Protocol S1 Analysis of genetic differentiation in MUM2

A total of 289 lines collected from 15 Norwegian, 6 Central Asian, 7 Spanish and 13 French populations, all previously described in [32], were phenotyped for the presence or absence of mucilage. These four broad regions are genetically differentiated [32] and reflect the species history of range expansion. The absence or presence of mucilage was considered as a binary trait. For the analysis of MUM2 differentiation, we focused on the 6 Central Asian and 15 Norwegian populations. We used primers muc1-F (5'-GAAGGAGGCATCGATGTGAT) and muc1-R (5'-GGTGAGTTTGGTCCAGGAAA) to amplify approximately a 1000 bp fragment in the 5' part of MUM2, including exons 3, 4 and 5 and introns 2, 3, 4 and 5. Genetic differentiation was quantified for the mucilage phenotype and the MUM2 gene and compared to the genetic differentiation observed at 20 microsatellite and 137 single nucleotide polymorphism (SNP) markers described previously [32]. Following recommendation from Kronholm et al. [32], the corrected estimator of genetic differentiation Φ_{ST} (Michalakis and Excoffier 1996) was used for multi-allelic markers, such as MUM2 alleles and microsatellites. The corrected estimator $\phi_{s\tau}$ takes into account the distances between alleles and has been shown to be the best estimator of differentiation for multi-allelic markers or haplotypes [32]. Differentiation was calculated between populations (F_{ST}) or between regions (F_{CT}), in a hierarchical setting taking into account the partition of genetic variation between populations within regions using the R package "hierfstat" (Goudet, 2005). Levels of differentiation for mucilage and MUM2 fell within the range of differentiation observed at neutral markers (Table S3).

- Goudet J (2005) hierfstat, a package for R to compute and test hierarchical F-statistics. Mol Ecol Notes 5: 184–186.
- Michalakis Y, Excoffier L (1996) A generic estimation of population subdivision using distances between alleles with special reference for microsatellite loci. Genetics 142: 1061–1064.