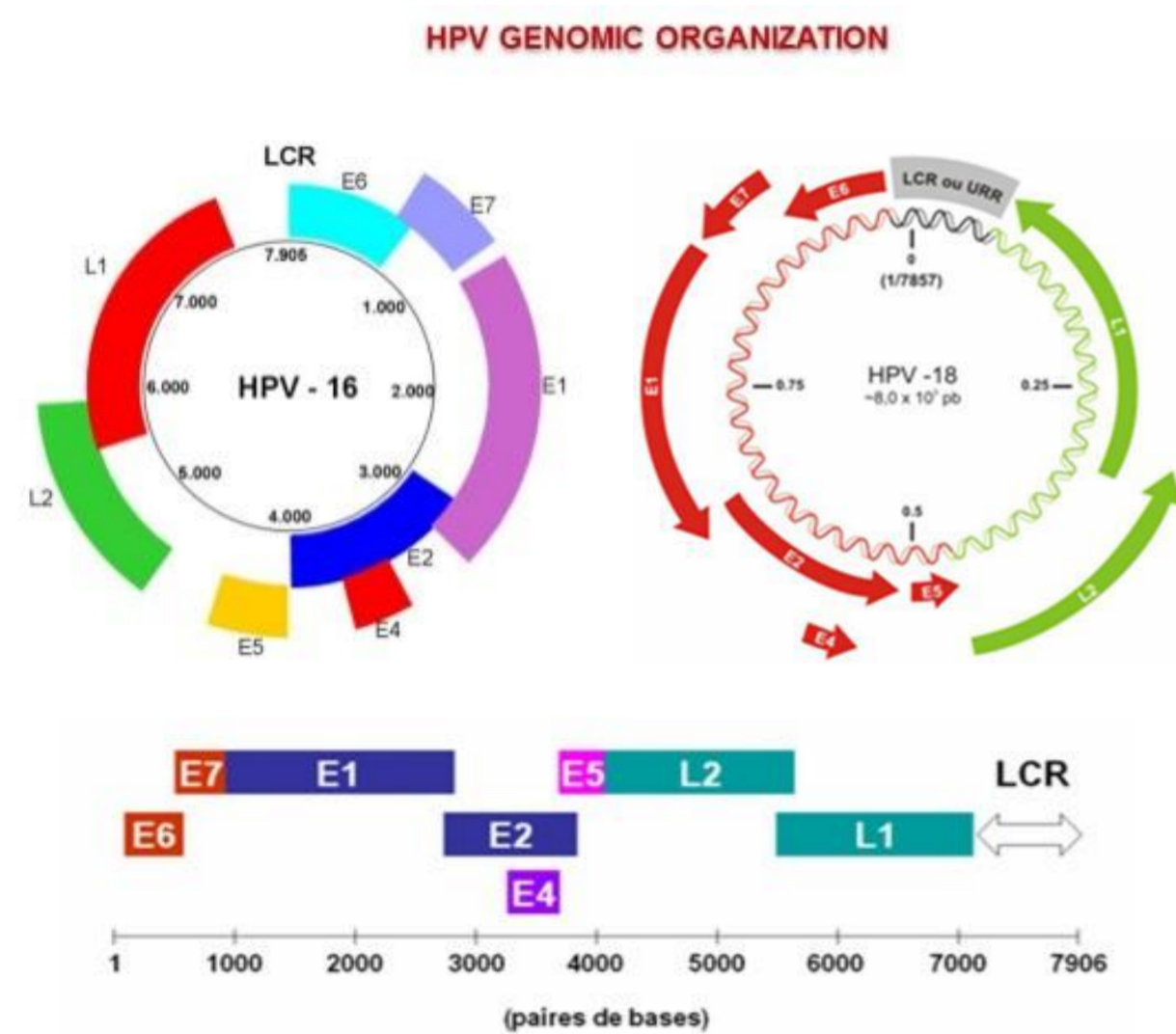
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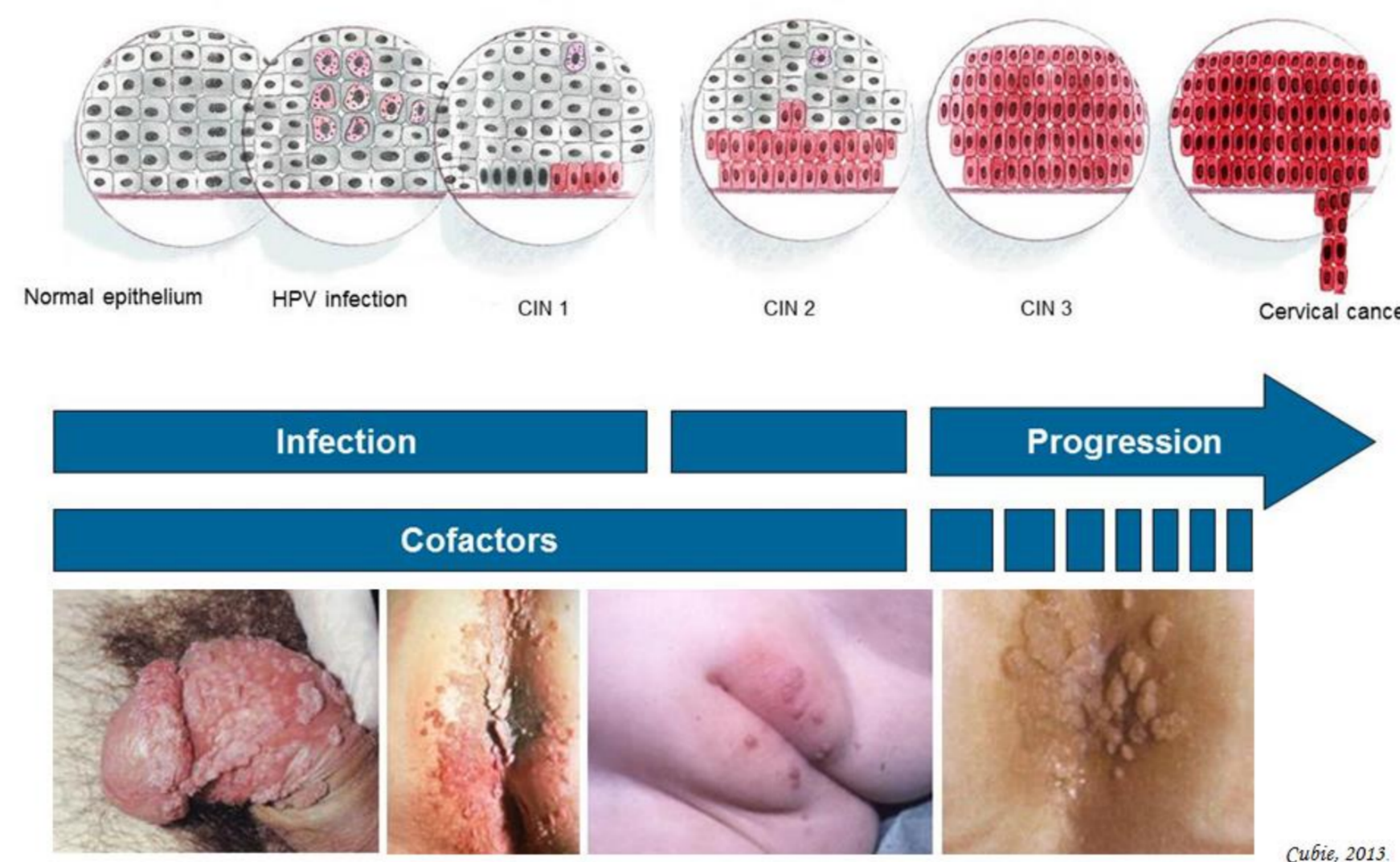
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### INTRODUCTION

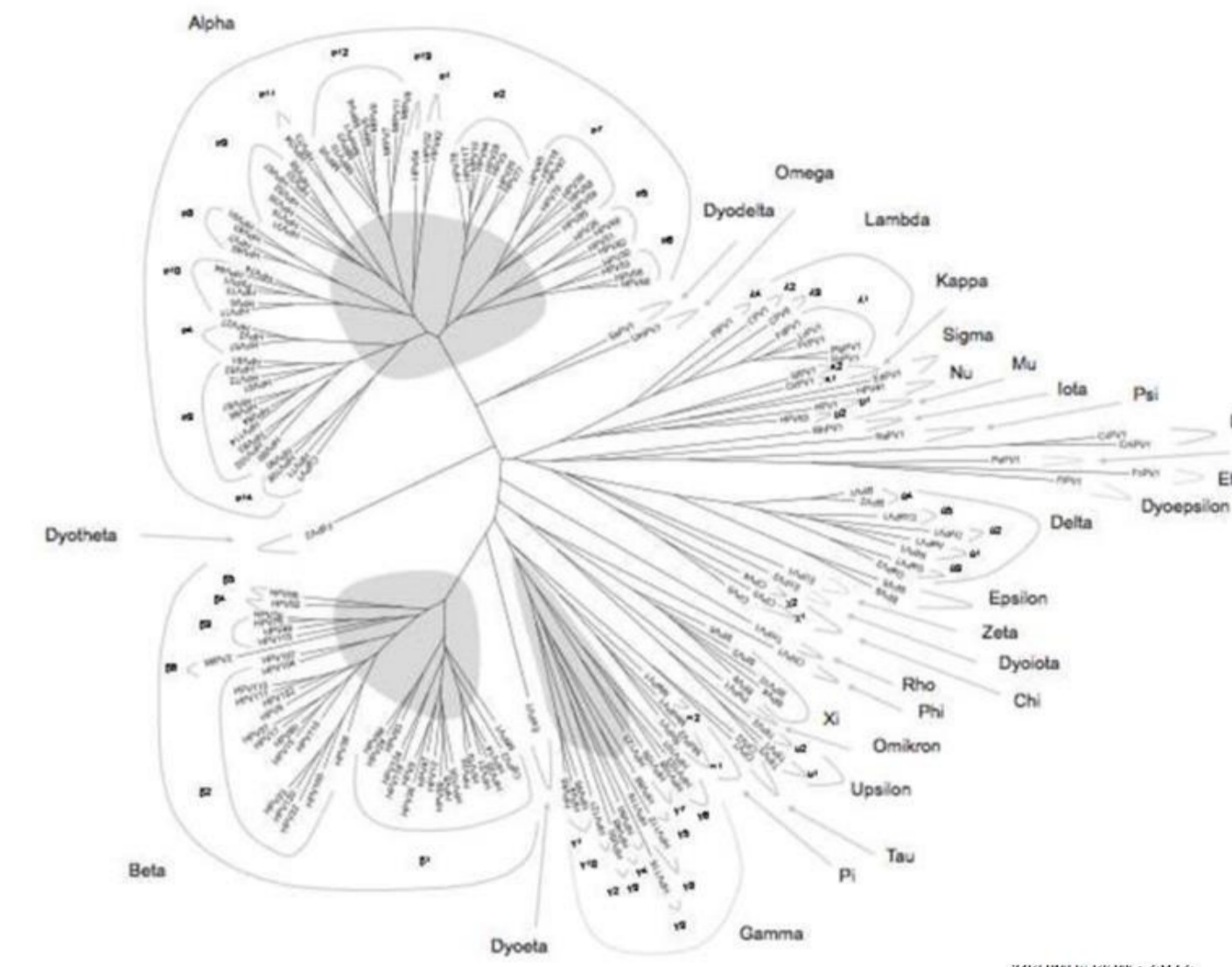
Cervical cancer is the most common cancer in developing countries induced by Papillomaviruses. Human papillomavirus (HPV) possesses a circular, non-enveloped double-stranded DNA genome of around 8 kb and belongs to the *Papillomaviridae* family. More than 200 HPV genotypes and several HPV types, associated to particular diseases such as oral lesions (Heck's disease, oropharyngeal carcinoma, laryngeal papillomas), anogenital warts (Bowenoid papulosis, Buschike-Lowenstein tumor), Epidermodysplasia verruciformis (plane warts, Pityriasis-like plaques, squamous cell carcinomas of sun-exposed skin) have been described. The aim of this study was to evaluate the prevalence of HPV in sexually active women. The demographic and behavior factors were also investigated as co-factors related to cervical cancer.



INFECTION TO CERVICAL CANCER AND CLINICAL LESIONS ASSOCIATED HPV TYPES

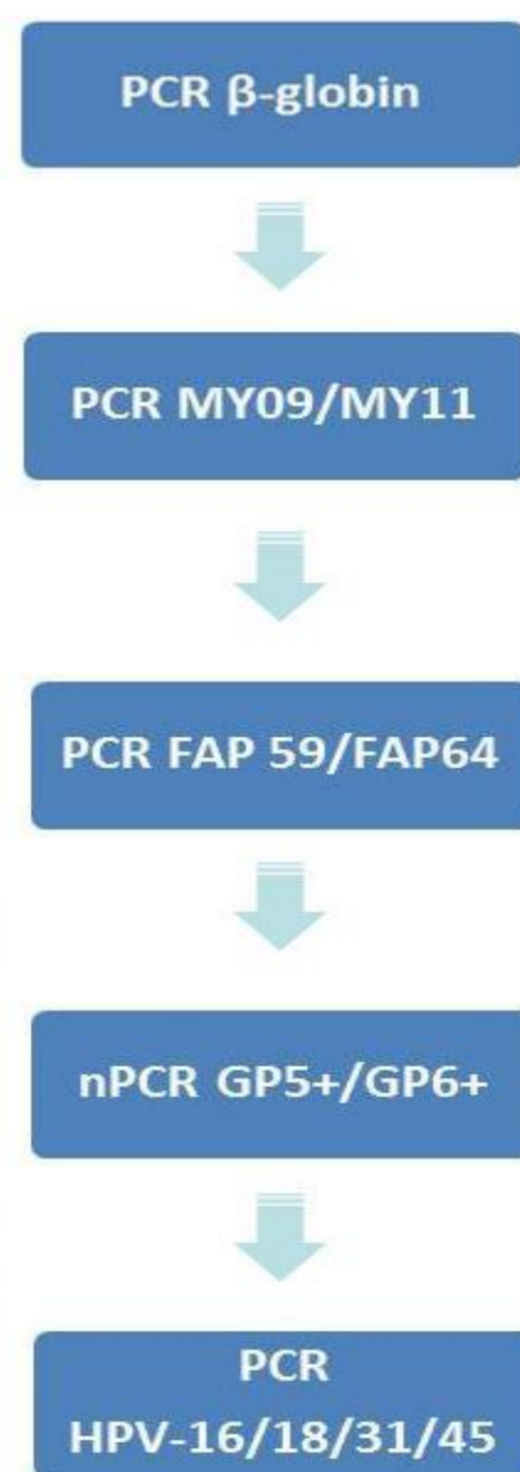
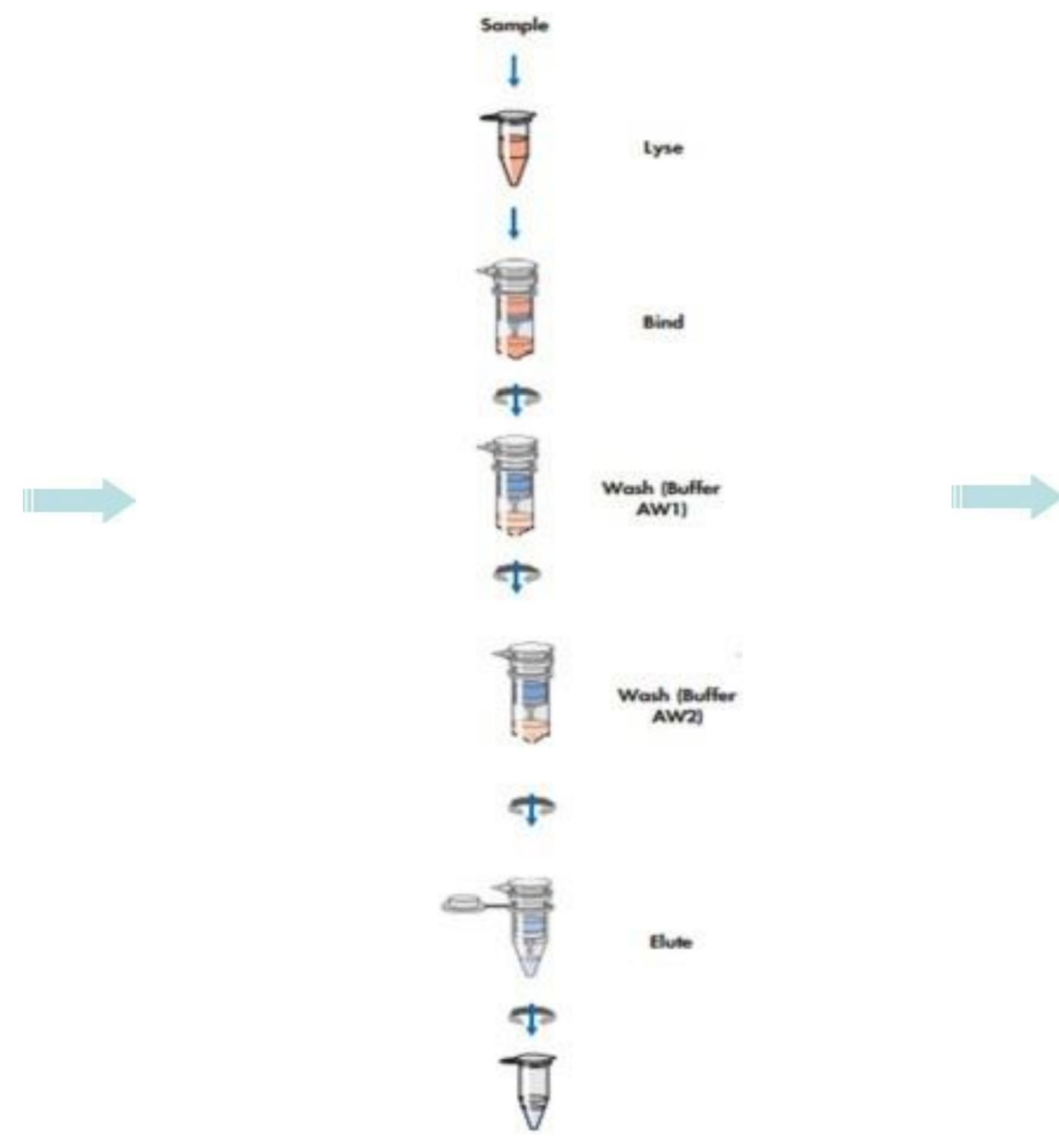


PHYLOGENETIC TREE OF 26 PAPILLOMAVIRUS GENERA



### MATERIAL AND METHODS

A cross-sectional study was conducted from 2014 to 2016 with randomly selected women from the Manguinhos Complex community in Rio de Janeiro city, who spontaneously accessed gynecology ambulatory. Cervical samples collected with a cytobrush were analyzed by PCR amplification of L1 ORF (450bp). HPV-DNA positive samples were detected by consensus (MY09/MY11), Nested PCR (GP5+/GP6+) and high-types specific primers (HPV16/18/31/45). In order to evaluate the viral DNA quality, swab samples collected were amplified by  $\beta$ -globin PCR primers (PC04/GH20). Restriction fragment length polymorphism (RFLP) assay patterns for mucosal HPVs were used for genotyping. Chi-square test was used to analyze the risk factors associated with HPV infection. The population study comprises 100 women, from 15 to 75 years and presenting normal cervical cytology.



CONSENSUS AND DEGENERATED PRIMERS USED IN THIS STUDY (ORF L1)

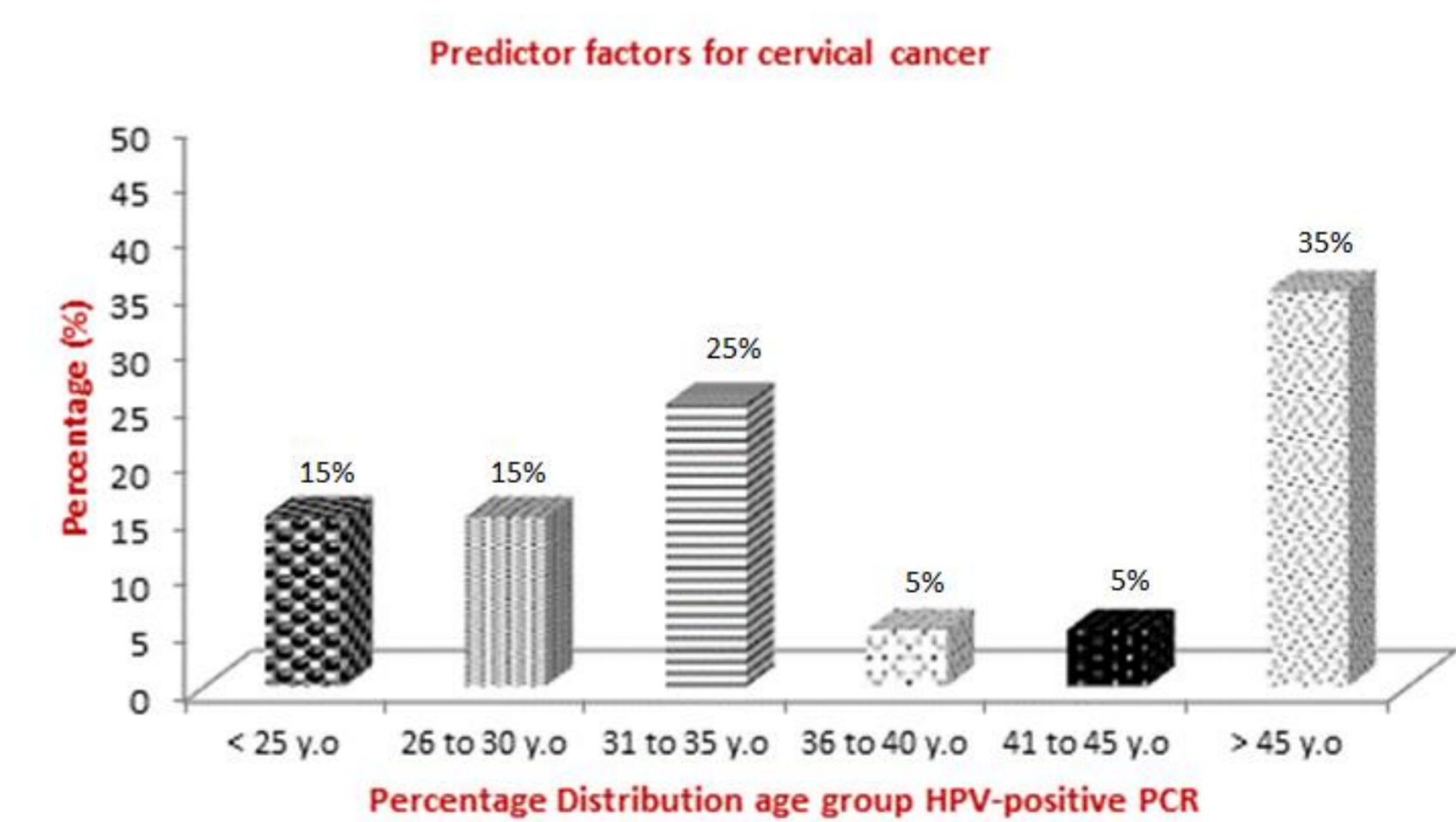
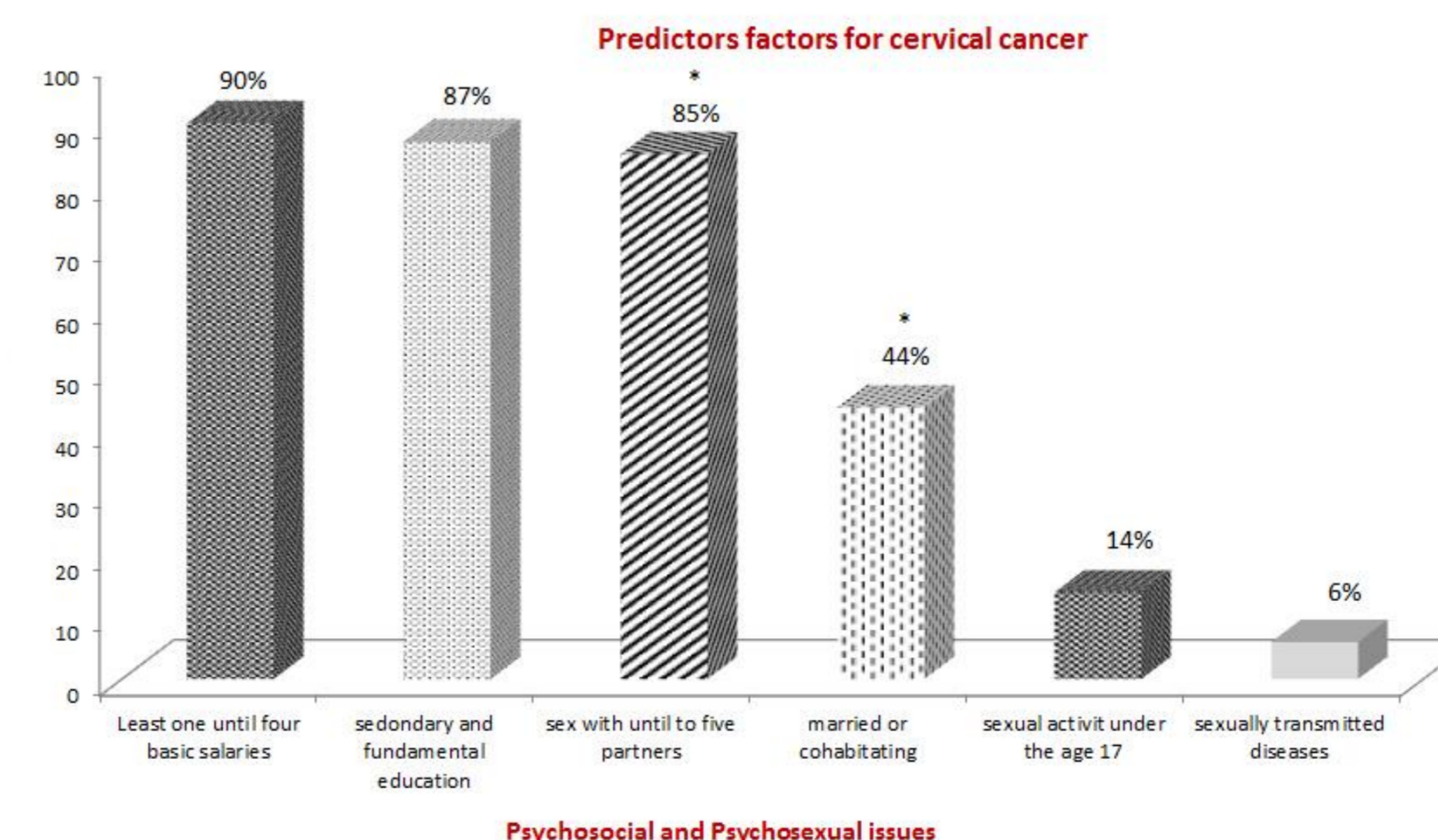
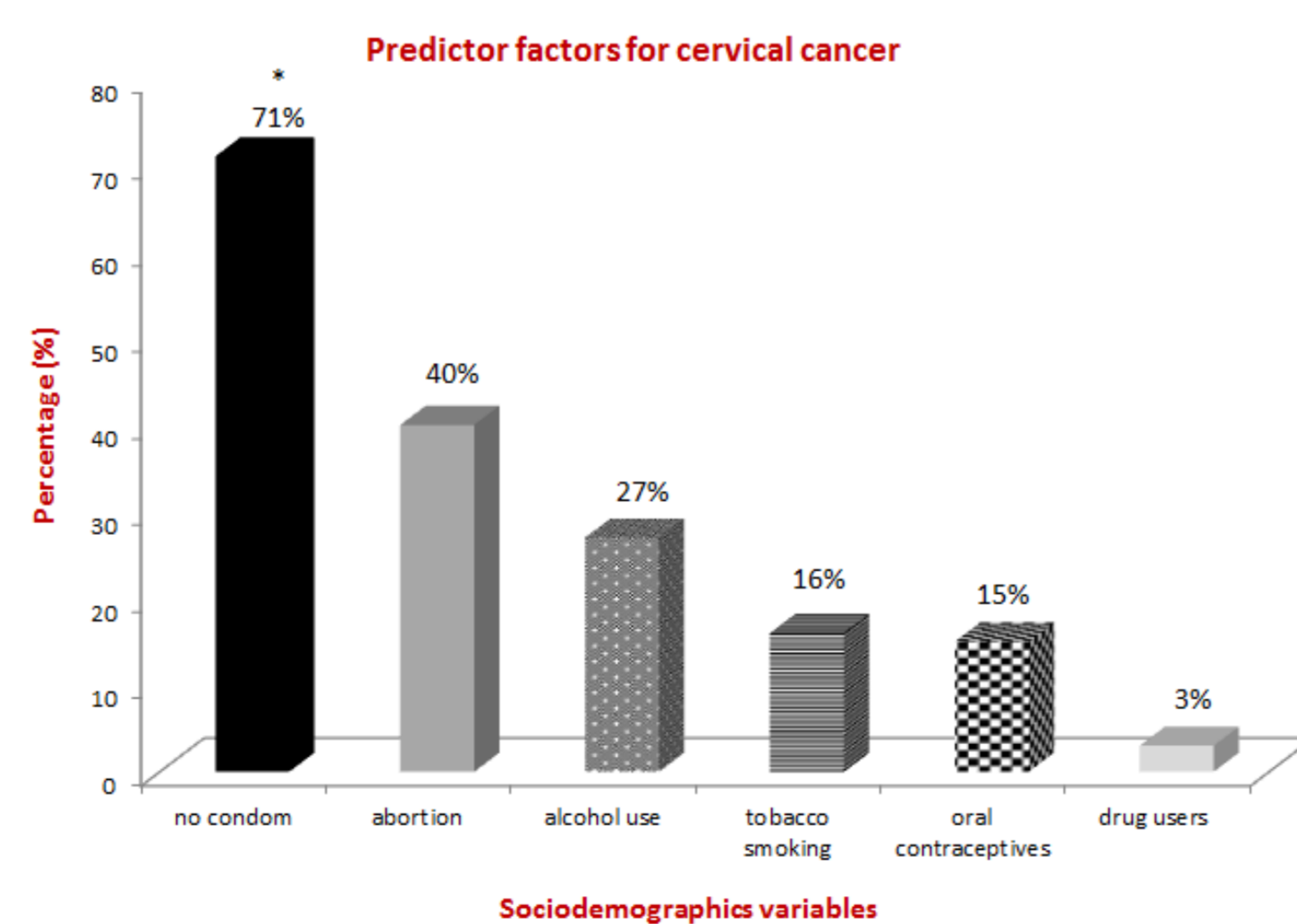
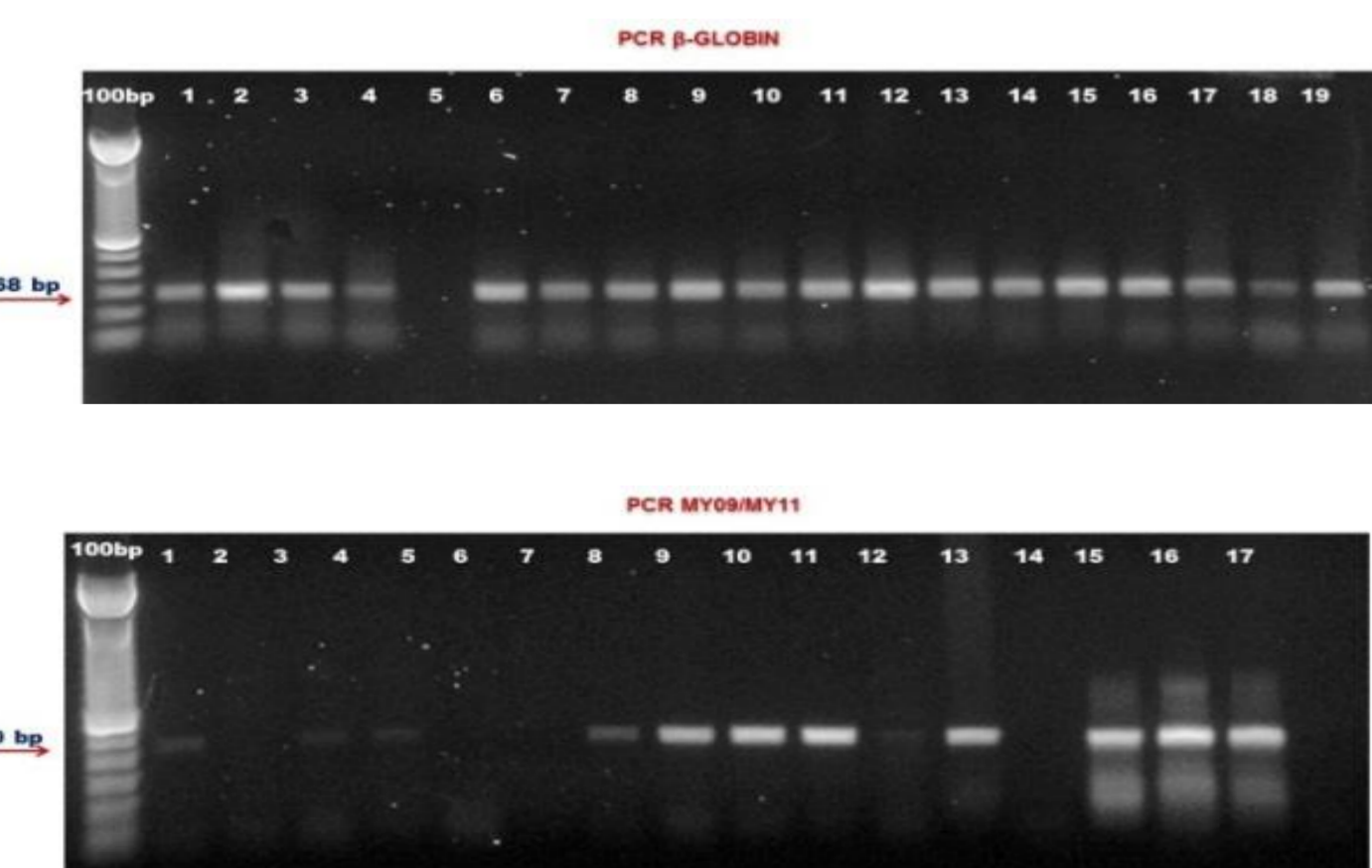
Primers	Sequence (5'-3')	Amplicon
PC04	CAACTTCATCCAGGTCACC	268 bp
GH 20	GAAGAGCCAGGACAGGATC	
MY 09	CTCCARRGGAACTGATC	450 bp
MY 11	GMCACGGGWCATATAAATGG	
FAP 59	TAAGCTGGGCAATCCAT	478 bp
FAP 64	CCWATATCWHATTCCATC	
GP 5+	TTGTACTGTGTGATGATC	150 bp
GP 6+	GAATAAATACTGTAAATCATTTC	
HPV 16	TAGGCTCGAGAAATTTTC	325 bp
HPV 18	CATTGTTGGGTAACCAAC	
HPV 31	TAAGCTAAAGAAATTTTC	425 bp
HPV 18	TGTTCTCGGATAATCAT	
HPV 31	CTAAATCTCGGAAATTTTC	514 bp
HPV 31	TATTGTTGGGCAATCAG	
HPV 45	TAGGTCACCACTCCAAATTTA	475 bp
HPV45	TAAATAGGCATATGTTACATAAG	

HPV type	DdeI	HaeIII	PstI	RsaI
HPV 16	452	444	216	310
Uncut: 452bp	8	210	72	70
HPV 18	432	455	242	135
Uncut: 450bp	23	213	125	85
			72	38
HPV 31	385	328	218	360
Uncut: 452bp	90	124	210	72
	77		28	
HPV 45	324	447	242	338
Uncut: 450bp	131	8	213	72
				45

### RESULTS AND CONCLUSIONS

Twenty percent of the samples were PCR-positive for cervical HPV was confirmed. HPV-18 was the most prevalent genotype (8%). About 16% reported being smokers and 3% drug users. Of all the participating women, 27% consume alcohol, 40% reported having had at least one abortion, 15% used oral contraceptives, while 71% did not use any type of condom ( $p < 0,03$ ). Most women were currently not married (56%), being 44% and married or cohabitating ( $p < 0,05$ ). This molecular epidemiological study estimates a high prevalence of HPV unimmunized women and it may be to contribute for the optimization of prevention strategies.



### FINANCIAL SUPPORT