

Population Genetics (and the status of sample 117493, bear #681)

To check for immigrants into the GYE, we performed a clustering analysis in the program Genetix, comparing your 20-locus genotypes to those of potential source populations. The 51 new grizzly bears (47 from g1172, 4 from Steve Gehman's project g1143) clustered with earlier genotypes from the GYE, once again suggesting that there have been no new immigrants into the GYE (Fig. 1).

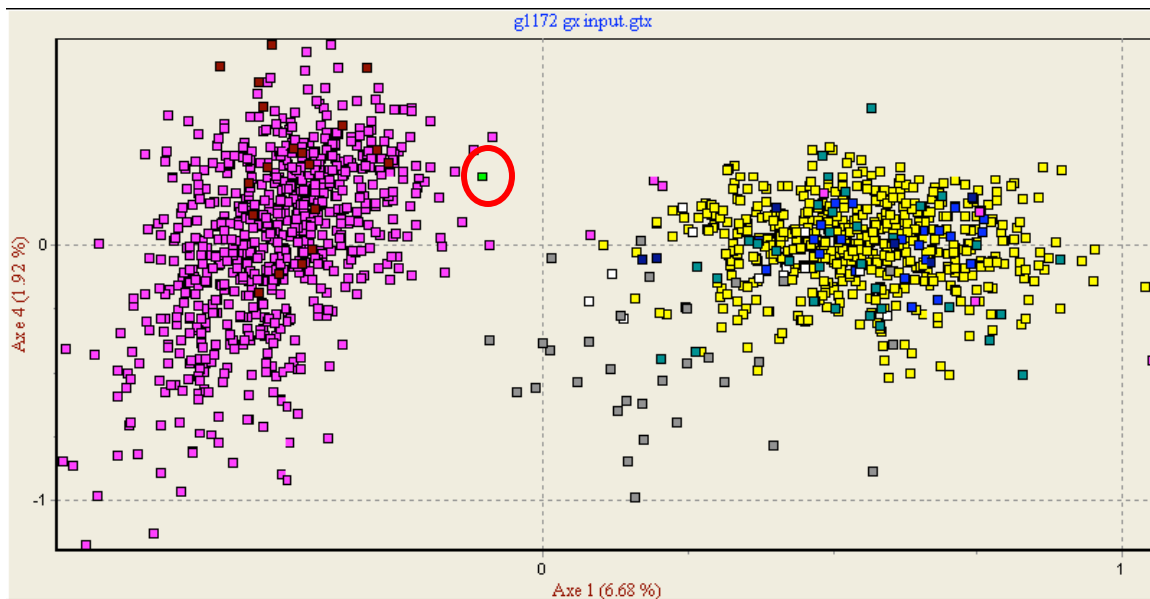


Fig. 1. Twenty-locus Genetix clustering for the 738 grizzly bears in our GYE database (pink), 19 of Steve Gehman's unique GYE individuals (rust), and reference animals from various populations to the north (Selkirks, Yaaks, NCDE, Cabinets and Purcells). Seven of Justin Teisberg's 'Yellowstone' bears are known to have one or two non-GYE parents, and these are easily identified as the 7 pink squares with positive values on axis 1. Individual 117493 (bright green) stood out in other analyses.

Following last year's template, we also pursued a more quantitative test for immigrants using the program GeneClass, which assigns probabilities to the hypothesis that each individual is a resident. This program is computationally intensive, so we limited the number of GYE bears being tested to 139 individuals from this year's project (g1172) and last year's g1005. This analysis confirmed that each GYE bear had a higher probability of occurrence in the GYE than in any of the more northerly populations to which we made comparison, but individual 117493 was an outlier, both visually (Fig. 2) and quantitatively ($P = 0.003$).

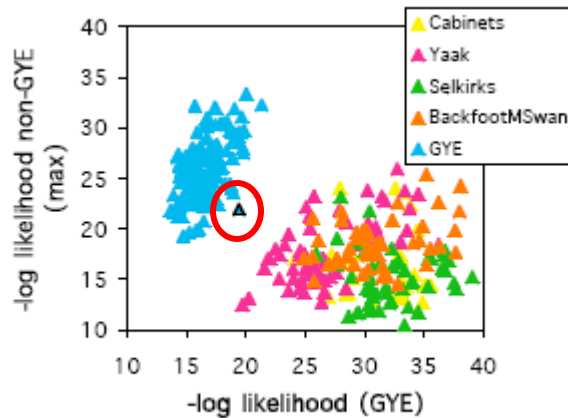


Fig. 2. Assignment plot for 139 20-locus GYE grizzly bear genotypes from g1005 and the current project (g1172), and for 20-locus genotypes from various potential source populations. All 139 GYE genotypes were more likely to have originated in the GYE than in any of the populations, but individual 117493 (blue triangle with black outline) was an outlier, sitting closer to Yaak bears than any other GYE bear.

The results did not suggest that 117493 was a first generation immigrant — otherwise it would have clustered with its source population in Fig. 1 and given a higher non-GYE probability than GYE probability in Fig. 2— but it did raise the possibility of a more derived immigrant status (i.e. its parent or grandparent could have been an immigrant).

The *P*-value of 0.003, while initially seeming impressive in a world where anything below 0.05 is considered meaningful, is actually ambiguous because of the large number of individuals ($n = 139$) whose status we tested; by definition, a *P* of 0.003 is expected to be observed in roughly 1 of every 300 residents whose status is tested (defined as Type I error), so to observe such a value after testing 139 residents sits within the range that is possible for outlying individuals of pure GYE ancestry.

As a test of the consistency of different analytical methods, we took the GYE and Yaak individuals from the GeneClass input file (Fig. 4) — the Yaak being the lost genetically similar population to the GYE, and having been identified as the most probable non-GYE source population for individual 117493 — and used the program Structure to estimate their proportional ancestry in a model with 2 populations (i.e. $k = 2$). The Structure results were fully compatible with the Genetix and GeneClass outputs, identifying 117493 as an unusual bear, but suggesting that more than half of its ancestry can be traced to the GYE (Fig. 3).

A final perspective on the status of 117493 (#681, Taylors Fork, 5 in 2011 when captured) is that he is identified as a likely offspring of 115079B (female #321, Hayden Valley, YNP) or 117420 (female #693, Hayden Valley, YNP). As the estimated age of #693 was 7 in 2011, she is not likely the mother of bear #681.

Compatible fathers for #681 are samples H1015 (Gehman ID, Male), BH963G (Gehman ID, Male), or 115191 (#320, Male). Male bear #320 is the only 1 of the 3 compatible fathers in our database that was known to have overlapped spatially with female #321. Added to the perspective from clustering programs (Figs. 1–3), which implies that 1 or 2 of the grandparents of 117493 were from the Yaak, and thus that 117493 is 1 or 2 generations removed from any putative immigration event, and we can see than any immigration event, if it did occur, took place some time ago.

In summary, 117493 may be the first or second generation descendent of an immigrant to the GYE, but the weak statistical result in GeneClass (once corrected for experimentwise error) suggests that it may also be an outlier, of the sort that one will occasionally encounter if one genotypes enough individuals.

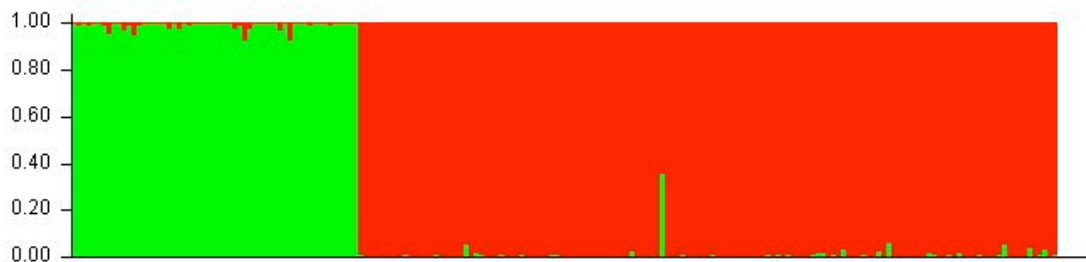


Fig. 3. Estimated proportion of ancestry in the Yaak (green) and GYE (red) for 56 grizzly bears sampled in the Yaak (leftmost columns) and 139 GYE grizzly bears (columns to the right). Only individual 117493 is flagged as having potentially mixed ancestry, being assigned 36% Yaak ancestry and 64% GYE ancestry (the obvious mixed column to right of center). Bear in mind that these values are estimates, subject to uncertain degrees of error.