Overview of Fellowship Project:
Infection with Human Papillomavirus (HPV) is known to play a central role in the development of cervical cancer [1,2]. Polymorphisms in the promoter region of the TNF-α gene have been associated with high (SNPs -307) and low (SNPs -237) cytokine production, and these functional differences may modulate the magnitude of immunological response following HPV infection but results are contradictory [3-11]. The province of Misiones (Argentina) is considered a region with a high prevalence of cervical carcinoma (12/100,000) compared to the urban areas of the country (Buenos Aires 3/100,000) [12-14]. Within Misiones, different ethnic groups inhabit specific regions of the province. The Guaraní Indian populations are concentrated in small communities in the rain forest, while the white populations (with a wide range of parental genetic contributions from Europe) live in the urban and rural areas [15-17].

The goal of this project was to analyze genetic variation in the TNF-α promoter (SNPs -237, -243, -307, -375) and examine its potential association with HPV infection and cervical cancer among different ethnic groups from Misiones. To this end, we have analyzed a sample of 123 urban and rural women (admixed populations of European descent) and compared the data with previous work involving American Indians from the region [18]. This approach has allowed us to undertake risk analysis in different ethnic groups. Polymorphisms in this gene were determined through PCR amplification and direct sequencing [18]. Our results showed no association between the presence of the -307 and -237 SNPs and HPV infection. However, the SNP distribution was statistically significantly different between study populations. In particular, we observed low genetic diversity in Amerindians that may be a result of small population size and random genetic drift associated with their particular history, cultural and geographical isolation. This study of human genetic variation in the TNF-α gene has provided new information about the genetic differences among Misiones populations. These differences may help us to better understand the role of genetic factors in the development of disease.

All work completed during the Fellowship period is being prepared for submission to a peer-reviewed journal.
ranks among the top 10 universities in the USA and, with more than 150 research centers and institutes on campus, offers a great opportunity for interdisciplinary study. During my fellowship, I had the opportunity to attend several seminars, workshops and lab meetings, as well as informal brainstorming sessions with members of the laboratory. Moreover, since the Annual Meeting of the American Society of Human Genetics was held in Philadelphia this year, I had the unique opportunity to attend to this important event. Besides the academic opportunities, the beautiful urban campus of UPenn, rich in green open spaces, museums, public art and architecture, made my stay a pleasant experience. I was privileged to meet the lab staff of Dr. Schurr, and, with their help, developed the skills to perform the experiments and enhance my understanding of human population genetics analysis. It was, indeed, a very productive experience. The Fellowship has enriched me in several ways, and I would like to thank the ISID for supporting this project.

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References: