Video Tutorial 15.1: A conversation with Professor Eric Wieschaus

In 1995 the Nobel Prize in Physiology or Medicine was awarded to Christiane Nüsslein-Volhard, Eric Wieschhaus, and Ed Lewis for their work elucidating the genetic control of early embryonic development. Their studies began in fruit flies but have provided profound insights into the development of all animals. In this video Eric Wieschhaus talks about genetic analysis and his work with Janni Nüsslein-Volhard on their ground-breaking embryonic patterning screen in the fruit fly Drosophila melanogaster.

What do you think were the essential features of your embryonic patterning gene screen that you did with Janni Nüsslein-Volhard that made it so successful?

I think one of the things was probably that it was simpler and pared down compared to what we thought we were going to do and compared to what the world thought was relevant in thinking about embryos and thinking about embryonic development. What we were somehow able to do was to pare down this to a mutagenesis screen that had a couple of cut-offs and look for genes that are required transcriptionally in the embryo such that if the embryo didn't have that gene it would die. And then then look at those dead embryos and fly embryos and look for ones where the there was a phenotype, meaning that you could distinguish that all the mutant embryos had something in common that was different from the random dead embryo on a plate and that thing that was in common was then our handle on what that gene was actually doing; the shared features of all the dead embryos in a particular stock kind of defines why that particular gene is needed and, therefore in a certain system, ultimately what that gene does. So being simple and paring things down to one or two simple criteria.

Before that people had tried to look for mutations that affected embryonic development but they felt an obligation to section, to do it at all different stages, to look at everything rather than staying really simple. Because staying really simple then allowed us to do the second thing which was to scan through the entire genome, something that wouldn't have been possible if we'd really focused on any particular gene. But by having the simple criteria, the simple set of cut-offs in the beginning, we could do a screen that actually said ok, we're going to try to look for all the genes. I think had we not set up simple criteria at the beginning nothing would have worked. We would have been still stuck with the first two hundred lines or first hundred lines, or I don't know how many. At what point, if we hadn't been driven by simplicity, we would have been distracted. Who knows?