Diversity of wild barley in 'Evolution Canyon'

J.R. Russell, R.C. Meyer, C.A. Hackett, P. Lawrence, G.R. Young, B.P. Forster & W. Powell

Lower Nahal Oren is a seasonally dry canyon on Mount Carmel in Israel. Although the geology of the canyon is uniform the opposing slopes, facing north and south, vary substantially in the amount of sunlight received. The south facing slope is hot and dry and characterised by a savannah ecosystem with typically African flora and fauna; the north facing slope is cooler and covered by a dense oak forest with associated European flora and fauna, hence the name "Evolution Canyon". Genetic diversity has been studied in several species in "Evolution Canyon", but wild barley, *Hordeum spontaneum* is of particular interest as it grows on both slopes.

The wild barley population in "Evolution Canyon" has been sampled by our collaborator, Prof. Eviatar Nevo (University of Haifa, Israel) at seven stations on a transect across the canyon: North High, North Middle, North Low, Canyon Bottom, South Low, South Middle and South High. Genetic diversity has been studied using single sequence repeat (SSR) variation in both nuclear and chloroplast DNA of 275 plants. Over 200 alleles were detected for 19 nuclear SSR loci and, in addition, 12 chloroplast haplotypes were detected in the population. A phylogenetic tree was constructed from the data: the branches of all individuals from the north facing slope have been coloured red, south facing slope individuals green branches and canyon bottom individuals blue (Figure 1). The tree shows that nuclear SSR variation in the canyon is non-randomly distributed, as there is a strong tendency for individuals to cluster together according to slope of origin. We have also colour-coded the 12 chloroplast haplotypes red, green, blue etc. and have placed these at the end of the branches of the phylogenetic tree. Linkage disequilibrium is evident between the nuclear and chloroplast data as colour-coded branches and disks match up in the majority of cases. Inter-slope contrasts for chloroplast haplotypes can be seen clearly when the frequency of the two most common haplotypes (red and green) is superimposed on the collection sites in the canyon (Figure 2). The pie charts shows a clear swing in haplotype dominance from one side of the canyon to the other.

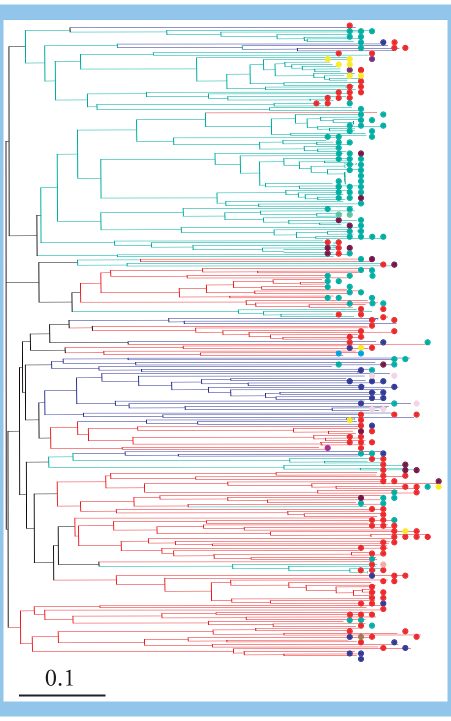

Figure 1 Phenogram of the genetic relationships among seven H. spontaneum subpopulations in "Evolution Canyon" based on UPGMA method branches are coloured based on their slope, SFS (green), NFS (red) and bottom (blue). Chloroplast haplotypes are represented by coloured disks, haplotypes A (green), C (red) and D (blue).

The inter-slope patterns of nuclear and chloroplast genetic variation suggest adaptive divergence to contrasting environmental conditions. Of the two slopes, greater SSR variation was found in the less stressed, north facing slope. In other studies, using anonymous genetic markers such as RAPDs and AFLPs, the opposite was found. The apparent discrepancy is probably due to the fact that SSRs sample a different portion of the genome as they are associated with genic regions. SSRs may, therefore, provide a valuable tool in searching for genes involved in adaptation and species divergence.

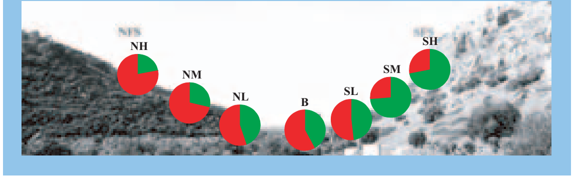

Figure 2 Chloroplast variation for haplotypes A (green), and C (red) in 'Evolution Canyon'.