

Science and technology

Babbage

Epigenetic anointment

Dec 23rd 2010, 16:21 by The Economist online

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LIFE in the hive is nasty, brutish and short—if you are a worker bee, that is. Workers spend the 20 days or so of their adulthoods constructing honeycomb, feeding larvae, foraging for nectar and pollen beyond the hive, and never producing offspring. The queen, by contrast, lives on for years in languor, fed and preened by workers as she lays up to 2,000 eggs a day for honeybee posterity.

Yet these starkly different fates emerge from the same genome. Who becomes royal and who a drudge depends on who gets fed with a fabulous substance called royal jelly. The jelly does this by modulating the expression of the insect’s genes, but the details have hitherto been obscure.

In a [study published in *PLoS Biology*](#), Ryszard Maleszka of the Australian National University and his colleagues illuminate some of those details. One of the ways that genes are regulated is by a process called methylation. This adds chemicals called methyl groups to DNA. These then obstruct the machinery responsible for turning genetic instructions into working proteins—a phenomenon known as epigenesis. Dr Maleszka has shown that royal jelly acts, at least in part, by changing the pattern of methylation. He and his team have produced a methylation map (a “methyloome”) of the DNA in honeybee brains.

They found 561 genes whose methylation patterns were different in queens and workers. Most of these genes encode humdrum proteins that regulate a cell’s metabolism or transmit molecular signals that keep it ticking over. Differences in these genes presumably explain the different body sizes and lifespans of queens and workers. A few of the affected genes, though, are involved in brain development and signalling between nerve cells. These would explain differences in behaviour.

A recurring theme was that the epigenetic marks found can pick and choose from alternative options offered by the genome. Genes are divvied up into pieces that may be swapped in or out of the final instructions for making a protein, allowing a cell to fine-tune a protein to its needs. Queens and workers differed in how methyl tags were clustered at the splicing sites between these pieces. For example, the splicing sites of the gene needed to make the short version of a protein called GB18602 (of unknown function, although its counterpart in fruit flies is involved in fat and sugar metabolism) were tagged with methyl groups in workers but not in queens. This strongly correlated with the meagre amounts of the short version of GB18602 found in workers and its abundance in queens.

How these precise patterns of methylation arise remains a mystery, which may involve some as yet unknown guidance molecules that instruct the methylating enzyme exactly where to tag the genome. This is a crucial question for human health, too, because epigenetic marks on certain genes can spur disease (the runaway cell division that causes cancer being one important example). With a genome a tenth the size of a human’s, and less crowded with methyl tags to boot, the honey bee may lead the way to the principles behind how these epigenetic patterns emerge—and ultimately determine fates beyond the hive.

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HardcoreKeynesian wrote:

Dec 24th 2010 12:40 GMT

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D. Sherman wrote:

Dec 24th 2010 2:06 GMT

This is a fascinating bit of research and it’s nice to have it reported in the popular press where a layman like myself might run across it. There aren’t too many new fields of research available these days, but this sounds like one of them. Whether or not it ever leads to a cure for cancer, which seems to be the popular definition of useful research, it definitely adds in a significant way to the body of human knowledge. That alone is good enough for me.

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tocharian wrote:

Dec 24th 2010 2:30 GMT

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Gurinder Shahi wrote:

Dec 24th 2010 2:50 GMT

Fascinating...

Beyond these findings in worker versus queen bees, a growing body of evidence suggests that epigenetic changes arising from differences in exposure to environmental factors may play a far greater role in shaping our destinies than we have generally recognized.

It is becoming increasingly clear, for example, that epigenetics plays a central role in such phenomena as cell differentiation where cells that eventually become, say, red blood cells or muscle cells follow very different developmental pathways even though they have essentially the same genetic make-up. Conversely, we are finding that it is possible to reverse epigenetic programming so relatively undifferentiated stem cells can be generated from previously specialized cells.

Even more intriguing is the likelihood that some epigenetic changes acquired during one’s lifetime might actually be passed on from one generation to the next, and that this “neo-Lamarckian” mechanism may be ubiquitous in helping organisms to evolve in response to changes in the environment.

The more we learn, the more we realize that there is much more to learn...as I see it, these are exciting times!

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Devils Advocate_2 wrote:

Dec 24th 2010 7:56 GMT

[tocharian wrote: Dec 24th 2010 2:30 GMT What are we gonna feed Kate Middleton?
(I’m just kidding!)]

With Suu Kyi’s?

Devi’s

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Chippe wrote:

Dec 25th 2010 10:22 GMT

Could it be that resveratrol acts in an epigenetic way to switch on the survival gene in organisms, even in mammals. Why is it that few people can believe this proven fact.

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Single Speak wrote:

Dec 26th 2010 1:09 GMT

Well, good to know that some are born to be genetically royal. Is there any similar traits in human gene?

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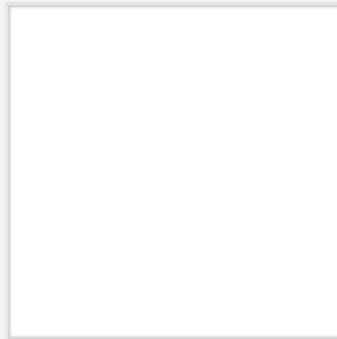
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