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Genomic surveillance in ulcerative colitis from promise to practice

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Discussion

We read with great interest the recent study by Al-Bakir et al., which explored the use of low-coverage whole-genome sequencing (lcWGS) to predict progression to advanced neoplasia in patients with Ulcerative Colitis (UC) and Low-Grade Dysplasia (LGD). The findings present a compelling advance in molecular risk stratification and may significantly improve surveillance decision-making.

However, the real-world implementation of lcWGS in routine clinical practice warrants careful consideration. While the sensitivity and negative predictive value reported are impressive, the feasibility of integrating genome-wide sequencing in standard dysplasia surveillance—particularly in resource-constrained settings—remains a concern. At present, histopathological evaluation remains the cornerstone of LGD risk assessment; thus, the proposed model should ideally complement rather than replace existing frameworks. Furthermore, cost-effectiveness data will be crucial in justifying broad application. As genomic technologies evolve, we encourage health economic modeling to assess whether lcWGS-guided surveillance strategies could reduce colorectal cancer incidence and healthcare costs over time.

Lastly, multicenter validation across diverse UC populations would help confirm generalizability and support its inclusion in future surveillance guidelines. This study is a significant step forward and raises important questions for translational research in IBD.

References

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