

# Chapter 3

## Genomic Epidemiology of Human Papillomavirus (HPV), Prostate Cancer, and Diabetes

### ABSTRACT

*Risk factors associated with prostate cancer were explored. The gene chromosomes which code for prostate cancer were discussed. The physical and financial implications of this disease were outlined and the interventions to prevent the onset of this disease were comprehensively discussed. HPV is a major life threatening sexually transmitted infection in United States. The disease is predominantly common among minority ethnic groups. If left untreated, HPV can become life threatening when it converts to cervical cancer. The primary preventive mechanism such as abstinence education and other primary preventive use of condom are known to convert the impact of this disease.*

### PART I: GENOMIC EPIDEMIOLOGY OF PROSTATE CANCER AND HPV

#### Introduction

Having read this chapter, the student should be able to:

- Explain specific genes' official symbols;
- Discuss the epidemiological web of causation of human papillomavirus (HPV);
- Outline the use of abstinence and comprehensive sex education to prevent HPV;
- Explain specific genes' official symbols for prostate cancer;
- Trace the role of family history as non-modifiable risk factor for prostate cancer;
- Document use of phytochemical nutrients in preventing the incipient stage of prostate cancer;
- Explain specific genes' official symbols for diabetes;
- Discuss the modifiable and non-modifiable risk factors for diabetes; and
- Illustrate the crucial reasons for using theoretical models by prevention research scientists.

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Epidemiological studies have identified HPVs as small, double-stranded DNA viruses that infect the cutaneous and mucosal epithelial tissues in multiple anogenital, skin regions, and the tracheobronchial and oral mucosa, principally due to oral sexual intercourse. Scientists argue that more than 100 types are diagnosed based on the genetic sequence of the outer capsid protein L1. The other 40 types infect the mucosal epithelium (Centers for Disease Control and Prevention [CDC], 2009). Reports from the CDC (2009) also revealed that 90% of cervical cancers are positive for HPV DNA and the subset of HPVs which are recognized as high-risk (HR) variant. These include HPV16 and HPV18, which are associated with cancer development (Muto et al., 2012). HPV is not only one of the over 100 viruses serving as the etiological agents of warts, but also for the majority of HPVs induced warts on the face, and fingers. High frequencies of HPV are confined to the genitalia, while others are commonly identified as the causative agents of cancer of the cervix and the anogenital regions. Predominantly, the HPVs associated with wart-like growth in the genitalia area is usually sexually transmitted.

The American Cancer Society (Adams et al., 2009) has estimated incidence of cervical cancer disease burden in United States alone to be 11,070 cases, with 3,870 deaths. Almost 100% of these cervical cancers cases are caused by one of the 40 HPV types which infect the mucosa region. Besides, the anogenital HPV is not only the most common sexually transmitted infection in the United States, but has a prevalence of an estimated 20 million among the sexually active patients. Currently, the incidence of 6.2 million cases occurs annually. Statistically, an estimated 80% of sexually active women are most likely infected in United States by age 50. The sexually active males are equally at risk of infection (CDC, 2009). Global epidemiological report on cervical cancer ranks this disease as the second most common cause of cancer death in American women, with an estimated 510,000 newly diagnosed cervical cancer with death rate of over 288,000 cases in the developing nations (Saslow et al., 2007).

## **Morbidity and Mortality of HPV Worldwide**

Modern epidemiological studies have revealed HPV as the most common sexually transmitted infection (STI) in the world. It is estimated at least 50% of sexually active individuals are at one time infected by at least one variant of HPV. Innovative genome mapping indicates more than 75% of HPV variants are recognized out of which 40 of them infect the urogenital area. HPV infects men and women in equal proportion; however, women are more likely to present more symptoms of the disease.

HPV is the causative agent of over 90% of all cervical cancers the second leading cause of death of women worldwide. Statistically, 1%–5% of women infected with HPV usually develop malignancies. In many patients, HPV is associated with genital warts and about 1%–2% of sexually active individuals experience visible genital warts infections. Advanced innovative genomic science continues to reveal copious scientific data on HPV. But in the resource-challenged developing nations, there is a dearth of knowledge, and so much to learn about the genomic spectrum, transmission patterns and infectivity of HPV in the developing and least-developed parts of the world (Bosch et al., 1995). In view of the lethal consequences of HPV and the associated morbidity in women of child-bearing age, we have used the health belief model (HBM) to explicate the exposure of at-risk population to HPV.

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