

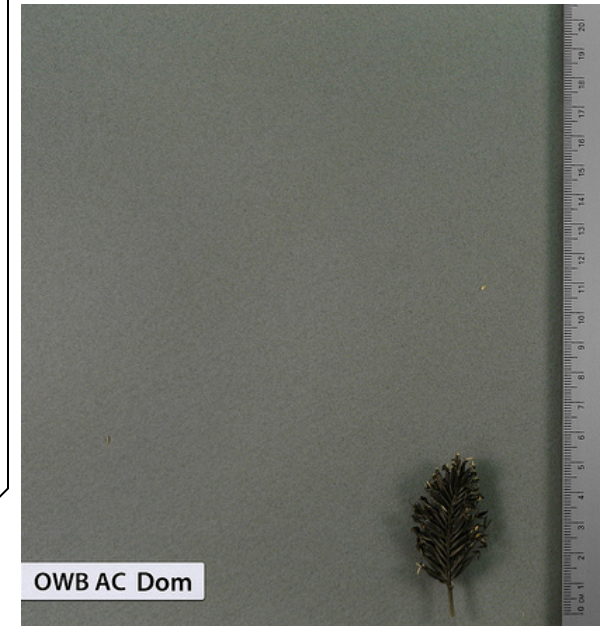
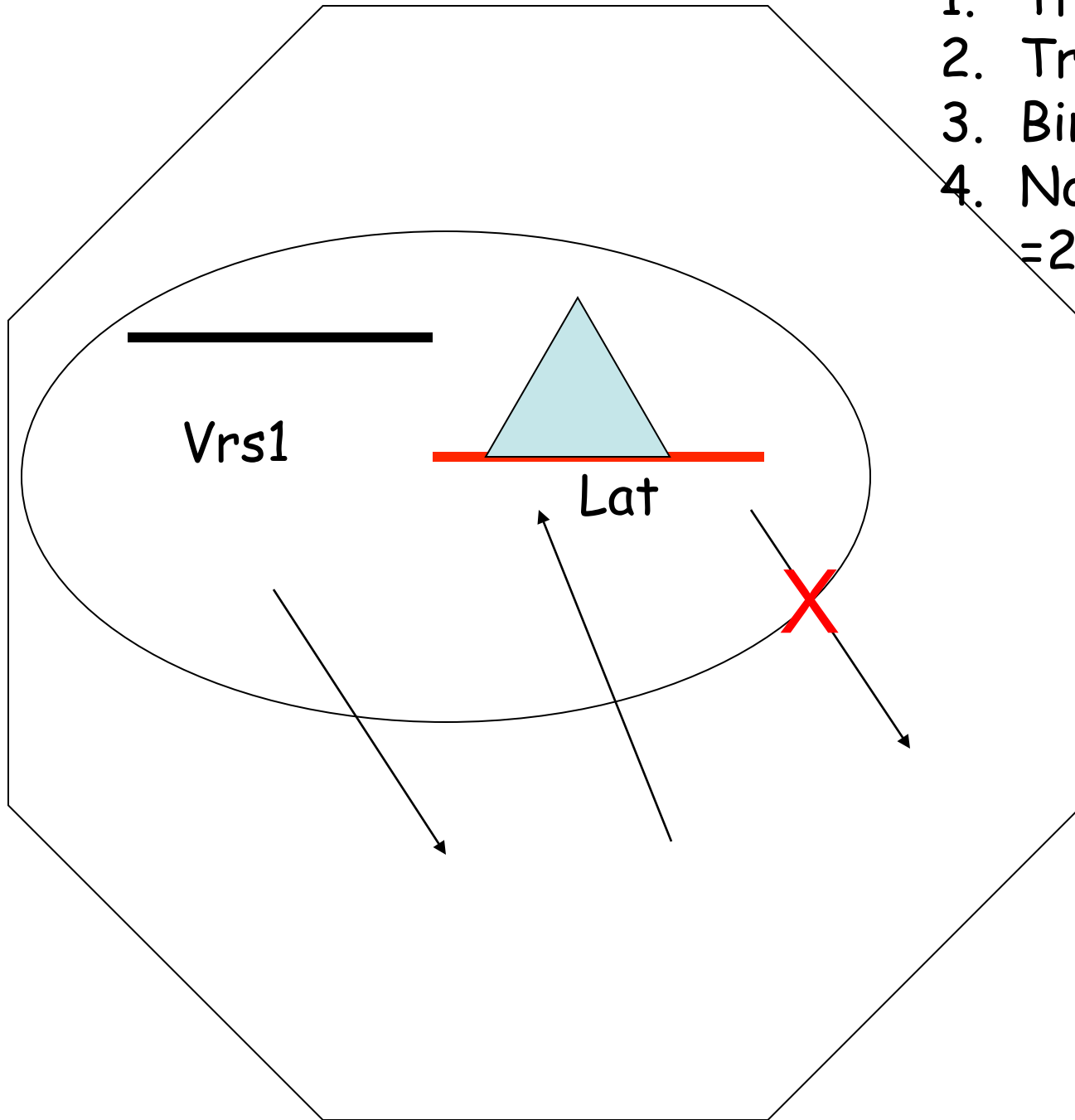
*“Six-rowed barley originated from a mutation in a.....
homeobox gene”*

- Two-rowed is ancestral (wild type)
- Homeobox genes are transcription factors - they encode proteins that bind to other genes and thus regulate the expression of other genes

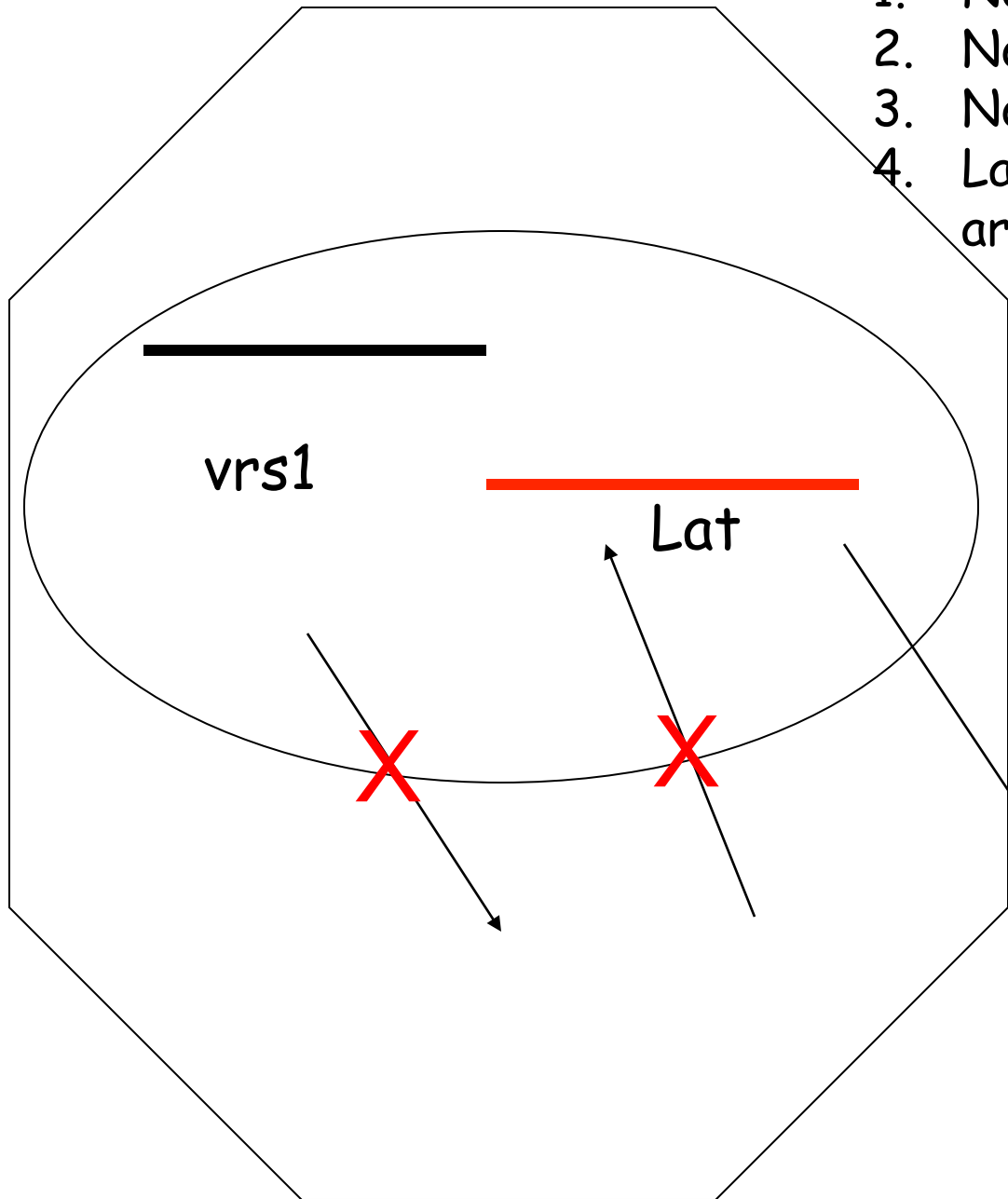
The “virtual” model -

- In a two-row, the product of *Vrs1* binds to another (unknown) gene (or genes) that determine the fertility of lateral florets. For convenience, the unknown gene will be abbreviated as *Lat*
- When there is no expression of *Lat*, lateral florets are sterile and thus the inflorescence has two rows of lateral florets

1. Transcription of Vrs1
2. Translation of Vrs1
3. Binding of Vrs1 to Lat
4. No expression of Lat
=2-row



1. No transcription of *vrs1* (or)
2. No translation of *vrs1*
3. No binding of *vrs1* to Lat
4. Lat expresses and lateral florets are fertile = 6-row



What happened to *Vrs1* to make it *vrs1*?

There are several scenarios that can lead to this loss-of-function.

- **Complete deletion** of the gene (- transcription, - translation = no protein)
- **Deletions of (or insertions into) key regions** of the gene leading to - transcription and/or + transcription but - translation, or incorrect translation = no protein
- **Nucleotide changes** leading to (+ transcription but incorrect translation = non-functional protein)

How many alleles are possible at a locus?

- Only two per diploid individual, but many are possible in a population of individuals
- New alleles arise through mutation
- Some mutations have no discernible effect on phenotype
- Different mutations in the same gene may lead to the same or different phenotypes

All this happened to *VRS1* in
the past 10,000 years!