How Can Economic Models Inform Decision-making About Screening?
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Questions Asked by Audience Members

1. How would HPV vaccination coverage change the results of your model? (you mentioned it would change with vaccination coverage)

Increasing HPV vaccination coverage would decrease the number of HPV infections, and therefore would decrease the number of women travelling through the algorithm after the initial HPV test. This would likely decrease the costs/test difference between the two arms.

2. [A comment fyi, not a question] - I would like to point out that it would be more inclusive to refer to the population as women and other people with a cervix (e.g. trans men, non-binary people)

Thank you for raising this – we will bear this in mind, the reason we originally referred to women is because this is how it is referenced in the CCO screening guidelines.

3. How would you account for opportunities for prevention (e.g. vaccination, sexual health counselling)?

The visit to a healthcare provider to take the sample would not change if HPV primary screening is introduced, and wouldn't be affected by the choice of screening assay. All screening visits present an opportunity for prevention activities.

Changes to cervical cancer prevention should be modelled separately if these are likely to affect the HPV positivity at the start of the model. These are currently not accounted for in the probability data from HORIZON (or any of the other mRNA vs DNA head to head studies).

4. Current cost of HPV test is $90 per patient. The cost will decrease if brought on for a population but did the model give a benefit for what range of cost per test?

The model accounted for possible changes to the cost of an HPV test in the deterministic sensitivity analysis (the cost was varied by 20%).

5. Why were the positivity rates between DNA and RNA so different in the Horizon, Gast, etc. studies? Is this due to lower sensitivity of RNA vs. DNA? Studies show that these are similar but your tables show difference?

The positivity rates differ for two main reasons. First, the underlying prevalence of infection can differ across different populations, for example in different age groups and in different geographical locations. Second, the specificity of the tests is also different for different assays. This difference in specificity will yield different

numbers of positive test results. The test result may not reflect the true underlying infection status of a woman, particularly if the specificity is low. The sensitivity across assays is broadly similar based on the published literature.

6. Have you calculated the number of colposcopies needed to detect 1 CIN 3 comparing RNA and DNA algorithms (using extended genotyping)?

This model has not calculated the number of colposcopies needed to detect 1 CIN 3 between the two tests. However, it is likely to be fewer in the mRNA arm, particularly as any CIN that is not picked up by mRNA tests will be early stage or regressing CIN (as they will not be actively replicating).

7. Can you comment on differences in sensitivity between DNA vs. RNA?

The literature show that the sensitivity across assays that are approved for use as screening tests are all very high and broadly similar. In particularly, both types of assays passed the Meijer criteria meaning they are of good enough performance for use in a screening program.

8. Where can we find the details for the model? Equations, etc.

The results of the UK model are published here: https://bmjopen.bmj.com/content/10/3/e031303

The Canadian results are being submitted for publication to a peer-reviewed journal. The results of the other models are yet unpublished, however are being prepared for submission.

9. I work in the HIV world and wondered if there has there been any modeling on HPV/HIV coinfections?

There is a lot of modelling work that has been done on HPV and HIV co-infections, focusing on different aspects (natural history, treatment, HPV vaccination, screening, etc.).

10. Great presentation. Have you done any modelling to look at genotyping vs. pooled hrHPV and differences in costs if a genotyping (ex: HPV 16 and 18 referred directly to colposcopy and other hrHPV positives triaged to cytology) is used for triage decisions?

One of the scenario analyses in this study looks at referring HPV16/18+ positive patients directly to colposcopy in the DNA arm. Aptima does not have the genotyping capability and therefore this was not included in the mRNA arm. The data used to parametrize this scenario was taken from the HORIZON study (as the breakdown of genotypes was not available from FOCAL), and the mRNA arm was still cost saving.

11. How different are the volunteers in BC from the total population in Ontario? How might this bias affect the conclusions?

The women in the FOCAL study were thought to be representative of that region. However as mentioned above, different populations may have different positivity rates.