EXECUTIVE SUMMARY of MSS243R

Characterization of the pattern and trends of HIV spread among newly diagnosed patients in Hong Kong

Objectives

With the aim of characterizing the risk of HIV spread in Hong Kong, this study involves the epidemiologic analyses of data derived from newly diagnosed HIV patients, with the objectives of: (a) defining the current pattern of HIV spread; (b) tracking the longitudinal trend of spread; and (c) assessing the population risks of subsequent dissemination in the medium term.

Project design

Between July 2016 and Dec 2019, newly diagnosed HIV positive patients were recruited from major HIV specialist clinics in Hong Kong for participation in the study. Enrolled patients were invited to complete a questionnaire survey to capture their behavioural and social network profiles shortly after one's diagnosis, supplemented by the transcription of anonymised clinical data. Blood samples were collected from recruited patients for molecular studies. With the collected data, epidemiologic analyses were conducted. Molecular clustering of HIV was explored, and modelling was performed to assess the effectiveness of measures for controlling the spread of HIV in Hong Kong.

Target population

HIV positive patients

Main results

The study has enrolled over 500 newly diagnosed HIV positive patients in Hong Kong. Between 2016 and 2018, the 2 major HIV subtype were B and CRF01_AE. The pattern of HIV virus diversity has changed over the years. Younger men who have sex with men (MSM) have been driving the ongoing epidemic, while chemsex, referring to the sexualised use of drugs, had contributed to new infections in recent years. Network clusters with newly diagnosed cases had a higher transmission speed and a wider age difference, signifying the presence of disassortative mixing by age. Newly diagnosed cases linking with past infections were more likely subtype B and younger. Newly diagnosed HIV positive MSM linking with past ones were less likely engaged in chemsex. Past infections linking new cases were younger, and were more connected in networks. Modelling results supported the hypothesis that sexual activity and the resultant HIV transmission were product of individual's networking pattern and preferences of sex partners. In terms of HIV prevention strategies, targeting MSM engaging in chemsex, gay dating app users, and those diagnosed with STI would be more effective than a non-targeted approach.

Conclusions

Through the adoption of an inter-disciplinary approach, the study has enabled the projection of Hong Kong's HIV epidemiologic patterns. The study results could be used for informing the development of evidence-based interventions

香港新感染愛滋病病毒人士的傳播趨勢和特徵

目標

本研究以新診斷愛滋病毒感染者的數據進行流行病學分析，從而表徵病毒在香港傳播的風險。目標是：（a）確定當前愛滋病毒傳播的方式；（b）追踪其傳播的縱向趨勢；（c）為病毒在人群傳播的風險作中期評估。

項目設計

在 2016 年 7 月至 2019 年 12 月之間，研究組在香港主要的愛滋病專科診所招募新診斷愛滋病毒感染者，邀請參加研究項目。受邀感染者需要填答一份問卷，用以收集個人行為和社交網絡概況數據，輔以轉錄匿名臨床數據，並收集參加者的血液樣本進行分子分析。數據在收集後經過整理，進行了流行病學分析。研究並包含探索愛滋病毒的分子簇，及進行建模以評估控制愛滋病毒在香港蔓延的措施的有效性。

目標人群

愛滋病毒感染者。

主要結果

研究項目在香港招募了 500 多名新診斷的愛滋病毒感染者。在 2016 年至 2018 年之間，本地兩種主要的愛滋病毒亞型分別是 B 和 CRF01_AE。多年來，愛滋病毒的多樣性模式已經改變。年輕的男男性接觸者（MSM）推動了愛滋病毒的流行，而 chemsex（指因性行為使用毒品）的普及，成為近幾年病毒傳播的因素。新診斷病例的網絡集群具有更高的傳播速度和更大的年齡差異，表明存在年齡差距的混合情況。與過往感染有關的新診斷者更有可能是 B 型，並且年齡較輕。新診斷受愛滋病毒感染的 MSM，較少與過去已診斷的 MSM 相關聯。過去已感染者如果與新病例相關，其年齡一般較輕，並且在網絡中的聯繫更加緊密。建模研究結果支持以下推斷：性活動和愛滋病毒傳播，與個人網絡模式和某形式的性伴侶偏好相關。就預防愛滋病毒傳播而言，針對 chemsex 使用者，同性約會應用程序用戶以及 MSM 性病患者，比非針對性的預防方法更為有效。

結論

透過跨學科方法，本項研究提供了數據預測香港的愛滋病毒流行病學模式。研究結果可應用於循證干預的發展。