

Advances in Clinical and Medical Research

Genesis-ACMR-3(1)-23
Volume 3 | Issue 1
Open Access

Gene Associated and Risk Factor of HPV Wharts: A Review Article

Gofur NRP^{1*}, Gofur ARP², Soesilaningtyas³, Gofur RNRP⁴, Kahdina M⁴ and Putri HM⁴

¹Department of Health, Faculty of Vocational Studies, Universitas Airlangga, Surabaya, Indonesia

²Faculty of Dental Medicine, Universitas Airlangga, Surabaya, Indonesia

³Department of Dental Nursing, Poltekkes Kemenkes, Surabaya, Indonesia

⁴Faculty of Medicine, Universitas Airlangga, Surabaya, Indonesia

***Corresponding author:** Gofur NRP, Department of Health, Faculty of Vocational Studies, Universitas Airlangga, Surabaya, Indonesia

Citation: Gofur NRP, Gofur ARP, Soesilaningtyas, Gofur RNRP, Kahdina M, et al. (2021) Department of Health, Faculty of Vocational Studies, Universitas Airlangga, Surabaya, Indonesia. 3(1):1-9.

Received: January 04, 2022 | **Published:** January 24, 2022

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Abstract

Introduction: HPV can infect basal epithelial cells of the skin or deep tissue and are categorized as either skin type or mucosal type. This skin type is epidermotropic and infects the surface of the keratinized skin, targeting the skin of the hands and feet. The type of mucosa that is infected is the lining of the mouth, throat, respiratory, or anogenital tract epithelium. The direct correlation between the number of sexual partners and the presence of HPV was shown to be independent of other risk factors such as age, race or use of oral contraceptives as well. Several genes and risk factors have been associated with genital HPV infection. The purpose of this review is to determine the genes and risk factors for Wharts.

Discussion: Detection of various genital HPV as many as 28 types that have been identified so far can use various methods. Identification of viral DNA or RNA by various hybridization techniques. Time to analyze the results is also very important to know the validity of the different HPV techniques, the sensitivity, specificity, and the spectrum of HPV types detected. Southern Blot hybridization is still used as the standard for DNA identification of various types of HPV. However, between 5000 and 50 000 copies of HPV DNA must be present in a clinical sample to be detected.

Conclusion: The seroprevalence of other types, including 18, 31, 33, 39, 58, and 59, ranging from 9% to 23%. In addition to VLP, HPV DNA is also most common in women under 25 years of age prevalence tends to peak in women over 25 years of age using HPV antibodies. Number of sexual partners was recognized as an independent risk factor for genital HPV infection in patients with immunosuppression will also be a risk factor for HPV infection, for example

in patients with autoimmune, HIV infection and organ transplantation.

Keywords

Gene; Riskfactor; HPV infection; Wharts disease

Introduction

HPV can infect basal epithelial cells of the skin or deep tissue and are categorized as either skin type or mucosal type. This skin type is epidermotropic and infects the surface of the keratinized skin, targeting the skin of the hands and feet. The type of mucosa that is infected is the lining of the mouth, throat, respiratory, or anogenital tract epithelium. Some HPVs are associated with transient warts whereas other manifestations may be risk factors for invasive cervical cancer and precancerous lesions. Currently, more than 150 types of HPV have been identified and about 40 can infect the epithelial lining of the anogenital tract and other mucosal areas of the human body [1].

The incidence rate of genital warts in Canada also increased significantly, 43,586 EGW events from 1999 to 2006, finding that the overall incidence slightly increased from 1.07 per 1,000 population in 1999 to 1.26 per 1,000 population in 2006. Overall incidence between years 1999 and 2006 were always higher in men than women, being 1.31 per 1,000 population in men and 1.21 in women. Both decline gradually with age. However, several studies have noted an increase in HPV infection in women after age 50 [2].

Transmission of HPV infection can be through two events, through direct sexual contact or without sexual contact. For condylomata acuminata the interval between exposure and clinical appearance of disease ranged from 3 weeks to 8 months. Incubation period data for subclinical and latent infection are unknown. The direct correlation between the number of sexual partners and the presence of HPV was shown to be independent of other risk factors such as age, race or use of oral contraceptives as well. Several genes and risk factors have been associated with genital HPV infection. The purpose of this review is to determine the genes and risk factors for Wharts [3].

Methods

A descriptive, cross-sectional, observational study in families of patients diagnosed with current SARS-CoV-2 infection. It was held at the facilities of the medical campus of the Autonomous University of Nuevo León, Mexico, from July to September 2020. Families of patients who had nuclear, extended, or single-parent family typology was included whose patient was present with SARS-CoV-2 infection was older than 18 years with and without comorbidities. Families of patients who were hospitalized or who had died from SARS-CoV-2 were not included.

Data Collection

1. FACES III questionnaire and was applied by medical personnel of the research team, in electronic format through Google Forms questionnaires who received training on:

- Conceptual aspects of family systems
- Instrument administration training. The training includes the self-application of FACES III.
- Protection measures under current sanitary recommendations.

The FACES III instrument, a self-applied scale of 20 Likert-type items with 5 options; 1 = never, 2 = almost never, 3 = sometimes, 4 = almost always, 5 = always. The instrument is validated in Spanish (37), achieving reliability of 70% and a Cronbach's alpha = 70%. This instrument has 8 questions for cohesion, corresponding to odd items, and 6 for adaptability, even items.

The total score of the instrument consists of the total sum of the cohesion and adaptability reagents where they are collated according to (Table 1). The results will be mapped in the matrix of (Table 2) to classify the family.

Cohesion	Classrange	Adaptability	Classrange
Unlinked	10-34	Rigid	10-19
Sem-linked	35-40	Organized	20-24
Linked	41-45	Flexible	25-28
Agglutinated	46-50	Chaotic	29-50

Table 1: Cohesion and adaptability classification.

		Adaptability			
		Rigid	Organized	Flexible	Chaotic
Cohesion	Unlinked	Rigid-unlinked	Organizedunlinked	Flexible unlinked	Chaoticunlinked
	Semi-linked	Rigidsemi-linked	Organizedsemi-linked	Flexible semi-linked	Chaoticsemi-linked
	Linked	Rigidlinked	Organizedlinked	Flexiblelinked	Chaoticlinked
	Agglutinated	Rigidagglutinated	Organizedagglutinated	Flexible agglutinated	Chaoticagglutinated
		Balanced	Intermediate	Extreme	

Table 2: Family class matrix.

Sociodemographic information was obtained from the subjects consisting of age, sex, education, marital status, type of economic income, place of residence, family structure, type of location, and degree of severity of the patient infected with SARS-CoV-2. The sample size from an infinite population was 99

patients with a precision of 10%, a power of 97.5%, and a significance level of 0.05. Verbal informed consent was applied to the relatives of patients for participation in the study.

Statistical Analysis

The IBM SPSS program was used in its most recent version for Windows where the frequencies of the different variables studied were calculated. Description of family functionality based on the 3 most common types of families (Nuclear, Extensive and single parent). The frequency of the families of patients infected with SARS-CoV-2 and their classification according to (Table 3) in the total population and for each age group was analyzed. Chi-square will be used to assess the association between the different categorical variables, being a significant value of $p < 0.05$ with a CI = 95%. The frequency of socio-demographic data was analyzed by sex and age group.

Variable	
Age (years)	33.2 ± 13.7
Sex	
Male	49 (50%)
Female	49 (50%)
Schooling	
Elementary	2 (2%)
Junior High	6 (6.1%)
Highschool	14 (14.3%)
College	76 (77.6%)
Civil status	
Single	56 (57.1%)
Married	38 (38.8%)
Divorced	3 (3.1%)
Common partner	1 (1%)
Economic input	-
Fixed employment	61 (62.2%)
Self employment	18 (18.4%)
Casual employment	12 (12.2%)
Retired	7 (7.1%)

Table 3: Sociodemographic characteristics.

Results

98 patients diagnosed with COVID-19 were surveyed. The mean age of the patients was 33.2 ± 13.7 years, 49 (50%) were women and 49 (50%) men. Most of the patients had a bachelor's degree (77.6%) and were single (57.1%) or married (38.8%). Most of the patients had a permanent job (62.2%) or their own (18.4%). The characteristics of the patients are summarized in (Table 3). By a relationship, the most

frequent type of family was simple nuclear in 71 (72.4%) patients, followed by extended family in 13 (13.3%) and single-parent in 8 (8.2%). All the patients belonged to an urban family (Table 4).

Family classification	
By relation	
Nuclear family	71 (72.4%)
Extended	13 (13.3%)
Monoparental	8 (8.2%)
Nuclear	3 (3.1%)
Monoparental extended	1 (1%)
Monoparental extendida composed	1 (1%)
Non parental	1 (1%)
By demography	
Urban	98 (100%)
Rural	0 (0%)

Table 4: Family classification.

According to the severity of the disease, most of the patients had the mild disease (64.3%), followed by moderate disease (20.4%) (Table 5).

Disease severity	
Asymptomatic	9 (9.2%)
Slight	63 (64.3%)
Mild	20 (20.4%)
Severe	6 (6.1%)

Table 5: Disease severity.

According to the FACES III instrument, by cohesion, the most frequent type of family was the related family in 42.9%, and the least frequent, the unrelated family (12.2%); and due to adaptability, the most frequent was the chaotic family in 54.1%, and the least frequent, the rigid one (4.1%) (Table 6).

The relationship of the type of family by kinship with the type of family by cohesion and adaptability, no statistically different relationship was found ($p = 0.957$ and $p = 0.78$, respectively) (Table 7).

No relationship was found between the severity of the COVID-19 disease and the cohesion and adaptability of the family according to FACES III ($P = 0.34$ and $P = 0.184$, respectively) (Table 8).

FACES III	
Cohesion	
Score	41.3 ± 5.3

Family class	
Unlinked	12 (12.2%)
Semi-linked	23 (23.5%)
Linked	42 (42.9%)
Agglutinated	21 (21.4%)
Adaptability	
Score	29.0 ± 5.6
Family class	
Rigid	4 (4.1%)
Organized	12 (12.2%)
Flexible	29 (29.6%)
Chaotic	53 (54.1%)

Table 6: FACES III results.

	Nuclear	Monoparental	Extended	P
Cohesion				0.957
Unlinked	9 (12.2%)	1 (10%)	2 (14.3%)	
Semi-linked	17 (23%)	2 (20%)	4 (28.6%)	
Linked	33 (44.6%)	5 (50%)	4 (28.6%)	
Agglutinated	15 (20.3%)	2 (20%)	4 (28.6%)	
Adaptability				0.78
Rigid	3 (4.1%)	0 (0%)	1 (7.1%)	
Organized	11 (14.9%)	1 (10%)	0 (0%)	
Flexible	21 (28.4%)	3 (30%)	5 (35.7%)	
Chaotic	39 (52.7%)	6 (60%)	8 (57.1%)	

Table 7: Association between Family classification and FACES III class.

	Asintomático	Leve	Moderado	Severa	P
Cohesion					0.34
Unlinked	1 (11.1%)	7 (11.1%)	4 (20%)	0 (0%)	
Semi-linked	4 (44.4%)	14 (22.2%)	3 (15%)	2 (33.3%)	
Linked	2 (22.2%)	32 (50.8%)	6 (30%)	2 (33.3%)	
Agglutinated	2 (22.2%)	10 (15.9%)	7 (35%)	2 (33.3%)	
Adaptability					0.184
Rigid	2 (22.2%)	1 (1.6%)	1 (5%)	0 (0%)	
Organized	0 (0%)	10 (15.9%)	2 (10%)	0 (0%)	
Flexible	2 (22.2%)	17 (27%)	7 (35%)	3 (50%)	
Chaotic	5 (55.6%)	35 (55.6%)	10 (50%)	3 (50%)	

Table 8: Association between FACES III class and disease severity.

Discussion

During the SARS-CoV-2 pandemic, the objective was to determine the level of cohesion and adaptability of the family of the patient infected with SARS-CoV-2. Family dynamics is a process that on many occasions can result in changes in its structure and functioning secondary to situations that act as generators of stress [15].

The accumulation of stressful situations in the family can produce unhealthy behavior patterns that can threaten the integrity of the family [16]. Families should receive interventions to reinforce adaptive behaviors and deflect unhealthy behaviors that lead to maladaptive [18]. No association was found between the family type by kinship and the severity of the COVID-19 disease with the adaptability and cohesion of the family, however, as an interesting finding in our work. We found a tendency for cohesion and high adaptability, being for cohesion related and agglutinated, and for adaptability, flexible and chaotic. It was not found that the type of family and the severity of the disease increased cohesion or adaptability in any way, however, we observed that in the population with SARS-CoV-2 infection there could be an increase in both, with a tendency to agglutination and chaos, to be able to handle the family situation through which it happens, in the middle of a global pandemic crisis. A comparative study is proposed to investigate the effect on the family. There is an emotional impact on the family after the presence of critically ill patients in the nucleus, mainly with the increase in the stay in intensive care [19]. In the case of the COVID-19 pandemic, an important role of physical distancing has also been observed in family dynamics, in such a way that there has been a decrease in support from formal and informal networks, a climate of sustained tension, and distribution of inequitable roles with female overload, the recurrent appearance of conflicts and changes in daily routines. In other diseases, such as HIV infection, there has been a trend towards less family cohesion, but greater adaptability and rigid and unrelated families have a poorer quality of life [20]. However, in this type of infection, due to its chronicity, the family has the opportunity to prepare for the possibility of fatal outcomes.

Contrary to this, in the case of abrupt diagnoses, there may be some type of arrangement of family dynamics similar to that presented by the COVID-19 disease, especially depending on the severity of the association of the infection. Similar to our work, AlviaMacías et al. have found that in diarrheal diseases, the agglutinated-chaotic family tends to prevail over the other family types and that the type of family cohesion and adaptability correlates with the level of knowledge of diarrheal diseases, so there may be some modification of family dynamics through educational interventions for the family [21].

In an earlier study by Clover et al., It has been found that family dynamics and family dysfunction can increase the prevalence of infections, such as influenza B infection, with the hypothesis that family dysfunction can alter the immune response, increasing the susceptibility of infection [20]. This may be relevant, especially in a scenario before the COVID-19 infection, because more than the response to the infection that a person can present, -since- the family can influence the health measures that are applied, promoting greater support in the family and the activation of family resources.

Conclusion

According to the family typology, by kinship, the main types of families identified in patients with COVID-19 disease were simple nuclear in 72.4%, followed by extended family in 13.3% and single parent in 8.2%. All the patients belonged to an urban family. We found 63.3% of patients with mild severity of COVID-19 disease, 20.4% with moderate severity, 6.1% severe, and 9.2% were asymptomatic.

We observe a greater tendency towards the type of family with high cohesion and adaptability, being by cohesion related and agglutinated, and by adaptability, flexible and chaotic, however, we did not find any association between the family type by kinship and the severity of the COVID-19 disease with the adaptability and cohesion of the family. The role of the family doctor in family support and the application of family interventions from the diagnosis of the disease, the follow-up, the recovery, and later is important, given the enormous psychosocial impact that the disease entails and the degree of stress and anxiety involved, as well as the relationship that the disease has on rearrangements in family dynamics and functionality.

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