

CORRESPONDENCE



Scientific refutation of ESHG statement on embryo selection

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European Journal of Human Genetics (2023) 31:278; <https://doi.org/10.1038/s41431-022-01237-0>

TO THE EDITOR:

Recently the European Society of Human Genetics (ESHG) published a Viewpoint article entitled *The use of polygenic risk scores in pre-implantation genetic testing: an unproven, unethical practice* [1].

It is important to clarify the scientific status of embryo selection using polygenic scores. The ESHG fails to cite many of the most important recent papers on this topic. Their statement therefore misrepresents the current scientific consensus and potential utility of this new technology.

It is a well-established result, replicated many times in the research literature, that polygenic scores can identify which of two siblings is at higher risk for a disease condition [2–7] (<https://twitter.com/ShaiCarmi/status/1487694576458481664>, https://twitter.com/hsu_steve/status/1487771721155452928), and that selection between them may confer disease risk reduction comparable to that of embryo selection for monogenic disease.

IVF embryos are potential siblings. Therefore the inference that polygenic scores can reduce health risks by embryo selection among those potential siblings is based on established scientific results.

The main benefit of PGT-P is identifying risk outliers – individuals with unusually high disease risk. These outliers can be detected among sibling IVF embryos using polygenic scores, with particularly beneficial risk reduction for families with a history of specific disease conditions.

Embryo screening for chromosome structure (e.g., Trisomy 21) or Mendelian risk variants with only partial penetrance (e.g., BRCA) has long been common practice, and called ethically justified by the ASRM ethics committee. Roughly 50% of US IVF embryos undergo some form of genetic screening today.

It would be morally wrong to hinder IVF families access to new technology that improves the chances for their children to have healthy lives.

We invite the authors of [1] to an open scientific discussion of the merits of embryo selection.

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REFERENCES

- Forzano F, Antonova O, Clarke A, de Wert G, Hentze S, Jamshidi Y, et al. The use of polygenic risk scores in pre-implantation genetic testing: an unproven, unethical practice. *Eur J Hum Genet.* 2022;30:493–5. <https://www.nature.com/articles/s41431-021-01000-x>.
- Lello L, Raben TG, Hsu SDH. Sibling validation of polygenic risk scores and complex trait prediction. *Sci Rep.* 2020;10:13190 <https://doi.org/10.1038/s41598-020-69927-7>.
- Turley P, Meyer MN, Wang N, Cesarini D, Hammonds E, Martin AR, et al. Problems with Using Polygenic Scores to Select Embryos. *N Engl J Med.* 2021;385:78–86.
- Lencz T, Backenroth D, Granot-Hershkovitz E, Green A, Gettler K, Cho J, et al. Utility of polygenic embryo screening for disease depends on the selection strategy. *eLife.* 2021;10:e64716.
- McGue M, Willoughby EA, Rustichini A, Johnson W, Iacono WG, Lee JJ. The contribution of cognitive and noncognitive skills to intergenerational social mobility. *Psychological Sci.* 2020;31:835–47. <https://doi.org/10.1177/0956797620924677>.
- Treff NR, Eccles J, Marin D, Messick E, Lello L, Gerber J, et al. Preimplantation genetic testing for polygenic disease relative risk reduction: evaluation of genomic index performance in 11,883 adult sibling pairs. *Genes (Basel).* 2020;11:648. <https://doi.org/10.3390/genes11060648>.
- Kumar A, Im K, Banjevic M, Ng PC, Tunstall T, Garcia G, et al. Whole-genome risk prediction of common diseases in human preimplantation embryos. *Nat Med.* 2022;28:513–6. <https://doi.org/10.1038/s41591-022-01735-0>.

AUTHOR CONTRIBUTIONS

The authors have all contributed to this manuscript equally.

FUNDING

Funding for this ESHG viewpoint article response comes from Genomic Prediction.

COMPETING INTERESTS

The authors declare the following interests: LT, NT, and SH are founders and shareholders of Genomic Prediction (GP). EW and LL are employees and shareholders of GP.

ADDITIONAL INFORMATION

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Received: 22 February 2022 Accepted: 13 June 2022
Published online: 12 December 2022