

ANSWERS Introgression Browser tutorial

EU-TransPLANT Training course: exploring plant variation data

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Q1 Answer: counted by hand; 13 different species, of which one unknown.

Q2 Answer: from white to black.

Q3 Answer: This data is on chromosome 6 only. It is a selection of a particular region emphasizing a recombination event.

Q4 Answer: 38.400.000, this is the second white block with 1785 SNPs.

Q5 Answer: marked reduction of the figure without accession names; reduced size allows for much easier assessment of patterns of large numbers of accessions.

Q6 Answer: they differ little from the reference chosen: it is all *S. lyc.* Note it does NOT mean that they are identical; it shows they have a relatively small SNP frequency.

Q7 Answer: *S. lyc.* TR0003; it has only one region that differs visibly from ref.

Q8 Answer: *S. pimp.* is a likely donor of this fragment in *S. lyc.*

Q9 Answer: It originates from Peru; Accession is identified as *S. pennelli*.

Q10 Answer: the data is not likely to come from a *S. pennelli*; it is difficult to tell which species it is without more data, therefore it was relabelled as *S. spp.*

Q11 Answer: it shows that there is a clear discrepancy between the sequencing data and the accession record. Possibly material was mixed in a greenhouse (such things happen....☹). There is no reason to conclude that the accession was mislabelled at the time of collection.

Q12 Answer: It is very close to two *S. che* accessions. There seems to be some confusion about the naming of these accessions; TGRC shows two taxon names (*S. gal* and *L. che*) that may not have been resolved properly in this accession list.

Q13 Answer: the distance plots suggest the occurrence of recombination/introgression events relative to most other *S. lyc.* accessions; in LA2463 the same event seems to have taken place.

Q14 Answer: iBrowser can give hints as to the source of the potential introgression and indicates the relative distance. A true inversion is better identified with direct sequence comparisons.

Q15 Answer: a MADS box transcription factor is at the 5' border. Transcription factors may be more prone to recombination events.