

人类双性恋性行为背后的基因变异对生殖有利

Genetic variants underlying human bisexual behavior are reproductively advantageous

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【摘要】 由于人类同性性行为 (SSB) 是可遗传的并且会导致后代减少, 因此 SSB 相关等位基因如何持续存在以及它们是否会保留在人类群体中引起人们的兴趣。在确认双性恋性行为 (BSB) 和排他性行为 (eSSB) 的遗传差异后, 我们利用英国生物库分别解决了这些问题。我们发现雄性 BSB 与后代数量在遗传上呈正相关。这种意想不到的现象可归因于男性冒险行为相关等位基因的水平多效性, 因为男性冒险行为在遗传上与 BSB 和后代数量呈正相关, 并且因为基因控制男性冒险行为消除了与 BSB 和后代数量之间的遗传相关性。相比之下, eSSB 在遗传上与后代数量呈负相关。我们的研究表明, 雄性 BSB 相关等位基因可能具有生殖优势, 这可以解释它们过去的持久性并预测它们未来的维持, 而 eSSB 相关等位基因目前可能会被选择。相比之下, eSSB 在遗传上与后代数量呈负相关。

[Abstract] Because human same-sex sexual behavior (SSB) is heritable and leads to fewer offspring, how SSB-associated alleles have persisted and whether they will remain in human populations are of interest. Using the UK Biobank, we address these questions separately for bisexual behavior (BSB) and exclusive SSB (eSSB) after confirming their genetic distinction. We discover that male BSB is genetically positively correlated with the number of offspring. This unexpected phenomenon is attributable to the horizontal pleiotropy of male risk-taking behavior-associated alleles because male risk-taking behavior is genetically positively correlated with both BSB and the number of offspring and because genetically controlling male risk-taking behavior abolishes the genetic correlation between male BSB and the number of offspring. By contrast, eSSB is genetically negatively correlated with the number of offspring. Our

results suggest that male BSB-associated alleles are likely reproductively advantageous, which may explain their past persistence and predict their future maintenance, and that eSSB-associated alleles are likely being selected against at present.

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