

Variation in pollen phenology in native populations of *Pinus sylvestris* in Scotland



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MOTIVATION:

A characteristic of most boreal and northern temperate tree species is the capacity for long distance pollen dispersal by wind and high levels of gene flow between populations are thought to be widespread. Studies based on neutral genetic markers suggest that there is little genetic variation between native populations of *Pinus sylvestris* in Scotland and propose that this is due to rampant outcrossing between populations. As such, Scottish populations of Scots pine are considered to be panmictic (Fig.1).

However, experimental studies have identified heritable variation in the timing of spring vegetative phenology in Scottish populations, which indicates that some degree of local adaptation is taking place

despite assumed constant gene flow.

These studies suggest that populations in colder environments require a lower heat sum to begin their years' shoot elongation. It seems plausible that flowering phenology would be serially correlated with shoot elongation, although variation in neither trait has been measured in wild populations.

The purpose of this study is to estimate the timing of pollen production in native pinewoods. We use data gained from field observations to test for synchrony of pollen shedding between populations. Asynchronous pollen shedding may suggest that some populations are temporally reproductively isolated from others, and possibly indicate local adaptation for flowering phenology.

SAMPLING:

Three sites were initially selected from an inventory of ancient semi-natural pine woodlands for this project (Figure 2,3). These were chosen because they are on a longitudinal gradient (largely correlated with temperature) and for ease of access enabling rapid sampling (Figure 4).

- 20 trees visited at each site 3 times with c. 10 day intervals during Spring.
- On each tree, 5 strobiles visually inspected and are assigned a developmental score, based on their morphology (see Figure 2).
- In 2015, a further two sites were added to the sample – to improve the fit of predictions.

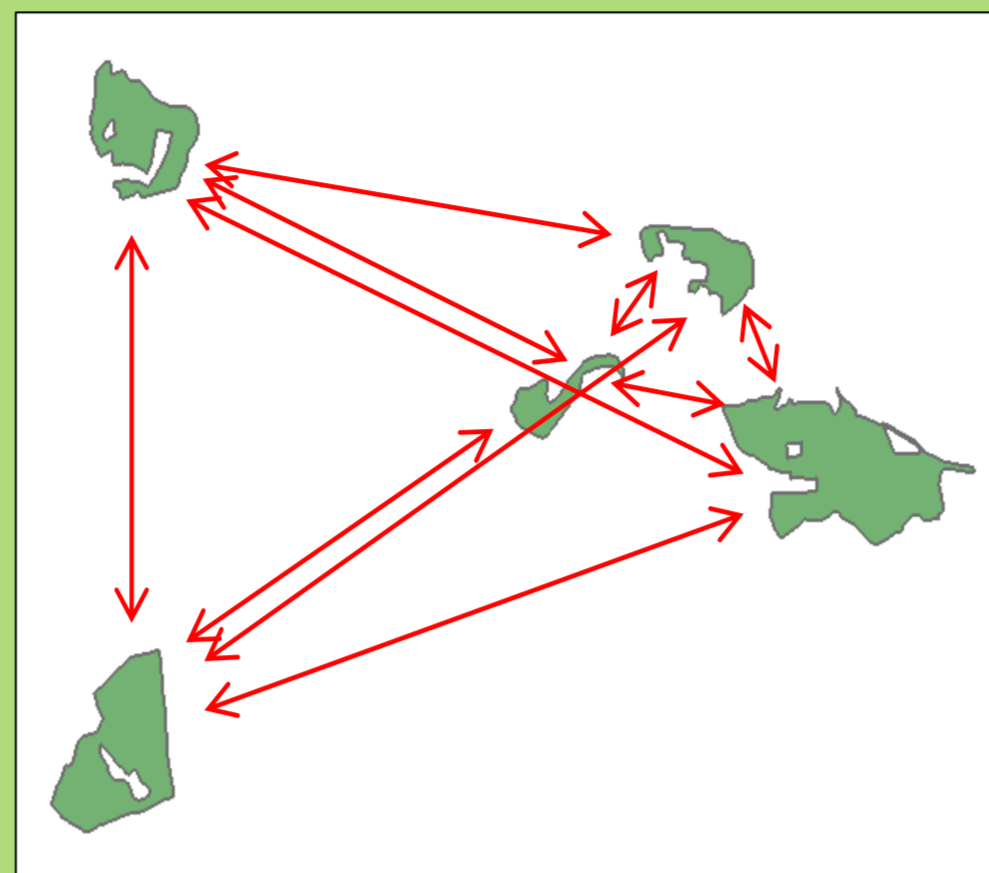


Figure 1. Diagrammatic representation of panmictic populations.

RESULTS:

ANOVA revealed significant differences between some populations for both 2014 ($F=191.51$, $df=2$, $p < 0.0001$) and 2015 ($F= 14.63$, $df= 4$, $p < 0.0001$) This seems to be due to much later anthesis at the coldest site, Allt Cul (Figures 5, 7).

In 2014, a very mild year, warmest populations reached anthesis first. A similar but less distinct pattern emerged in 2015, a cooler but very typical year (Figure 6), there seemed to be less variation between and within populations. This inference has not been tested.

Location of sampling sites within northern Scotland

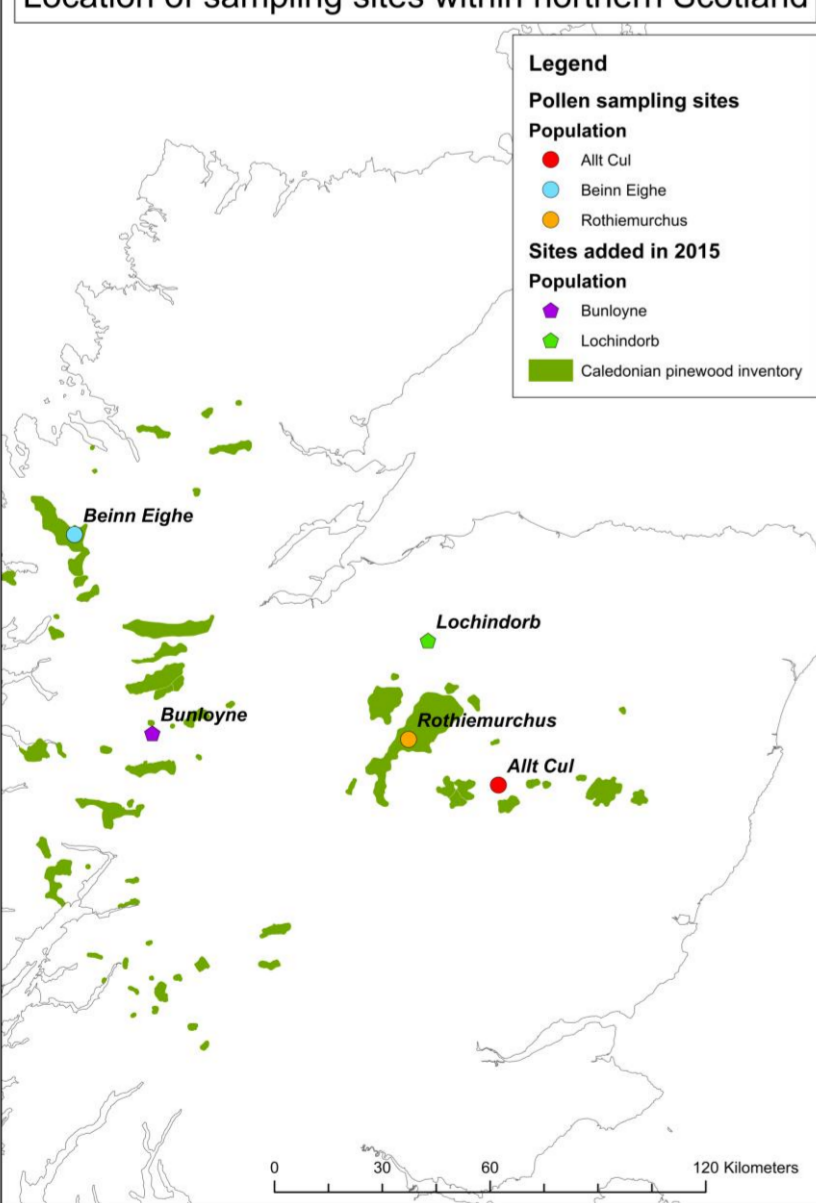


Figure 2. Map of sampling locations within Scotland

Kriged long-term average GDD for native pinewoods.

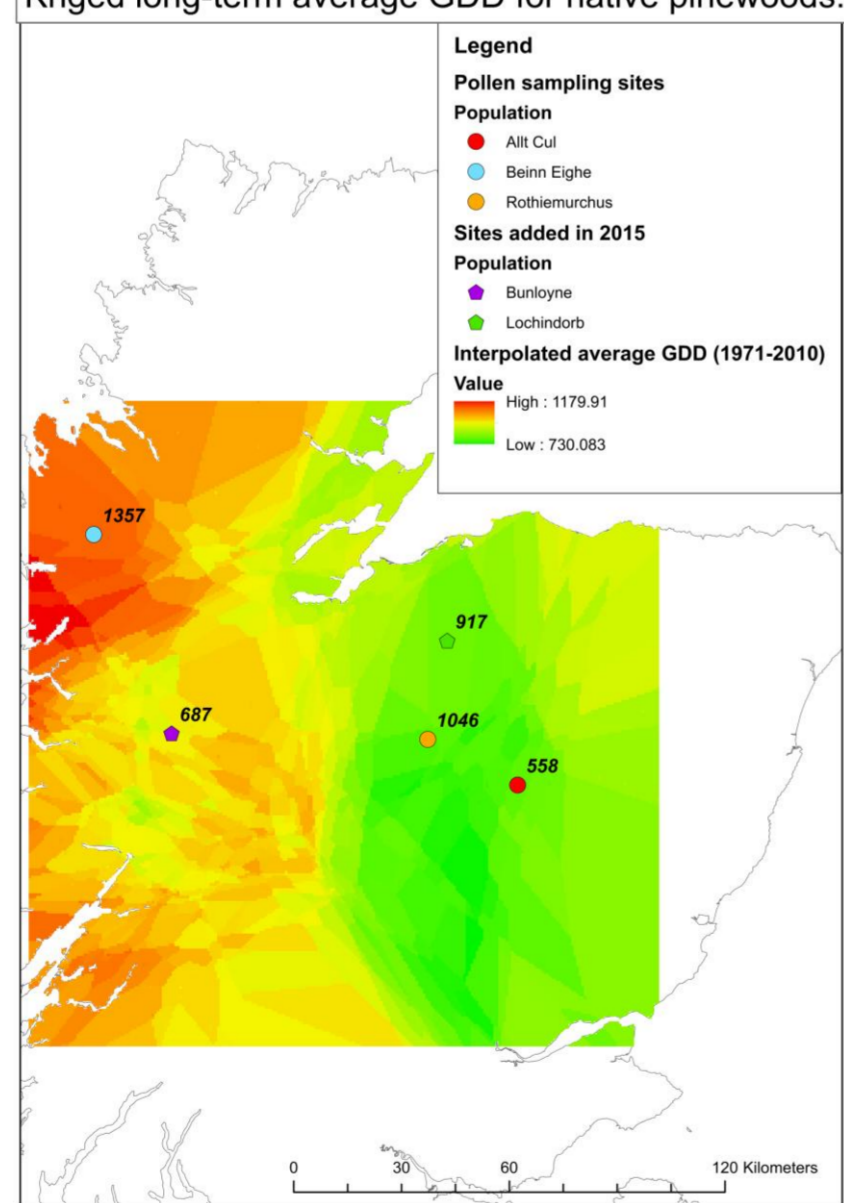


Figure 3. Average growing degree day surface for native pinewoods. Numerical values are the average annual GDD for each sample site.

1



Bud dormant, no indication of initiation of development

2



Bud beginning to swell but remaining entirely closed

3



Bud scales beginning to open

4



Most scales have shed although no pollen shedding yet

5



Peak pollen shedding, strobilus bright yellow

6



Past peak but shedding continues weakly

7



Past shedding, strobilus brown

Figure 4. Modal scale of development

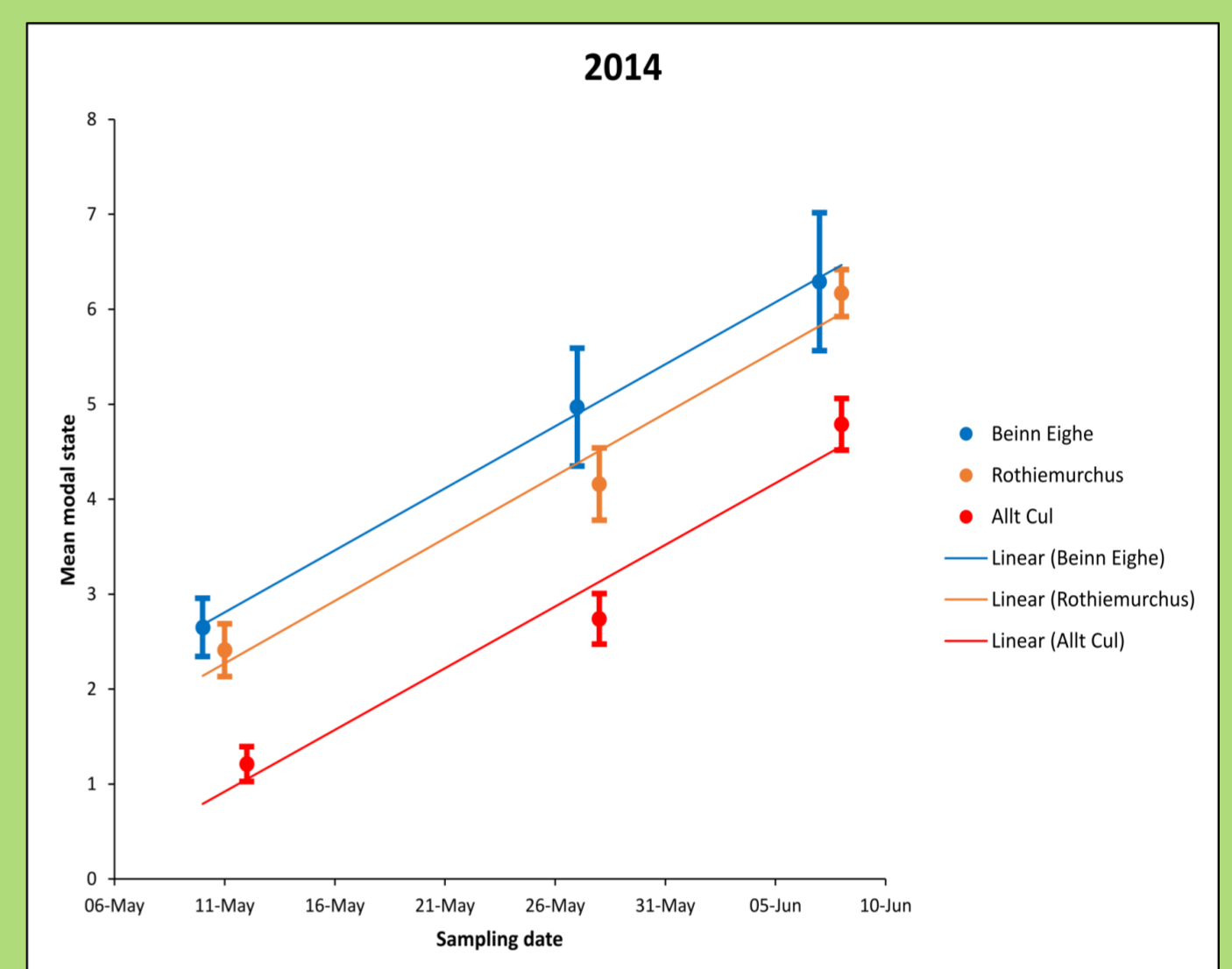


Figure 5. Mean modal state observed on each sampling date +/- 95% confidence intervals for 2014.

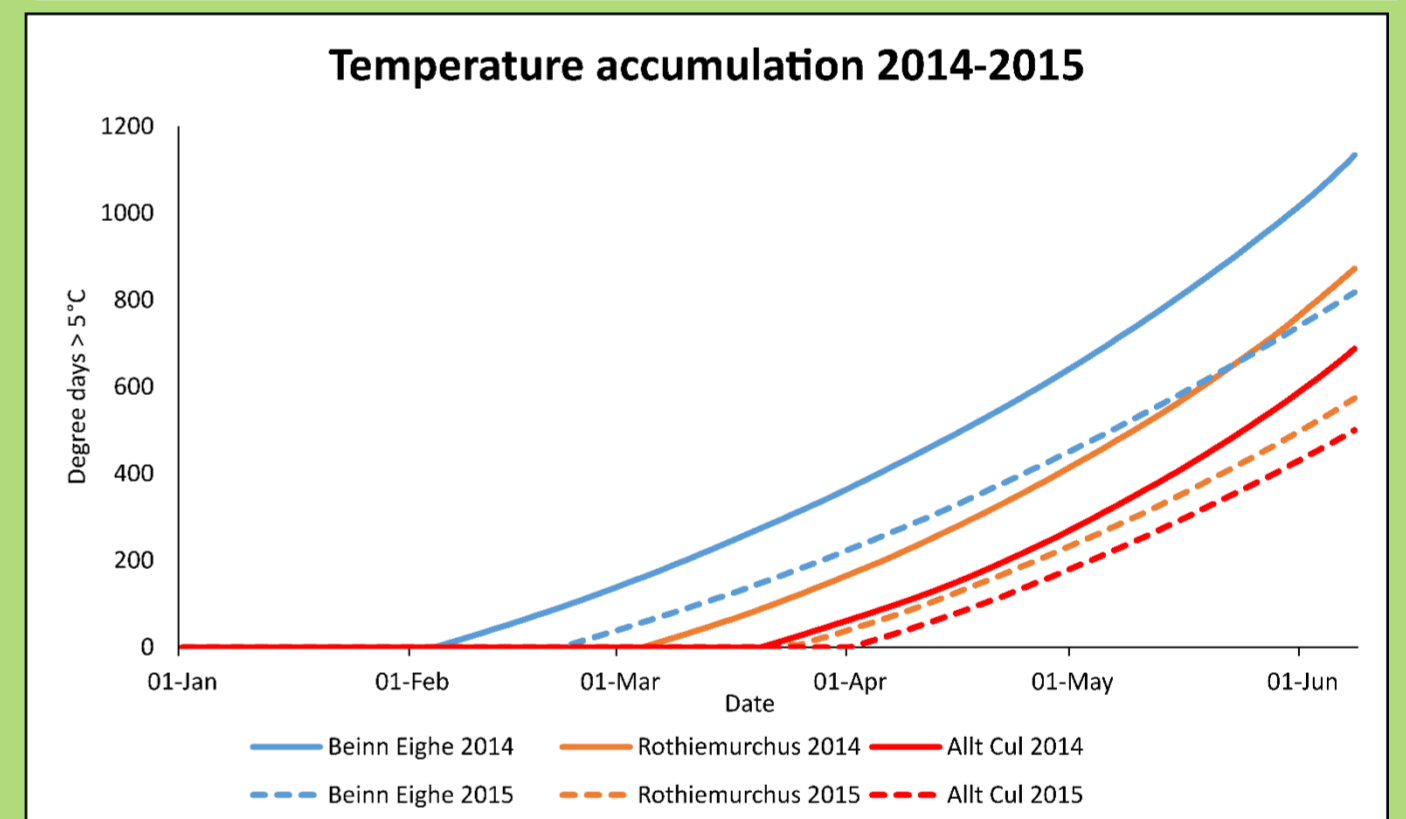


Figure 6. Temperature accumulation curves for 2014 and 2015. Units are degree days > 5°C.

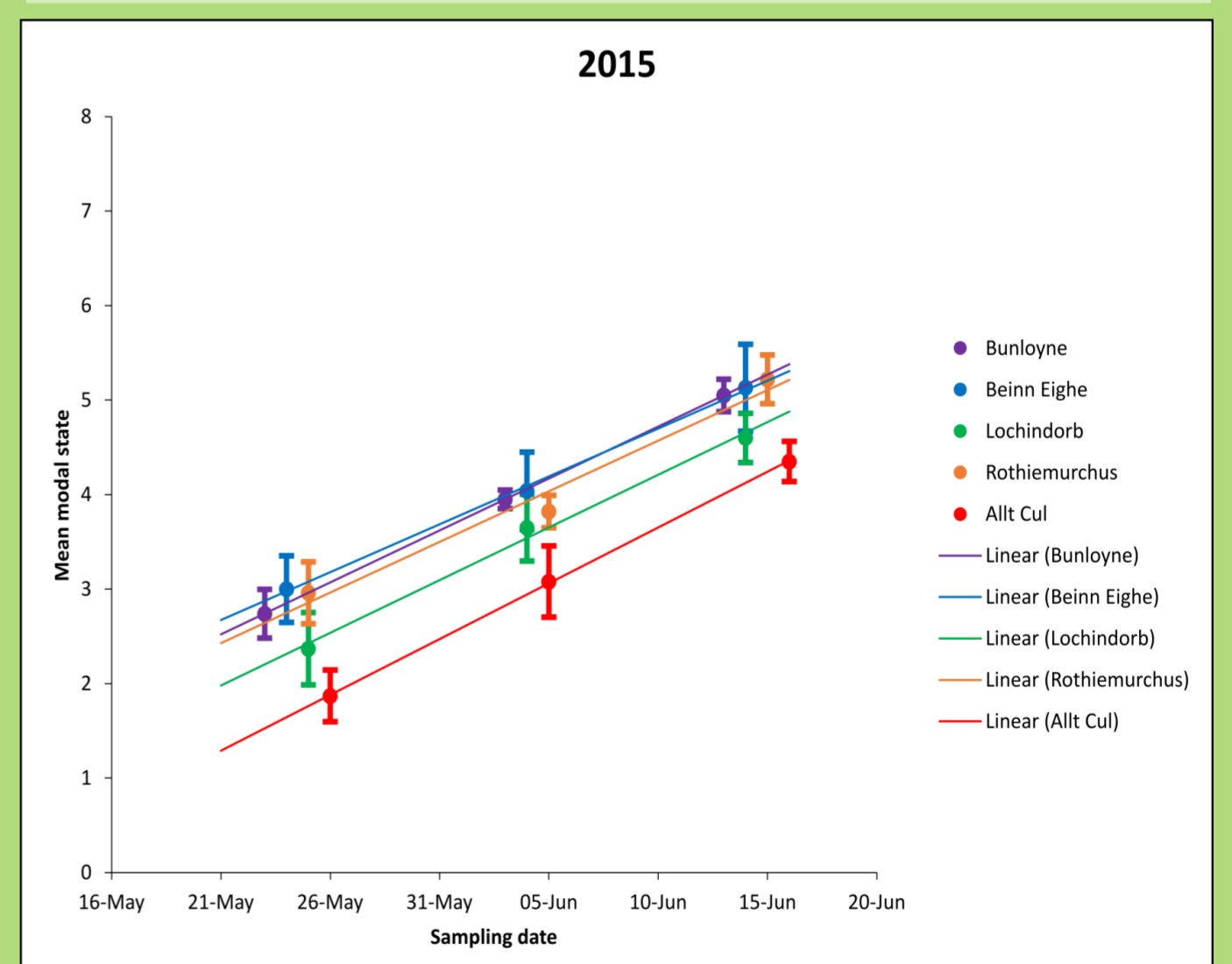


Figure 7. Mean modal state observed on each sampling date +/- 95% confidence intervals for 2015

CONCLUSIONS AND NEXT STEPS:

- It seems as though there are differences in the timing of pollen production between some populations and that timing differs from year-to-year.
- A relationship between timing of anthesis and temperature seems plausible. Further work may enable the development of predictive functions.
- A predictive function will be built into multiple population, spatially explicit individual-based models, to simulate the rate of phenotypic adaptation to environmental change.
- Quantifying the permeability of the landscape, dispersal distances and wind patterns will help to build a more complete picture of pollen transfer between populations.