

Raisa C. S. Raulino¹, Juliana D. Siqueira¹, Adriana C. Branco¹, Brunna M. Alves¹, Esmeralda A. Soares¹, Hector N. Seuánez^{2,3}, Gulnar A. Silva⁴, Marcelo Alves Soares^{1,3}

¹Programa de Oncovirologia, Instituto Nacional de Câncer, Rio de Janeiro, RJ, Brazil; ²Programa de Genética, Instituto Nacional de Câncer, Rio de Janeiro, RJ, Brazil;

³Departamento de Genética, Universidade Federal do Rio de Janeiro, Rio de Janeiro, RJ, Brazil; ⁴Universidade Estadual do Rio de Janeiro, Rio de Janeiro, RJ, Brazil.

INTRODUCTION

Human papillomavirus (HPV) infection is the most common sexually transmitted disease worldwide and represents a major public health problem because of its high prevalence and transmissibility. The prevalence of HPV infection among women varies between different regions of the world and of Brazil. Virus infection is a necessary factor, but not enough, for the development of cervical cancer. This type of cancer is the second most frequent type among women, and presents a greater potential of prevention and cure when diagnosed early. HPV is a small double-stranded DNA viruses infecting human epithelial cells, and more than 200 genotypes ('types') are known, which are divided into low-risk or high-risk groups depending on their oncogenic potential. The identification of the infecting HPV types is very important, since different types have distinct roles in carcinogenesis. In addition, simultaneous infection with multiple HPV types and persistence of HPV infection are two risk factors that contribute to the development of cervical dysplasia. Reverse hybridization kits are capable of detecting several types of HPVs among high- and low-risk genotypes, through amplification with specific primers. The aim of this study is to analyze follow-up samples of women attended by the Family Health Strategy (FHS) in Juiz de Fora, MG, in order to evaluate and compare the results regarding HPV diversity five years after the first study, a period that included the implementation of the HPV vaccine.

METHODOLOGY

The main study of this subproject was approved by the Ethics Committee of the Institute of Social Medicine of the University of the State of Rio de Janeiro (UERJ), according to CAAE 8067815.2.0000.5260 / opinion number 1.323.441, and followed all the proposed recommendations.

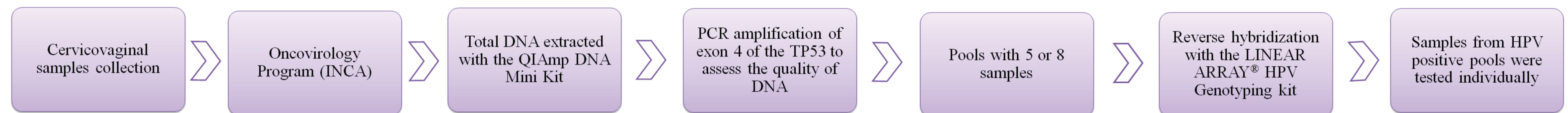


Figure 1. Flowchart

RESULTS

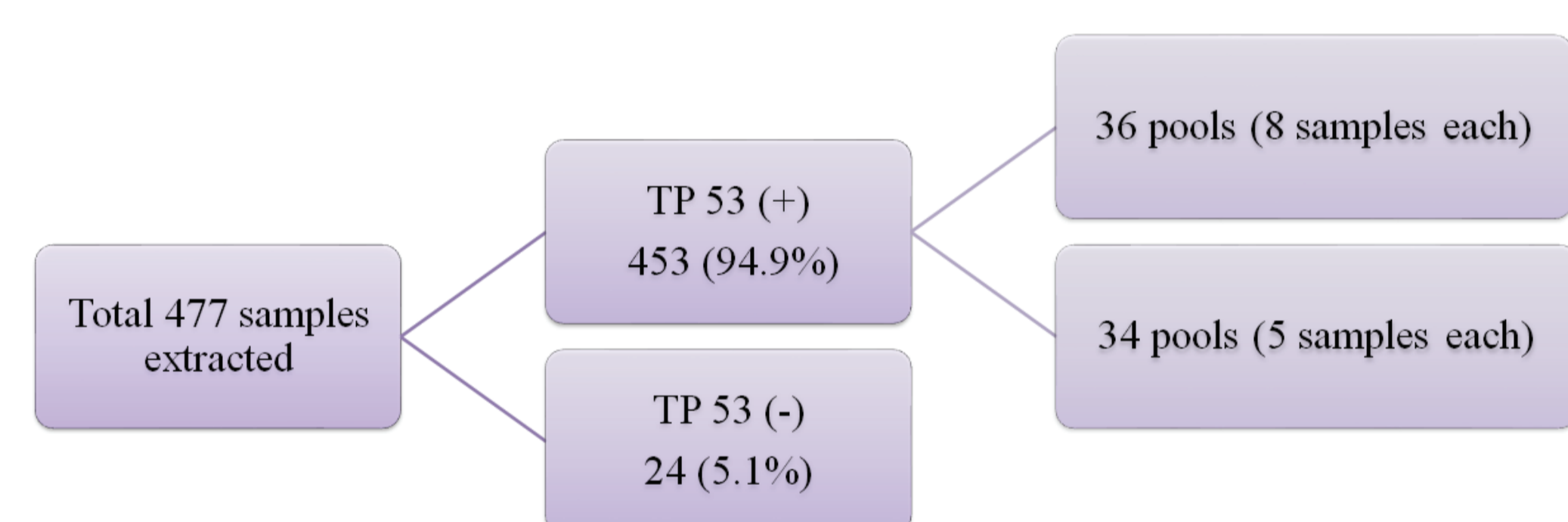


Figure 2. Flowchart of sample collection and processing

Overall, 16 pools (22.8%) were positive, and until present samples from 6 positive pools have already been tested.

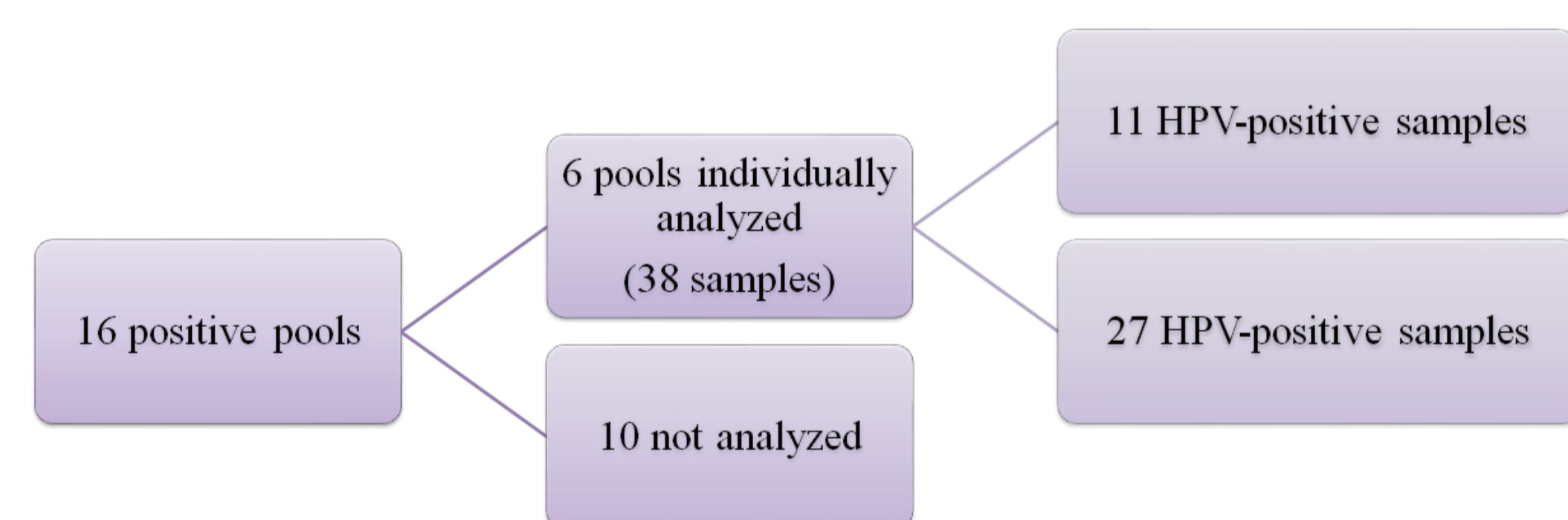


Figure 3. Flowchart of HPV-positive sample analysis

Table 1. HPV type distribution in positive pools

POOLS (+)	N° of samples	HIGH-RISK	LOW-RISK
P3	5	59	-
P5	5	16	-
P6	5	31/52/59	53
P11	5	33	-
P23	8	16/52/58	-
P27	8	16	-
P30	8	52	61/81/83/84
P37	8	59/53	-
P38	8	-	81
P45	5	-	62
P51	5	52/58	-
P54	5	52/33/35/58	61
P55	5	52	61
P56	5	-	84
P57	5	16	62
P58	5	18/45	-

Highlighted are the pools that the samples were tested individually

Table 2. HPV type distribution in positive samples

SAMPLES	HIGH-RISK HPV types*	LOW-RISK HPV types#
ID 184	58	-
ID 185	16/45	-
ID 186	33/35	-
ID 216	16/59	54/70/89
ID 217	-	61
ID 241	16	6/61/83/84
ID 245	52	81
ID 296	-	70
ID 297	53/59	-
ID 299	16	81
ID 300	35	-

*Probably high-risk HPV types are in the high-risk column; # HPV types with undetermined risk are in the low-risk column.

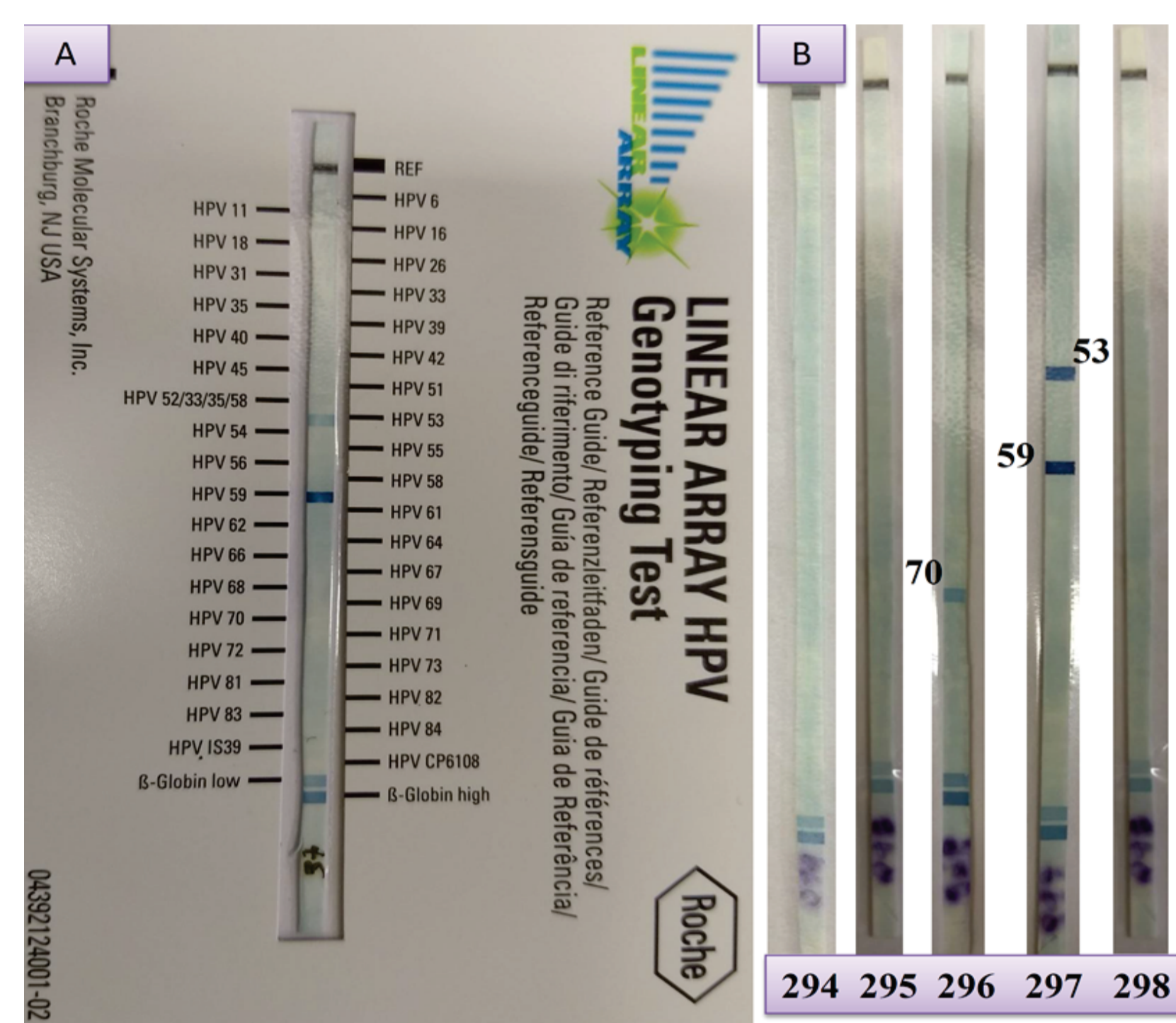


Figure 4. Representative results with LINEAR ARRAY® HPV kit Genotyping: Panel A, result of pool 37 (5 samples). Panel B presents results from the individual analysis of samples contained in the pool 37.

Table 3. HPV prevalence and type distribution in single and multiple infections

HPV PREVALENCE/TYPE	N, %		
HPV-NEGATIVE	27/38 (73.6)		
HPV-POSITIVE	11/38 (26.3)		
	SINGLE	MULTIPLE	TOTAL
	4/11 (36.3)	7/11 (63.6)	11 (100)
High-risk HPV			
16	0	4	4 (36.3)
33	0	1	1 (9.0)
35	1	1	2 (18.1)
45	0	1	1 (9.0)
52	0	1	1 (9.0)
58	1	0	1 (9.0)
59	0	0	2 (18.1)
Probably high-risk			
53	0	1	1 (5.8)
Low-risk HPV			
6	0	1	1 (9.0)
54	0	1	1 (9.0)
61	1	0	1 (9.0)
70	1	1	1 (5.8)
81	0	2	2 (18.1)
83	0	1	1 (9.0)
84	0	1	1 (9.0)
89	0	1	1 (9.0)