

ANALYSING FRUIT FLIES; FROM DNA TO DATA

What hope of control?



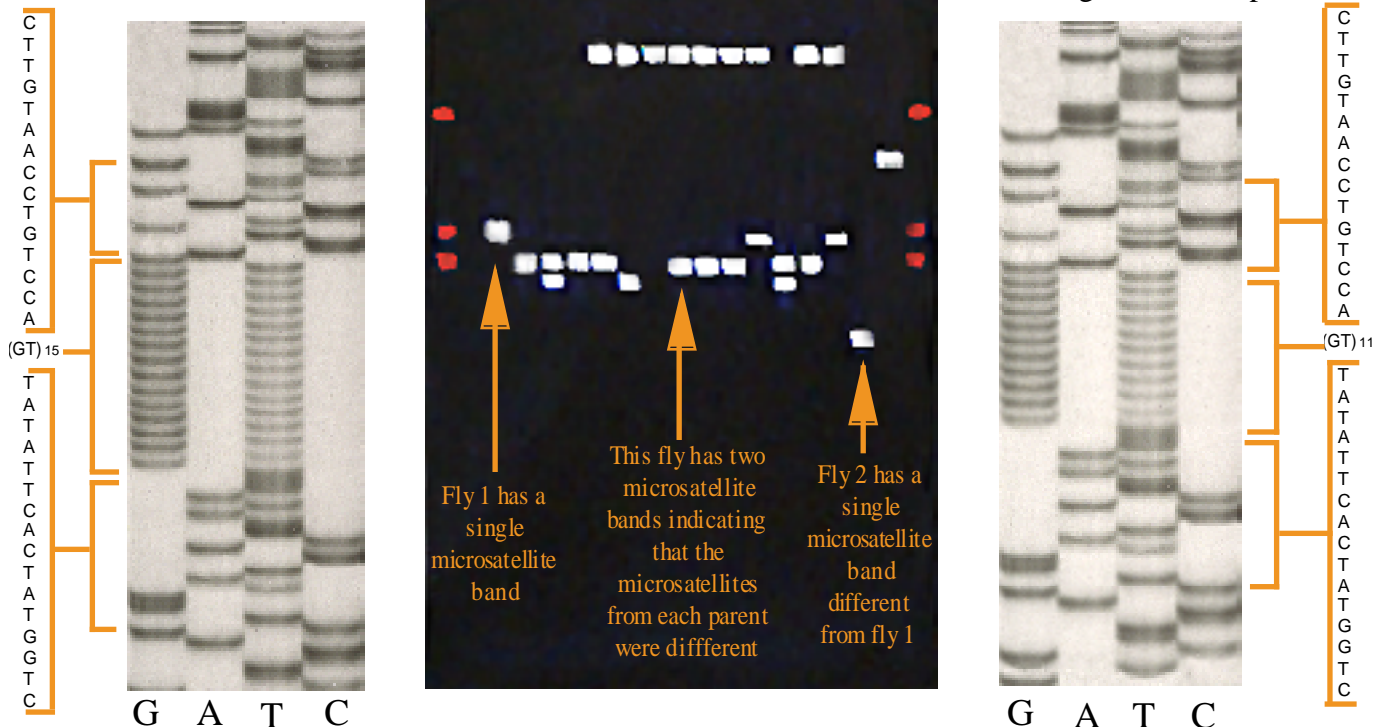
This work by the Fruit Fly Research Centre was supported for 6 years by Woolworths Supermarkets, horticultural industries and Horticulture Australia Ltd



How can you tell where flies come from?

Fly 1 was trapped in Batlow by NSW Agriculture inspectors.

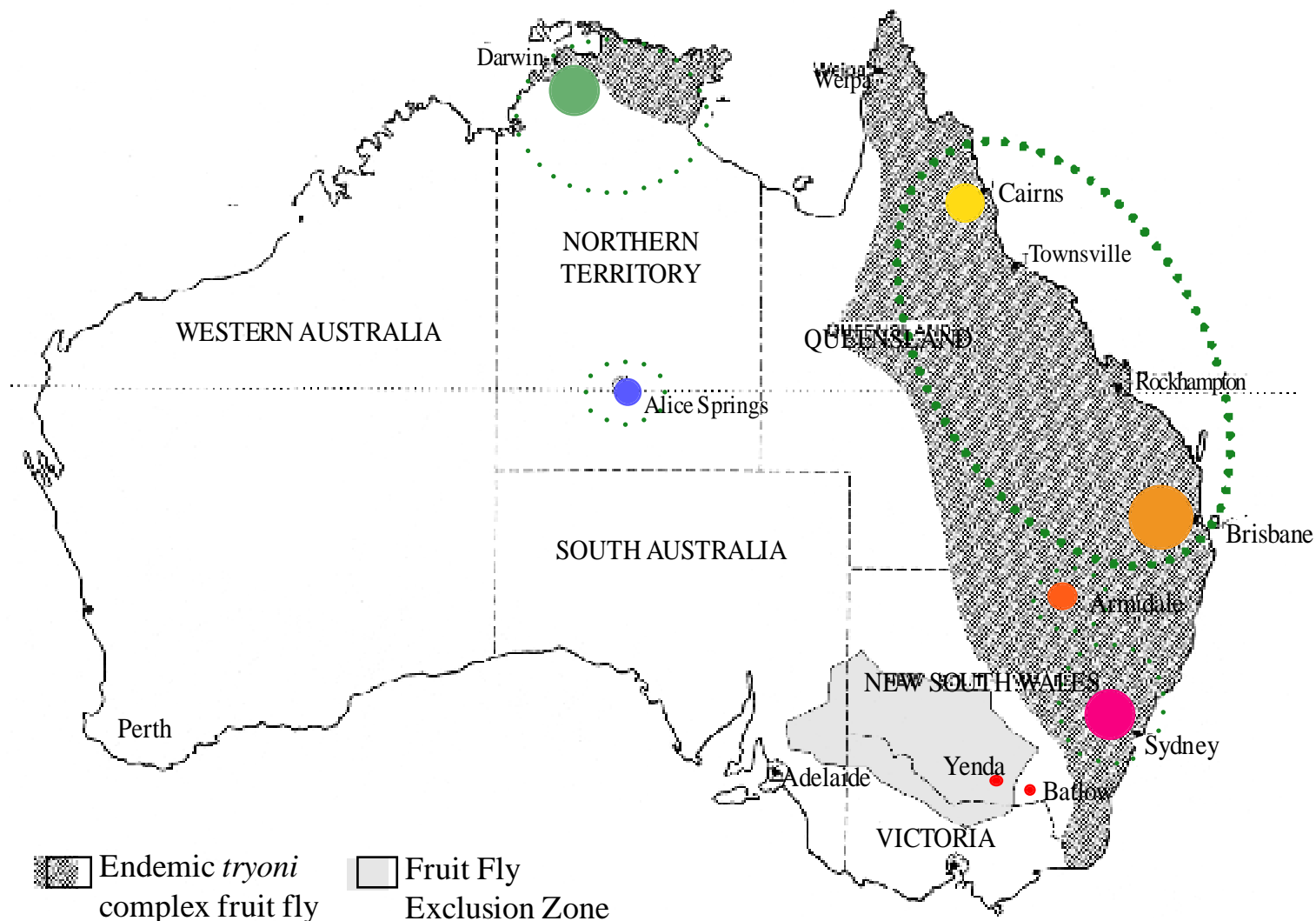
Fly 2 was trapped in Yenda by NSW Agriculture Inspectors.



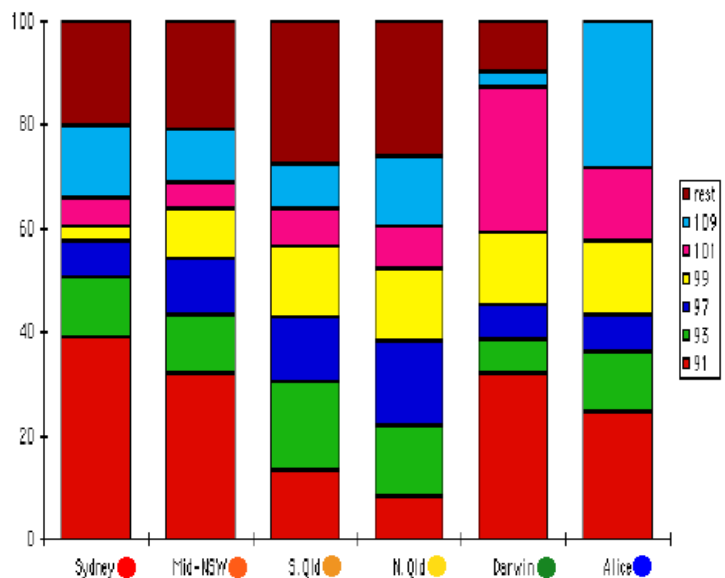
The fly on the left was found by NSW Department of Agriculture in a cuelure trap in Batlow on 21 January 1998 and sent by post to the Fruit Fly Research Centre for microsatellite analysis. After being catalogued the fly was stored at -70°C to ensure that its DNA did not degrade. In May 1999 the Fruit Fly Research Centre extracted DNA from the head of this fly and analysed 6 microsatellites. The DNA banding pattern for microsatellite *Bt32* is shown on the left. There are 15 repeats. Each fly has two strands of DNA and so two copies of this microsatellite, one from its maternal parent and one from its paternal parent. If both copies of microsatellite *Bt32* have the same number of repeats there is a single band on an acrylamide gel (shown on the right). Only the microsatellite is seen on an acrylamide gel since the unique ends of a microsatellite (primers) attach to this unique section of the fly DNA. The two copies of microsatellite *Bt32* for the fly (above left) are in the first column with white banding from the left of the gel. There is only one band at this position.

Fly 2 was trapped by NSW Department of Agriculture in Yenda on 9 June 1998. The microsatellite *Bt32* DNA of this fly has 11 repeats in both strands of its *Bt32* microsatellite - seen as DNA on the right, and seen on an acrylamide gel on the left (column 2 of white banding from right). Since the number of repeats is less than fly 1 (11 repeats in fly 2 compared with 15 repeats in fly 1), the band of fly 2 is at a different, lower, position on the gel. It may be seen that the DNA for microsatellite *Bt32* of the fly in column 5 from the right has two bands at different positions to either fly 1 or 2. This fly has different numbers of repeats in each strand of microsatellite *Bt32* of DNA - the parents of this fly had different microsatellite repeats, $(\text{GT})_{13}$ and $(\text{GT})_{14}$.

Microsatellite profiles using up to 30 variable DNA microsatellites have been obtained for thousands of *B. tryoni* flies from endemic and outbreak regions of Australia and used to analyse the population.



Since 1993 the Fruit Fly Research Centre has collaborated with hundreds of members of the CSIRO Double Helix Club to collect fruit flies in the endemic areas of Australia. These flies have been analysed for six microsatellites. We have found that the pattern of microsatellites in flies from Queensland are significantly different from the pattern in the Sydney region, and significantly different from the pattern in the Northern Tablelands of New South Wales (as seen by the frequencies of various alleles of *Bt32* in histogram on the right). Of great interest is that the pattern of microsatellites in Queensland and the Sydney region have not changed over the five years of the project. However, the flies from NSW Northern Tablelands, after remaining stable for four years, changed in 1998 to be Queensland-like.



Flies from the Darwin region are significantly different from all other regions.

The Alice Springs sub-population is different from all other regions; it does not have a “rest” band (frequency of rare microsatellite alleles). This indicates that the Alice Springs population built up from a small genetic base, and if this sub-population is eradicated it is unlikely to re-establish.

This work confirmed the South Australian Department of Primary Industry claim that fruit fly outbreaks in Adelaide in successive years had different origins, that sterile insect technique eradication was successful and that new outbreak flies arrived from elsewhere.