

Should biologists keep invasive CRISPR mutations in check?

On 28 December 2014, Valentino Gantz and Ethan Bier checked on the fruit flies that had just hatched in their lab at the University of California (UC), San Diego. By the classic rules of Mendelian genetics, only one out of four of the newborn flies should have shown the effects of the mutation their mothers carried, an X-linked recessive trait that causes a loss of pigmentation similar to albinism. Instead, nothing but pale yellow flies kept emerging. “We were stunned,” says Bier, who is Gantz’s Ph.D. adviser. “It was like the sun rose in the west rather than the east.” They hammered out a paper and submitted it to *Science* 3 days later.

In the study, published online (<http://scim.ag/VMGantz>), Gantz and Bier report that the introduced mutation disabled both normal copies of a pigmentation gene on the fruit fly chromosomes, transmitting itself to the next generation with 97% efficiency—a near-complete invasion of the genome. The secret of its success: an increasingly popular gene-editing toolkit called CRISPR, which Gantz and Bier adapted to give the mutation an overwhelming advantage. The technique is the latest—and some say, most impressive—example of gene drive: biasing inheritance to spread a gene rapidly through a population, or even an entire species. At this level of efficiency, a single mosquito equipped with a parasite-blocking gene could in theory spread malaria resistance through an entire breeding population in a single season.

The paper comes amid intense soul-searching among gene drive researchers, with calls for public dialogue and self-policing for the technology. George Church, a geneticist at Harvard Medical School in Boston who is a leader in the field, believes the new study should not have been published, because it does not include measures to restrain the spread of unintended mutations. “It is a step too far,” he says.

Read full original article: Biologists devise invasion plan for mutations