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Randomised recruitment in estimating genital human papillomavirus prevalence

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Authors' reply

We thank Dan Shan and colleagues for their letter highlighting the importance of representativeness when pooling data to generate prevalence estimates. The authors suggest that random sampling is the primary way of doing this. We would argue, as do others,[1] that representativeness can be achieved not only by means of representative sampling using appropriate methods, including randomisation, but also by interpreting studies' findings as generalisable on the basis of solid premises and scientific knowledge.

Our paper presents estimates of genital human papillomavirus (HPV) infection in the general population of men based on a meta-analysis.[2] We took great care to include only studies that

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were representative of the general male population, which in some cases meant including only a subsample of the study. Study methods and results were scrutinised to ensure there were sufficient sociodemographic and behavioural data to assess whether the study population differed in characteristics from the general male population and to check that there were no incentives that would skew participation towards individuals at high risk for HPV infection. Non-randomisation was one of the variables in our risk of bias score, and in our subgroup meta-analyses no difference was observed by risk of bias score. We also performed an influence analysis (data not published) and no influential studies were identified.

Shan and colleagues make reference to two studies included in our review. In neither study is there any reason to suspect that volunteer selection bias might have skewed the prevalence estimates upwards. One study[3] was conducted in men attending an outpatient clinic for reasons unrelated to HPV or other sexually transmitted infections, and the other[4] was a study of HPV prevalence and type distribution in men and women in the general population recruited through a media campaign. Both studies have large sample sizes (3690 and 2309 respectively), participation was voluntary, and there were no apparent incentives that might skew participation towards those self-identifying as being at high risk for HPV.

Our estimates, that almost one in three men worldwide are infected with at least one genital HPV type and around one in five men are infected with one or more high-risk HPV types, are consistent with previous observations and HPV natural history studies. We did not present these estimates as a cause for concern or alarm but as data to improve understanding of the disease burden and transmission risk of HPV and to highlight the importance of incorporating men in comprehensive HPV prevention strategies.

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