Biog5: A bioinformatic system for the analysis of the Human Papillomavirus

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BACKGROUND

Human papillomavirus (HPV) is classified according to its oncogenic potential into different types of risk which are low, high and undetermined. Currently, there are more than 100 different types but just the most prevalent and high-risk ones (nine of them) are currently covered by available vaccines. In addition, there are several less common strains that can still cause cancer and be resistant to vaccines.

Biog5 is a tool that integrates multiple computational biology and bioinformatics tools to find correlations between all requested HPV strains in sequence analysis and structural data of L1, L2, E1, E2 and E7 proteins. This allows us to assist in diagnostic and outbreak investigations to address the virulence and likelihood of vaccine resistance of the less prevalent strains.

RESULTS

Biog5 uses public databases and alignment algorithms, Hidden Markov Models, phylogenetic trees, and conservation analysis to predict whether a selected HPV strain can cause a serious health condition and whether available vaccines might be effective.

Component testing on HPV strains of well-known phenotypes yields correct classification to risk groups and high similarity between strains of the same group.

CONCLUSIONS

The trend and accessibility of sequencing technologies hint at their potential use within our healthcare systems. With this in mind, Biog5 was conceived as a tool that could be useful, for example, in epidemiological surveillance, that is, for the planning, implementation and evaluation of public health programs based on the phenotypes of local HPV strains. In addition, it could also be used in patients with HPV, for the prognosis of the outcome of the disease.