GENETIC ANALYSIS OF EURASIAN POPULATIONS OF *TAENIATHERUM CAPUT-MEDUSAE* SUBSPECIES *ASPERUM*: BIOGEOGRAPHY OF AN INVASIVE, SELF-POLLINATING, ANNUAL GRASS IN ITS NATIVE RANGE

by

Peter Guerdan

A thesis
submitted in partial fulfillment
of the requirements for the degree of
Master of Science in Biology
Boise State University

August 2016

BOISE STATE UNIVERSITY GRADUATE COLLEGE

DEFENSE COMMITTEE AND FINAL READING APPROVALS

of the thesis submitted by

Peter Guerdan

Thesis Title: Genetic Analysis of Eurasian Populations of *Taeniatherum caput-medusae* subspecies *asperum*: Biogeography of an Invasive, Self-Pollinating, Annual Grass in Its Native Range

Date of Final Oral Examination: 4 May 2016

The following individuals read and discussed the thesis submitted by student Peter Guerdan, and they evaluated his presentation and response to questions during the final oral examination. They found that the student passed the final oral examination.

Stephen Novak, Ph.D.	Chair, Supervisory Committee
James F. Smith, Ph.D.	Member, Supervisory Committee
René Sforza, Ph.D.	Member, Supervisory Committee

The final reading approval of the thesis was granted by Stephen Novak, Ph.D., Chair of the Supervisory Committee. The thesis was approved for the Graduate College by Jodi Chilson, M.F.A., Coordinator of Theses and Dissertations.

DEDICATION

To my brothers, without whom I would not be here to do this thesis. I am forever in your debt. Eddie, Jeff, Alex, Ryan, Nate, Steve, Justin, Brandon, Tyler, Cory, Paul, Bobby, Rob, Clayton, and Chris. *Dagaz Maidan, De Oppresso Liber!*

To my fallen brothers: Matt Ferrara, Tim Cunningham, Nick Dewhirst, Ray Munden, Brandon Pepper, Andrew “PK” Pedersen-Keel, and Roberto “Tico” Skelt, be thou at peace.

ACKNOWLEDGEMENTS

The support of many great people made this thesis possible. I'd first like to thank my major advisor, Dr. Steve Novak, whose tireless assistance, guidance, and motivation made this an incredibly informative and enjoyable process. Steve, the gratitude I have for your help at every step of this project cannot be overstated. Thank you for giving me the opportunity to pursue this project and for providing sound counsel. I would also like to thank Dr. Jim Smith for his help along the way, especially with the molecular techniques in the lab. Dr. René Sforza, thank you for seeing the value in this research and for your collection efforts over the last 15 years. I would also like to thank Dr. John Gaskin and Kim Mann from the United States Department of Agriculture (USDA) Agricultural Research Service (ARS) for helpful conversations regarding AFLP best practices and on interpreting the genetic data. Finally, I appreciate the funding provided by the USDA ARS Area-Wide Management of Agricultural Pests Project, the Boise State University Department of Biology, the Boise State University Dean of the College of Arts and Sciences, Dr. Tony Roark, and the Boise State University Vice President for Research and Economic Development, Dr. Mark Rudin.

ABSTRACT

Understanding species' distributions provides a comprehensive biogeographical framework with which to evaluate theoretical and applied ecological and evolutionary questions. To date, few studies have used amplified fragment length polymorphisms (AFLPs) to assess the biogeographical patterns of a broadly distributed grass species, and none that I have found used AFLPs to specifically study biogeographical patterns of an invasive annual grass in its native range. The overall objective of my study was to assess the biogeographic pattern of the invasive, self-pollinating, annual grass *Taeniatherum caput-medusae* subspecies *asperum* (medusahead) in its native range in Eurasia using AFLPs. Seventy populations of medusahead from 13 countries in Eurasia were analyzed in this study with 110 AFLP loci. The populations of medusahead analyzed in this study possessed low to moderate levels of range-wide genetic diversity, which was largely partitioned among populations (i.e., high levels of genetic structure). In addition, my results indicated that genetic diversity was distributed randomly across the species' native range thus providing no support for the Central-Marginal hypothesis. These AFLP results are concordant with a previous study that analyzed the same populations of medusahead using allozymes, with the AFLP method employed in this study providing a finer scale assessment of genetic structure. Finally, these results for medusahead are consistent with results reported for another highly self-pollinating, annual grass species that is broadly distributed across much of Eurasia.

Keywords: AFLPs, biogeography, Central-Marginal hypothesis, medusahead, Eurasia

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

INTRODUCTION

A central aspect of biology involves assessing the myriad factors that influence the geographic distribution of species. An understanding of a species' distribution can provide a comprehensive biogeographical framework with which to evaluate a range of theoretical and applied ecological and evolutionary questions (Bridle and Vines 2007; Kawecki 2008; Sexton *et al.* 2009; Cahill and Levinton 2016). Biogeographic studies describe and explain both the present distribution of organisms and changes in their distribution over time (Hengeveld 1988). Therefore, gaining knowledge of the processes determining a species' range boundaries, when boundaries are stable and dynamic (i.e., when populations are actively expanding or contracting across the landscape), is one of the goals of biogeographic analyses (Holt *et al.* 2005). A species' current range limits occur in space as individuals of that species are no longer able to survive under the conditions beyond their range boundary (Fisher 1930). Range limits are influenced by multiple interacting factors: dispersal capability, biotic and abiotic environmental conditions, establishment success, population demographic parameters such as survival and reproductive rates, gene flow, and the potential for local adaptation to occur (Brown and Lomolino 1998). In addition, variation in the level and structure of genetic diversity across a species' range is the sum of multiple evolutionary and demographic forces: natural selection, gene flow, the effective population size, and *in situ* mutation (Eckert *et al.* 2008; Keller and Taylor 2008; Allendorf and Luikart 2007). Thus, deciphering the multiple factors that determine the abundance and distribution of a species and its range limits requires, by necessity, both an ecological and a genetic approach (Antonovics 1976 a,b).

The abundance of individuals in a population reflects the degree to which different localities fulfill a species' niche requirements (Brown 1984; Brown *et al.* 1995). Closer to a species' range limits, the abundance of individuals in its populations will be reduced, compared with populations near the center of the species' distribution, as environmental conditions at the range limit deviate from the 'ideal' niche requirements of the species (Sagarin and Gaines 2002; Brussard 1984; Lawton 1993; Vucetich and Waite 2003; Hengeveld and Haeck 1982; Brown 1984; Brown *et al.* 1995). This distribution pattern is referred to as the "Abundant Center" model, and it is one of the prevailing models describing population and ecological dynamics across a species' range (Sagarin and Gaines 2002; Andrewartha and Birch 1954; Kendeigh 1974; Brown and Gibson 1983; Cox and Moore 1985; Gaston *et al.* 1997, Hengeveld and Haeck 1982; Cotgreave 1993; Hochberg and Ives 1999). There is however mixed support for this concept in the literature; Sagarin and Gaines (2002) found support for this pattern in only 39% of the studies they reviewed.

The Abundant Center model also holds implications for the level and structure of genetic diversity across a species' distribution (Duncan *et al.* 2015), with these implications leading to the development of the Central-Marginal hypothesis. For a thorough discussion of the Abundant Center model and the Central-Marginal hypothesis, see Eckert *et al*. (2008), but a brief summary is provided here. Under both concepts, central populations that exhibit the highest abundance, survival, and reproductive success are predicted to have higher values for the effective population size (N_e) and gene flow (*m*) relative to populations located elsewhere in the distribution of a species (Eckert *et al.* 2008). In addition, density-dependent migration will likely promote an asymmetric pattern of gene flow in which more migrants disperse from central populations to marginal or peripheral populations (Hansson 1991; Hanski *et al.* 1994; Hartl and Clark 1997; Kubisch *et al.* 2011; Duncan *et al.* 2015). This asymmetric pattern of gene flow may have negative consequences for local adaptation to occur within populations that have dispersed to localities at and/or beyond the range boundary of a species (Hoffmann and Blows 1994; Garcia-Ramos and Kirkpatrick 1997; Kirkpatrick and Barton 1997; Kawecki and Holt 2002; Bridle and Vines 2007; Eckert *et al.* 2008; Munwes *et al.* 2010; Duncan *et al.* 2015). Based on these conditions, marginal populations should exhibit lower genetic diversity within populations and higher population genetic structure, compared with central populations (Eckert *et al.* 2008). Stochastic processes such as genetic drift, founder effects, and population bottlenecks are likely to play a more important role in these relatively smaller, marginal populations (Carson 1959; Mayr 1965; Templeton 1980; Brussard 1984).

The Central-Marginal hypothesis is not only important for understanding the ecology and evolution of a species' range characteristics, it is also important for conservation and management of species in decline (Micheletti and Storfer 2015). Conservation of populations across the geographic distribution of a species is critical to maintaining the adaptations resident in genetically distinct populations. The loss of such populations could reduce the potential of a species to experience range shifts as the result of global change (Millar and Libby 1991; Lesica and Allendorf 1995; Pouget *et al.* 2013; Micheletti and Storfer 2015).

Several alternative models have been proposed to describe the pattern of genetic diversity and genetic structure across a species' geographic distribution. In the first alternative model, genetic diversity may be highest in populations at the range margin because these populations are likely to experience fluctuating selection pressures, compared with populations located at the center of a species distribution (Fisher 1930; Lesica and Allendorf 1995; Volis *et al.* 1998; Munwes *et al.* 2010). The second alternative model proposes no significant differences in genetic diversity between central and marginal populations, and this pattern has been detected in several studies (Mayr 1965; Brussard 1984; Safriel *et al.* 1994; Kark *et al.* 2001; Garner *et al.* 2004; Cahill and Levington 2016). For instance, Garner *et al.* (2004) found no significant difference in the genetic diversity of central and marginal populations of *Rana latastei* (the Italian agile frog), which they suggested was the result of asymmetric range expansion and contraction during periodic, large-scale climate fluctuations. The third alternative model states that populations residing between a species range center and range margins, or at the 'sub-periphery' of the range, should exhibit the highest genetic diversity because populations in such locations would be expected to receive gene flow from multiple core populations (Kark *et al.* 2008; Duncan *et al.* 2015).

Taeniatherum caput-medusae (L.) Nevski, (medusahead, Poaceae) is an invasive, self-pollinating, annual grass native to most of Europe, northern Africa, and southwest Asia (Frederiksen 1986). In Eurasia, three subspecies have been recognized: *T. caput-medusae* subspecies *caput-medusae, T. caput-medusae* subspecies *crinitum* (Schreb.) Melderis, and *T. caput-medusae* subspecies *asperum* (Simk.) Melderis (Frederiksen 1986; Frederiksen and Von Bothmer 1986; Linde-Laursen and Frederiksen 1989) (Fig. 1). The grass is a diploid, winter annual that is primarily self-pollinating (McKell *et al.* 1962; Frederiksen 1986). Most of the pollen grains this plant produces are dispersed within the floret, with each of the short anthers producing only a moderate number of pollen grains. Cleistagomous flowers, as found in this species, promote self-pollination, but some cross-pollination by wind has been suggested in this species (Frederiksen and Von Bothmer 1986; Brock 1998). In southern France, one portion of the species' native range, *Taeniatherum caput-medusae* is listed as a weed in vineyards, without causing much crop damage (Blank and Sforza 2007). Across the plant's distribution in the Mediterranean Basin, it is typically found in "garrigue" habitats, which are characterized as low scrublands on limestone soils (Blank and Sforza 2007). Other native plants growing in the garrigues include *Thymus vulgaris* L. (thyme), *Rosmarinus officinalis* L. (rosemary), and *Ficus carica* L. (fig tree) (Blank and Sforza 2007).

Only *T. caput-medusae* subspecies *asperum* (hereafter referred to as medusahead) is believed to have been introduced into the western United States (US) (Young 1992), where it is a destructive invader of rangelands in California, Idaho, Nevada, Oregon, Utah, and Washington (Invaders Database System 1997-2014; Novak and Rausch 2009). Due to its high silica content, the plant is almost worthless as forage for cattle, sheep, and wildlife, which probably contributes to its ability to displace native vegetation (Miller *et al.* 1999). The biomass of medusahead and other introduced annuals such as *Bromus tectorum* L. (cheatgrass, Poaceae) can build up over several growing seasons, which leads to an accumulation of fine fuel in areas that are heavily infested. The presence of these grasses, and the fuel they produce, has led to an alteration of the fire regime such that fires in western rangelands now occur more frequently and are more severe, compared to range fires prior to European settlement (Whisenant 1990; Novak and Rausch 2009).

Due to the negative ecological consequences associated with the invasion of medusahead across the western US, recent studies have been conducted by Peters (2013) and Skaar (2015) using allozymes to determine the level and structure of genetic diversity within and among native populations, compare the genetic diversity of native populations with that of invasive populations, and identify putative source populations or regions in the native range. Peters (2013) analyzed 34 populations of the grass from across its native range (from Morocco and Spain to Iran), while Skaar (2015) analyzed 48 populations from a smaller geographic area (southeastern Europe and south-central Turkey). Both studies found relatively low levels of within-population genetic diversity, and relatively high levels of genetic structure, compared with other diploid seed plants (Hamrick and Godt 1996). However, each of these studies also reported higher amounts of genetic diversity across native populations (e.g., allelic richness and number of polymorphic loci) and within native populations than in invasive populations, thus providing evidence for founder effects among invasive populations. Finally, results from these two studies suggest that geographic origins for this invasion may have been drawn from across the native range of the grass, with putative source populations occurring in France, Sardinia (Italy), Albania, Macedonia, Greece, Romania, Bulgaria, Turkey, and the Crimean Peninsula of Ukraine.

Despite the analysis of populations from across the Eurasian range of medusahead, neither of these studies explicitly tested any of the biogeographic patterns (e.g., the Central-Marginal hypothesis) mentioned above. The overall objective of my study was to assess the biogeographic pattern of medusahead in its native range in Eurasia using a molecular approach, amplified fragment length polymorphisms analysis (AFLPs). The specific goals of my research are to: (1) determine the level of genetic diversity across and within native populations of medusahead, (2) determine the genetic and geographic structure of native populations of this grass, (3) evaluate these genetic data in the context of the Central-Marginal hypothesis, and other models used to describe biogeographic patterns, and (4) compare and combine AFLP results with previously reported allozyme data to more fully assess the demographic and evolutionary forces that have shaped the genetic diversity of medusahead in its native range.

To date, few studies have used AFLPs to assess the biogeographical patterns of a broadly distributed grass (e.g., Wagner *et al.* 2011), and none that this author have found have used AFLPs to specifically study biogeographical patterns of an invasive annual grass in its native range.

METHODS

Plant Collections

In order to assess the biogeographic pattern of medusahead in its native range, my goal was to analyze populations across Eurasia. A total of 70 populations of medusahead from 13 countries were analyzed in this study, with populations ranging from Morocco to Russia (Fig. 2, Table 1). Mature spikes with caryopses (hereafter referred to as seeds) from each of these populations were collected from 2001 to 2013 by Dr. Rene F. H. Sforza and Dr. Stephen J. Novak. Populations in my study ranged from 13 m to 1984 m in elevation, from 29° North to 45° North latitude, and 8° West to 39° East longitude. For the complete population locality information, see Table 1. In order to maximize the total number of populations analyzed in this study, I capped the number of individuals sampled within populations at 10. This sampling strategy is believed to optimize the detection of within- and among-population genetic diversity (Wagner *et al.* 2011; Prinz *et al.* 2009). Spikes from 20-30 individuals were collected in each population, and each spike was placed into a separate paper envelopes and stored at room temperature until DNA extraction.

DNA Extraction and AFLP Procedures

Because many of the medusahead seeds used in this study could no longer germinate, DNA was extracted directly from seed tissues. In order to maximize DNA yield, seeds were allowed to imbibe distilled water for 24 h prior to DNA extraction.

Total genomic DNA was extracted from the imbibed seeds using the Qiagen DNeasy Plant Mini prep kits (Valencia, California). The DNA extraction procedures I used generally followed the manufacturer's recommendations with a slight modification (Qiagen 2015). This modification involved the incubation of samples in a 65° C water bath for 2 h.

The Amplified Fragment Length Polymorphism protocol was conducted on the extracted DNA using the protocol developed by Vos *et al.* (1995), with slight modifications described by Lucardi (2012). To ensure the appropriate conditions were maintained, restriction enzyme digests with *EcoR*1 and *Mse*1, and the ligation of the corresponding AFLP adaptor pairs were performed in a BioRad PTC-200 Thermocycler (Hercules, California). A pilot study was conducted prior to the start of conducting the AFLP procedure on sampled populations to determine the most polymorphic selective primer pairs. Three primer pairs were tested (see Table 2) with the two most polymorphic primers used in the AFLP procedure.

The restriction enzyme double digest reactions were set up as follows: 15 µl of extracted DNA were added to 9.58 µl H_20, 2.5 µl NEB 4 buffer (New England Biolabs, Ipswich, Massachusetts), 0.25 µl BSA (10 mg/ml) (Promega Corp., Madison, Wisconsin), 1.67 µl *EcoR*1 (12 u/µl) (Promega Corp.), and 1.0 µl *Mse*1 (10,000 u/ml) (New England Biolabs), for a total volume of 25 µl. The reaction was incubated for 2 h at 37° C, followed by 15 m at 70° C. The ligation reaction had a total volume of 20 µl and was set up as follows: 10 µl of a restricted DNA solution was added to 5.0 µl water, 2.0 µl T4 ligase buffer (Promega Corp.), 1.0 µl T4 ligase (3 u/µl) (Promega Corp.), 1.0 µl *Mse*1 adaptor pair, and 1.0 µl *EcoR*1 adaptor pair (see Table 2 for the sequences). The ligation reaction was incubated for 3 h at 37° C. Pre-selective amplification consisted of the following reaction: 3.0 µl of ligated DNA were added to 7.1 µl water, 4.0 µl 5X Go*Taq* buffer (Promega Corp.), 2.5 µl dNTPs (0.2 mM) (Promega Corp.), 1.2 µl $MgCl_2$ (25 mM) (Promega Corp.), 1.0 µl *Mse*1 + C primer (10 µM) (Eurofins Operon, Huntsville, Alabama), 1.0 µl *EcoR*1 + A primer (10 µM) (Eurofins Operon), and 0.2 µl Go*Taq* Flexi DNA Polymerase (5 u/µl) (Promega Corp.). The reaction was heated to 94º C for 1 m, and 30 PCR cycles were conducted as follows: 30 s at 94º C, 1 m at 56º C, and 1 m at 72º C. A final elongation step conducted for 2 m at 72° C. A 1:20 dilution of pre-selective amplification products was conducted. Selective amplification reactions consisted of the following: 3.0 µl of diluted pre-selective amplification products added to 6.05 µl water, 4.0 µl 5X Go*Taq* Buffer, 2.5 µl dNTPs (0.2 mM), 3.7 µl $MgCl_2$ (25 mM), 1.0 µl *Mse*1 + CXX primer (5 µM), 1.0 µl *EcoR*1 + AXX primer (1 µM), and 0.2 µl Go*Taq* Flexi DNA Polymerase (5 u/µl). The reaction was conducted for 2 m at 94° C, 10 cycles of (30 s at 94° C, 30 s at 65° C, 1 m at 72° C), 30 cycles of (30 s at 94° C, 30 s at 56° C, 1 m at 72°C), and a final step for 30 s at 72° C.

AFLP Loci Selection and Error Rate Estimation

AFLP bands were visualized, selected, and scored using the default algorithm in the program Peak Scanner 2 (Applied Biosystems Industries, Waltham, Massachusetts) and using a custom panel created in the program GeneMarker (SoftGenetics, State College, Pennsylvania). The AFLP loci selected to be scored in this analysis were chosen by visualizing the entire sample set and determining which loci were unequivocally present in at least one population using both the “Score” and “Intensity” functions of GeneMarker to assist in calling bands. Loci between 60 and 400 base pairs (bp) size range were considered present when the eletropherogram showed an intensity value greater than 75 relative fluorescent units (rfu) and displayed a discrete “peak” shape. These loci selection criteria have been employed in other AFLP studies (e.g., Wolf *et al.* 2004; Trybush *et al*. 2006; Bjerregaard and Wolf 2008; Zhang and Hare 2012; Voss *et al.* 2012; Preite *et al.* 2015). Once 110 AFLP loci were selected from both primer pairs, individual AFLP electropherograms were scored as present or absent (“1” or “0”, respectively). Restricting the fragment size range from 60 to 400 bp mitigates the effects of AFLP band homoplasy while maximizing the potential of detecting polymorphisms (Vekemans *et al.* 2002).

In order to calculate an AFLP error rate, samples were chosen for replicate reactions from the entire set of successfully amplified samples in my analysis. Twenty percent (20%) of the individuals originally analyzed were randomly selected (99 individuals) and reanalyzed using the AFLP procedures described above, beginning with the restriction digestion step. The replication error rate was calculated to be 2.009%, which was then used to determine the maximum number of loci by which individuals could differ and still be considered genetically identical (Gaskin *et al.* 2013; Hufford *et al.* 2013). With an error rate of 2.009% for 110 scored AFLP loci, individuals differing at 2.2 loci would still be considered genetically identical.

Data Analysis

The program AFLP-SURV (Vekemans 2002) estimates genetic diversity, population genetic structure, and genetic distance values for dominant molecular markers such as AFLPs. Because medusahead has cleistogamous florets, and the results of a mating system study revealed that the plant has a predominantly self-pollinating mating system which results in significant deviation from Hardy-Weinberg equilibrium (S.J. Novak, unpublished data), “option 1 – fragment frequencies (homozygous at marker loci)” was chosen to calculate allelic frequencies in AFLP-SURV. AFLP-SURV uses the dominant marker bi-allelic coding system derived in GeneMarker to compute the number of polymorphic loci (P), the percentage of polymorphic loci (%P), and Nei’s (1978) gene diversity (H_T) values for each population. Nei’s gene diversity is equivalent to expected heterozygosity (H_E) when it is calculated with bi-allelic data, as is the case with AFLPs (Lynch and Milligan 1994; Nybom 2004). AFLP-SURV can also be used to conduct a hierarchical analysis of how the total gene diversity (H_T) is partitioned within and among populations. The parameter H_S describes the amount of the total gene diversity that is partitioned within populations, while D_{ST} describes the amount of the total gene diversity that is portioned among populations. These parameters are related by the equation $H_T = H_S + D_{ST}$. G_{ST} is a parameter that describes the proportion of the total gene diversity that is partitioned among populations, and it is calculated as $G_{ST} = D_{ST}/H_T$. Pairwise population F_{ST} values and pairwise population genetic distance values were estimated using one thousand permutations with one thousand bootstrap replicates. AFLP-SURV computes pairwise population F_{ST} values and genetic distance values that can be inputted into other population genetics programs such as STRUCTURE and PHYLIP.

The program AFLPdat was used to create input files for use in HICKORY (Ehrich 2006). HICKORY was used to independently calculate measures of genetic diversity, including H_E, and to calculate F-statistics, including F_{IS}, which describes the level of inbreeding within populations (Holsinger and Lewis 2003). STRUCTURE 2.3.4 uses an iterative model-based algorithm to assign individuals within a population to genetic clusters (Pritchard *et al.* 2000). Because AFLPs are a dominant molecular marker, which generate a pseudo-haploid data matrix, and STRUCTURE is designed for diploid data, AFLP-SURV produces an input file for STRUCTURE with the second allelic state recorded as missing data (-9). I used the "No Admixture" model in the Ancestry model as input parameters, as recommended by AFLP-SURV. I used a burn-in of 10,000 and 50,000 Monte Carlo Markov Chains (MCMC) iterations to determine the number of genetic clusters in my AFLP data. I calculated delta K using the method of Evanno *et al.* (2005) using Microsoft Excel where [L"(K)] equals the second order mean logarithmic probability of assignment with the formula ΔK = ([L"(K)]) / (StdDev L(K)). I confirmed this calculation using the applet STUCTURE HARVESTER (Earl and vonHoldt 2012). My first STRUCTURE analysis testing population assignments of K = 1 to K = 20 with 10 replicates per K value, a burn-in of 10,000 iterations, and 50,000 MCMC iterations yielded results that supported a K = 10, but this result was somewhat equivocal. I reran STRUCTURE testing population assignments of K = 6 through K = 14 with the same parameters described above. This analysis found a K = 9 to be the best supported.

The program GenoType assigns individuals in a population a genotypic identity based on a shared AFLP banding patterns (Meirmans and Van Tienderen 2004). GenoType is designed to genotype asexually reproducing organisms and is therefore better suited than other programs for analyzing primarily self-pollinating plants such as medusahead. As recommended for AFLP data by Meirmans and Van Tienderen (2004), I used the "infinite allele model" for the distance option, and treated missing data as "not counted." GenoType requires the user to enter an integer threshold value, which determines how many loci an individual can differ at and still be considered genetically identical. Based on my previously calculated AFLP error rate of 2.009%, or a mismatch of 2.2 AFLP loci, I used a threshold of three loci for this analysis. GenoType produces an input file for its complementary program, GenoDive (Meirmans and Van Tienderen 2004). The program GenoDive calculates diversity indices after GenoType assigns individuals to genotypes. Several genetic parameters are computed by GenoDive: s is the number of genotypes, n is the sample size, and p_i is the frequency of genotype i in the sample. Indices include Nei's (1987) genetic diversity corrected for sample size (Simpson's diversity index) using the formula $(n/(n\text{-}1))*(1\text{-}\Sigma p_i^2)$. Simpson's evenness was calculated using the formula $(1/S)*(1/(\Sigma p_i^2))$. The Shannon-Wiener (or Shannon-Weaver) diversity index was calculated using the formula $–\Sigma p_i*logp_i$.

The program PHYLIP 3.695 was used to create unrooted Neighbor-Joining trees based on Nei's genetic distance (Felsenstein 2004). The program GenAlEx was used to conduct an Analysis of Molecular Variance (AMOVA) to determine how genetic diversity was partitioned within and among populations and regions (Peakall and Smouse 2006, 2012). Two separate AMOVAs were conducted: the first AMOVA investigated the partitioning of genetic variance among and within populations, and the second AMOVA was based on the hierarchical arrangement of populations into five regions based on their geographical locations and apparent barriers to gene flow (Fig. 2). Region 1 included populations from Spain and Morocco, separated from the remainder of populations by the Pyrenees Mountains and the Mediterranean Sea. Region 2 included populations from France and Italy (including Sardinian populations), separated from other populations by the Pyrenees Mountains, the Mediterranean Sea, and the Adriatic

Sea. Region 3 included populations from Albania, Bulgaria, Greece Macedonia, Romania, western Turkey, and Serbia, separated from other populations by the Adriatic Sea, the Black Sea, and the Carpathian Mountains. Region 4 included populations from the Ukraine and Russia, separated from other populations by the Carpathian Mountains, Caucasus Mountains, and the Black Sea. Region 5 included Anatolian Turkish populations and is separated from other populations by the Aegean Sea, the Sea of Marmara, the Bosporus and Dardanelles Straits, and the Black Sea. R 3.1.2 (R Core Development Team 2014) was used to generate descriptive statistics, execute correlation tests, test univariate linear regression models, produce genetic diversity indices, and prepare software input files in AFLPdat.

Evaluating the Central-Marginal Hypothesis

Based on the recommendations provided by Eckert *et al*. (2008), I did not employ qualitative criteria for the categorical assignment of populations to central or marginal groups. Instead, I evaluated the Central-Marginal hypothesis among populations of medusahead across its native range using three quantitative approaches. In the first approach, I identified the geographic centroid of the locality polygon of all 70 populations included in this study using Google Earth and Microsoft Excel to analyze the GPS coordinates of all 70 populations. Geographic coordinates were visually inspected and confirmed with the collectors when necessary. The mean latitude and longitude values of populations included in this study were computed in Excel, which resulted in the determination of the geographic centroid of my populations. The Euclidean distance of each population to the geographic centroid was calculated using the “ruler” function of Google Earth and were confirmed using the two-plane Euclidean distance equation $d(p,q)$

$= \sqrt{((q_1-p_1)^2 + (q_2-p_2)^2)}$ where p = latitude and q = longitude. A univariate linear regression model in R was used to assess the relationship between the H_E value of a population and its distance to the geographic centroid. The second method employed to evaluate the Central-Marginal hypothesis used the same univariate regression model described above, but analyzed the relationship between the %P value of a population and its distance to the geographic centroid. The third method employed to evaluate the Central-Marginal hypothesis used a univariate linear regression model in R to assess how genetic diversity in medusahead was distributed over a longitudinal gradient. Because the geographic distribution of medusahead in its native range mainly occurs along an east-west axis (see Frederiksen 1986), this test of the Central-Marginal hypothesis is appropriate.

Comparing Molecular Markers: AFLPs and Allozymes

One of the specific goals of this research is to compare the estimates of genetic diversity obtained using AFLPs with the estimates previously reported using allozymes. Allozyme genetic data comes from two recent studies: Peters (2013) analyzed 956 individuals in 34 populations of medusahead and Skaar (2015) analyzed 1084 individuals in 48 populations of medusahead from southeastern Europe and south-central Turkey. Because values of H_E and other genetic parameters were not normally distributed, statistical comparison of AFLP- and allozyme-based estimates of genetic diversity were conducted using non-parametric Spearman rank correlation analysis in R (R Core Development Team 2014).

RESULTS

In this study, the level and structure of genetic diversity within and among populations from across much of the native range of medusahead was estimated based on the analysis of 495 individuals from 70 populations (Fig. 2, Table 1). My goal was to analyze 10 individuals per population, but because DNA could not be successfully extracted from all seeds, the actual sample size was an average of 7.2 individuals per population. The smallest number of individuals sampled in any population (two) occurred for Tizi n'test, Morocco, while 10 individuals were analyzed in several populations (Table 1). Because I was concerned that estimates of genetic diversity might be positively correlated with population size, I conducted a correlation analysis of the number of AFLP multilocus genotypes (MLGs) detected in each population (without using the AFLP error rate) and the sample size (n) of each population and a correlation analysis of the H_E and the sample size of each population. This analysis indicated that there was no significant correlation between the number of AFLP MLGs and population sample size ($y = 0.1693x + 1.2787$, $P > 0.5$) (Fig. 3), nor a significant correlation between H_E and population sample size ($y = 0.0010x + 0.0409$, $P > 0.5$) (data not shown). Therefore, I do not believe that my estimates of genetic diversity within these 70 native populations of medusahead were influenced by population sample sizes.

Genetic Diversity

Based on the criteria described above, 110 AFLP loci were scored to generate estimates of range-wide and within-population genetic diversity. Of the 110 AFLP loci selected for scoring, 104 loci (94.5%) were polymorphic across all individuals and populations of medusahead across its native range (Table 3). A moderate level of genetic diversity was discovered across all individuals across the native range of the grass (H_E = 0.166). Among the 70 populations of medusahead analyzed in this study, the populations from Bancizaray, Ukraine (38 polymorphic loci, 34.5 %P, and 0.188 H_E), Tenevo, Bulgaria (38 polymorphic loci, 34.5 %P, and 0.135 H_E), and Tleta tassrit, Morocco (33 polymorphic loci, 30.0 %P, and 0.158 H_E), exhibited the highest level of genetic diversity; while the population located near Poggiorsini, Italy, had the lowest amount of genetic diversity (1 polymorphic locus, 0.9 %P, and 0.004 H_E) (Table 3). The mean value for these three parameters across all 70 populations was 7.82 polymorphic loci, 11.72 %P, and 0.049 H_E (Table 3). The mean value for the coefficient of inbreeding (F_{IS}) across all populations was 0.991 (SD = 0.0097).

Populations from Region 1 and Region 3 had the highest genetic diversity, the populations from Regions 4 and 5 had intermediate levels of genetic diversity, and the populations from Region 2 exhibited the lowest amount of genetic diversity (Table 4). Estimates of H_E and %P for all 70 populations of medusahead analyzed in this study using AFLPs were significantly and positively correlated ($P<0.001$, data not shown).

Genetic Structure

Nei’s total gene diversity (H_T) was 0.171, and the value for the amount of gene diversity distributed among populations (D_{ST}) was 0.122 (Table 5). Thus, the proportion of the total gene diversity distributed among populations (G_{ST}) was 0.716, indicating that 71.6% of the total gene diversity of these 70 populations of medusahead was distributed among populations. The mean value of Wright's F_{ST} for all populations (0.717) (Table 5) was in close agreement with the G_{ST} values reported above. The highest population pairwise F_{ST} value was 0.974, and this value occurred for the Tizi n'tishka, Morocco and Poggiorsini, Italy, population pair (Appendix A). The lowest population pairwise F_{ST} value (0.012) occurred between Sudak and Trudalyubivka, Ukraine. The mean genetic distance value for all 70 populations of medusahead was 0.145 (Appendix B). The highest population pairwise genetic distance value was 0.643 and occurred for the Kakcaveli, Ukraine and Izvorishte, Bulgaria, population pair. The lowest population pairwise genetic distance value (0.004) occurred for the Sudak and Trudalyubivka, Ukraine populations.

Analysis of molecular variance (AMOVA) was used to partition genetic diversity 1) within and among populations and 2) within and among populations within regions and among regions. In the first AMOVA analysis, genetic diversity was partitioned at two hierarchical levels, and 29.92% of the variation was partitioned within individuals and 70.08% of the variation was partitioned among populations (Table 6A). In the second AMOVA analysis, 32.11% of the genetic diversity was partitioned within populations, 39.41% of the diversity was partitioned among populations within the five regions, and 28.48% of the diversity was partitioned among the five regions (Table 6B).

The genetic relationships among the 70 populations of medusahead sampled in this study were assessed using an un-rooted neighbor-joining tree (Fig. 4). This analysis clustered populations based on Nei's genetic distance values. The neighbor-joining tree showed some clustering of populations based on geographical proximity, but the tree revealed that many clusters are composed of populations from the five different geographical regions. The most genetically distinct populations on the neighbor-joining tree are Lodine, Sardinia, Italy, and three distinct clusters that include populations from Spain, Morocco and two from Ukraine (Bancizaray and Kakcevelli) (Fig. 4). In addition, with the exception of the population from Lodine, the remaining five populations from Italy formed a cluster. For evidence that populations from the different regions are genetically similar, note the distribution of populations from Regions 2 and 4 within multiple clusters throughout the neighbor-joining tree. Genetic clustering in the neighbor-joining tree presented a similar pattern to that of the pairwise F_{ST} and pairwise genetic distance matrices (Appendices A and B, respectively).

Based on the methods of Pritchard *et al.* (2000) and Evanno *et al.* (2005), a K = 9 clusters had the strongest support (Fig. 5), and the assignment of the 70 populations of medusahead to these nine clusters are shown in Fig. 6 A & B. The genetic cluster indicated by the blue color had the highest occurrence among the medusahead populations analyzed in this study, with at least one individual assigned to this genetic cluster in 41 of 70 (58.6%) populations. The order of occurrence of the genetic clusters are teal (57.1% of populations), purple (44.3% of populations), orange (38.9% of populations), yellow (14.3% of populations), red-striped (7.1% of populations), green (5.7% of populations), pink (4.3% of populations), and red (2.9% of populations). Twenty-one populations were completely assigned to only one genetic cluster, with the remaining 49 populations having at least two individuals assigned to different genetic clusters (Fig. 6B). Sozopol, Bulgaria had the highest number of individuals assigned to different genetic clusters, with five different genetic clusters identified. Ten populations had individuals assigned to four genetic clusters, 17 populations had individuals assigned to three genetic clusters, and 21 populations had individuals assigned to two genetic clusters.

Multilocus Genotypes

Initially, 419 AFLP MLGs were identified across the 495 individuals in the 70 populations analyzed in this study. Employing an AFLP error rate of 2.009%, 132 ALFP MLGs were detected in this analysis. The mean number of MLGs detected per population was 2.6, and a maximum of 10 genotypes occurred in the Tenevo, Bulgaria population (Tables 7 & 8). Several populations (28) possessed only one MLG. However, there was no significant correlation between the number of MLGs identified in a population and its sample size (Fig. 3). The most common AFLP MLG across the range of medusahead was MLG #1, found in 275 of 495 (55.6%) of individuals. Henceforth, this genotype is referred to as the Most Common Genotype (MCG). The MCG was detected in 46 of 70 (65.7%) populations surveyed in this study. The only countries in which the MCG was not found were Italy, Morocco, and Spain. The majority of MLGs detected in this study, 110 of 132 (83.3%) genotypes, were singletons (detected in just one individual) (Tables 7 & 8). For MLGs detected in more than one individual, that number ranged from two individuals (nine MLGs) to 13 individuals (MLG #30).

The mean value for the Simpson’s diversity index across all 70 populations of medusahead was 0.360, with values ranging from 0.0 to 1.0 among these populations (Table 8). Populations that were monomorphic for a MLG had a Simpson’s diversity index value of 0.0, for such populations Simpson’s evenness values can’t be calculated.

The mean value for Simpson's evenness across all populations was 0.859. The populations from Slava Rus, Romania and Izvorishte, Bulgaria had the lowest evenness values (0.48), with several populations having the maximum evenness value of 1.0. The mean value for the Shannon-Wiener diversity index was 0.254, with these values ranging from 0.0 to 1.0 (1.0 for the Tenevo, Bulgaria population).

Biogeographical Patterns

All three methods I used to evaluate the Central-Marginal hypothesis in this study yielded non-significant results (Fig. 7). The first method of evaluating the hypothesis used a linear regression analysis of AFLP H_E and distance to the geographic centroid, and indicated a slightly positive, yet non-significant relationship ($y = 0.000003x + 0.0453$, $P > 0.1$) (Fig. 7A). The second method of assessing the hypothesis used a linear regression analysis of AFLP H_E and longitude, and indicated a slightly positive, but non-significant relationship ($y = 0.0002x + 0.0427$, $P > 0.5$) (Fig. 7B). The third method used a linear regression analysis of AFLP %P and distance to the geographic centroid, and indicated a slightly negative, but non-significant relationship ($y = 0.0005x + 11.239$, $P > 0.5$) (Fig. 7C). In order to compare these findings concerning the test of the Central-marginal hypothesis using AFLP data, I evaluated this hypothesis using previously reported allozyme data (Peters 2013; Skaar 2015). In this analysis, a linear regression analysis of H_E obtained using allozyme data and distance to the geographic centroid yielded a slightly positive, but non-significant relationship ($y = 0.000002x + 0.0299$, $P > 0.5$) (Fig. 8).

Comparison of Molecular Markers

Based on a comparison of the populations of medusahead previously analyzed using allozymes and this AFLP analysis, a total of 65 populations were analyzed using both molecular markers. A significant, positive correlation was detected between AFLP H_E and allozyme H_E ($y = 0.2373x + 0.0384$, $P < 0.05$) (Fig. 9). The mean value of H_E using AFLPs (0.049) was significantly higher than the mean values obtained using allozymes (0.03) (Wilcoxon rank sum test, $P<0.001$) (Table 9). A total of 66 allozyme MLGs (1.94 MLGs per population) were reported among 34 native populations by Peters (2013), and 35 allozyme MLGs (0.73 MLGs per population) were reported among 48 native populations by Skaar (2015). My analysis with AFLPs, using the error rate calculation, yielded a total of 132 MLG in 70 populations (1.89 MLG per population), and I found a significant positive correlation between the number of MLGs discovered per country between my AFLP data and the previous allozyme data ($y = 1.34x + 1.58$, $P < 0.05$) (Fig. 10). Estimates of Nei's gene diversity statistics calculated in this study with AFLPs show conflicting results when compared to the estimates using allozyme data (Table 9). The value for the total gene diversity (H_T) in my study was 0.171, compared with the values of 0.262 and 0.248 previously reported by Peters (2013) and Skaar (2015), respectively, using allozymes. The value of G_{ST} in this AFLP analysis was 0.715, compared with the values of 0.745 and 0.417 previously reported by Peters (2013) and Skaar (2015), respectively (Table 9).

The STRUCTURE analysis of AFLP data for the 70 native populations of medusahead revealed the presence of nine genetic clusters (Figs. 5 & 6). In a STRUCTURE analysis of 48 native populations of medusahead analyzed using allozymes, Skaar (2015) detected two genetic clusters. I obtained AFLP data for the same 48 populations analyzed by Skaar (2015), and I subjected the AFLP results for these 48 populations to a STRUCTURE analysis and found support for six genetic clusters among these 48 populations (Fig. 11). Results of this comparison indicated that AFLPs were a more polymorphic molecular marker compared with allozymes, and that AFLPs provided a higher degree of resolution for detecting finer-scale genetic structure among the native populations of medusahead analyzed in this study (Fig. 11).

DISCUSSION

The 70 populations of medusahead analyzed using 110 AFLP loci allow me to make broad inferences across much of this species' Eurasian range, using a highly polymorphic molecular marker. The populations of medusahead analyzed in this study show low to moderate levels of range-wide genetic diversity that is largely partitioned among populations (i.e., high levels of genetic structure) (Nybom 2004). In addition, my results indicated that genetic diversity is distributed randomly across the species' native range thus providing no support for the Central-Marginal hypothesis. These AFLP results are generally consistent with a previous study that analyzed the same populations of medusahead using allozymes. Finally, these results for medusahead are similar to the results reported for *Lolium rigidum*, another self-pollinating, annual grass species that is broadly distributed across much of Eurasia.

Genetic Diversity

A critical goal of this research was to determine the level and structure of genetic diversity of medusahead across its range in Eurasia. To accomplish this goal, my experimental design primarily focused on analyzing as many populations as possible because increasing the number of populations increases the statistical power for detecting a biogeographical pattern (Eckert *et al.* 2008). Thus, if sufficient plant material existed for two or more individuals to be successfully amplified using the AFLP procedure, the population was included in the analysis. Conversely, increasing the number of individuals sampled per population increases the statistical reliability of within-population estimates of genetic diversity (e.g., expected heterozygosity). A similar sampling strategy has been employed in other studies assessing genetic diversity and genetic differentiation of broadly distributed species (e.g., Wagner *et al.* 2011; Prinz *et al.* 2009; Gaskin *et al*. 2013). Moreover, the non-significant relationship between population sample size and the number of MLGs (Fig. 3) and sample size and values of H_E (data not shown) indicated that sample sizes did not limit the estimates of genetic diversity reported here.

A previous study estimated that the mean value for the inbreeding coefficient (*F*) for native populations of medusahead using allozymes was 0.997 (S.J. Novak, unpublished data), and this value was consistent with the value for the inbreeding coefficient (F_{IS}) calculated for the 70 populations of medusahead analyzed in this study using AFLPs (0.991). Values of *F* obtained using these two marker systems were the product of the high rate of self-pollination occurring within populations of this species, and indicated that significant deviations from Hardy-Weinberg equilibrium exist within these populations. Several parameters commonly used to evaluate the amount and distribution of genetic diversity in populations of a species, such as total Nei's genetic diversity and expected heterozygosity, indicated that the populations of medusahead analyzed in the current study have relatively low genetic diversity (Tables 3, 4, & 5). In a review of 307 studies that used dominant, multilocus molecular markers such as Random Amplified Polymorphic DNA (RAPD) and AFLPs, Nybom (2004) found mean values of within population genetic diversity associated with different plant life-history traits. Plants with an annual life form, a widespread geographic range, a primarily selfing mating system, gravity seed dispersal, and an early successional status had a mean expected heterozygosity of 0.166, which is higher than the value I obtained in this study ($H_E = 0.049$). Using AFLPs, Voss *et al.* (2012) reported a mean H_E value of 0.005 (Standard Error = 0.0012) in native populations of *Ceratocapnos claviculata*, a primarily selfing plant species. The value of H_E reported here for medusahead is approximately 10-fold greater than the value reported by Voss *et al.* (2012). Additionally, the values of Simpson's genotypic diversity index and Simpson's evenness for medusahead (0.36 and 0.859, respectively) (Table 8) were considerably lower than the values reported for *Chondrilla juncea* (0.99 and 0.96, respectively) by Gaskin *et al.* (2013), indicating that these populations of medusahead demonstrate relatively low levels of multilocus genotype diversity (Tables 8).

The number and distribution of AFLP Multilocus Genotypes (MLG) is a measure of the level and distribution of genetic diversity among native populations of medusahead. My analysis of 495 individuals detected 132 MLGs (utilizing the error rate) (Tables 7 & 8), which resulted in a G/N value (G/N is the proportion of distinct multilocus genotypes detected) of 0.267, which is considerably lower than the value of 0.650 reported by Gaskin *et al.* (2013) in a range-wide genetic analysis of *Chondrilla juncea* using AFLPs. More in-keeping with my data, Voss *et al.* (2012) discovered 39 MLGs among the 207 native individuals of *Ceratocapnos claviculata* they sampled, which produced a G/N value of 0.188. The studies of Voss *et al.* (2012) and Gaskin *et al.* (2013) indicate that the MLG values reported here for medusahead fall within the range previously reported across populations of these two broadly-distributed plant species, using AFLPs. Several life history traits could potentially contribute to the reduced number of MLGs discovered for medusahead, compared with that reported for *Chondrilla juncea* (Gaskin *et al*. 2013). *Chondrilla juncea* is a perennial herbaceous plant that is believed to reproduce both sexually and asexually in its native range in Eurasia, but which appears to reproduce asexually through gametophytic apomixis throughout its invasive range in North America, Australia, and Argentina (Panetta and Dodd 1987; Chaboudez 1994; McVean 1996; Gaskin *et al.* 2013). Thus, even infrequent bouts of sexual reproduction and genetic recombination in *Chondrilla juncea* would lead to a higher level of genetic variation within and among native populations, compared with native populations of medusahead. In addition, the study conducted by Gaskin *et al.* (2013) analyzed populations of the entire species of *Chondrilla* j*uncea*, whereas my study analyzed populations from a single subspecies of medusahead (*T. caput-medusae* subspecies *asperum*). Genetic analyses that include taxa from different taxonomic levels might lead to the detection of higher amounts of genetic diversity in *Chondrilla juncea.* While the native ranges of medusahead and *Chondrilla juncea* overlap longitudinally, *Chondrilla juncea* occurs across a greater latitudinal range throughout much of Eurasia. This larger geographical distribution of *Chondrilla juncea* compared to medusahead, and its resulting occupancy of a variety of habitats and potentially more diverse ecological niches, may be associated with the overall higher levels of genetic diversity detected for *Chondrilla juncea* compared with medusahead.

Genetic Structure

The populations of medusahead sampled in this study had relatively high genetic structure, as exemplified by the G_{ST} (0.716) and F_{ST} (0.717) values reported for all 70 native populations (Table 5). These values indicate that 71.6% and 71.7% of the total genetic diversity for populations of medusahead is partitioned among populations: a pattern of partitioning genetic diversity that is often associated with plants that have a primarily self-pollinating mating system (Barrett and Husband 1990; Novak and Mack 1993; Nybom 2004, Voss *et al.* 2012; Pajkovic *et al.* 2014). Results from both AMOVA runs provided results similar to the G_{ST} and F_{ST} values mentioned above, and indicated that the majority of the genetic diversity is partitioned among population (70.1%, Table 6A), or partitioned among populations within regions (39.4%) or among regions (28.5%) (Table 6B). These data indicate 28.5% of the total genetic variance of medusahead is partitioned among the five geographic regions described in Fig. 2. This result probably stems from the primarily self-pollinating mating system of medusahead and from barriers to gene flow such as mountain ranges and bodies of water that are present across the Eurasian range of medusahead.

The Neighbor-Joining tree (Fig. 4), which is based on Nei’s genetic distance values, reveals most clusters consist of populations from different geographic regions. For instance, populations from Region 1 occur in one cluster, although this cluster also included two populations from Region 4. As a further way of visualizing this pattern, note the distribution of populations from Bulgaria and Turkey in various clusters throughout the neighbor-joining tree. The occurrence of populations from different countries in the same cluster indicates that there is little relationship between geographic distance and genetic distance.

Results from the STRUCTURE analysis revealed a pattern similar to that of the neighbor-joining tree: populations from different regions were assigned to the same genetic cluster (or group). First, the methods of Pritchard *et al.* (2000) and Evanno *et al.*

(2005) both identified the same number of genetic clusters (K = 9) (Fig. 5). Second, several genetic clusters exhibited a restricted geographical distribution and were only present in some populations from Morocco, Italy and Bulgaria (Fig. 6). Third, populations assigned to the genetic cluster indicated by the yellow color exhibited a disjunct distribution, occurring in Region 1 (Spain and Morocco) and Region 4 (Ukraine). Finally, populations in the central and eastern portions of the native range of medusahead included individuals possessing various frequencies of four different genetic clusters (blue, teal, purple, and orange) (Fig. 6). Populations in these regions exhibited a high degree of genetic admixture that likely resulted from gene flow between these populations, most probably due to seed dispersal leading to the establishment of populations following disturbance events.

Biogeographical Pattern

Range-wide tests of the Central-Marginal hypothesis are rare. The meta-analysis of Eckert *et al.* (2008) revealed the existence of only 28 such studies; with most studies examining only one region of a species' distribution, or analyzing populations located only at the center of a species' distribution, only at the species' range boundary, or only disjunct populations. In order to maximize the possibility of detecting genetic patterns at geographically meaningful scales, I attempted to maximize the number of populations analyzed across the entire Eurasian range of medusahead. The most common genetic diversity parameters used to test the Central-Marginal hypothesis are expected heterozygosity (H_E), percentage of polymorphic loci (%P), and allelic richness (Eckert *et al.* 2008). Although the majority of studies (87%) that reported both H_E and allelic richness found that both parameters were interrelated and provided similar results, this was not a uniform outcome (Eckert *et al.* 2008). Therefore, my study was designed to evaluate the tenets of the Central-Marginal hypothesis using two parameters, H_E and %P, in order to independently investigate the species' distribution using a genetic approach. Eckert *et al*. (2008) found that 60.5% of the studies that used some statistical analysis found support for either 1) a decline in genetic diversity or 2) an increase in genetic differentiation in marginal versus central populations. These results included studies that categorically assigned populations to "central" or "marginal" groups. Conversely, studies that used a quantitative measure of centrality such as distance to centroid and statistical analysis found that only 47% of studies yielded evidence in support of the two tenants of the Central-Marginal hypothesis described above (Eckert *et al.* 2008). Despite the lower support for the Central-Marginal hypothesis using a quantitative measure of centrality, Eckert *et al*. (2008) recommended the use of this approach when testing this hypothesis. Therefore, my evaluation of the Central-Marginal hypothesis was conducted on medusahead populations using a quantitative approach in which populations were analyzed as being continuously distributed across the species' range. The results reported here provide support for a random distribution pattern of genetic diversity, and this result is in agreement with 53% of studies reviewed in Eckert *et al.* (2008).

Results of my evaluation of the distribution of genetic diversity across medusahead's native range support the hypothesis proposed by Safriel *et al.* (1994): there is no significant difference in genetic diversity between central and marginal populations of the species (Fig. 7, Table 3). In addition, Fisher (1930) described an alternative hypothesis in which the highest level of genetic diversity for a species would occur within populations at the edge of its distribution, in contrast to populations at the central portion of its distribution. My results may provide partial support for the Fisher hypothesis because the genetic diversity of populations from Region 1, which included Spanish and Moroccan populations at the species' westernmost range boundary, exhibited on average the highest levels of genetic diversity (Table 4). In addition to testing the Central-Marginal hypothesis using AFLP data, I wanted to test this hypothesis using previously reported (Peters 2013; Skaar 2015) allozyme data. Results using AFLP data (Fig. 7) and allozyme data (Fig. 8) were in agreement, and indicate that genetic diversity is randomly distributed across the native range of medusahead. These results for medusahead using both allozymes and AFLPs are one of only two studies I am aware of that have tested the Central-Marginal hypothesis in the same species (same populations), using two different molecular markers. In the other study, allozymes and RAPDs revealed a significant decline in the genetic diversity of populations of *Pinus contorta* subspecies *latifolia* (lodgepole pine) towards the range margin of the species (Yeh and Layton 1979; Yeh *et al.* 1985; Fazekas and Yeh 2001). These findings for lodgepole pine are in direct contrast to my results for medusahead. Similar to my results for medusahead, a study with the regionally distributed species *Pinus edulis*, using allozymes, did not reveal a statistically significant decline in the genetic diversity of populations as distance from the range center increased (Betancourt *et al.* 1991). These findings for two different *Pinus* species highlight the results reported by Eckert *et al.* (2008): different species exhibit different biogeographical patterns and it can be difficult *a priori* to predict what that pattern will be.

Comparison with Other Studies Assessing Biogeographic Pattern

The Central-Marginal hypothesis has been used as a framework to test the biogeographical pattern of many taxa (see Eckert *et al.* 2008). The pattern of genetic variation among 55 European populations of *Ceratocapnos claviculata* reported by Voss *et al.* (2012) was not consistent with the Central-Marginal hypothesis. Garner *et al.* (2004) found that the centrality of the population failed to explain significant differences in the level of genetic diversity observed among 19 populations of *Rana latastei*, the Italian agile frog. Munwes *et al.* (2010) reported an increase in the genetic diversity of populations of the eastern spadefoot toad (*Pelobates syriacus*) at the species' range boundary, results consistent with the hypothesis of Fisher (1930) described above.

While the studies cited above provide tests of the Central-Margin hypothesis that can be compared to my results, it would probably be more appropriate to compare my results to those of a species with similar life-history traits as medusahead. In a range-wide assessment of genetic diversity within and among native populations of *Lolium rigidum*, a self-pollinating, annual grass that is broadly distributed across Eurasia, Balfourier *et al.* (1998) found a non-significant statistical relationship between both H_E and allelic richness and longitude. These results indicate a random distribution of genetic diversity across the native range of *L. rigidum*, similar to that reported here for medusahead. The near continuous sampling of populations across the Eurasian range of both medusahead and *L. rigidum* greatly assisted in uncovering range-wide biogeographical patterns.

The random pattern I uncovered for the level and distribution of genetic diversity of native populations of medusahead could be the result of two different scenarios associated with the geographical distribution of the grass: 1) the expansion of primitive agriculture from the Middle East across Europe in the last 10,000 years, or 2) colonization of European populations from glacial refugia which were established just prior to the last glacial episode (Balfourier *et al.* 1998; Balfourier *et al.* 2000; Salamini *et al.*2002; Fuller *et al.* 2011). The expansion of primitive agriculture following the domestication of cereal crops from the Middle East is generally believed to have occurred along two routes; a southwestern expansion towards Mediterranean countries, and a northwestern expansion towards northern Poland, Germany, France, and ultimately the United Kingdom and Scandinavia (Balfourier *et al.* 1998; Balfourier *et al.* 2000; Fuller *et al.* 2011). Using cpDNA sequence data, Balfourier *et al.* (2000) concluded that the random distribution of genetic diversity within Eurasian populations of *L. rigidum* is based on human-mediated dispersal following the spread of primitive agriculture along the southwestern expansion route described previously. The second scenario of recolonization from glacial refugia has been documented in many plant and animal species distributed across Europe (Balfourier *et al.* 1998; Sharbel *et al.* 2000). My AFLP data does not allow me to differentiate between the two alternate scenarios described above. The fact that medusahead is a ruderal species and is an agricultural weed (Frederiksen 1986; Blank and Sforza 2007; Fuller *et al.* 2011) suggests that seeds of the plant could have inadvertently been transported by humans during the spread of agriculture from the Middle East within the last 10,000 years. Future analyses should attempt to provide data (e.g., nucleotide sequences) that can be used to identify the biogeographical processes that have resulted in the current distribution of genetic diversity within native populations of medusahead.

Comparison of AFLP and Allozyme Results

My research analyzed many of the same populations of medusahead analyzed by Peters (2013) and Skaar (2015) using allozymes, and therefore provides an opportunity to compare estimates of genetic diversity obtained using two molecular marker systems. In my study, I assessed genetic diversity in native populations of medusahead using 110 AFLP loci, whereas 23 loci were used in the two allozyme studies (Peters 2013; Skaar 2015). One hundred and four of 110 AFLP loci (94.5%) were polymorphic, compared to 15 and seven (65.2% and 30.4%, respectively) polymorphic allozyme loci. Even with the higher number of polymorphic AFLP loci, the AFLP and allozyme data shared some similarities. The significant correlation between AFLP and allozyme H_E values detected among the 65 populations analyzed using both markers similar estimates for the pattern of genetic diversity in these populations of medusahead (Fig. 9). In addition, the two populations with the highest value of H_E (Sozopol, Bulgaria and Tleta tassrit, Morocco) and the population displaying the lowest value of H_E (Monesterio, Spain) (Table 3 of the current study and Peters 2013 and Skaar 2015) were the same using each of these molecular markers. The STRUCTURE analysis revealed nine genetic clusters with AFLP data (Figs. 5 & 6), but only two genetic clusters were revealed by the allozyme data (Skaar 2015). To provide a better comparison of the STRUCTURE results of AFLP and allozyme date, I performed a STRUCTURE analysis of only the 48 populations of medusahead from Regions 3, 4, and 5 (Fig. 2) that were common to my study and the study of Skaar (2015). The analysis of this group of 48 populations, for which two genetic clusters were detected with the allozyme data, revealed six genetic clusters using the AFLP data (Fig. 11). These results for the same populations stem from the higher level of genetic diversity associated with AFLP data compared to the genetic diversity contained in the allozyme data. The differences in genetic diversity estimated described here through the comparison of AFLP and allozyme data (higher H_E, greater number of MLGs, and finer-scale genetic structure associated with AFLPs) is consistent with other studies that have used both marker systems (see Wolf and Sinclair 1997; Bjerregaard and Wolf 2008; Johnson 2009; Gaskin *et al.* 2013; Hufford *et al.* 2013). At least two reasons have been presented to explain this pattern: 1) a larger number of loci are assayed in the majority of AFLP studies compared with allozyme analyses, and 2) AFLP loci are assumed to be distributed across the entire genome of an organism rather than just a few specific locations as occurs for allozyme loci (Vos *et al.* 1995; Vekemans *et al.* 2002; Bjerrergaard and Wolf 2008).

Conclusions

The AFLP analysis of native populations of medusahead, a primarily self-pollinating annual grass species with a wide geographic distribution, revealed low to moderate levels of genetic diversity, high genetic structure, and a random pattern for the distribution of genetic diversity across its range. The results of this study support the biogeographical species distribution model proposed by Safriel *et al.* (1994) in which no significant genetic diversity pattern occurs across this species' wide geographic range. My assessment of the level and structure of genetic diversity of native populations of medusahead using AFLPs is largely concordant with previous studies by Peters (2013) and Skaar (2015), who analyzed almost all of the same populations using allozymes. The AFLP method employed in this study however provided a finer scale assessment of genetic structure. These results should encourage future studies that examine the historical and demographic processes that influence the geographical distribution of medusahead in Eurasia. Finally, this analysis of the genetic diversity of medusahead in its native range is the requisite first step for assessing the genetic consequences of the invasion of medusahead in western US rangelands.

LITERATURE CITED

Allendorf FW, Luikart G (2007) Units of conservation. *Conservation and the genetics of populations*, 380-420.

Andrewartha HG, Birch LC (1954) *The distribution and abundance of animals*. University of Chicago press, Chicago, IL.

Antonovics J (1976a) The nature of the limits to natural selection. *Annals of the Missouri Botanical Garden*, 63, 224-247.

Antonovics J (1976b) The input from population genetics: ‘the new ecological genetics.’ *Systematic Botany*, 1, 233-245.

Balfourier F, Charmet G, Ravel C (1998) Genetic differentiation within and between natural population of perennial and annual ryegrass (*Lolium perenne* and *L. rigidum*). *Heredity*, 81, 100-110.

Balfourier F, Imbert C, Charmet G (2000) Evidence for phylogeographic structure in *Lolium* species related to the spread of agriculture in Europe. A cpDNA study. *Theoretical Applied Genetics*, 101, 131-138.

Barrett SCH, Husband BC (1990) Variation in outcrossing rates in *Eichhornia paniculata*: the role of demographic and reproductive factors. *Plant Species Biology*, 5, 41-55.

Betancourt JL, Schuster WS, Mitton JB, Anderson RS (1991) Fossil and genetic history of a Pinyon Pine (*Pinus edulis*) isolate. *Ecological Society of Amerca*, 72(5), 1685-1697.

Bjerregaard L, Wolf PG (2008) Strong genetic differentiation among neighboring populations of a locally endemic primrose. *Western North American Naturalist*, 68(1), 66-75.

Blank RF, Sforza R (2007) Plant-soil relationships of the invasive annual grass *Taeniatherum caput-medusae*: a reciprocal transplant experiment. *Plant Soil*, 298, 7-19.

Bridle JR, Vines TH (2007) Limits to evolution at range margins: when and why does adaptation fail? *Trends in Ecology and Evolution*, 22, 140-147.

Brock JH (1998) Ecological characteristics of invasive alien plants. In: *The future of arid grasslands: identifying issues, seeking solutions: Proceedings;* 1996 October 9-13; Tuscon, AZ. Eds Tellman B, Finch D, Edminster C, Hamre R. Proceedings RMRS-P-3. Fort Collins, CO: US Department of Agriculture, Forest Service, Rocky Mountain Research Station: 137-143.

Brown JH (1984) On the relationship between abundance and distribution of species. *American Naturalist*, 124, 255-279.

Brown JH, Gibson AH (1983) *Biogeography*. St. Louis, MO: C. V. Mosby.

Brown JH, Mehlman DW, Stevens GC (1995) Spatial variation in abundance. *Ecology*, 76, 2028-2043.

Brown JH, Lomolino MV (1998) *Biogeography*. Sinaur associates. Sunderland, Massachusetts.

Brussard PF (1984) Geographical patterns and environmental gradients: the central-marginal model in *Drosophila* revisited. *Annual Review of Ecology and Systematics*, 15, 25-64.

Cahill AE, Levinton JS (2016) Genetic differentiation and reduced genetic diversity at the northern range edge of two species with different dispersal modes. *Molecular Ecology*, 25, 515-526.

Carson HL (1959) Genetic conditions which promote or retard the formation of species. *Cold Spring Harbor Symposia on Quantitative Biology*, 24, 87-105.

Chaboudez P (1994) Patterns of clonal variation in skeleton weed (*Chondrilla juncea*), and apomictic species. *Australian Journal of Botany*, 42, 283-295.

Cotgreave P (1993) The relationship between body size and population abundance in animals. *Trends in Ecology and Evolution*, 8, 7, 244-248.

Cox CB, Moore PD (1985) *Biogeography: an ecological and evolutionary approach*, 4th edn. Blackwell Scientific Publications, Oxford.

Duncan SI, Crespi EJ, Mattheus NM, Rissler LJ (2015) History matters more when explaining genetic diversity within the context of the core-periphery hypothesis. *Molecular Ecology*, 24, 4323-4336.

Earl DA, vonHoldt BM (2012) STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. *Conservation Genetics Resources*, 4, 359-361.

Eckert CG, Samis KE, Lougheed SC (2008) Genetic variation across species' geographical ranges: the central-margin hypothesis and beyond. *Molecular Ecology*, 17, 1170-1188.

Ehrich D (2006) AFLPdat: a collection of R functions for convenient handling of AFLP data. *Molecular Ecology Notes*, 6, 603-604.

Evanno G, Regnaut S, Goudet J (2005) Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology, 14, 2611-2620.*

Fazekas AJ, Yeh FC (2001) Random amplified polymorphic DNA diversity of marginal and central populations in *Pinus contorta* subsp. *Latifolia. Genome*, 44, 13-22.

Fisher RA (1930) *The Genetical Theory of Natural Selection.* Clarendon Press, Oxford.

Felsenstein J (2004) *PHYLIP (Phylogeny Inference Package) version 3.6*. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

Frederiksen S (1986) Revision of *Taeniatherum* (Poaceae). *Nordic Journal of Botany,* 6, 389-397.

Frederiksen S, Von Bothmer R (1986) Relationships in *Taeniatherum* (Poaceae). *Canadian Journal of Botany,* 64(10), 2343-2347.

Fuller DQ, Wollcox G, Allaby RG (2011) Early agricultural pathways: moving outside the ‘core area’ hypothesis in Southwest Asia. *Journal of Experimental Botany*, 63(2), 617-633.

Garcia-Ramos G, Kirkpatrick M (1997) Genetic models of adaptation and gene flow in peripheral populations. *Evolution*, 51, 21-28.

Garner TWJ, Pearman PB, Angelone S (2004) Genetic diversity across a vertebrate species’ range: a test of the central-peripheral hypothesis. *Molecular Ecology*, 13, 1047-1053.

Gaskin JF, Schwarzlander M, Kinter CL, Smith JF, Novak SJ (2013) Propagule pressure, genetic structure, and geographic origins of *Chondrilla Juncea* (Asteraceae): an apomictic invader on three continents. *American Journal of Botany*, 100(9), 1871-1882.

Gaston KJ, Blackburn TM, Lawton JH (1997) Interspecific abundance-range size relationships: an appraisal of mechanisms. *Journal of Animal Ecology*, 66, 579-601.

Hamrick JL, Godt MJW (1996) Effects of life history traits on genetic diversity in plant species. *Philosophical Transactions: Biological Sciences*, 351(1345), 1291-1298.

Hanski I, Kuussaari M, Nieminen M (1994) Metapopulation structure and migration in the butterfly *Melitaea cinxia*. *Ecology*, 75, 747-762.

Hansson L (1991) Dispersal and connectivity in metapopulations. *Biological Journal of the Linnean Society*, 42, 89-103.

Hartl DL, Clark AG (1997) *Principles of Population Genetics*, Vol 116. Sinauer Associates, Sunderland, Massachusetts.

Hengeveld R (1988) Mechanisms of biological invasions. *Journal of Biogeography*, 819-828.

Hengeveld R, Haenck J (1982) The distribution of abundance. 1. Measurements. *Journal of Biogeography*, 9, 303-316.

Hochberg ME, Ives AR (1999) Can natural enemies enforce geographical range limits? *Ecography*, 22(3), 268-276.

Hoffman AA, Blows MW (1994) Species borders: ecological and evolutionary perspectives. *Trends in Ecology and Evolution*, 9, 223-227.

Holsinger KE, Lewis PO (2003) HICKORY: A package for analysis of population genetic data. Distributed by the authors. Department of Ecology and Evolutionary Biology, University of Connecticut.

Holt RD, Keitt TH, Lewis MA, Maurer BA, Taper ML (2005) Theoretical models of species' borders: single species approaches. *Oikos*, 108, 18-27.

Hufford KM, Mazer SJ, Hodges SA (2013) Genetic variation among mainland and island populations of a native perennial grass used in restoration. *Annals of Botany Plants*, 6, plt055.

Invaders Database System (1997-2014). http://invader.dbs.umt.edu, Division of Biological Sciences, University of Montana – Missoula.

Johnson RL (2009) A comparison of genetic structuring of Yellowcheek Darters (*Etheostoma moorei*) using AFLPs and allozymes. *Biochemical Systematics and Ecology*, 37, 298-303.

Kark S, Hadeny L, Safriel WK (2008) How does genetic diversity change towards the range periphery? An empirical and theoretical test. *Evolutionary Ecology Research*, 10, 391-414.

Kark S, Safriel UN, Tabarroni C, Randi E (2001) Relationship between heterozygosity and asymmetry: a test across the distribution range. *Heredity*, 86, 119-127.

Kawecki TJ (2008) Adaptation to marginal habitats. *Annual Review of Ecology Evolution Systematics*, 39, 321-342.

Kawecki TJ, Holt RD (2002) Evolutionary consequences of asymmetric dispersal rates. *The American Naturalist*, 160, 333-347.

Keller S, Taylor D (2008) History, chance, and adaptation during biological invasion: separating stochastic phenotypic evolution from response to selection. *Ecology Letters*, 11, 852-866.

Kendeigh SC (1974) *Ecology with special reference to animals and man*. Prentice-Hall, New Jersey.

Kirkpatrick M, Barton NH (1997) Evolution of a species' range. *American Naturalist*, 150, 1-23.

Kubisch A, Poethke HJ, Hovestadt T (2011) Density-dependent dispersal and the formation of range borders. *Ecology*, 34, 1002-1008.

Lawton JH (1993) Range, population abundance and conservation. *Trends in Ecology and Evolution*, 8, 409-413.

Lesica P, Allendorf FW (1995) When are peripheral populations valuable for conservation? *Conservation Biology*, 9, 753-760.

Linde-Laursen IB, Frederiksen S (1989) Giemsa C-banded karyotypes of three subspecies of *Taeniatherum caput-medusae* and two intergeneric hybrids with *Psathyrostachys* spp. (Poaceae). *Hereditas*, 110(3), 283-288.

Lucardi RD (2012) Multi-scale population genetic analysis of Cogongrass (*Imperata cylindrica*) in the southeastern United States: introduction history, range expansion, and hybridization. PhD dissertation, Mississippi State, MS. Mississippi State University.

Lynch M, Milligan BG (1994) Analysis of population genetic structure with RAPD markers. *Molecular Ecology*, 3, 91-99.

Mayr E (1965) *Populations Species and Evolution. An Abridgement of Animal Species and Evolution.* Belknap Press, Cambridge, MA.

McKell CM, Robinson JP, Major J (1962) Ecotypic variation in medusahead, an introduced annual grass. *Ecology*, 43, 686-698.

McVean DN (1996) Ecology of Chondrilla juncea L. in south-eastern Australia. Journal of Ecology, 54, 345-365.

Meirmans PG, Van Tienderen PH (2004) GENOTYPE and GENODIVE: two programs for the analysis of genetic diversity of asexual organisms. Molecular Ecology Notes, 4, 792-794.

Micheletti SJ, Storfer A (2015) A test of the central-marginal hypothesis using population genetics and ecological niche modelling in an endemic salamander (*Ambystoma barbouri*). *Molecular Ecology*, 24, 967-979.

Millar CI, Libby WJ (1991) Strategies for conserving clinal, ecotypic, and disjunct population diversity in widespread species. In: *Genetics and Conservation of Rare Plants* (eds Falk DA, Holsinger KE), pp 149-170. Oxford University Press, New York.

Miller HC, Clausnitzer D, Borman MM (1999) Medusahead. Pages 271-281 *in* RL Sheley and JK Petroff, eds. Biology and Management of Noxious Rangeland Weeds. Corvalis, OR: Oregon State University Press.

Munwes I, Geffen E, Roll U, Friedmann A, Daya A, Tikochinski Y, Gafny S (2010) The change in genetic diversity down the core-edge gradient in the eastern spadefoot toad (*Pelobates syriacus*). *Molecular Ecology*, 19, 2675-2689.

Nei M (1978) Estimation of average heterozygosity and genetic distance from a small number of individuals. *Genetics*, 89, 583-590.

Nei M (1987) *Molecular evolutionary genetics*. Columbia University Press, New York.

Novak SJ, Mack RN (1993) Genetic variation in *Bromus tectorum* (Poaceae): comparison between native and introduced populations. *Heredity*, 71, 167-176.

Novak SJ, Rausch JH (2009) Use of field surveys, distributed data and genetic analyses to monitor alien species: *Taeniatherum caput-medusae* as an example of the approach. *Biological Invasions: Towards a Synthesis. Neobiota*, 8, 169-182.

Nybom, H (2004) Comparison of different nuclear DNA markers for estimating intraspecific genetic diversity in plants. *Molecular Ecology*, 13, 1143-1155.

Pajkovic M, Lappe S, Barman R, Parisod C, Neuenschwander S, Goudet J, Alvarez N, Guadagnuolo R, Felber F, Arrigo N (2014) Wheat alleles introgress into selfing wild relatives: empirical estimates from approximate Bayesian computation in *Aegilops triuncialis*. *Molecular Ecology*, 23, 5089-5101.

Panetta FD, Dodd J (1987) The biology of Australian weeds 16. *Chondrilla juncea* L. *Journal of the Australian Institute of Agricultural Science*, 53, 83-95.

Peakall R, Smouse PE (2006) GenAlEx 6: genetic analysis in Excel. Population genetic software for teaching and research. *Molecular Ecology Notes*, 6, 288-295.

Peakall R, Smouse PE (2012) GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research – an update. *Bioinformatics*, 28, 2537-2539.

Peters ML (2013) Genetic and morphological variation in *Taeniatherum caput-medusae* (Medusahead): Taxonomic diversity, geographic origins, multiple introductions, and founder effects. M.S. Thesis, Boise State University, Boise, ID.

Pouget M, Youssef S, Migliore J, Juin M, Medail F, Baumel A (2013) Phylogeography sheds light on the central-marginal hypothesis in a Mediterranean narrow endemic plant. *Annals of Botany*, 112, 1409-1420.

Preite V, Snoek LB, Oplaat C, Bierre A, Van Der Putten WH, Verhoeven KJF (2015) The epigenetic footprint of poleward range-expanding plants in apomictic dandelions. *Molecular Ecology*, 24, 4406-4418.

Pritchard JK, Stephens M, Donnelly P (2000) Inference of population structure using multilocus genotype data. *Genetics*, 155, 945-959.

Prinz K, Weising K, Hensen I (2009) Genetic structure of coastal and inland populations of the annual halophyte *Suaeda maritima* (L.) Dumort. in Central Europe, inferred from amplified fragment length polymorphism (AFLP) markers. *Plant Biology*, 11, 812-820.

Qiagen (2015) DNeasy Plant Handbook and Technical Manual.

R Core Development Team, R Foundation of Statistical Computing (2014) R version 3.1.2 “Pumpkin Helmet.”

Safriel UN, Volis S, Kark S (1994) Core and peripheral populations and global climate change. *Israel Journal of Plant Sciences*, 42, 331-345.

Sagarin RD, Gaines SD (2002) The ‘abundant centre’ distribution: to what extent is it a biogeographic rule? *Ecology letters*, 5, 137-147.

Salamini F, Ozkan H, Brandolini A, Schafer-Pregl R, Martin W (2002) Genetics and geography of wild cereal domestication in the Near East. *Nature Reviews*, 3, 429-441.

Sharbel TF, Haubold B, Mitchell-Olds T (2000) Genetic isolation by distance in *Arabidopsis thaliana*: biogeography and postglacial colonization of Europe. *Molecular Ecology*, 9, 2109-2118.

Sexton JP, McIntyre PJ, Angert AL, Rice KJ (2009) Evolution and ecology of species range limits. *Annual Review of Ecology Evolutionary Systematics*, 40, 415-436.

Skaar SK (2015) Identifying the geographic origins for the introduction of *Taeniatherum caput-medusae* subspecies *asperum* (Medusahead) in the western United States. M.S. Thesis, Boise State University, Boise, ID.

Templeton AR (1980) The theory of speciation via the founder principle. *Genetics*, 94, 1011-1038.

Trybush S, Hanley S, Cho KH, Jahodova S, Grimmer M, Emelianov I, Bayon C, Karp A (2006) Getting the most out of fluorescent amplified fragment length polymorphism. *Canadian Journal of Botany*, 84, 1347-1354.

Vekemans X (2002) *AFLP-SURV version 1.0*. Distributed by the author, Universite Libre de Bruxelles, Belgium. Laboratoire de Genetique et Ecologie Vegetale.

Vekemans X, Beauwens T, Lemaire M, Roldan-Ruiz I (2002) Data from amplified fragment length polymorphisms (AFLPs) markers show indication of size homoplasy and of a relationship between degree of homoplasy and fragment size. *Molecular Ecology*, 11, 139-151.

Volis S, Mendlinger S, Olsvig-Whittaker L, Safriel UN, Orlovski N (1998) Phenotypic variation and stress resistance in core and peripheral population of *Hordeum spontaneum. Biodiversity and conservation*, 7, 799-813.

Vos P, Hogers R, Bleeker M, Reijans M, Lee T, Hornes M, Frijters A, Pot J, Peleman J, Kuiper M, Zabeau M (1995) AFLP: a new technique for DNA fingerprinting. *Nucleic Acid Research*, 23, 4407-4414.

Voss N, Eckstein RL, Durka W (2012) Range expansion of a selfing polyploid plant despite widespread genetic uniformity. *Annals of Botany*, 110, 585-593.

Vucetich JA, Waite TA (2003) Spatial patters of demography and genetic processes across the species' range: null hypotheses for landscape conservation genetics. *Conservation Genetics*, 4, 639-645.

Wagner V, Durka W, Hensen I (2011) Increased genetic differentiation but no reduced genetic diversity in peripheral vs. central populations of a steppe grass. *American Journal of Botany*, 98(7), 1173-1179.

Whisenant SG (1990) Postfire population dynamics of *Bromus japonicus*. *The American Midland Naturalist*, 123(2), 301-308.

Wolf PG, Doche B, Gielly L, Taberlet P (2004) Genetic structure of *Rhododendron ferrugineum* at a wide range of spatial scales. *Journal of Heredity*, 95(4), 301-308.

Wolf PG, Sinclair RB (1997) Highly differentiated populations of the narrow endemic plant Maguire primrose (*Primula maguirei*). *Conservation Biology*, 11, 375-381.

Yeh FC, Layton C (1979) The organization of genetic variability in central and marginal populations of lodgepole pine (*Pinus contorta* ssp. *latifolia*). *Canadian Journal of Genetics and Cytology*, 21, 487-503.

Yeh FC, Cheliak WM, Dancik BP, Illingworth K, Trust DC, Pryhitka BA (1985) Populations differentiation in lodgepole pine, *Pinus contorta* spp. *Latifolia* – a discriminant analysis of allozyme variation. *Canadian Journal of Genetics and Cytology*, 27, 210-218.

Young JA (1992) Ecology and management of medusahead (*Taeniatherum caput-medusae* ssp. *asperum* [Simk.] Melderis). *Great Basin Natur.*, 52, 245-252.

Zhang H, Hare MP (2012) Identifying and reducing AFLP genotyping error: an example of tradeoffs when comparing population structure in broadcast spawning versus brooding oysters. *Heredity*, 108, 616-625.

TABLES AND FIGURES

Table 1 Locality Data for 70 native populations of *Taeniatherum caput-medusae* subspecies *asperum* analyzed in this study. Also included is each population's Euclidian distance from the calculated geographic centroid.

Population Number	Country	Locality	Code	Number of Individuals (n)	Latitude	Longitude	Elevation (m)	Collection Date	Distance to Geographic Centroid (km)
1	Albania	Bilisti	BAL	9	40.6680	20.8222	878	7/14/2011	277.45
2		Struga	SAL	9	41.0777	20.6069	1016	6/26/2011	295.78
3	Bulgaria	Beronovo	BBG	8	42.8275	26.7094	358	10/4/2010	312.06
4		Devnja	DEBG	6	43.2322	27.5425	128	10/4/2010	390.96
5		Dripclevo	DBG	4	41.9947	26.1958	461	7/3/2011	218.19
6		Galabets	GBG	10	41.8275	25.4508	322	7/4/2011	159.34
7		Harmanli	HBG	7	41.9675	25.9950	241	10/3/2010	203.28
8		Izgrev	IGBG	5	42.1447	27.8105	137	10/5/2010	343.64
9		Izvorishte	IBG	10	42.6586	27.4352	278	7/3/2011	344.62
10		Izvorsko	IZBG	5	43.2797	27.7825	323	7/2/2011	408.99
11		Orizare	OBG	5	42.7119	27.6177	77	10/4/2010	359.69
12		Razlog	RBG	9	41.9030	23.5013	834	10/2/2010	129.33
13		Rudnik	RUBG	4	42.9861	27.7883	75	7/12/2003	389.29
14		Sozopol	SBG	10	42.3686	27.6852	50	10/5/2010	345.01
15		Sredec	SRBG	7	42.2136	27.0363	332	10/5/2010	289.71
16		Staro Orjahovo	SOBG	7	42.9863	27.7880	65	10/4/2010	289.42
17		Tenevo	TBG	10	42.3605	26.5719	145	7/3/2011	268.26
18		Zvezdel	ZBG	10	41.4711	25.5400	572	7/4/2011	142.09
19	France	Pezenes Les Mines	PMFR	7	43.6030	3.26250	361	11/9/2009	1749.02
20	Greece	Askos	AGR	6	40.7575	23.4530	398	7/8/2011	55.66

21		Edessa	EGR	10	40.7850	21.8888	587	6/25/2011	187.3
22		Kokinochoma	KGR	9	40.924	24.2900	73	7/7/2011	19.61
23		Komotini	KMGR	6	41.0872	25.7416	113	7/7/2011	140.36
24		Sapes	SGR	7	40.9952	25.6613	84	7/7/2011	132.03
25	Greece	Thermi	TGR	9	40.5713	23.0608	300	8/18/2001	92.8
26	Italy	Altamura	ALIT	7	40.9350	16.5008	507	7/3/2009	640.43
27		Dorgali	DSA	10	40.3050	9.5716	270	9/17/2009	1230.67
28		Minervino Murge	MMIT	3	41.0452	16.1825	572	7/4/2009	669.94
29		Orosei	OSA	10	40.3969	9.7183	26	9/17/2009	1220.3
30		Poggiorsini	PIT	5	40.9763	16.2541	601	7/4/2009	662.85
31		Lodine	18IT	5	40.1625	9.2361	860	9/16/2009	1260.4
32	Macedonia	Bitola	BMC	7	41.0377	21.3794	645	6/25/2011	235.69
33		Lavazzalady	LMC	10	41.0530	21.2802	761	6/26/2011	239.79
34		Umin Dol	YDMC	7	42.0391	21.6011	535	6/27/2011	252.17
35	Morocco	Tafroute	TRMO	5	29.7377	8.8344	1626	10/6/2004	3218.5
36		Timahdite	TMO	5	33.2838	5.0758	1820	10/1/2004	2714.58
37		Tizi n'test	TZMO	2	30.9163	8.2927	1560	10/5/2004	3114.36
38		Tizi n'tishka	TIMO	8	31.2372	7.4141	1984	10/4/2004	3015.41
39		Tleta tassrit	TLMO	6	29.6163	8.9233	1670	10/7/2004	3256.43
40	Romania	Slava Rus	CRO	10	44.9736	28.6458	43	7/1/2011	592.55
41		Drobetia	DRO	5	44.8069	28.6458	100	6/28/2011	579.42
42		Sacele	SRO	5	44.6416	22.6213	73	7/1/2011	442.82
43		Schela	SCRO	6	44.4791	28.6475	54	7/1/2011	551.62
44	Russia	Taman Bay	TBRU	9	45.3277	36.8097	22	4/5/2002	1147.36
45	Serbia	Kladovo	KSR	10	44.6336	22.5605	95	6/28/2011	443.48
46	Spain	Castillejo de Martin Viejo	CMSP	6	40.6963	6.6600	597	9/15/2009	2589.47
47		Monesterio	MSP	6	38.0958	6.2108	745	6/19/2009	2615.92
48		Pedraza de la Sierra	PSP	9	41.1308	3.8075	1039	6/14/2009	2339.4
49		Robledillo	RSP	7	41.5341	4.9469	1230	9/14/2009	2425.17

50	Turkey	Alseki	ATR	8	37.1213	31.7969	1271	6/26/2013	783.36
51		Corlu	CTR	5	40.0516	27.7322	13	7/6/2011	306.27
52		Havsa	HTR	8	41.4013	26.4780	73	7/5/2011	208.78
53		Ipsala	IPT	9	40.8797	26.4194	50	7/5/2011	194.83
54	Turkey	Kesan	KTR	7	40.7350	26.7225	104	7/6/2011	221.72
55		Poyrali	PTR	5	41.6280	27.6055	329	7/6/2011	306.38
56		Seydishir	SETR	9	37.4047	31.8350	1239	6/26/2013	767.43
57		Sarigol	STU	5	38.2480	28.6700	311	6/23/2005	484.5
58		Urunlu	UTR	6	41.6741	26.9980	132	7/5/2011	260.82
59		Uzunkopru North	UNTR	6	41.3158	26.5733	118	7/5/2011	215.15
60		Yalihuyuk	YTR	10	37.3138	32.1050	1102	6/27/2013	792.84
61		Yorukler	YTU	7	41.1186	27.2402	105	7/6/2011	266.08
62	Ukraine	Alushta	AUK	9	44.7047	34.4316	190	7/8/2013	948.54
63		Bahate	BUK	8	45.02778	34.7658	303	7/8/2013	986.78
64		Bancizaray	BCUK	6	34.1250	44.4827	180	8/15/2002	912.07
65		Izobilne	IUK	9	44.7013	34.3505	217	7/9/2013	942.42
66		Kakceveli	KUK	10	33.9622	44.4000	150	8/15/2002	900.45
67		Pryvitne	PUK	5	44.8219	34.7297	279	7/8/2013	975.42
68		Sudak	SUK	6	44.8861	35.0944	176	7/8/2013	1004.44
69		Trudalyubivka	TUK	6	44.7805	33.9975	190	7/10/2013	919.36
70		Yalta	YUK	8	44.4811	34.1255	281	7/9/2013	917.91

Table 2 (A) Amplified Fragment Length Polymorphism (AFLP) Adaptor Pair, Pre-Selective Amplification, and Selective Amplification Sequences. (B) Selective Amplification Primer pair combinations.

(A)

Oligonucleotide Name	Sequence
Mse1 Forward Adaptor	GAC GAT GAG TCC TGA G
Mse1 Reverse Adaptor	TAC TCA GGA CTC AT
EcoR1 Forward Adaptor	CTC GTA GAC TGC GTA CC
EcoR1 Reverse Adaptor	AAT TGG TAC GCA GTC TAC
Mse1 + C Pre-Selective Amplification Primer	GAT GAG TCC TGA GTA AC
EcoR1 + A Pre-Selective Amplification Primer	GAC TGC GTA CCA ATT CA
Mse1 + CTC Selective Amplification Primer	GAT GAG TCC TGA GTA ACT C
Mse1 + CAC Selective Amplification Primer	GAT GAG TCC TGA GTA ACA C
Mse1 + CAT Selective Amplification Primer	GAT GAG TCC TGA GTA ACA T
EcoR1 + ACC Selective Amplification Primer	GAC TGC GTA CCA ATT CAC C
EcoR1 + ACT Selective Amplification Primer	GAC TGC GTA CCA ATT CAC T
EcoR1 + AGC Selective Amplification Primer	GAC TGC GTA CCA ATT CAG C

(B)

Selective Amplification Primer Combination 1	
EcoR1 + ACC	Mse1 + CTC
Selective Amplification Primer Combination 2	
EcoR1 + ACT	Mse1 + CAC
Selective Amplification Primer Combination 3 (Only used in pilot study)	
EcoR1 + AGC	Mse1 + CAT

Table 3 Within-population genetic diversity parameters based on 110 AFLP loci for 70 native populations of *Taeniatherum caput-medusae* subspecies *asperum*.

Population Number	Country	Locality	Code	Number of Individuals (n)	AFLP %P	AFLP H_E	Standard Error of AFLP H_E
1	Albania	Bilisti	BAL	9	12.7	0.042	0.011
2		Struga	SAL	9	10.9	0.044	0.013
		MEAN		9	11.8	0.043	0.012
3	Bulgaria	Beronovo	BBG	8	13.6	0.058	0.01
4		Devnja	DEBG	6	5.5	0.030	0.012
5		Dripclevo	DBG	4	4.5	0.027	0.012
6		Galabets	GBG	10	9.1	0.032	0.011
7		Harmanli	HBG	7	10.9	0.053	0.015
8		Izgrev	IGBG	5	10	0.042	0.012
9		Izvorishte	IBG	10	18.2	0.051	0.012
10		Izvorsko	IZBG	5	6.4	0.024	0.009
11		Orizare	OBG	5	12.7	0.065	0.017
12		Razlog	RBG	9	13.6	0.043	0.011
13		Rudnik	RUBG	4	14.5	0.055	0.013
14		Sozopol	SBG	10	19.1	0.078	0.016
15		Sredec	SRBG	7	9.1	0.041	0.013
16		Staro Orjahovo	SOBG	7	18.2	0.077	0.017
17		Tenevo	TBG	10	34.5	0.135	0.019
18		Zvezdel	ZBG	10	16.4	0.061	0.014
		MEAN		7.31	13.52	0.054	0.013
19	France	Pezenes Les Mines	PMFR	7	5.5	0.020	0.009

20	Greece	Askos	AGR	6	9.1	0.037	0.011
21		Edessa	EGR	10	20	0.073	0.015
22		Kokinochoma	KGR	9	6.4	0.023	0.009
23		Komotini	KMGR	6	6.4	0.024	0.009
24		Sapes	SGR	7	18.2	0.070	0.015
25		Thermi	TGR	9	13.6	0.050	0.013
		MEAN		7.83	12.28	0.046	0.012
26	Italy	Altamura	ALIT	7	9.1	0.031	0.010
27		Dorgali	DSA	10	19.1	0.058	0.013
28		Minervino Murge	MMIT	3	6.4	0.038	0.014
29		Orosei	OSA	10	6.4	0.028	0.011
30		Poggiorsini	PIT	5	0.9	0.004	0.004
31		Lodine	18IT	5	12.7	0.073	0.018
		MEAN		6.67	9.1	0.039	0.011
32	Macedonia	Bitola	BMC	7	8.2	0.037	0.012
33		Lavazzalady	LMC	10	3.6	0.012	0.006
34		Umin Dol	YDMC	7	14.5	0.055	0.014
		MEAN		8	8.77	0.035	0.011
35	Morocco	Tafroute	TRMO	5	16.4	0.086	0.019
36		Timahdite	TMO	5	16.4	0.072	0.016
37		Tizi n'test	TZMO	2	2.7	0.021	0.012
38		Tizi n'tishka	TIMO	8	2.7	0.011	0.007
39		Tleta tassrit	TLMO	6	30	0.158	0.023
		MEAN		5.2	13.64	0.069	0.015

40	Romania	Slava Rus	CRO	10	22.7	0.073	0.014
41		Drobetia	DRO	5	14.5	0.063	0.015
42		Sacele	SRO	5	10.9	0.051	0.014
43		Schela	SCRO	6	11.8	0.040	0.011
		MEAN		6.5	14.98	0.057	0.013
44	Russia	Taman Bay	TBRU	9	7.3	0.034	0.012
45	Serbia	Kladovo	KSR	10	7.3	0.028	0.010
46	Spain	Castillejo de Martin Viejo	CMSP	6	7.3	0.030	0.010
47		Monesterio	MSP	6	4.5	0.018	0.008
48		Pedraza de la Sierra	PSP	9	19.1	0.082	0.017
49		Robledillo	RSP	7	7.3	0.035	0.012
		MEAN		7	9.55	0.041	0.012
50	Turkey	Alseki	ATR	8	7.3	0.031	0.011
51		Corlu	CTR	5	15.5	0.068	0.016
52		Havsa	HTR	8	10.9	0.045	0.013
53		Ipsala	IPT	9	15.5	0.060	0.014
54		Kesan	KTR	7	15.5	0.054	0.013
55		Poyrali	PTR	5	7.3	0.037	0.013
56		Seydishir	SETR	9	10	0.044	0.013
57		Sarigol	STU	5	8.2	0.040	0.013
58		Urunlu	UTR	6	8.2	0.037	0.012
59		Uzunkopru North	UNTR	6	6.4	0.024	0.009
60		Yalihuyuk	YTR	10	18.2	0.063	0.014
61		Yorukler	YTU	7	11.8	0.061	0.016

		MEAN		7.08	11.23	0.047	0.013
62	Ukraine	Alushta	AUK	9	4.5	0.001	0.004
63		Bahate	BUK	8	6.4	0.024	0.009
64		Bancizaray	BCUK	6	34.5	0.188	0.025
65		Izobilne	IUK	9	8.2	0.031	0.010
66		Kakceveli	KUK	10	10	0.038	0.012
67		Pryvitne	PUK	5	10.9	0.045	0.013
68		Sudak	SUK	6	6.4	0.024	0.009
69		Trudalyubivka	TUK	6	18.2	0.061	0.012
70		Yalta	YUK	8	5.5	0.021	0.009
		MEAN		7.44	11.62	0.049	0.012
RANGE	OVERALL	MEAN		7.2	11.72	0.049	0.013

Table 4 Within-population genetic diversity parameters based on 110 AFLP loci for 70 native populations of *Taeniatherum caput-medusae* subspecies *asperum* based on their assignment to five geographic regions. See text for a description of these geographic regions.

Region	Countries	Number of Populations	Average Number of Individuals (n)	AFLP %P	AFLP H_E	Standard Error of AFLP H_E
1	Morocco and Spain	9	6	11.822	0.057	0.014
2	France and Italy	7	6.7	8.586	0.036	0.011
3	Albania, Bulgaria, Greece, Macedonia, Romania, Serbia, and Turkey	40	7.4	12.455	0.049	0.013
4	Russia and Ukraine	10	7.6	11.190	0.047	0.012
5	Turkey	4	8	10.925	0.045	0.013

Table 5 Nei's genetic diversity statistics for 70 native populations of *Taeniatherum caput-medusae* subspecies *asperum*. A description of the parameters H_T, H_S, D_{ST}, G_{ST}, and F_{ST} is provided in the text.

Statistic:	H_T	H_S	D_{ST}	G_{ST}	F_{ST}
	0.171	0.049	0.122	0.716	0.717
Standard Error:	0.004	0.016	0.042		

Table 6 Analysis of Molecular Variance (AMOVA) for 70 native populations of *Taeniatherum caput-medusae* subspecies *asperum*. AMOVA hierarchically partitioning genetic diversity within populations and among populations (A). AMOVA hierarchically partitioning genetic diversity within populations, among populations within regions and among five geographic regions (B). See the text for a description of the populations assigned to the five regions. (P<0.001 for both analyses).

(A) Population AMOVA

Source	Degrees of Freedom	Sums of Squares	Variance Component	Percentage of Variation
Among Populations	69	3344.36	6.471	70.08%
Within Populations	425	1173.94	2.762	29.92%
Total	494	4518.29	9.233	-

(B) Regional AMOVA

Source	Degrees of Freedom	Sums of Squares	Variance Component	Percentage of Variation
Among Regions	4	1026.14	2.947	28.48%
Among Populations Within Regions	65	2080.18	4.078	39.41%
Within Populations	425	1411.97	3.322	32.11%
Total	494	4518.29	10.347	-

Table 7 Distribution and frequency of AFLP Multilocus Genotypes (MLGs) within Populations of *Taeniatherum caput-medusae* subspecies *asperum.* See text for descriptions of AFLP MLG ID.

Population Number	Population	Number of Individuals	Genotype ID	Number of Individuals with Genotype ID	Genotypic Frequency
1	BAL	9	1	8	0.889
			20	1	0.111
2	SAL	8	1	7	0.875
			77	1	0.125
3	BBG	8	1	7	0.875
			21	1	0.125
4	DEBG	5	1	5	1.000
5	DBG	3	1	2	0.667
			37	1	0.333
6	GBG	10	1	10	1.000
7	HBG	7	1	6	0.857
			50	1	0.142
8	IGBG	5	1	5	1.000
9	IBG	10	51	7	0.700
			52	1	0.100
			53	1	0.100
			54	1	0.100
10	IZBG	5	1	5	1.000
11	OBG	5	1	3	0.600
			60	1	0.200
			61	1	0.200
12	RBG	8	1	6	0.750
			70	1	0.125

			71	1	0.125
13	RUBG	6	1	1	0.167
			74	3	0.500
			75	1	0.167
			76	1	0.167
14	SBG	10	78	1	0.100
			79	1	0.100
			80	1	0.100
			81	2	0.200
			82	1	0.100
			83	1	0.100
			84	1	0.100
			85	1	0.100
			86	1	0.100
15	SRBG	7	1	7	1.00
16	SOBG	7	1	1	0.143
			74	2	0.286
			90	1	0.143
			91	1	0.143
			92	1	0.143
			93	1	0.143
17	TBG	10	102	1	0.100
			103	1	0.100
			104	1	0.100
			105	1	0.100
			106	1	0.100
			107	1	0.100

			108	1	0.100
			109	1	0.100
			110	1	0.100
			111	1	0.100
18	ZBG	10	1	9	0.900
			147	1	0.100
19	PMFR	7	1	7	1.000
20	AGR	6	1	6	1.000
21	EGR	10	1	3	0.300
			43	1	0.100
			44	1	0.100
			45	1	0.100
			46	1	0.100
			47	1	0.100
			48	1	0.100
			49	1	0.100
22	KGR	9	1	8	0.889
			56	1	0.111
23	KMGR	6	1	6	1.000
24	SGR	7	1	5	0.714
			88	1	0.143
			89	1	0.143
25	TGR	7	1	6	0.857
			113	1	0.143
26	ALIT	7	18	6	0.857
26			19	1	0.143
27	DSA	10	41	9	0.900

			42	1	0.100
28	MMIT	3	18	1	0.333
			59	2	0.667
29	OSA	10	62	10	1.000
30	PIT	5	63	5	1.000
31	18IT	5	16	3	0.600
			17	2	0.400
32	BMC	7	1	6	0.857
			28	1	0.143
33	LMC	10	1	10	1.000
34	YDMC	7	131	3	0.429
			132	1	0.143
			133	2	0.286
			134	1	0.143
35	TRMO	5	125	1	0.200
			126	1	0.200
			127	1	0.200
			128	2	0.400
36	TMO	5	121	1	0.200
			122	2	0.400
			123	1	0.200
			124	1	0.200
37	TZMO	2	130	2	1.000
38	TIMO	7	114	7	1.000
39	TLMO	6	115	1	0.167
			116	1	0.167
			117	1	0.167

			118	1	0.167
			119	1	0.167
			120	1	0.167
40	CRO	10	1	7	0.700
			31	1	0.100
			32	1	0.100
			33	1	0.100
41	DRO	5	1	2	0.400
			38	1	0.200
			39	1	0.200
			40	1	0.200
42	SRO	5	94	1	0.200
			95	1	0.200
			96	1	0.200
			97	1	0.200
			98	1	0.200
43	SCRO	6	1	5	0.833
			87	1	0.167
44	TBRU	9	1	3	0.333
			112	6	0.667
45	KSR	10	1	10	1.000
46	CMSP	6	29	1	0.167
			30	5	0.833
47	MSP	6	30	6	1.000
48	PSP	9	30	2	0.222
			64	1	0.111
			65	2	0.222

			66	1	0.111
			67	1	0.111
			68	1	0.111
			69	1	0.111
49	RSP	5	72	4	0.800
			73	1	0.200
50	ATR	8	1	8	1.000
51	CTR	5	1	2	0.400
			34	1	0.200
			35	1	0.200
			36	1	0.200
52	HTR	8	1	8	1.000
53	IPT	9	1	8	0.889
			55	1	0.111
54	KTR	7	1	6	0.857
			57	1	0.143
55	PTR	5	1	5	1.000
56	SETR	9	1	9	1.000
57	STU	5	99	2	0.400
			100	2	0.400
			101	1	0.200
58	UTR	5	1	5	1.000
59	UNTR	6	1	6	1.000
60	YTR	10	135	1	0.100
			136	4	0.400
			137	1	0.100
			138	1	0.100

			139	1	0.100
			140	1	0.100
			141	1	0.100
61	YTU	7	1	2	0.286
			142	1	0.143
			143	1	0.143
			144	1	0.143
			145	1	0.143
			146	1	0.143
62	AUK	9	1	9	1.000
63	BUK	8	1	8	1.000
64	BCUK	6	22	1	0.167
			23	1	0.167
			24	1	0.167
			25	1	0.167
			26	1	0.167
			27	1	0.167
65	IUK	9	1	9	1.000
66	KUK	9	58	9	1.000
67	PUK	5	1	5	1.000
68	SUK	6	1	6	1.000
69	TUK	6	1	5	0.833
			129	1	0.167
70	YUK	8	1	8	1.000

Table 8 Simpson's and Shannon-Wiener genotypic diversity indices for 70 native populations of *Taeniatherum caput-medusae* subspecies *asperum*. See text for a description of these parameters.

Population number	Code	Sample size (n)	Number of AFLP genotypes	Simpson's genotypic diversity index	Simpson's evenness	Shannon-Wiener genotypic diversity index
1	BAL	9	2	0.222	0.623	0.152
2	SAL	8	2	0.250	0.640	0.164
3	BBG	8	2	0.250	0.640	0.164
4	DEBG	5	1	0	-	0
5	DBG	3	2	0.667	0.900	0.276
6	GBG	10	1	0	-	0
7	HBG	7	2	0.286	0.662	0.178
8	IGBG	5	1	0	-	0
9	IBG	10	4	0.533	0.481	0.408
10	IZBG	5	1	0	-	0
11	OBG	5	3	0.700	0.758	0.413
12	RBG	8	3	0.464	0.561	0.320
13	RUBG	6	4	0.800	0.750	0.540
14	SBG	10	9	0.978	0.926	0.940
15	SRBG	7	1	0	-	0
16	SOBG	7	6	0.952	0.907	0.759
17	TBG	10	10	1.000	1.000	1.000
18	ZBZ	10	2	0.200	0.607	0.141
19	PMFR	7	1	0	-	0
20	AGR	6	1	0	-	0
21	EGR	10	8	0.933	0.781	0.857
22	KGR	9	2	0.222	0.623	0.152
23	KMGR	6	1	0	-	0

24	SGR	7	3	0.524	0.605	0.346
25	TGR	7	2	0.286	0.662	0.178
26	ALIT	7	2	0.286	0.662	0.178
27	DSA	10	2	0.200	0.610	0.141
28	MMIT	3	2	0.667	0.900	0.276
29	OSA	10	1	0	-	0
30	PIT	5	1	0	-	0
31	18IT	5	2	0.600	0.962	0.292
32	BMC	7	2	0.286	0.662	0.178
33	LMC	10	1	0	-	0
34	YDMC	7	4	0.810	0.817	0.555
35	TRMO	5	4	0.900	0.893	0.579
36	TMO	5	4	0.900	0.893	0.579
37	TZMO	2	1	0	-	0
38	TIMO	7	1	0	-	0
39	TLMO	6	6	1.000	1.000	0.778
40	CRO	10	4	0.533	0.481	0.408
41	DRO	5	4	0.900	0.893	0.579
42	SRO	5	5	1.000	1.000	0.699
43	SCRO	6	2	0.333	0.692	0.196
44	TBRU	9	2	0.500	0.900	0.276
45	KSR	10	1	0	-	0
46	CMSP	6	2	0.333	0.692	0.196
47	MSP	6	1	0	-	0
48	PSP	9	7	0.944	0.890	0.821
49	RSP	5	2	0.400	0.735	0.217
50	ATR	8	1	0	-	0

51	CTR	5	4	0.900	0.893	0.579
52	HTR	8	1	0	-	0
53	IPT	9	2	0.222	0.623	0.152
54	KTR	7	2	0.286	0.662	0.178
55	PTR	5	1	0	-	0
56	SETR	9	1	0	-	0
57	STU	5	3	0.800	0.926	0.458
58	UTR	5	1	0	-	0
59	UNTR	6	1	0	-	0
60	YTR	10	7	0.867	0.649	0.759
61	YTU	7	6	0.952	0.907	0.759
62	AUK	9	1	0	-	0
63	BUK	8	1	0	-	0
64	BCUK	6	6	1.000	1.000	0.778
65	IUK	9	1	0	-	0
66	KUK	9	1	0	-	0
67	PUK	5	1	0	-	0
68	SUK	6	1	0	-	0
69	TUK	6	2	0.333	0.692	0.196
70	YUK	8	1	0	-	0
	Mean					

Table 9 Range-wide genetic diversity parameters comparing the results obtained using two different molecular markers, AFLPs and allozyme. See text for descriptions of the previous studies.

	Sample Size (Populations)	Molecular Marker	H_E	H_T	H_S	D_{ST}	G_{ST}	F_{ST}
This Study								
Native Populations	70	AFLPs	0.166	0.171	0.049	0.122	0.715	0.717
Previous Studies								
Native Populations	48	Allozymes	0.03	0.248	0.1	0.147	0.417	
Native Populations	34	Allozymes	0.025	0.262	0.043	0.194	0.745	
Invasive Populations	46	Allozymes	0.006	0.224	0.028	0.203	0.907	

Figure 1 Images of *Taeniatherum caput-medusae* plants from the species' native range. *Taeniatherum caput-medusae* subsp. *asperum* (A), *T. caput-medusae* subsp. *caput-medusae* (B), *T. caput-medusae* subsp. *crinitum* (C)

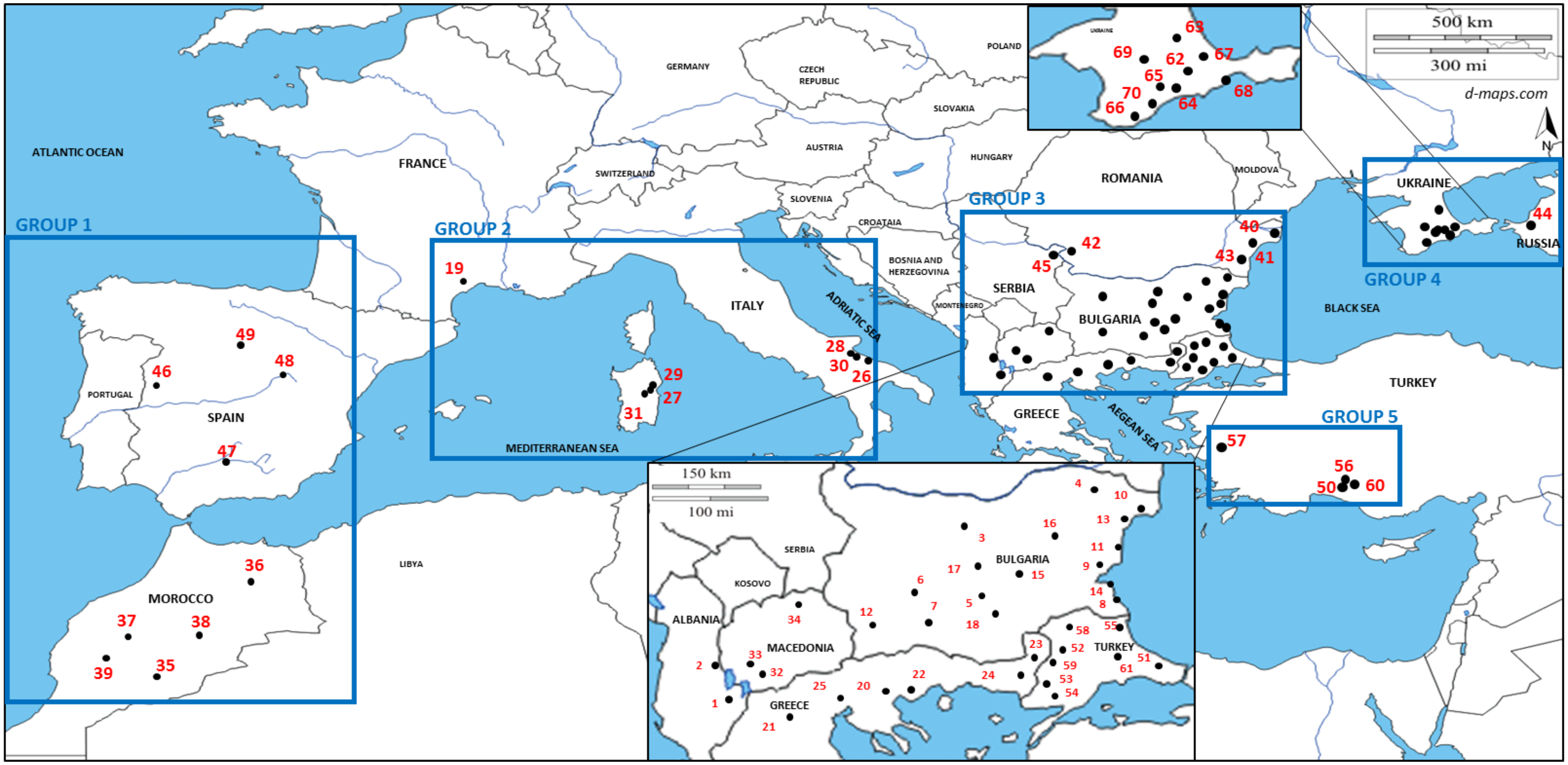


Figure 2 Collection locations for 70 native populations of *Taeniatherum caput-medusae* subspecies *asperum*. Populations were grouped into five geographic regions as shown here.

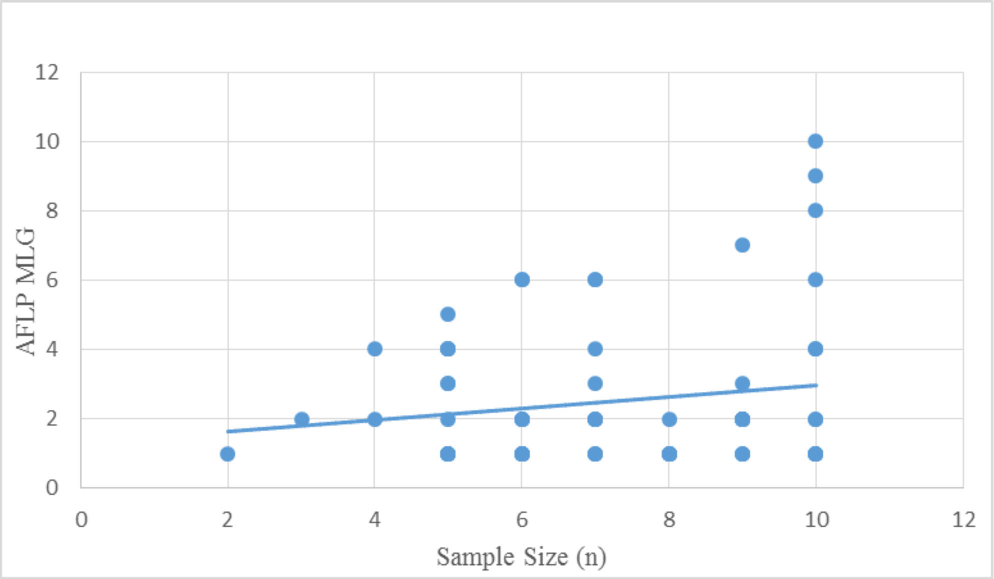


Figure 3 **Correlation between the number of AFLP MLG and population sample size (n).**

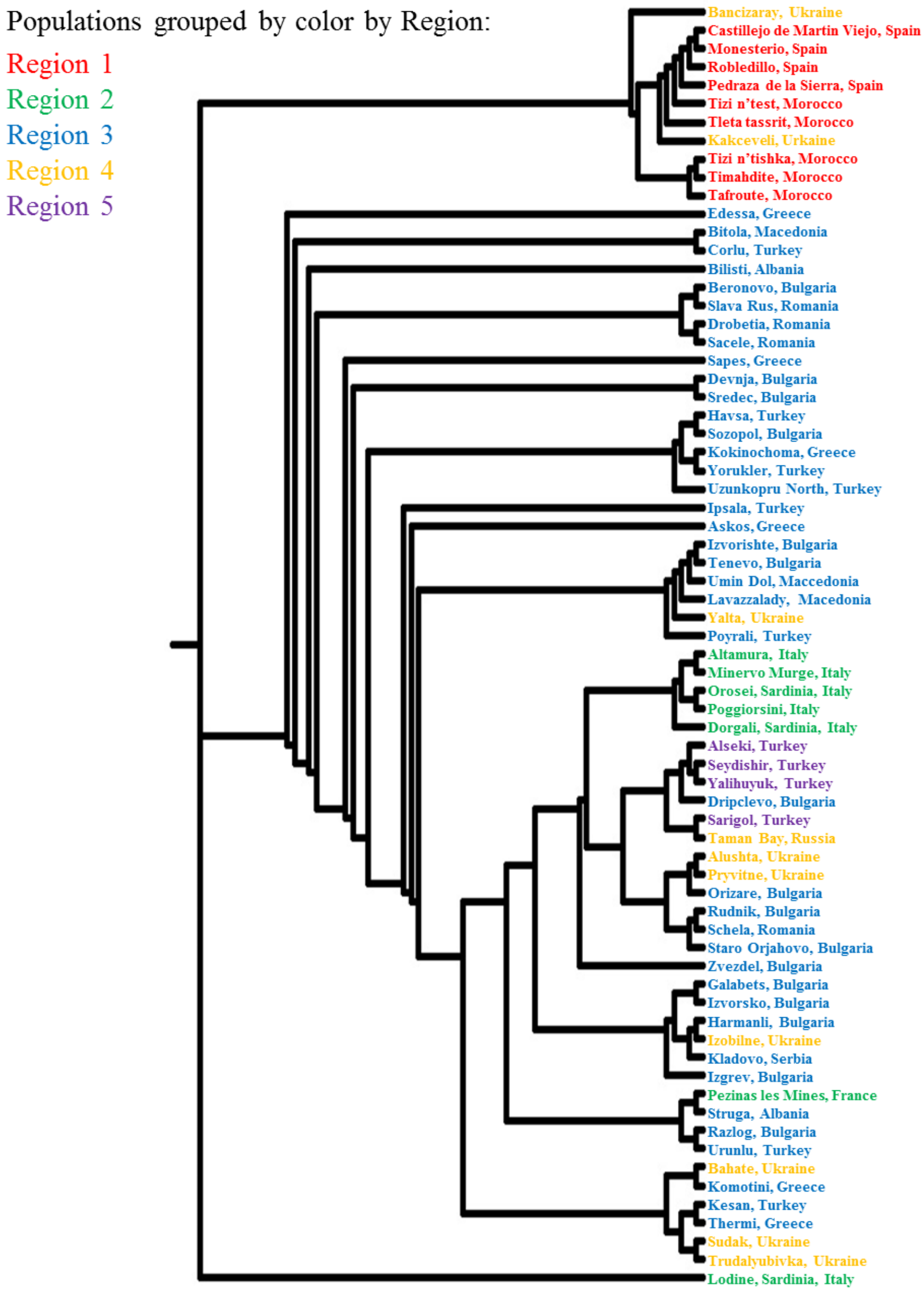
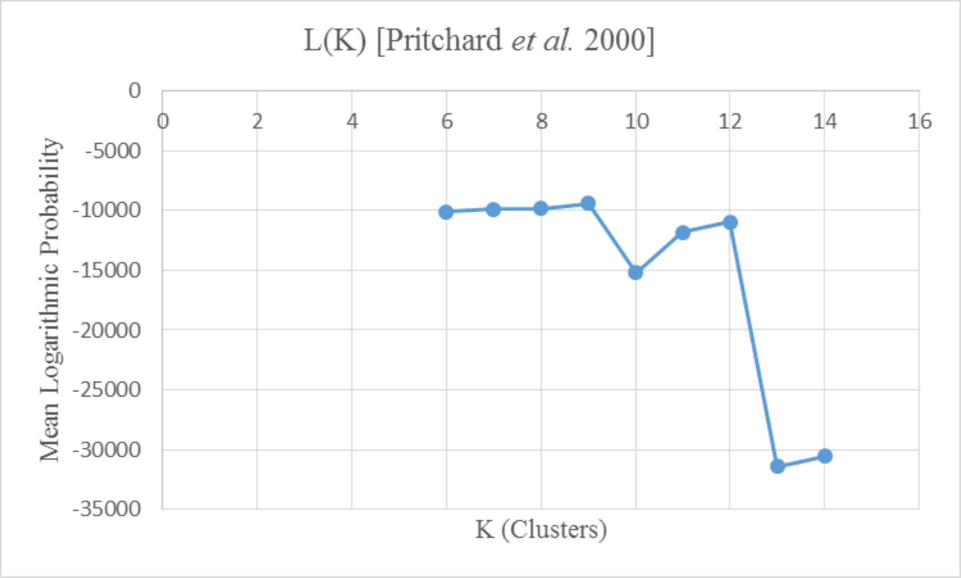


Figure 4 Neighbor-Joining tree the genetic relationships of 70 native populations of *Taeniatherum caput-medusae* subspecies *asperum*. Figure created with PHYLIP 3.695. Note that the populations from each Region are grouped by color.

(A)



(B)

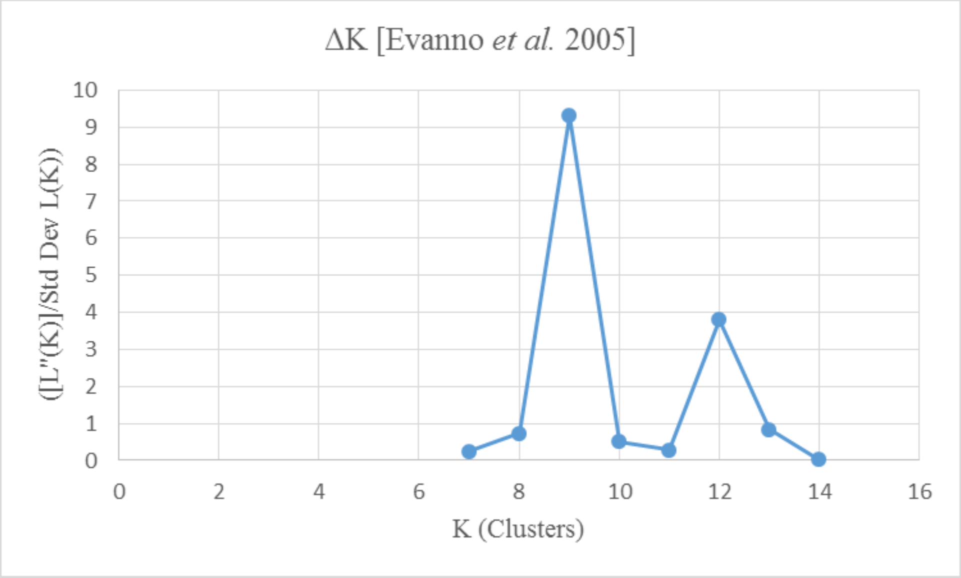
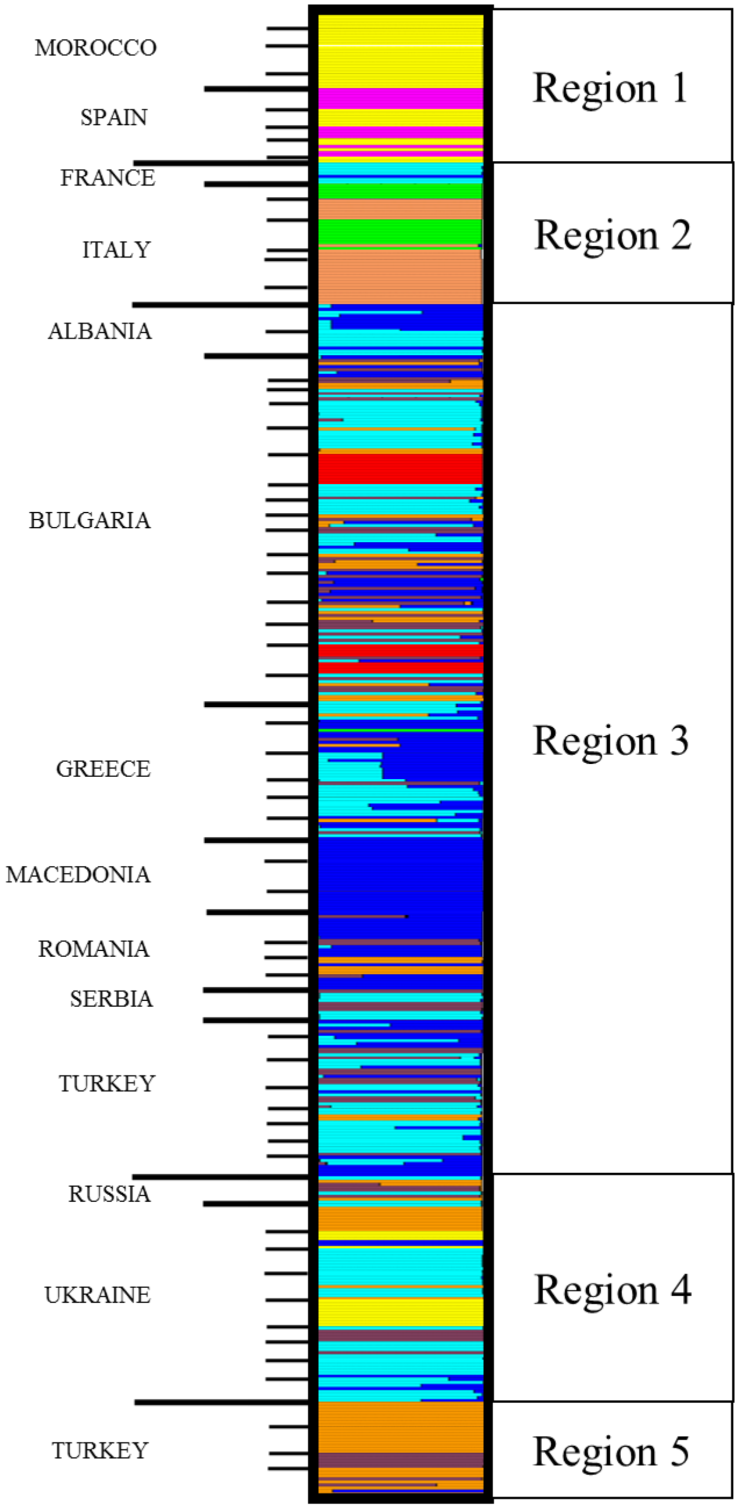


Figure 5 Results of the logarithmic probability of clustering of native populations of *Taeniatherum caput-medusae* subspecies *asperum*. See text for discussion of inferring the true value of K (clusters). Logarithmic probability L(K) of K based on the method of Pritchard *et al.* (2000) (A), and the ΔK method described by Evanno *et al.* (2005) (B).

(A)


MOROCCO
SPAIN
FRANCE
ITALY
ALBANIA
BULGARIA
GREECE
MACEDONIA
ROMANIA
SERBIA
TURKEY
RUSSIA
UKRAINE
TURKEY
Region 1
Region 2
Region 3
Region 4
Region 5

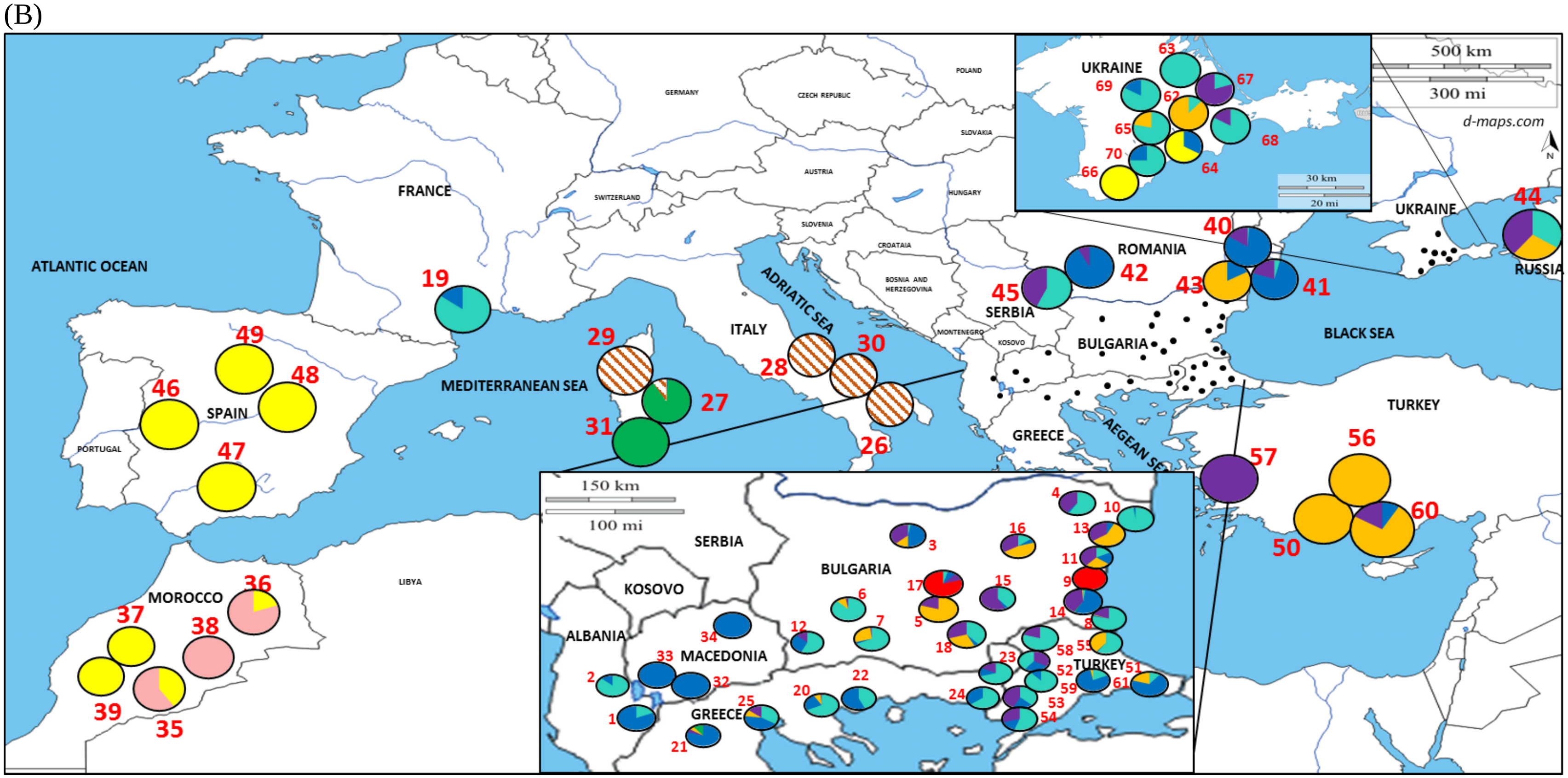
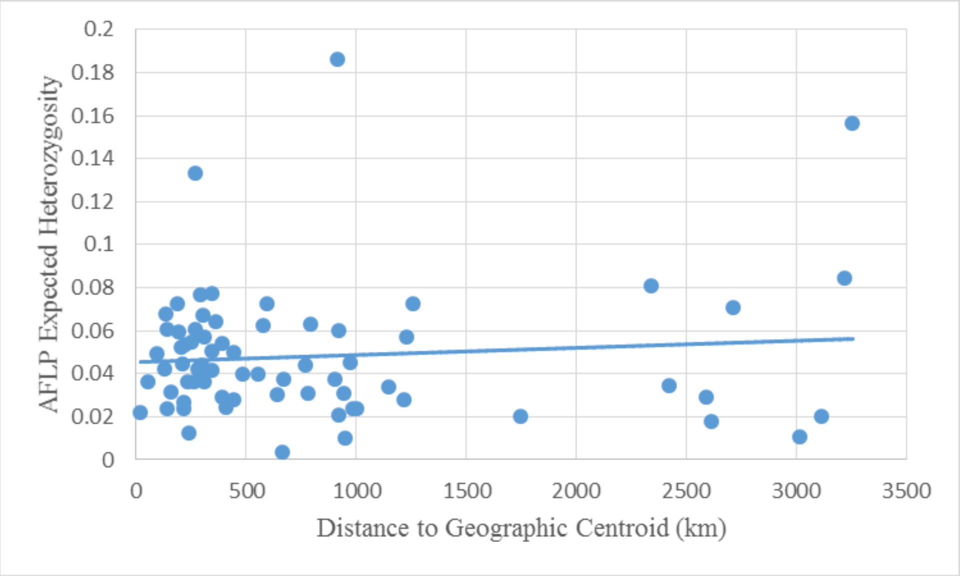
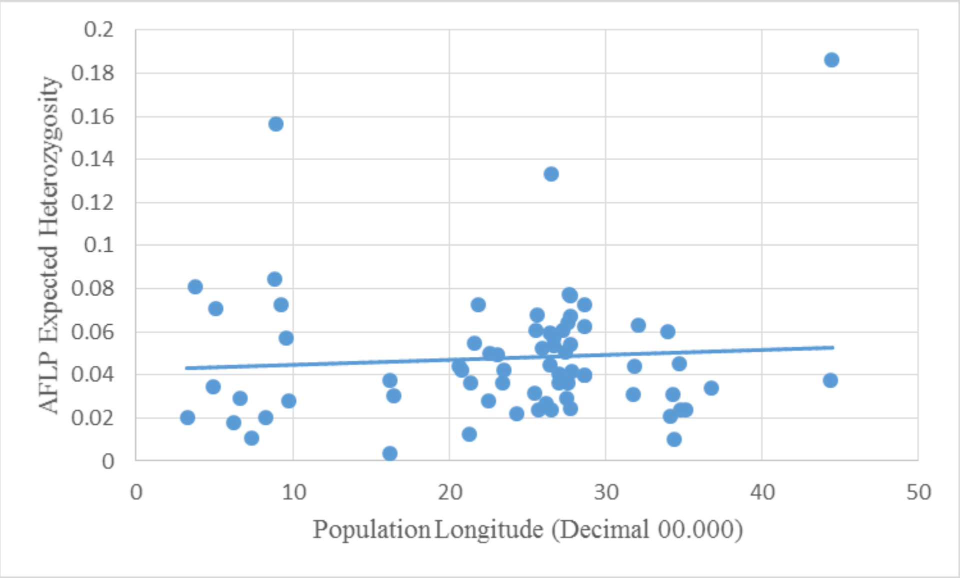


Figure 6 Population genetic structure analysis based on K = 9. STRUCTURE cluster assignments for each of the 495 individuals from 70 native populations of *Taeniatherum caput-medusae* subspecies *asperum* (A). STRUCTURE cluster assignments for the 70 native populations of *Taeniatherum caput-medusae* subspecies *asperum* (B).

(A)


AFLP Expected Heterozygosity
0.2
0.18
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0
500
1000
1500
2000
2500
3000
3500
Distance to Geographic Centroid (km)

(B)


AFLP Expected Heterozygosity
0.2
0.18
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0
10
20
30
40
50
Population Longitude (Decimal 00.000)

(C)

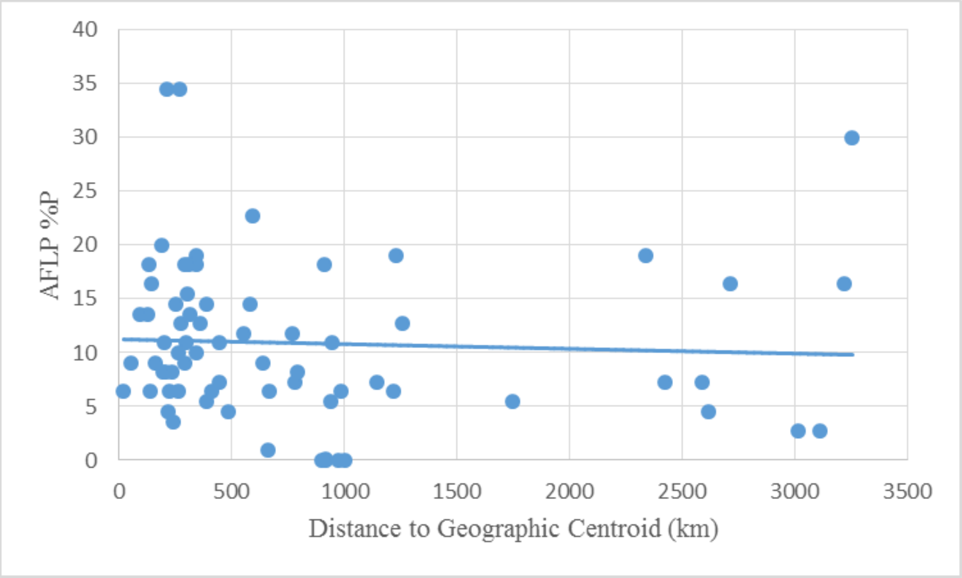


Figure 7 Analyses of the Central-Marginal Hypothesis with AFLP molecular data. Linear regression analysis of AFLP expected heterozygosity (H_E) and Euclidean distance to the geographic centroid (A), linear regression analysis of AFLP expected heterozygosity (H_E) and longitude (B), and linear regression analysis of AFLP percent polymorphic loci (%P) and Euclidean distance to the geographic centroid (C).

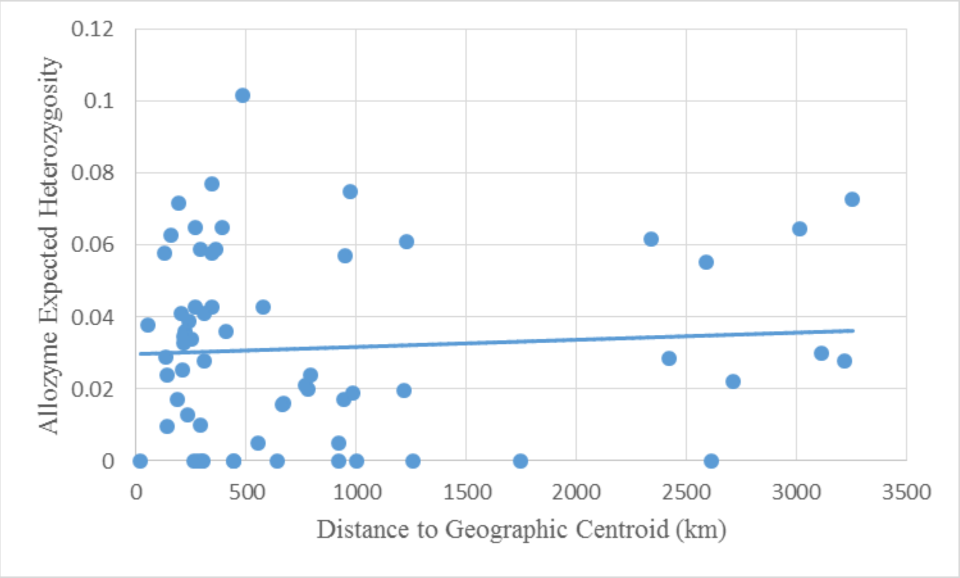


Figure 8 **Linear regression analysis of allozyme expected heterozygosity (H_E) and Euclidean distance to the geographic centroid.**

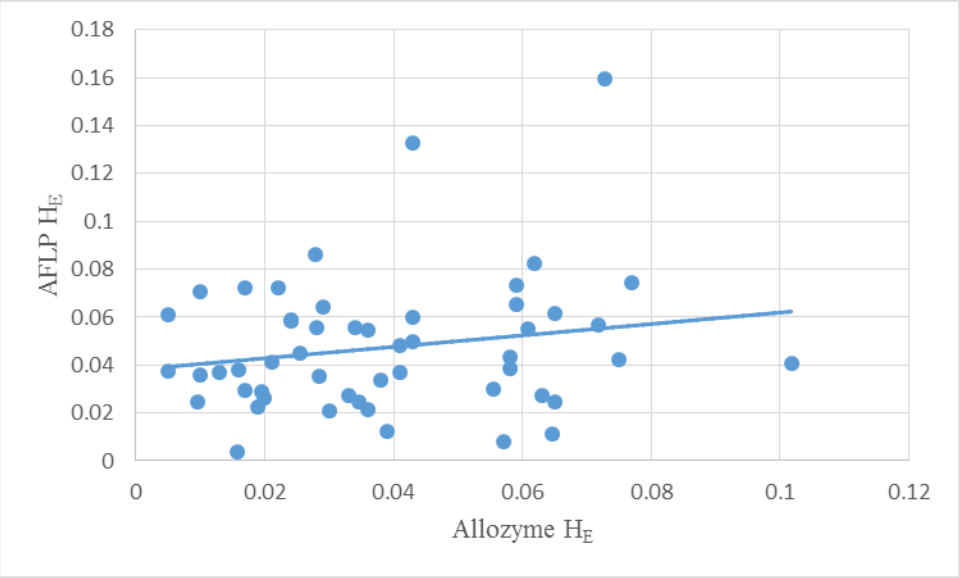


Figure 9 **Correlation between AFLP expected heterozygosity (H_E) values detected in this study and the allozyme expected heterozygosity (H_E) values reported by Peters (2013) and Skaar (2015).**

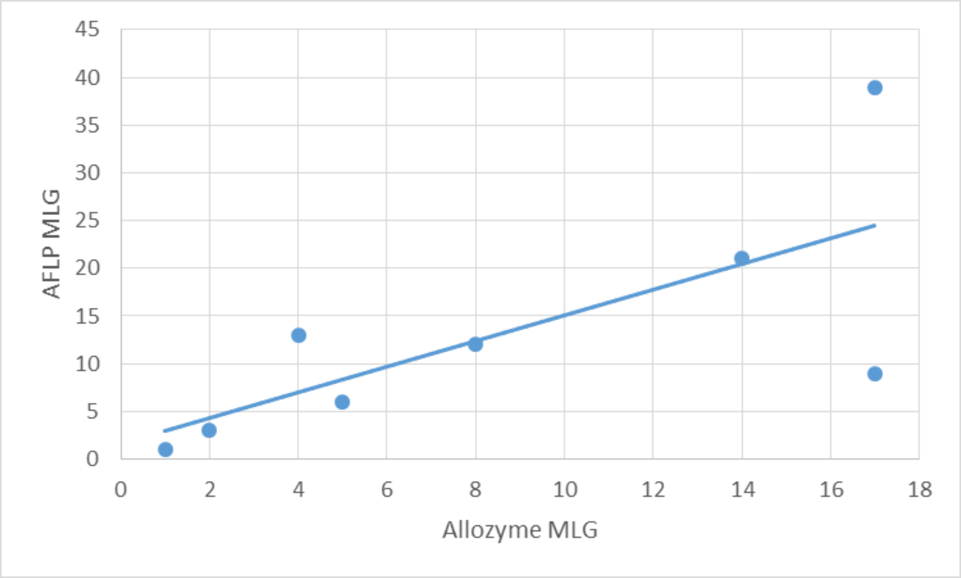


Figure 10 Correlation between the number of allozyme MLGs reported per country by Skaar (2015) and the number of AFLP MLGs discovered using AFLP data.

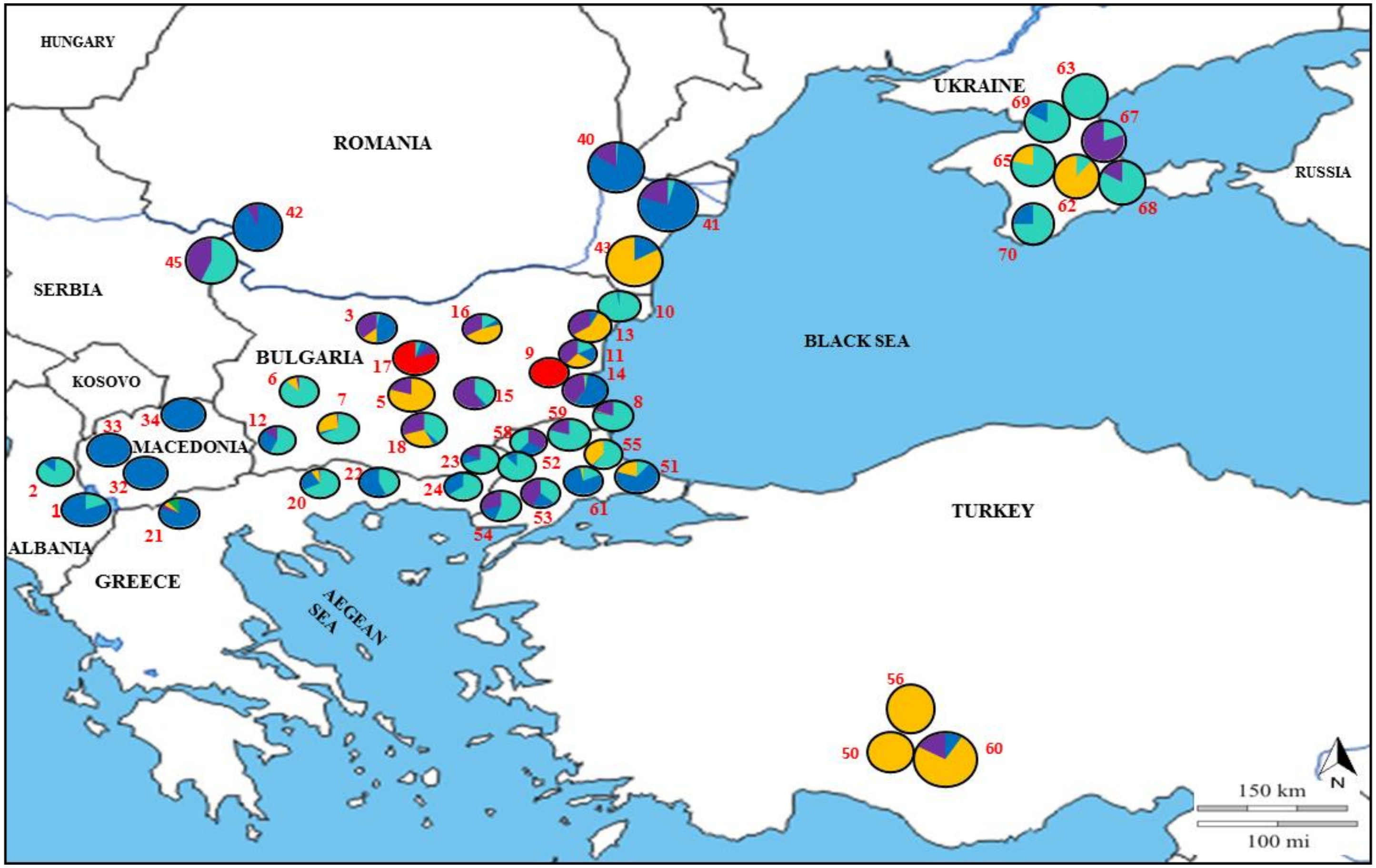


Figure 11 STRUCTURE analysis using AFLP data of the 48 native populations of *T. caput-medusae* subsp. *asperum* from Regions 3, 4 and 5 (see text) that were previously analyzed using allozymes. A K = 6 was best supported with the AFLP data, compared with a K = 2 using allozyme data (see Skaar 2015).

APPENDIX A

Population Pairwise F_{ST} values. Population Pairwise Comparisons Are Ordered in Each Population's List of Values in the Order Following the Population Codes to the Left of Each Block of Data.

```
18IT  0      0.5878 0.6806 0.6549 0.7354 0.5772 0.5934 0.4158 0.6163 0.7227 0.8174
      0.6088 0.5742 0.669  0.6333 0.6491 0.4172 0.4754 0.6661 0.6351 0.6628 0.7729
      0.6484 0.5888 0.6987 0.7314 0.6908 0.7047 0.6983 0.6522 0.8517 0.7263 0.7328
      0.8529 0.6241 0.6561 0.7437 0.6971 0.7482 0.6454 0.6986 0.6753 0.8141 0.6056
      0.5861 0.5166 0.6344 0.6391 0.5554 0.547  0.636  0.6286 0.6934 0.7047 0.5943
      0.6753 0.6338 0.7725 0.6295 0.6165 0.6442 0.5839 0.8454 0.6723 0.6624 0.6592
      0.5833 0.6026 0.6527 0.5789

AGR   0.5878 0      0.659  0.4596 0.6329 0.2624 0.3727 0.4896 0.4191 0.3928 0.8724
      0.5443 0.4506 0.4984 0.3543 0.516  0.3906 0.378  0.1939 0.1664 0.3909 0.7995
      0.2423 0.0903 0.3639 0.3817 0.6053 0.467  0.2691 0.3217 0.9008 0.5674 0.6718
      0.9053 0.3067 0.6934 0.7743 0.3648 0.8251 0.0948 0.5259 0.3687 0.8762 0.4708
      0.2206 0.4263 0.4633 0.4108 0.1522 0.2403 0.2695 0.5402 0.5875 0.2411 0.566
      0.4641 0.2073 0.8705 0.7553 0.7434 0.7509 0.094  0.905  0.3106 0.1793 0.6104
      0.366  0.3458 0.0698 0.1538

ALIT  0.6806 0.659  0      0.7577 0.7863 0.68   0.717  0.5915 0.7819 0.7434 0.9044
      0.7226 0.7157 0.7254 0.7363 0.7593 0.6712 0.6521 0.7037 0.6941 0.7379 0.8509
      0.6588 0.6603 0.7485 0.7809 0.7987 0.7313 0.7745 0.6438 0.9273 0.8512 0.3887
      0.9356 0.6316 0.5806 0.6719 0.7874 0.8592 0.7242 0.702  0.7181 0.9088 0.6614
      0.7141 0.6224 0.636  0.7212 0.5594 0.5709 0.7494 0.7093 0.7295 0.7619 0.6884
      0.7289 0.6497 0.9125 0.7809 0.7819 0.7907 0.5832 0.934  0.7322 0.7333 0.7664
      0.6833 0.6775 0.7537 0.6028

ATR   0.6549 0.4596 0.7577 0      0.7118 0.6575 0.6064 0.6096 0.7062 0.6706 0.9181
      0.6915 0.6974 0.4523 0.6415 0.6668 0.5336 0.5123 0.5406 0.366  0.5916 0.859
      0.3715 0.4536 0.4031 0.7065 0.7209 0.7703 0.6005 0.5554 0.9314 0.7773 0.7638
      0.9459 0.4239 0.8005 0.8675 0.7343 0.8734 0.4384 0.6507 0.6648 0.9198 0.4893
      0.6192 0.4943 0.4677 0.2222 0.5188 0.1476 0.5864 0.6999 0.6069 0.5895 0.6468
      0.5188 0.493  0.927  0.8012 0.8086 0.8082 0.3814 0.9475 0.6384 0.5865 0.7202
      0.3284 0.5744 0.6257 0.4

AUK   0.7354 0.6329 0.7863 0.7118 0      0.696  0.7168 0.6284 0.8325 0.6648 0.9283
      0.7408 0.7391 0.6519 0.7837 0.7756 0.6766 0.6862 0.7114 0.661  0.7681 0.8871
      0.6433 0.6491 0.715  0.8312 0.8348 0.742  0.761  0.6737 0.9487 0.8946 0.7301
      0.9592 0.5197 0.8459 0.9064 0.8288 0.887  0.6985 0.5798 0.7505 0.9381 0.6427
      0.7213 0.6788 0.5649 0.5636 0.6138 0.5148 0.7534 0.7646 0.7625 0.745  0.7129
      0.7354 0.6435 0.9407 0.8138 0.8149 0.8049 0.5368 0.9644 0.7273 0.7043 0.7863
      0.5549 0.7125 0.7801 0.5809

BAL   0.5772 0.2624 0.68   0.6575 0.696  0      0.2567 0.3983 0.3383 0.5551 0.8344
      0.381  0.2716 0.665  0.4758 0.4562 0.5136 0.3545 0.5105 0.502  0.5518 0.799
      0.5248 0.4033 0.5993 0.627  0.6306 0.5217 0.5481 0.5161 0.8821 0.635  0.7057
      0.8741 0.4778 0.7153 0.7829 0.6083 0.7745 0.5119 0.5975 0.5482 0.8372 0.5505
      0.4006 0.5404 0.5526 0.624  0.2028 0.4271 0.4831 0.5329 0.6921 0.5364 0.6033
      0.6499 0.4431 0.8402 0.6949 0.6925 0.7052 0.3419 0.873  0.4811 0.4865 0.6292
      0.5608 0.4021 0.4245 0.438

BBG   0.5934 0.3727 0.717  0.6064 0.7168 0.2567 0      0.4606 0.4499 0.6323 0.8484
      0.3213 0.3777 0.6728 0.3742 0.2698 0.5238 0.3123 0.5293 0.508  0.548  0.819
```

0.5493 0.4238 0.5566 0.6249 0.6374 0.6558 0.5262 0.5678 0.8838 0.7359 0.7354
0.8836 0.3964 0.7125 0.7982 0.6835 0.7905 0.5947 0.5497 0.6071 0.8487 0.4138
0.5405 0.5097 0.4588 0.5733 0.2372 0.3429 0.4218 0.4303 0.6131 0.6061 0.6242
0.5836 0.547 0.8499 0.7168 0.7268 0.737 0.4452 0.8849 0.5328 0.5731 0.6715
0.4796 0.4406 0.558 0.4609

BCUK 0.4158 0.4896 0.5915 0.6096 0.6284 0.3983 0.4606 0 0.4449 0.5979 0.5802
0.4249 0.3576 0.6262 0.5333 0.4463 0.5292 0.3733 0.5675 0.5484 0.5402 0.6467
0.5557 0.5156 0.6054 0.6134 0.5756 0.5871 0.6011 0.5487 0.759 0.5915 0.6179
0.6386 0.5169 0.6061 0.682 0.5896 0.5203 0.5726 0.5887 0.5603 0.6186 0.5245
0.5312 0.4839 0.5544 0.5957 0.4228 0.5017 0.5484 0.4643 0.6194 0.5977 0.5182
0.6157 0.5266 0.629 0.3647 0.4587 0.4962 0.4745 0.5939 0.5331 0.566 0.505
0.5224 0.4615 0.5442 0.5139

BMC 0.6163 0.4191 0.7819 0.7062 0.8325 0.3383 0.4499 0.4449 0 0.7213 0.8877
0.5545 0.3407 0.7582 0.4778 0.5223 0.6086 0.3106 0.6181 0.5535 0.5526 0.8324
0.5749 0.4652 0.6684 0.7162 0.6298 0.7441 0.6805 0.5977 0.9141 0.6907 0.8148
0.922 0.5763 0.8001 0.876 0.7096 0.8375 0.6117 0.7262 0.6449 0.8921 0.6471
0.5281 0.5325 0.7078 0.708 0.3469 0.4783 0.5512 0.5924 0.7779 0.6776 0.6253
0.7446 0.5642 0.9048 0.7541 0.7699 0.765 0.4752 0.9196 0.5213 0.6172 0.6949
0.5908 0.3793 0.5092 0.5251

BUK 0.7227 0.3928 0.7434 0.6706 0.6648 0.5551 0.6323 0.5979 0.7213 0 0.9188
0.6734 0.6229 0.667 0.6461 0.6682 0.6417 0.6186 0.464 0.4419 0.5634 0.8487
0.3771 0.3951 0.4755 0.6156 0.7385 0.4824 0.5481 0.4084 0.9367 0.7816 0.7534
0.9472 0.4959 0.8157 0.8764 0.6167 0.8779 0.4891 0.6076 0.5469 0.9229 0.6352
0.5135 0.5641 0.5724 0.6205 0.4383 0.4408 0.5845 0.6639 0.7285 0.3444 0.6447
0.6383 0.3214 0.9294 0.8119 0.8081 0.8131 0.1742 0.951 0.3898 0.4288 0.7044
0.6274 0.5058 0.5313 0.4203

CMSP 0.8174 0.8724 0.9044 0.9181 0.9283 0.8344 0.8484 0.5802 0.8877 0.9188 0
0.8397 0.8403 0.9185 0.8871 0.846 0.8627 0.8116 0.9019 0.8833 0.897 0.8909
0.8878 0.8698 0.9095 0.9278 0.9122 0.9219 0.9124 0.8778 0.9202 0.9363 0.9094
0.0278 0.8327 0.9138 0.9448 0.9248 0.2991 0.9117 0.8751 0.8899 0.5261 0.8441
0.8846 0.8401 0.8752 0.896 0.8302 0.8327 0.8903 0.8375 0.8978 0.9224 0.8002
0.9111 0.8782 0.9183 0.4872 0.75 0.7068 0.8475 0.689 0.8972 0.901 0.8542
0.8594 0.8741 0.9121 0.8531

CRO 0.6088 0.5443 0.7226 0.6915 0.7408 0.381 0.3213 0.4249 0.5545 0.6734 0.8397
0 0.4369 0.7354 0.532 0.4716 0.6351 0.4485 0.6121 0.6108 0.6075 0.8
0.6145 0.5527 0.6487 0.6906 0.6688 0.6979 0.6579 0.6128 0.8914 0.7254 0.7427
0.8776 0.5256 0.7397 0.822 0.7297 0.7805 0.691 0.6055 0.6712 0.8436 0.5144
0.618 0.5629 0.5654 0.6648 0.3473 0.4717 0.5885 0.5676 0.7142 0.6831 0.6136
0.6677 0.5627 0.855 0.6997 0.6997 0.7035 0.5313 0.8754 0.5915 0.6617 0.6837
0.5914 0.49 0.6657 0.5559

CTR 0.5742 0.4506 0.7157 0.6974 0.7391 0.2716 0.3777 0.3576 0.3407 0.6229 0.8403
0.4369 0 0.7294 0.5091 0.4832 0.5998 0.3769 0.6036 0.565 0.5218 0.7984
0.5672 0.4836 0.6673 0.6813 0.6234 0.6153 0.6405 0.5674 0.8796 0.7269 0.7449
0.8776 0.5546 0.7135 0.8067 0.6514 0.7826 0.6239 0.6499 0.5871 0.8424 0.5666

	0.5276	0.4855	0.6115	0.6848	0.3181	0.4949	0.5309	0.5262	0.7357	0.6525	0.6227
	0.7073	0.5592	0.8391	0.6951	0.7058	0.7115	0.4821	0.8729	0.4679	0.5643	0.6275
	0.5955	0.3519	0.5661	0.4913							
DBG	0.669	0.4984	0.7254	0.4523	0.6519	0.665	0.6728	0.6262	0.7582	0.667	0.9185
	0.7354	0.7294	0	0.6384	0.7257	0.507	0.586	0.5376	0.5037	0.6494	0.8601
	0.4531	0.4574	0.5868	0.6961	0.7776	0.7617	0.6298	0.5186	0.9369	0.8177	0.7306
	0.9471	0.478	0.784	0.8334	0.7269	0.8742	0.4529	0.5885	0.6582	0.9228	0.6163
	0.574	0.5535	0.5578	0.4032	0.5666	0.3496	0.6219	0.7417	0.617	0.5651	0.6506
	0.5819	0.4559	0.9253	0.8047	0.8051	0.8052	0.3896	0.9522	0.6688	0.5508	0.7265
	0.4596	0.666	0.6604	0.4166							
DEBG	0.6333	0.3543	0.7363	0.6415	0.7837	0.4758	0.3742	0.5333	0.4778	0.6461	0.8871
	0.532	0.5091	0.6384	0	0.5121	0.5385	0.4791	0.3679	0.4357	0.413	0.8215
	0.4677	0.2101	0.5779	0.4191	0.6375	0.6878	0.4805	0.458	0.9157	0.7494	0.7705
	0.9181	0.4234	0.7026	0.812	0.6082	0.8379	0.5544	0.5495	0.5445	0.8891	0.504
	0.4789	0.4345	0.6252	0.6159	0.2309	0.3449	0.2098	0.5141	0.6452	0.5788	0.5775
	0.5869	0.4974	0.8995	0.7715	0.7853	0.7821	0.4305	0.9222	0.4364	0.488	0.7024
	0.494	0.4642	0.4946	0.3262							
DRO	0.6491	0.516	0.7593	0.6668	0.7756	0.4562	0.2698	0.4463	0.5223	0.6682	0.846
	0.4716	0.4832	0.7257	0.5121	0	0.6207	0.3455	0.5991	0.5863	0.563	0.8226
	0.5795	0.517	0.5957	0.6727	0.6418	0.7393	0.6311	0.588	0.8824	0.7667	0.7789
	0.8824	0.5211	0.7778	0.8462	0.7171	0.7898	0.6625	0.6586	0.6534	0.8482	0.5688
	0.6094	0.5434	0.5914	0.659	0.4269	0.4673	0.5554	0.3817	0.7084	0.6408	0.647
	0.6593	0.575	0.8465	0.7119	0.7164	0.7517	0.4542	0.8799	0.5526	0.6467	0.6496
	0.5887	0.4722	0.6321	0.5634							
DSA	0.4172	0.3906	0.6712	0.5336	0.6766	0.5136	0.5238	0.5292	0.6086	0.6417	0.8627
	0.6351	0.5998	0.507	0.5385	0.6207	0	0.4663	0.5063	0.4799	0.6222	0.8106
	0.5165	0.4607	0.5881	0.6193	0.6781	0.6738	0.5708	0.5603	0.8929	0.7228	0.6974
	0.8947	0.4763	0.661	0.7262	0.5895	0.8068	0.4793	0.6201	0.5538	0.8633	0.5568
	0.4418	0.5244	0.538	0.4942	0.4385	0.4016	0.5521	0.6493	0.6124	0.5952	0.613
	0.5718	0.5185	0.8374	0.7319	0.7102	0.7287	0.4367	0.8933	0.5954	0.529	0.6855
	0.4643	0.5924	0.5584	0.4126							
EGR	0.4754	0.378	0.6521	0.5123	0.6862	0.3545	0.3123	0.3733	0.3106	0.6186	0.8116
	0.4485	0.3769	0.586	0.4791	0.3455	0.4663	0	0.5414	0.5092	0.4727	0.7825
	0.4883	0.445	0.5542	0.6457	0.5723	0.6633	0.6043	0.509	0.8608	0.6296	0.678
	0.8508	0.4893	0.6946	0.767	0.6344	0.7498	0.5151	0.6399	0.5737	0.8124	0.5247
	0.5028	0.4415	0.4914	0.5498	0.3807	0.3889	0.502	0.455	0.627	0.5592	0.5939
	0.5977	0.4532	0.8078	0.6664	0.6659	0.6815	0.3798	0.8415	0.4569	0.555	0.5587
	0.4374	0.3696	0.4908	0.4635							
GBG	0.6661	0.1939	0.7037	0.5406	0.7114	0.5105	0.5293	0.5675	0.6181	0.464	0.9019
	0.6121	0.6036	0.5376	0.3679	0.5991	0.5063	0.5414	0	0.1512	0.4613	0.815
	0.1483	0.1579	0.3645	0.1295	0.6696	0.5776	0.2372	0.26	0.9253	0.6901	0.7158
	0.9313	0.3209	0.7577	0.8104	0.3836	0.8569	0.2754	0.4875	0.3642	0.9044	0.531
	0.3129	0.4708	0.5228	0.4445	0.2189	0.251	0.3879	0.5825	0.5873	0.3585	0.5605

```
     0.4152 0.2356 0.901  0.792  0.7765 0.7868 0.2185 0.9339 0.4025 0.1917 0.6539
     0.4737 0.5119 0.3417 0.1139

HBG  0.6351 0.1664 0.6941 0.366  0.661  0.502  0.508  0.5484 0.5535 0.4419 0.8833
     0.6108 0.565  0.5037 0.4357 0.5863 0.4799 0.5092 0.1512 0      0.4547 0.7953
     0.122  0.1821 0.2056 0.2867 0.6442 0.5529 0.1745 0.3581 0.906  0.5509 0.6974
     0.9125 0.1897 0.7319 0.782  0.3734 0.8386 0.1626 0.4916 0.342  0.8854 0.4652
     0.3185 0.4162 0.4604 0.3036 0.2721 0.0994 0.3657 0.5657 0.53   0.3636 0.5583
     0.3886 0.2711 0.8763 0.7721 0.7568 0.7654 0.2198 0.9114 0.453  0.1702 0.5756
     0.3704 0.4745 0.295  0.1117

HTR  0.6628 0.3909 0.7379 0.5916 0.7681 0.5518 0.548  0.5402 0.5526 0.5634 0.897
     0.6075 0.5218 0.6494 0.413  0.563  0.6222 0.4727 0.4613 0.4547 0      0.8224
     0.2908 0.1859 0.5429 0.5989 0.5615 0.6924 0.5508 0.2884 0.9213 0.7525 0.7519
     0.9278 0.5347 0.7472 0.8503 0.5742 0.8493 0.5074 0.6069 0.4979 0.8999 0.5462
     0.5206 0.2573 0.625  0.6277 0.4151 0.4077 0.2898 0.5906 0.6926 0.4173 0.5853
     0.6288 0.3448 0.9119 0.7782 0.7951 0.7939 0.2896 0.9303 0.2895 0.4291 0.6664
     0.5072 0.2424 0.4582 0.3126

IBG  0.7729 0.7995 0.8509 0.859  0.8871 0.799  0.819  0.6467 0.8324 0.8487 0.8909
     0.8    0.7984 0.8601 0.8215 0.8226 0.8106 0.7825 0.815  0.7953 0.8224 0
     0.7998 0.7797 0.8357 0.8491 0.8557 0.8567 0.8331 0.7892 0.906  0.8598 0.862
     0.9181 0.7818 0.8647 0.8927 0.8392 0.8524 0.8334 0.8248 0.8003 0.8978 0.8048
     0.7915 0.7658 0.8279 0.8386 0.7654 0.7639 0.8193 0.8063 0.8514 0.8483 0.4624
     0.8364 0.7856 0.9089 0.7967 0.7997 0.7943 0.7743 0.9193 0.8266 0.8116 0.7818
     0.8102 0.8131 0.8333 0.7665

IGBG 0.6484 0.2423 0.6588 0.3715 0.6433 0.5248 0.5493 0.5557 0.5749 0.3771 0.8878
     0.6145 0.5672 0.4531 0.4677 0.5795 0.5165 0.4883 0.1483 0.122  0.2908 0.7998
     0      0.1615 0.2415 0.3732 0.579  0.5674 0.326  0.1662 0.9107 0.6167 0.6523
     0.917  0.3671 0.7288 0.7731 0.3818 0.8417 0.1519 0.4863 0.3632 0.8892 0.4872
     0.3508 0.3793 0.4869 0.3745 0.3208 0.2135 0.4002 0.5981 0.5577 0.2311 0.5434
     0.421  0.1358 0.8825 0.7742 0.7616 0.7703 0.1262 0.9158 0.3479 0.1785 0.5889
     0.4048 0.3753 0.3285 0.1034

IPT  0.5888 0.0903 0.6603 0.4536 0.6491 0.4033 0.4238 0.5156 0.4652 0.3951 0.8698
     0.5527 0.4836 0.4574 0.2101 0.517  0.4607 0.445  0.1579 0.1821 0.1859 0.7797
     0.1615 0      0.3464 0.2958 0.5579 0.4882 0.186  0.2126 0.8976 0.5808 0.6768
     0.9    0.3494 0.662  0.7491 0.3627 0.8225 0.1726 0.4555 0.3337 0.8715 0.4511
     0.2656 0.301  0.51   0.4418 0.244  0.2424 0.0287 0.5107 0.5411 0.1831 0.5169
     0.4255 0.2    0.8682 0.7544 0.7542 0.7603 0.1471 0.9013 0.2867 0.1107 0.5766
     0.3691 0.3187 0.1352 0.1077

IUK  0.6987 0.3639 0.7485 0.4031 0.715  0.5993 0.5566 0.6054 0.6684 0.4755 0.9095
     0.6487 0.6673 0.5868 0.5779 0.5957 0.5881 0.5542 0.3645 0.2056 0.5429 0.8357
     0.2415 0.3464 0      0.4835 0.6963 0.6834 0.363  0.4492 0.9228 0.6944 0.7543
     0.9359 0.3474 0.8074 0.8556 0.6267 0.8707 0.3741 0.5637 0.5624 0.9126 0.5345
     0.5194 0.5136 0.4635 0.3662 0.4211 0.2311 0.5176 0.6368 0.5922 0.3879 0.6019
     0.4325 0.3627 0.9146 0.8058 0.8042 0.8076 0.2356 0.9364 0.5531 0.4729 0.6742
     0.4623 0.5198 0.4937 0.3852
```

IZBG 0.7314 0.3817 0.7809 0.7065 0.8312 0.627 0.6249 0.6134 0.7162 0.6156 0.9278
0.6906 0.6813 0.6961 0.4191 0.6727 0.6193 0.6457 0.1295 0.2867 0.5989 0.8491
0.3732 0.2958 0.4835 0 0.7708 0.7218 0.3637 0.4332 0.9459 0.8127 0.811
0.9561 0.3872 0.822 0.8903 0.5534 0.8872 0.52 0.5707 0.4878 0.9321 0.6141
0.4664 0.5374 0.6313 0.6048 0.3137 0.3731 0.5089 0.6403 0.6895 0.5827 0.616
0.555 0.4242 0.9421 0.8224 0.8192 0.8215 0.3837 0.9605 0.5577 0.4254 0.722
0.596 0.6205 0.5502 0.3073

KGR 0.6908 0.6053 0.7987 0.7209 0.8348 0.6306 0.6374 0.5756 0.6298 0.7385 0.9122
0.6688 0.6234 0.7776 0.6375 0.6418 0.6781 0.5723 0.6696 0.6442 0.5615 0.8557
0.579 0.5579 0.6963 0.7708 0 0.7956 0.7455 0.5869 0.9272 0.8281 0.8207
0.9405 0.648 0.7997 0.8833 0.728 0.8692 0.6978 0.7309 0.7017 0.9148 0.6486
0.6355 0.5655 0.7124 0.7297 0.5214 0.5384 0.6437 0.6774 0.7916 0.7087 0.6425
0.7588 0.6265 0.9171 0.7959 0.8071 0.791 0.5204 0.9408 0.6033 0.6909 0.7609
0.6461 0.5017 0.6907 0.5563

KMGR 0.7047 0.467 0.7313 0.7703 0.742 0.5217 0.6558 0.5871 0.7441 0.4824
0.9219 0.6979 0.6153 0.7617 0.6878 0.7393 0.6738 0.6633 0.5776 0.5529 0.6924
0.8567 0.5674 0.4882 0.6834 0.7218 0.7956 0 0.632 0.5444 0.9408 0.7969
0.7517 0.9523 0.5214 0.8099 0.864 0.7055 0.8765 0.5825 0.6238 0.6019 0.9259
0.6267 0.5674 0.6345 0.6365 0.7011 0.3979 0.4848 0.6356 0.6354 0.759 0.6509
0.6363 0.7292 0.5371 0.9349 0.8015 0.7992 0.8073 0.4373 0.9574 0.5992 0.5178
0.7024 0.6761 0.609 0.557 0.4487

KSR 0.6983 0.2691 0.7745 0.6005 0.761 0.5481 0.5262 0.6011 0.6805 0.5481 0.9124
0.6579 0.6405 0.6298 0.4805 0.6311 0.5708 0.6043 0.2372 0.1745 0.5508 0.8331
0.326 0.186 0.363 0.3637 0.7455 0.632 0 0.413 0.9314 0.7304 0.7785
0.9404 0.3067 0.8028 0.8519 0.5458 0.869 0.3743 0.4722 0.4649 0.915 0.5312
0.401 0.4913 0.5627 0.4719 0.3673 0.3044 0.3327 0.6172 0.5561 0.4251 0.5965
0.4276 0.3663 0.9197 0.8024 0.8012 0.8086 0.3287 0.9451 0.5679 0.2248 0.6522
0.4933 0.5962 0.421 0.2399

KTR 0.6522 0.3217 0.6438 0.5554 0.6737 0.5161 0.5678 0.5487 0.5977 0.4084 0.8778
0.6128 0.5674 0.5186 0.458 0.588 0.5603 0.509 0.26 0.3581 0.2884 0.7892
0.1662 0.2126 0.4492 0.4332 0.5869 0.5444 0.413 0 0.9033 0.6569 0.6459
0.9072 0.442 0.7193 0.762 0.3905 0.8324 0.3718 0.5089 0.3779 0.8798 0.5533
0.3744 0.408 0.5574 0.5416 0.3644 0.3691 0.3905 0.5798 0.5912 0.248 0.5493
0.503 0.1527 0.8762 0.7678 0.7592 0.7723 0.1735 0.9105 0.3179 0.269 0.6063
0.5248 0.4196 0.3768 0.2074

KUK 0.8517 0.9008 0.9273 0.9314 0.9487 0.8821 0.8838 0.759 0.9141 0.9367 0.9202
0.8914 0.8796 0.9369 0.9157 0.8824 0.8929 0.8608 0.9253 0.906 0.9213 0.906
0.9107 0.8976 0.9228 0.9459 0.9272 0.9408 0.9314 0.9033 0 0.9535 0.9383
0.9462 0.8762 0.9315 0.9584 0.9421 0.8785 0.9292 0.9121 0.9174 0.9216 0.8759
0.9082 0.8716 0.9012 0.9178 0.8723 0.8617 0.9158 0.8778 0.9228 0.9386 0.8128
0.9302 0.9094 0.9481 0.803 0.8516 0.8517 0.8796 0.9484 0.9225 0.9235 0.8964
0.8951 0.898 0.9322 0.8849

LMC 0.7263 0.5674 0.8512 0.7773 0.8946 0.635 0.7359 0.5915 0.6907 0.7816 0.9363
0.7254 0.7269 0.8177 0.7494 0.7667 0.7228 0.6296 0.6901 0.5509 0.7525 0.8598

	0.6167	0.5808	0.6944	0.8127	0.8281	0.7969	0.7304	0.6569	0.9535	0	0.8668
	0.966	0.5929	0.8944	0.9409	0.8044	0.8928	0.6262	0.7731	0.7086	0.9411	0.7294
	0.6183	0.6895	0.7696	0.7414	0.5756	0.5066	0.7243	0.7406	0.823	0.7474	0.6187
	0.7968	0.537	0.9618	0.8147	0.8166	0.8189	0.5225	0.9704	0.7421	0.67	0.6488
	0.6904	0.6917	0.6118	0.5819							
MMIT	0.7328	0.6718	0.3887	0.7638	0.7301	0.7057	0.7354	0.6179	0.8148	0.7534	0.9094
	0.7427	0.7449	0.7306	0.7705	0.7789	0.6974	0.678	0.7158	0.6974	0.7519	0.862
	0.6523	0.6768	0.7543	0.811	0.8207	0.7517	0.7785	0.6459	0.9383	0.8668	0
	0.942	0.5848	0.7061	0.6991	0.8028	0.866	0.734	0.6347	0.726	0.9196	0.6562
	0.7357	0.6794	0.6371	0.6928	0.5993	0.5726	0.7601	0.7458	0.7435	0.77	0.6905
	0.7249	0.6609	0.9182	0.7973	0.7909	0.7893	0.5979	0.9423	0.7526	0.7371	0.7728
	0.6371	0.725	0.7685	0.5909							
MSP	0.8529	0.9053	0.9356	0.9459	0.9592	0.8741	0.8836	0.6386	0.922	0.9472	0.0278
	0.8776	0.8776	0.9471	0.9181	0.8824	0.8947	0.8508	0.9313	0.9125	0.9278	0.9181
	0.917	0.9	0.9359	0.9561	0.9405	0.9523	0.9404	0.9072	0.9462	0.966	0.942
	0	0.864	0.9444	0.9734	0.9546	0.4525	0.9411	0.9052	0.9203	0.6111	0.8769
	0.916	0.873	0.9069	0.9256	0.8655	0.8629	0.9206	0.8736	0.9257	0.9505	0.8277
	0.9383	0.9098	0.959	0.5811	0.8037	0.7667	0.8796	0.8681	0.9285	0.9308	0.8889
	0.8922	0.9069	0.9429	0.8846							
OBG	0.6241	0.3067	0.6316	0.4239	0.5197	0.4778	0.3964	0.5169	0.5763	0.4959	0.8327
	0.5256	0.5546	0.478	0.4234	0.5211	0.4763	0.4893	0.3209	0.1897	0.5347	0.7818
	0.3671	0.3494	0.3474	0.3872	0.648	0.5214	0.3067	0.442	0.8762	0.5929	0.5848
	0.864	0	0.6687	0.6978	0.5099	0.7896	0.4155	0.27	0.4354	0.8441	0.3688
	0.4593	0.4979	0.341	0.2747	0.2527	0.087	0.4248	0.4772	0.4101	0.4985	0.5659
	0.3589	0.4098	0.8085	0.7264	0.7012	0.713	0.3498	0.865	0.5051	0.4064	0.5857
	0.3026	0.5262	0.4694	0.2519							
OSA	0.6561	0.6934	0.5806	0.8005	0.8459	0.7153	0.7125	0.6061	0.8001	0.8157	0.9138
	0.7397	0.7135	0.784	0.7026	0.7778	0.661	0.6946	0.7577	0.7319	0.7472	0.8647
	0.7288	0.662	0.8074	0.822	0.7997	0.8099	0.8028	0.7193	0.9315	0.8944	0.7061
	0.9444	0.6687	0	0.6859	0.8004	0.8665	0.7799	0.731	0.7542	0.9172	0.6292
	0.7287	0.6091	0.7114	0.7699	0.6062	0.6089	0.7182	0.7291	0.7621	0.8198	0.6853
	0.7814	0.742	0.9323	0.7898	0.8141	0.8133	0.6756	0.9453	0.7703	0.7659	0.8017
	0.6774	0.7092	0.7991	0.6095							
PIT	0.7437	0.7743	0.6719	0.8675	0.9064	0.7829	0.7982	0.682	0.876	0.8764	0.9448
	0.822	0.8067	0.8334	0.812	0.8462	0.7262	0.767	0.8104	0.782	0.8503	0.8927
	0.7731	0.7491	0.8556	0.8903	0.8833	0.864	0.8519	0.762	0.9584	0.9409	0.6991
	0.9734	0.6978	0.6859	0	0.8793	0.8985	0.835	0.7503	0.8117	0.9479	0.7129
	0.7779	0.7474	0.7699	0.8131	0.6858	0.6483	0.8202	0.8041	0.8011	0.8833	0.6964
	0.8265	0.7926	0.9664	0.8282	0.8365	0.84	0.7375	0.979	0.8571	0.8186	0.8223
	0.7595	0.8291	0.8654	0.658							
PMFR	0.6971	0.3648	0.7874	0.7343	0.8288	0.6083	0.6835	0.5896	0.7096	0.6167	0.9248
	0.7297	0.6514	0.7269	0.6082	0.7171	0.5895	0.6344	0.3836	0.3734	0.5742	0.8392
	0.3818	0.3627	0.6267	0.5534	0.728	0.7055	0.5458	0.3905	0.9421	0.8044	0.8028
	0.9546	0.5099	0.8004	0.8793	0	0.8816	0.4915	0.6635	0.4011	0.9293	0.671

```
     0.2151 0.5174 0.6826 0.6668 0.431  0.4829 0.5668 0.6838 0.7423 0.5692 0.596
     0.6749 0.3832 0.9382 0.8135 0.8055 0.8129 0.3606 0.9592 0.5376 0.3187 0.6933
     0.6269 0.6076 0.5088 0.2337

PSP  0.7482 0.8251 0.8592 0.8734 0.887  0.7745 0.7905 0.5203 0.8375 0.8779 0.2991
     0.7805 0.7826 0.8742 0.8379 0.7898 0.8068 0.7498 0.8569 0.8386 0.8493 0.8524
     0.8417 0.8225 0.8707 0.8872 0.8692 0.8765 0.869  0.8324 0.8785 0.8928 0.866
     0.4525 0.7896 0.8665 0.8985 0.8816 0      0.8676 0.833  0.845  0.4151 0.7854
     0.8371 0.7867 0.8253 0.8521 0.7779 0.7807 0.841  0.7821 0.8484 0.8808 0.7514
     0.8682 0.8309 0.8545 0.2932 0.6457 0.6298 0.8013 0.5815 0.8519 0.8541 0.7961
     0.8146 0.8268 0.8676 0.8009

PTR  0.6454 0.0948 0.7242 0.4384 0.6985 0.5119 0.5947 0.5726 0.6117 0.4891 0.9117
     0.691  0.6239 0.4529 0.5544 0.6625 0.4793 0.5151 0.2754 0.1626 0.5074 0.8334
     0.1519 0.1726 0.3741 0.52   0.6978 0.5825 0.3743 0.3718 0.9292 0.6262 0.734
     0.9411 0.4155 0.7799 0.835  0.4915 0.8676 0      0.5973 0.4603 0.9148 0.5647
     0.3126 0.4901 0.5484 0.3929 0.3792 0.2674 0.4514 0.6563 0.6392 0.2851 0.5856
     0.5324 0.2414 0.9175 0.7958 0.7902 0.7953 0.1443 0.9427 0.502  0.1864 0.6294
     0.4191 0.4994 0.1709 0.2021

PUK  0.6986 0.5259 0.702  0.6507 0.5798 0.5975 0.5497 0.5887 0.7262 0.6076 0.8751
     0.6055 0.6499 0.5885 0.5495 0.6586 0.6201 0.6399 0.4875 0.4916 0.6069 0.8248
     0.4863 0.4555 0.5637 0.5707 0.7309 0.6238 0.4722 0.5089 0.9121 0.7731 0.6347
     0.9052 0.27   0.731  0.7503 0.6635 0.833  0.5973 0      0.5701 0.8868 0.4461
     0.5922 0.5534 0.5105 0.5037 0.4211 0.3715 0.5386 0.6284 0.5558 0.6048 0.6061
     0.5442 0.5428 0.8658 0.769  0.763  0.7591 0.4939 0.9109 0.6395 0.527  0.6879
     0.4616 0.6305 0.6406 0.3826

RBG  0.6753 0.3687 0.7181 0.6648 0.7505 0.5482 0.6071 0.5603 0.6449 0.5469 0.8899
     0.6712 0.5871 0.6582 0.5445 0.6534 0.5538 0.5737 0.3642 0.342  0.4979 0.8003
     0.3632 0.3337 0.5624 0.4878 0.7017 0.6019 0.4649 0.3779 0.9174 0.7086 0.726
     0.9203 0.4354 0.7542 0.8117 0.4011 0.845  0.4603 0.5701 0      0.8934 0.6137
     0.4095 0.4738 0.5775 0.6183 0.3964 0.416  0.4999 0.5734 0.6533 0.502  0.5884
     0.6158 0.364  0.8871 0.7811 0.7617 0.7789 0.3545 0.9228 0.4898 0.239  0.5687
     0.5909 0.5513 0.4629 0.2624

RSP  0.8141 0.8762 0.9088 0.9198 0.9381 0.8372 0.8487 0.6186 0.8921 0.9229 0.5261
     0.8436 0.8424 0.9228 0.8891 0.8482 0.8633 0.8124 0.9044 0.8854 0.8999 0.8978
     0.8892 0.8715 0.9126 0.9321 0.9148 0.9259 0.915  0.8798 0.9216 0.9411 0.9196
     0.6111 0.8441 0.9172 0.9479 0.9293 0.4151 0.9148 0.8868 0.8934 0      0.8413
     0.8871 0.8398 0.8762 0.9013 0.8326 0.8309 0.8919 0.8394 0.8975 0.9261 0.8037
     0.913  0.8812 0.9349 0.5664 0.7745 0.7589 0.8507 0.8446 0.9013 0.903  0.8542
     0.8706 0.8779 0.9165 0.8527

RUBG 0.6056 0.4708 0.6614 0.4893 0.6427 0.5505 0.4138 0.5245 0.6471 0.6352 0.8441
     0.5144 0.5666 0.6163 0.504  0.5688 0.5568 0.5247 0.531  0.4652 0.5462 0.8048
     0.4872 0.4511 0.5345 0.6141 0.6486 0.6267 0.5312 0.5533 0.8759 0.7294 0.6562
     0.8769 0.3688 0.6292 0.7129 0.671  0.7854 0.5647 0.4461 0.6137 0.8413 0
     0.616  0.4715 0.3764 0.451  0.3642 0.234  0.4693 0.5377 0.5088 0.6282 0.5845
```

0.5147 0.576 0.847 0.7129 0.7285 0.7342 0.5067 0.8739 0.6034 0.5782 0.6541
0.3738 0.5273 0.6083 0.3678

SAL 0.5861 0.2206 0.7141 0.6192 0.7213 0.4006 0.5405 0.5312 0.5281 0.5135 0.8846
0.618 0.5276 0.574 0.4789 0.6094 0.4418 0.5028 0.3129 0.3185 0.5206 0.7915
0.3508 0.2656 0.5194 0.4664 0.6355 0.5674 0.401 0.3744 0.9082 0.6183 0.7357
0.916 0.4593 0.7287 0.7779 0.2151 0.8371 0.3126 0.5922 0.4095 0.8871 0.616
0 0.4587 0.6 0.5567 0.338 0.3949 0.4548 0.6133 0.6675 0.4138 0.5528
0.5866 0.2759 0.8803 0.7696 0.7495 0.7601 0.2763 0.9175 0.463 0.2151 0.5937
0.5429 0.5085 0.3135 0.2629

SBG 0.5166 0.4263 0.6224 0.4943 0.6788 0.5404 0.5097 0.4839 0.5325 0.5641 0.8401
0.5629 0.4855 0.5535 0.4345 0.5434 0.5244 0.4415 0.4708 0.4162 0.2573 0.7658
0.3793 0.301 0.5136 0.5374 0.5655 0.6345 0.4913 0.408 0.8716 0.6895 0.6794
0.873 0.4979 0.6091 0.7474 0.5174 0.7867 0.4901 0.5534 0.4738 0.8398 0.4715
0.4587 0 0.5345 0.5227 0.4272 0.3742 0.3666 0.5196 0.5646 0.492 0.5745
0.543 0.3999 0.8411 0.7085 0.7281 0.7287 0.3849 0.8685 0.4366 0.4222 0.5839
0.4297 0.3351 0.4956 0.3336

SCRO 0.6344 0.4633 0.636 0.4677 0.5649 0.5526 0.4588 0.5544 0.7078 0.5724 0.8752
0.5654 0.6115 0.5578 0.6252 0.5914 0.538 0.4914 0.5228 0.4604 0.625 0.8279
0.4869 0.51 0.4635 0.6313 0.7124 0.6365 0.5627 0.5574 0.9012 0.7696 0.6371
0.9069 0.341 0.7114 0.7699 0.6826 0.8253 0.5484 0.5105 0.5775 0.8762 0.3764
0.6 0.5345 0 0.3886 0.4004 0.2445 0.5985 0.576 0.5181 0.5993 0.6456
0.4936 0.5127 0.863 0.7543 0.7368 0.7546 0.4113 0.9067 0.6269 0.574 0.6453
0.4727 0.5701 0.6364 0.436

SETR 0.6391 0.4108 0.7212 0.2222 0.5636 0.624 0.5733 0.5957 0.708 0.6205 0.896
0.6648 0.6848 0.4032 0.6159 0.659 0.4942 0.5498 0.4445 0.3036 0.6277 0.8386
0.3745 0.4418 0.3662 0.6048 0.7297 0.7011 0.4719 0.5416 0.9178 0.7414 0.6928
0.9256 0.2747 0.7699 0.8131 0.6668 0.8521 0.3929 0.5037 0.6183 0.9013 0.451
0.5567 0.5227 0.3886 0 0.4671 0.1902 0.5644 0.6719 0.5071 0.5666 0.6302
0.3953 0.4801 0.8899 0.7831 0.7734 0.7686 0.3998 0.9257 0.6373 0.5145 0.6875
0.2177 0.6142 0.5859 0.3543

SGR 0.5554 0.1522 0.5594 0.5188 0.6138 0.2028 0.2372 0.4228 0.3469 0.4383 0.8302
0.3473 0.3181 0.5666 0.2309 0.4269 0.4385 0.3807 0.2189 0.2721 0.4151 0.7654
0.3208 0.244 0.4211 0.3137 0.5214 0.3979 0.3673 0.3644 0.8723 0.5756 0.5993
0.8655 0.2527 0.6062 0.6858 0.431 0.7779 0.3792 0.4211 0.3964 0.8326 0.3642
0.338 0.4272 0.4004 0.4671 0 0.1994 0.3489 0.4098 0.5712 0.4516 0.5299
0.4709 0.3517 0.8118 0.7075 0.6822 0.6988 0.2636 0.8605 0.3382 0.3623 0.6071
0.4234 0.3067 0.3191 0.2085

SOBG 0.547 0.2403 0.5709 0.1476 0.5148 0.4271 0.3429 0.5017 0.4783 0.4408 0.8327
0.4717 0.4949 0.3496 0.3449 0.4673 0.4016 0.3889 0.251 0.0994 0.4077 0.7639
0.2135 0.2424 0.2311 0.3731 0.5384 0.4848 0.3044 0.3691 0.8617 0.5066 0.5726
0.8629 0.087 0.6089 0.6483 0.4829 0.7807 0.2674 0.3715 0.416 0.8309 0.234
0.3949 0.3742 0.2445 0.1902 0.1994 0 0.3487 0.4615 0.4134 0.3947 0.527
0.3242 0.3287 0.8068 0.715 0.6954 0.7097 0.2503 0.8574 0.4322 0.337 0.5434
0.2647 0.3926 0.3752 0.1619

SRBG 0.636 0.2695 0.7494 0.5864 0.7534 0.4831 0.4218 0.5484 0.5512 0.5845 0.8903
0.5885 0.5309 0.6219 0.2098 0.5554 0.5521 0.502 0.3879 0.3657 0.2898 0.8193
0.4002 0.0287 0.5176 0.5089 0.6437 0.6356 0.3327 0.3905 0.9158 0.7243 0.7601
0.9206 0.4248 0.7182 0.8202 0.5668 0.841 0.4514 0.5386 0.4999 0.8919 0.4693
0.4548 0.3666 0.5985 0.5644 0.3489 0.3487 0 0.5354 0.6007 0.445 0.5728
0.5441 0.4235 0.9046 0.7731 0.7927 0.7923 0.3519 0.9256 0.4385 0.3464 0.6542
0.4284 0.4408 0.3644 0.2502

SRO 0.6286 0.5402 0.7093 0.6999 0.7646 0.5329 0.4303 0.4643 0.5924 0.6639 0.8375
0.5676 0.5262 0.7417 0.5141 0.3817 0.6493 0.455 0.5825 0.5657 0.5906 0.8063
0.5981 0.5107 0.6368 0.6403 0.6774 0.6354 0.6172 0.5798 0.8778 0.7406 0.7458
0.8736 0.4772 0.7291 0.8041 0.6838 0.7821 0.6563 0.6284 0.5734 0.8394 0.5377
0.6133 0.5196 0.576 0.6719 0.4098 0.4615 0.5354 0 0.6556 0.6776 0.6191
0.6646 0.6047 0.8379 0.6981 0.7113 0.746 0.5245 0.8719 0.5617 0.6094 0.5473
0.6001 0.5288 0.598 0.5213

STU 0.6934 0.5875 0.7295 0.6069 0.7625 0.6921 0.6131 0.6194 0.7779 0.7285 0.8978
0.7142 0.7357 0.617 0.6452 0.7084 0.6124 0.627 0.5873 0.53 0.6926 0.8514
0.5577 0.5411 0.5922 0.6895 0.7916 0.759 0.5561 0.5912 0.9228 0.823 0.7435
0.9257 0.4101 0.7621 0.8011 0.7423 0.8484 0.6392 0.5558 0.6533 0.8975 0.5088
0.6675 0.5646 0.5181 0.5071 0.5712 0.4134 0.6007 0.6556 0 0.6916 0.6454
0.4512 0.6035 0.9084 0.7728 0.7962 0.8045 0.5654 0.9305 0.7178 0.6163 0.7086
0.5039 0.7036 0.713 0.4702

SUK 0.7047 0.2411 0.7619 0.5895 0.745 0.5364 0.6061 0.5977 0.6776 0.3444 0.9224
0.6831 0.6525 0.5651 0.5788 0.6408 0.5952 0.5592 0.3585 0.3636 0.4173 0.8483
0.2311 0.1831 0.3879 0.5827 0.7087 0.6509 0.4251 0.248 0.9386 0.7474 0.77
0.9505 0.4985 0.8198 0.8833 0.5692 0.8808 0.2851 0.6048 0.502 0.9261 0.6282
0.4138 0.492 0.5993 0.5666 0.4516 0.3947 0.445 0.6776 0.6916 0 0.6218
0.5841 0.1142 0.9357 0.8135 0.8171 0.8205 0 0.955 0.4324 0.2846 0.6897
0.5593 0.4813 0.3466 0.3321

TBG 0.5943 0.566 0.6884 0.6468 0.7129 0.6033 0.6242 0.5182 0.6253 0.6447 0.8002
0.6136 0.6227 0.6506 0.5775 0.647 0.613 0.5939 0.5605 0.5583 0.5853 0.4624
0.5434 0.5169 0.6019 0.616 0.6425 0.6363 0.5965 0.5493 0.8128 0.6187 0.6905
0.8277 0.5659 0.6853 0.6964 0.596 0.7514 0.5856 0.6061 0.5884 0.8037 0.5845
0.5528 0.5745 0.6456 0.6302 0.5299 0.527 0.5728 0.6191 0.6454 0.6218 0
0.6099 0.5578 0.794 0.697 0.682 0.685 0.556 0.8229 0.609 0.5743 0.6004
0.5911 0.602 0.5838 0.4984

TBRU 0.6753 0.4641 0.7289 0.5188 0.7354 0.6499 0.5836 0.6157 0.7446 0.6383 0.9111
0.6677 0.7073 0.5819 0.5869 0.6593 0.5718 0.5977 0.4152 0.3886 0.6288 0.8364
0.421 0.4255 0.4325 0.555 0.7588 0.7292 0.4276 0.503 0.9302 0.7968 0.7249
0.9383 0.3589 0.7814 0.8265 0.6749 0.8682 0.5324 0.5442 0.6158 0.913 0.5147
0.5866 0.543 0.4936 0.3953 0.4709 0.3242 0.5441 0.6646 0.4512 0.5841 0.6099
0 0.4841 0.9099 0.7998 0.789 0.7976 0.4332 0.9406 0.6356 0.5336 0.7165
0.447 0.6512 0.6296 0.3752

TGR 0.6338 0.2073 0.6497 0.493 0.6435 0.4431 0.547 0.5266 0.5642 0.3214 0.8782
0.5627 0.5592 0.4559 0.4974 0.575 0.5185 0.4532 0.2356 0.2711 0.3448 0.7856

```
     0.1358 0.2    0.3627 0.4242 0.6265 0.5371 0.3663 0.1527 0.9094 0.537  0.6609
     0.9098 0.4098 0.742  0.7926 0.3832 0.8309 0.2414 0.5428 0.364  0.8812 0.576
     0.2759 0.3999 0.5127 0.4801 0.3517 0.3287 0.4235 0.6047 0.6035 0.1142 0.5578
     0.4841 0      0.8797 0.7622 0.743  0.7568 0.0401 0.9118 0.3181 0.193  0.5543
     0.4955 0.3967 0.3012 0.2317

TIMO 0.7725 0.8705 0.9125 0.927  0.9407 0.8402 0.8499 0.629  0.9048 0.9294 0.9183
     0.855  0.8391 0.9253 0.8995 0.8465 0.8374 0.8078 0.901  0.8763 0.9119 0.9089
     0.8825 0.8682 0.9146 0.9421 0.9171 0.9349 0.9197 0.8762 0.9481 0.9618 0.9182
     0.959  0.8085 0.9323 0.9664 0.9382 0.8545 0.9175 0.8658 0.8871 0.9349 0.847
     0.8803 0.8411 0.863  0.8899 0.8118 0.8068 0.9046 0.8379 0.9084 0.9357 0.794
     0.9099 0.8797 0      0.7194 0.4072 0.6072 0.8382 0.9665 0.9088 0.9015 0.8555
     0.8555 0.8843 0.9253 0.8358

TLMO 0.6295 0.7553 0.7809 0.8012 0.8138 0.6949 0.7168 0.3647 0.7541 0.8119 0.4872
     0.6997 0.6951 0.8047 0.7715 0.7119 0.7319 0.6664 0.792  0.7721 0.7782 0.7967
     0.7742 0.7544 0.8058 0.8224 0.7959 0.8015 0.8024 0.7678 0.803  0.8147 0.7973
     0.5811 0.7264 0.7898 0.8282 0.8135 0.2932 0.7958 0.769  0.7811 0.5664 0.7129
     0.7696 0.7085 0.7543 0.7831 0.7075 0.715  0.7731 0.6981 0.7728 0.8135 0.697
     0.7998 0.7622 0.7194 0      0.4602 0.5159 0.7306 0.5375 0.7847 0.7864 0.7086
     0.7416 0.7454 0.7949 0.7373

TMO  0.6165 0.7434 0.7819 0.8086 0.8149 0.6925 0.7268 0.4587 0.7699 0.8081 0.75
     0.6997 0.7058 0.8051 0.7853 0.7164 0.7102 0.6659 0.7765 0.7568 0.7951 0.7997
     0.7616 0.7542 0.8042 0.8192 0.8071 0.7992 0.8012 0.7592 0.8516 0.8166 0.7909
     0.8037 0.7012 0.8141 0.8365 0.8055 0.6457 0.7902 0.763  0.7617 0.7745 0.7285
     0.7495 0.7281 0.7368 0.7734 0.6822 0.6954 0.7927 0.7113 0.7962 0.8171 0.682
     0.789  0.743  0.4072 0.4602 0      0.4165 0.7183 0.7926 0.7875 0.7758 0.6855
     0.7484 0.7629 0.7975 0.7164

TRMO 0.6442 0.7509 0.7907 0.8082 0.8049 0.7052 0.737  0.4962 0.765  0.8131 0.7068
     0.7035 0.7115 0.8052 0.7821 0.7517 0.7287 0.6815 0.7868 0.7654 0.7939 0.7943
     0.7703 0.7603 0.8076 0.8215 0.791  0.8073 0.8086 0.7723 0.8517 0.8189 0.7893
     0.7667 0.713  0.8133 0.84   0.8129 0.6298 0.7953 0.7591 0.7789 0.7589 0.7342
     0.7601 0.7287 0.7546 0.7686 0.6988 0.7097 0.7923 0.746  0.8045 0.8205 0.685
     0.7976 0.7568 0.6072 0.5159 0.4165 0      0.735  0.7478 0.7876 0.7856 0.7376
     0.7348 0.76   0.7993 0.7299

TUK  0.5839 0.094  0.5832 0.3814 0.5368 0.3419 0.4452 0.4745 0.4752 0.1742 0.8475
     0.5313 0.4821 0.3896 0.4305 0.4542 0.4367 0.3798 0.2185 0.2198 0.2896 0.7743
     0.1262 0.1471 0.2356 0.3837 0.5204 0.4373 0.3287 0.1735 0.8796 0.5225 0.5979
     0.8796 0.3498 0.6756 0.7375 0.3606 0.8013 0.1443 0.4939 0.3545 0.8507 0.5067
     0.2763 0.3849 0.4113 0.3998 0.2636 0.2503 0.3519 0.5245 0.5654 0      0.556
     0.4332 0.0401 0.8382 0.7306 0.7183 0.735  0      0.8772 0.2494 0.2175 0.5537
     0.4226 0.2717 0.1912 0.2281

TZMO 0.8454 0.905  0.934  0.9475 0.9644 0.873  0.8849 0.5939 0.9196 0.951  0.689
     0.8754 0.8729 0.9522 0.9222 0.8799 0.8933 0.8415 0.9339 0.9114 0.9303 0.9193
     0.9158 0.9013 0.9364 0.9605 0.9408 0.9574 0.9451 0.9105 0.9484 0.9704 0.9423
     0.8681 0.865  0.9453 0.979  0.9592 0.5815 0.9427 0.9109 0.9228 0.8446 0.8739
```

0.9175 0.8685 0.9067 0.9257 0.8605 0.8574 0.9256 0.8719 0.9305 0.955 0.8229
0.9406 0.9118 0.9665 0.5375 0.7926 0.7478 0.8772 0 0.9304 0.9344 0.8871
0.8857 0.9021 0.9455 0.8849

UNTR 0.6723 0.3106 0.7322 0.6384 0.7273 0.4811 0.5328 0.5331 0.5213 0.3898 0.8972
0.5915 0.4679 0.6688 0.4364 0.5526 0.5954 0.4569 0.4025 0.453 0.2895 0.8266
0.3479 0.2867 0.5531 0.5577 0.6033 0.5992 0.5679 0.3179 0.9225 0.7421 0.7526
0.9285 0.5051 0.7703 0.8571 0.5376 0.8519 0.502 0.6395 0.4898 0.9013 0.6034
0.463 0.4366 0.6269 0.6373 0.3382 0.4322 0.4385 0.5617 0.7178 0.4324 0.609
0.6356 0.3181 0.9088 0.7847 0.7875 0.7876 0.2494 0.9304 0 0.4114 0.6904
0.5575 0.2685 0.4343 0.3442

UTR 0.6624 0.1793 0.7333 0.5865 0.7043 0.4865 0.5731 0.566 0.6172 0.4288 0.901
0.6617 0.5643 0.5508 0.488 0.6467 0.529 0.555 0.1917 0.1702 0.4291 0.8116
0.1785 0.1107 0.4729 0.4254 0.6909 0.5178 0.2248 0.269 0.9235 0.67 0.7371
0.9308 0.4064 0.7659 0.8186 0.3187 0.8541 0.1864 0.527 0.239 0.903 0.5782
0.2151 0.4222 0.574 0.5145 0.3623 0.337 0.3464 0.6094 0.6163 0.2846 0.5743
0.5336 0.193 0.9015 0.7864 0.7758 0.7856 0.2175 0.9344 0.4114 0 0.5744
0.5066 0.5094 0.2608 0.0911

YDMC 0.6592 0.6104 0.7664 0.7202 0.7863 0.6292 0.6715 0.505 0.6949 0.7044
0.8542 0.6837 0.6275 0.7265 0.7024 0.6496 0.6855 0.5587 0.6539 0.5756 0.6664
0.7818 0.5889 0.5766 0.6742 0.722 0.7609 0.7024 0.6522 0.6063 0.8964 0.6488
0.7728 0.8889 0.5857 0.8017 0.8223 0.6933 0.7961 0.6294 0.6879 0.5687 0.8542
0.6541 0.5937 0.5839 0.6453 0.6875 0.6071 0.5434 0.6542 0.5473 0.7086 0.6897
0.6004 0.7165 0.5543 0.8555 0.7086 0.6855 0.7376 0.5537 0.8871 0.6904 0.5744
0 0.6533 0.6648 0.642 0.5549

YTR 0.5833 0.366 0.6833 0.3284 0.5549 0.5608 0.4796 0.5224 0.5908 0.6274 0.8594
0.5914 0.5955 0.4596 0.494 0.5887 0.4643 0.4374 0.4737 0.3704 0.5072 0.8102
0.4048 0.3691 0.4623 0.596 0.6461 0.6761 0.4933 0.5248 0.8951 0.6904 0.6371
0.8922 0.3026 0.6774 0.7595 0.6269 0.8146 0.4191 0.4616 0.5909 0.8706 0.3738
0.5429 0.4297 0.4727 0.2177 0.4234 0.2647 0.4284 0.6001 0.5039 0.5593 0.5911
0.447 0.4955 0.8555 0.7416 0.7484 0.7348 0.4226 0.8857 0.5575 0.5066 0.6533
0 0.5097 0.5133 0.3394

YTU 0.6026 0.3458 0.6775 0.5744 0.7125 0.4021 0.4406 0.4615 0.3793 0.5058 0.8741
0.49 0.3519 0.666 0.4642 0.4722 0.5924 0.3696 0.5119 0.4745 0.2424 0.8131
0.3753 0.3187 0.5198 0.6205 0.5017 0.609 0.5962 0.4196 0.898 0.6917 0.725
0.9069 0.5262 0.7092 0.8291 0.6076 0.8268 0.4994 0.6305 0.5513 0.8779 0.5273
0.5085 0.3351 0.5701 0.6142 0.3067 0.3926 0.4408 0.5288 0.7036 0.4813 0.602
0.6512 0.3967 0.8843 0.7454 0.7629 0.76 0.2717 0.9021 0.2685 0.5094 0.6648
0.5097 0 0.4426 0.4148

YUK 0.6527 0.0698 0.7537 0.6257 0.7801 0.4245 0.558 0.5442 0.5092 0.5313 0.9121
0.6657 0.5661 0.6604 0.4946 0.6321 0.5584 0.4908 0.3417 0.295 0.4582 0.8333
0.3285 0.1352 0.4937 0.5502 0.6907 0.557 0.421 0.3768 0.9322 0.6118 0.7685
0.9429 0.4694 0.7991 0.8654 0.5088 0.8676 0.1709 0.6406 0.4629 0.9165 0.6083
0.3135 0.4956 0.6364 0.5859 0.3191 0.3752 0.3644 0.598 0.713 0.3466 0.5838

0.6296 0.3012 0.9253 0.7949 0.7975 0.7993 0.1912 0.9455 0.4343 0.2608 0.642
0.5133 0.4426 0 0.2873

ZBG 0.5789 0.1538 0.6028 0.4 0.5809 0.438 0.4609 0.5139 0.5251 0.4203 0.8531
0.5559 0.4913 0.4166 0.3262 0.5634 0.4126 0.4635 0.1139 0.1117 0.3126 0.7665
0.1034 0.1077 0.3852 0.3073 0.5563 0.4487 0.2399 0.2074 0.8849 0.5819 0.5909
0.8846 0.2519 0.6095 0.658 0.2337 0.8009 0.2021 0.3826 0.2624 0.8527 0.3678
0.2629 0.3336 0.436 0.3543 0.2085 0.1619 0.2502 0.5213 0.4702 0.3321 0.4984
0.3752 0.2317 0.8358 0.7373 0.7164 0.7299 0.2281 0.8849 0.3442 0.0911 0.5549
0.3394 0.4148 0.2873 0

APPENDIX B

Population Pairwise Nei's Genetic Distance. Population Pairwise Comparisons Are Ordered in Each Population's List of Values in the Order Following the Population Codes to the Left of Each Block of Data.

```
18IT  0      0.1154 0.1493 0.1259 0.1658 0.1184 0.1276 0.1163 0.1147 0.1751 0.3375
      0.1366 0.1184 0.1318 0.1321 0.164  0.061  0.0872 0.146  0.1435 0.143  0.3093
      0.1482 0.1237 0.1738 0.1711 0.1563 0.1487 0.1622 0.1599 0.4509 0.1497 0.1836
      0.3678 0.1701 0.1245 0.1566 0.1416 0.2674 0.1231 0.1987 0.1627 0.3154 0.1449
      0.1092 0.102  0.1436 0.1333 0.1211 0.1266 0.1323 0.1571 0.1742 0.1551 0.2023
      0.1489 0.1397 0.1913 0.2119 0.1603 0.194  0.1338 0.3195 0.1492 0.1424 0.1687
      0.1216 0.1221 0.1233 0.1268

AGR   0.1154 0      0.0922 0.0372 0.0637 0.0222 0.0375 0.1337 0.0352 0.0277 0.3622
      0.0767 0.0527 0.0424 0.0289 0.0679 0.0408 0.0443 0.0117 0.0114 0.0314 0.2634
      0.0177 0.0061 0.0285 0.024  0.072  0.0344 0.0168 0.0283 0.5054 0.0447 0.0894
      0.3926 0.0329 0.0999 0.1126 0.0221 0.3248 0.0046 0.0661 0.0311 0.356  0.0618
      0.0152 0.0534 0.0505 0.0361 0.0127 0.0246 0.0191 0.0801 0.0753 0.013  0.1437
      0.0415 0.0146 0.2451 0.3291 0.2319 0.262  0.0071 0.3502 0.0218 0.0106 0.0989
      0.0362 0.03   0.0031 0.0121

ALIT  0.1493 0.0922 0      0.1068 0.0984 0.1137 0.1379 0.188  0.1433 0.0964 0.3857
      0.1419 0.139  0.0862 0.1219 0.1739 0.1107 0.1196 0.094  0.11   0.1116 0.3137
      0.0887 0.1023 0.1215 0.1054 0.1481 0.0799 0.1264 0.0903 0.5482 0.1416 0.0201
      0.4197 0.1126 0.0446 0.0434 0.1085 0.3457 0.0924 0.1168 0.1121 0.3809 0.1163
      0.1122 0.1019 0.0841 0.1094 0.0783 0.0918 0.1288 0.1425 0.1147 0.1024 0.2241
      0.1027 0.0862 0.2608 0.3318 0.2433 0.2826 0.0838 0.3463 0.1076 0.1084 0.1759
      0.1155 0.0993 0.1027 0.0872

ATR   0.1259 0.0372 0.1068 0      0.0583 0.0965 0.0771 0.1987 0.087  0.0612 0.4313
      0.1141 0.1195 0.024  0.0714 0.1008 0.0572 0.0621 0.0423 0.0253 0.0519 0.3167
      0.0247 0.04   0.0245 0.0635 0.0867 0.0901 0.0493 0.058  0.5354 0.0745 0.0974
      0.4598 0.0445 0.1235 0.1275 0.0723 0.3741 0.0246 0.0858 0.0805 0.4077 0.0525
      0.0671 0.0562 0.039  0.0108 0.0629 0.0106 0.0551 0.1286 0.0598 0.0408 0.1753
      0.0371 0.0416 0.2845 0.368  0.2785 0.3053 0.0342 0.3983 0.0633 0.0506 0.1275
      0.0236 0.0589 0.0503 0.0354

AUK   0.1658 0.0637 0.0984 0.0583 0      0.0979 0.1095 0.1999 0.1481 0.0452 0.3792
      0.1245 0.1257 0.0417 0.1211 0.1518 0.0907 0.116  0.0721 0.0731 0.0972 0.3486
      0.0637 0.0772 0.0751 0.0967 0.1362 0.0558 0.0832 0.0816 0.5749 0.1247 0.0608
      0.4096 0.0576 0.1291 0.1187 0.0934 0.3557 0.0576 0.0523 0.1012 0.4133 0.0867
      0.0888 0.1088 0.0484 0.0401 0.0816 0.0606 0.0988 0.1562 0.1033 0.0633 0.2221
      0.0773 0.0649 0.226  0.3581 0.25   0.2576 0.0564 0.3717 0.0769 0.0685 0.1565
      0.052  0.0915 0.083  0.0644

BAL   0.1184 0.0222 0.1137 0.0965 0.0979 0      0.0235 0.0941 0.0274 0.0607 0.2867
      0.0422 0.0256 0.0974 0.0531 0.0577 0.0741 0.0431 0.0574 0.0645 0.0678 0.2895
      0.0685 0.0458 0.0845 0.0758 0.0898 0.0486 0.0628 0.0706 0.4534 0.0688 0.1189
      0.3147 0.0748 0.1257 0.1387 0.0693 0.2482 0.0529 0.098  0.0723 0.2788 0.0931
      0.0398 0.0928 0.08   0.0973 0.0195 0.0637 0.054  0.0842 0.1345 0.0544 0.1803
      0.1015 0.0494 0.2178 0.2478 0.1898 0.2178 0.0392 0.2833 0.0504 0.0516 0.1175
      0.0891 0.0419 0.0355 0.0573

BBG   0.1276 0.0375 0.1379 0.0771 0.1095 0.0235 0      0.1242 0.0445 0.0851 0.3259
      0.0324 0.0422 0.1016 0.0348 0.0251 0.0776 0.0356 0.0623 0.0664 0.067  0.3387
```

0.0761 0.0502 0.0708 0.0755 0.093 0.0872 0.0576 0.088 0.4656 0.1135 0.1399
0.3523 0.0532 0.1245 0.1544 0.0984 0.2775 0.0753 0.0801 0.0934 0.3102 0.0528
0.0715 0.0818 0.0544 0.0784 0.024 0.0442 0.0421 0.0552 0.0934 0.0735 0.1993
0.0759 0.0762 0.2384 0.2804 0.2292 0.2614 0.0614 0.3254 0.0627 0.0742 0.1438
0.0638 0.0495 0.062 0.0632

BCUK 0.1163 0.1337 0.188 0.1987 0.1999 0.0941 0.1242 0 0.1006 0.1865 0.1762
0.1061 0.0789 0.2123 0.1547 0.1163 0.1685 0.092 0.1739 0.1739 0.1533 0.2806
0.176 0.1567 0.2086 0.1922 0.1742 0.1702 0.1958 0.1774 0.4617 0.1629 0.2039
0.2051 0.1765 0.1934 0.2469 0.1712 0.1566 0.1698 0.2108 0.1754 0.206 0.1729
0.1555 0.1482 0.1792 0.2029 0.1141 0.1708 0.1642 0.1306 0.2273 0.1836 0.224
0.2139 0.1556 0.1917 0.1037 0.1344 0.1654 0.1405 0.1597 0.1482 0.1719 0.1482
0.1624 0.1176 0.1464 0.1632

BMC 0.1147 0.0352 0.1433 0.087 0.1481 0.0274 0.0445 0.1006 0 0.092 0.3362
0.0684 0.0282 0.111 0.0406 0.0596 0.0872 0.0284 0.0671 0.0617 0.0504 0.2823
0.0646 0.0466 0.0857 0.0796 0.065 0.0927 0.0818 0.0774 0.4721 0.0581 0.1595
0.364 0.0918 0.1452 0.1772 0.0761 0.2996 0.0582 0.1396 0.0832 0.3303 0.1136
0.0514 0.0722 0.1251 0.1084 0.0333 0.0647 0.0539 0.0861 0.1611 0.0711 0.1692
0.1194 0.0626 0.2614 0.2883 0.2352 0.2484 0.0557 0.3039 0.0441 0.0661 0.1248
0.0795 0.0294 0.0361 0.0656

BUK 0.1751 0.0277 0.0964 0.0612 0.0452 0.0607 0.0851 0.1865 0.092 0 0.4248
0.1028 0.0829 0.0578 0.0716 0.0999 0.0898 0.0964 0.0303 0.0343 0.0452 0.2823
0.0249 0.0309 0.0324 0.0407 0.093 0.0236 0.0388 0.0311 0.5836 0.0739 0.0895
0.4562 0.0592 0.1337 0.1334 0.0403 0.3863 0.0296 0.0696 0.0473 0.4182 0.0964
0.0422 0.0743 0.0591 0.062 0.0445 0.0502 0.0536 0.1062 0.1042 0.0144 0.1719
0.0601 0.0197 0.2851 0.3955 0.2735 0.3125 0.0112 0.4162 0.022 0.0259 0.1155
0.0828 0.0436 0.033 0.038

CMSP 0.3375 0.3622 0.3857 0.4313 0.3792 0.2867 0.3259 0.1762 0.3362 0.4248 0
0.3012 0.3082 0.4151 0.3769 0.3169 0.3791 0.2934 0.4108 0.414 0.3807 0.4716
0.4134 0.3955 0.4698 0.4258 0.4293 0.3856 0.4281 0.408 0.4599 0.3901 0.3602
0.0006 0.3621 0.3884 0.4111 0.3972 0.0201 0.4091 0.3853 0.3964 0.0346 0.3541
0.3811 0.3612 0.3798 0.4083 0.3356 0.3904 0.3837 0.3211 0.4199 0.4278 0.4465
0.4471 0.3752 0.2681 0.0763 0.195 0.1673 0.3758 0.0444 0.3792 0.3999 0.3303
0.3596 0.3631 0.3844 0.3759

CRO 0.1366 0.0767 0.1419 0.1141 0.1245 0.0422 0.0324 0.1061 0.0684 0.1028 0.3012
0 0.0542 0.1398 0.0672 0.0617 0.1255 0.0646 0.0885 0.1026 0.0863 0.2927
0.1007 0.0857 0.1058 0.1025 0.1076 0.1066 0.1019 0.1069 0.5127 0.1071 0.1456
0.3288 0.0916 0.144 0.1825 0.1244 0.259 0.1171 0.1018 0.1253 0.296 0.0803
0.0996 0.1023 0.0847 0.1178 0.0414 0.077 0.0842 0.0978 0.1513 0.1045 0.1896
0.1107 0.0814 0.2493 0.2548 0.1976 0.2165 0.0878 0.2922 0.0802 0.11 0.1526
0.1019 0.0606 0.0995 0.094

CTR 0.1184 0.0527 0.139 0.1195 0.1257 0.0256 0.0422 0.0789 0.0282 0.0829 0.3082
0.0542 0 0.1376 0.062 0.0654 0.1085 0.0482 0.0866 0.0853 0.0609 0.2935
0.0831 0.065 0.1172 0.0997 0.0886 0.0738 0.0955 0.0889 0.4505 0.1102 0.15
0.3359 0.1046 0.1272 0.167 0.0859 0.2663 0.0869 0.1261 0.0868 0.2983 0.1012

```
     0.0686 0.0748 0.1048 0.1318 0.0366 0.0857 0.0669 0.083  0.1726 0.092  0.1996
     0.1369 0.0812 0.2217 0.251  0.2065 0.2285 0.0723 0.2915 0.0486 0.0725 0.1184
     0.1051 0.0343 0.0651 0.0726

DBG  0.1318 0.0424 0.0862 0.024  0.0417 0.0974 0.1016 0.2123 0.111  0.0578 0.4151
     0.1398 0.1376 0      0.0682 0.132  0.05   0.0828 0.0404 0.0437 0.0646 0.3102
     0.0338 0.0397 0.0505 0.0576 0.1147 0.0817 0.0539 0.0484 0.5736 0.0913 0.0777
     0.4415 0.0545 0.1064 0.0898 0.0664 0.3656 0.0251 0.0634 0.0757 0.4087 0.0877
     0.0536 0.0703 0.0549 0.0248 0.0752 0.0335 0.0622 0.1568 0.0605 0.0354 0.1757
     0.0464 0.0347 0.2585 0.3706 0.265  0.2916 0.0346 0.4161 0.0702 0.0421 0.1283
     0.0405 0.0858 0.0564 0.0371

DEBG 0.1321 0.0289 0.1219 0.0714 0.1211 0.0531 0.0348 0.1547 0.0406 0.0716 0.3769
     0.0672 0.062  0.0682 0      0.0617 0.0697 0.0632 0.0259 0.0412 0.0312 0.2826
     0.0451 0.0151 0.0631 0.0249 0.0745 0.0785 0.0384 0.0468 0.5557 0.0909 0.134
     0.4029 0.0516 0.093  0.1227 0.0539 0.3286 0.0508 0.067  0.059  0.362  0.0658
     0.0459 0.0514 0.0917 0.0771 0.0199 0.0388 0.0125 0.0665 0.0882 0.0514 0.1431
     0.0622 0.0516 0.2884 0.3428 0.2799 0.2975 0.0495 0.38   0.0343 0.0424 0.1404
     0.0572 0.0455 0.0379 0.0302

DRO  0.164  0.0679 0.1739 0.1008 0.1518 0.0577 0.0251 0.1163 0.0596 0.0999 0.3169
     0.0617 0.0654 0.132  0.0617 0      0.1172 0.0413 0.0833 0.0919 0.071  0.347
     0.0861 0.0735 0.0832 0.0935 0.0944 0.132  0.0897 0.0955 0.4544 0.1345 0.18
     0.3447 0.0896 0.1798 0.2203 0.1158 0.2748 0.1016 0.1292 0.1147 0.307  0.1007
     0.0955 0.0939 0.0944 0.1142 0.0583 0.0754 0.0728 0.0447 0.1462 0.0853 0.2218
     0.106  0.0854 0.2297 0.2718 0.2156 0.2847 0.0635 0.3051 0.0677 0.1022 0.129
     0.1004 0.0561 0.0849 0.0967

DSA  0.061  0.0408 0.1107 0.0572 0.0907 0.0741 0.0776 0.1685 0.0872 0.0898 0.3791
     0.1255 0.1085 0.05   0.0697 0.1172 0      0.0702 0.0572 0.0596 0.0931 0.3201
     0.067  0.059  0.0817 0.0745 0.1137 0.096  0.0701 0.086  0.5313 0.1072 0.1159
     0.4104 0.0751 0.0977 0.1022 0.065  0.3151 0.047  0.1096 0.0751 0.3617 0.0968
     0.0479 0.0877 0.0762 0.0569 0.0618 0.0577 0.0729 0.1421 0.0939 0.0709 0.1902
     0.073  0.0683 0.2174 0.3083 0.2108 0.2509 0.0597 0.366  0.0824 0.0623 0.1555
     0.0603 0.094  0.0627 0.0521

EGR  0.0872 0.0443 0.1196 0.0621 0.116  0.0431 0.0356 0.092  0.0284 0.0964 0.2934
     0.0646 0.0482 0.0828 0.0632 0.0413 0.0702 0      0.0774 0.0773 0.0579 0.3053
     0.0687 0.063  0.0826 0.1012 0.0834 0.1102 0.0956 0.0795 0.4467 0.0841 0.126
     0.3219 0.0891 0.1375 0.1611 0.0955 0.2501 0.0643 0.1382 0.0947 0.2826 0.0957
     0.0713 0.07   0.0721 0.0834 0.0545 0.0611 0.0687 0.0699 0.117  0.0726 0.192
     0.0959 0.06   0.2176 0.2402 0.1903 0.2194 0.0529 0.2744 0.054  0.0813 0.1
     0.0615 0.0424 0.0562 0.073

GBG  0.146  0.0117 0.094  0.0423 0.0721 0.0574 0.0623 0.1739 0.0671 0.0303 0.4108
     0.0885 0.0866 0.0404 0.0259 0.0833 0.0572 0.0774 0      0.0087 0.0352 0.2493
     0.0082 0.0099 0.024  0.0046 0.0791 0.0433 0.0117 0.018  0.5885 0.0592 0.0897
     0.4421 0.0311 0.1135 0.1059 0.0192 0.3627 0.014  0.0484 0.0259 0.3959 0.0693
     0.0209 0.0564 0.0553 0.035  0.0175 0.0231 0.0278 0.0834 0.0632 0.0187 0.1272
```

0.0282 0.0147 0.2553 0.3761 0.248 0.2898 0.0169 0.4024 0.0274 0.0096 0.1036
0.0493 0.0516 0.0182 0.0074

HBG 0.1435 0.0114 0.11 0.0253 0.0731 0.0645 0.0664 0.1739 0.0617 0.0343 0.414
0.1026 0.0853 0.0437 0.0412 0.0919 0.0596 0.0773 0.0087 0 0.0413 0.2575
0.0077 0.0138 0.0129 0.0156 0.0863 0.0494 0.0097 0.0336 0.5525 0.0422 0.1021
0.4427 0.0174 0.1229 0.1195 0.0231 0.3674 0.0087 0.0578 0.0278 0.4001 0.0607
0.0254 0.0515 0.0503 0.0226 0.0269 0.0085 0.0302 0.0897 0.0596 0.0238 0.1396
0.0305 0.021 0.2634 0.3699 0.2529 0.2887 0.0196 0.3894 0.0409 0.01 0.0856
0.0372 0.0521 0.018 0.0084

HTR 0.143 0.0314 0.1116 0.0519 0.0972 0.0678 0.067 0.1533 0.0504 0.0452 0.3807
0.0863 0.0609 0.0646 0.0312 0.071 0.0931 0.0579 0.0352 0.0413 0 0.2621
0.0193 0.0121 0.0499 0.0467 0.0489 0.0717 0.0466 0.0206 0.5397 0.0808 0.1079
0.4078 0.0773 0.1059 0.1416 0.0417 0.3349 0.038 0.0793 0.0448 0.3684 0.0734
0.0502 0.0214 0.0848 0.0746 0.045 0.0483 0.0177 0.0859 0.1013 0.0239 0.1414
0.0681 0.0251 0.2923 0.3392 0.2799 0.303 0.0247 0.3696 0.0164 0.0305 0.1092
0.0563 0.0154 0.0296 0.0265

IBG 0.3093 0.2634 0.3137 0.3167 0.3486 0.2895 0.3387 0.2806 0.2823 0.2823 0.4716
0.2927 0.2935 0.3102 0.2826 0.347 0.3201 0.3053 0.2493 0.2575 0.2621 0
0.2554 0.2508 0.2987 0.256 0.3262 0.2756 0.2661 0.2561 0.5734 0.2417 0.3162
0.5086 0.3137 0.3269 0.317 0.2331 0.4295 0.2604 0.3275 0.244 0.4878 0.3349
0.2338 0.2672 0.332 0.3179 0.2691 0.2959 0.2735 0.3281 0.3582 0.2714 0.0938
0.2855 0.2344 0.4133 0.4509 0.3453 0.3595 0.2763 0.4637 0.2697 0.2407 0.2501
0.3145 0.2879 0.2485 0.252

IGBG 0.1482 0.0177 0.0887 0.0247 0.0637 0.0685 0.0761 0.176 0.0646 0.0249 0.4134
0.1007 0.0831 0.0338 0.0451 0.0861 0.067 0.0687 0.0082 0.0077 0.0193 0.2554
0 0.0115 0.0152 0.0221 0.0619 0.0498 0.0213 0.0115 0.5596 0.0525 0.0783
0.4429 0.0424 0.1149 0.1058 0.0228 0.3619 0.0076 0.0545 0.0294 0.3955 0.0644
0.0283 0.0426 0.054 0.0299 0.033 0.0206 0.0336 0.0997 0.0641 0.0118 0.1276
0.0335 0.0085 0.2625 0.3644 0.252 0.2885 0.0097 0.3854 0.025 0.0101 0.0874
0.0416 0.0331 0.0201 0.0074

IPT 0.1237 0.0061 0.1023 0.04 0.0772 0.0458 0.0502 0.1567 0.0466 0.0309 0.3955
0.0857 0.065 0.0397 0.0151 0.0735 0.059 0.063 0.0099 0.0138 0.0121 0.2508
0.0115 0 0.0288 0.018 0.0649 0.0418 0.0113 0.0173 0.548 0.0536 0.1018
0.4235 0.0429 0.0954 0.1116 0.0244 0.3478 0.0101 0.0535 0.0289 0.3816 0.061
0.0212 0.0327 0.0663 0.0448 0.0246 0.0266 0.0016 0.0761 0.0676 0.0101 0.1224
0.0388 0.0151 0.2769 0.3483 0.2662 0.298 0.0128 0.3903 0.0213 0.0065 0.0923
0.0395 0.0287 0.0072 0.0086

IUK 0.1738 0.0285 0.1215 0.0245 0.0751 0.0845 0.0708 0.2086 0.0857 0.0324 0.4698
0.1058 0.1172 0.0505 0.0631 0.0832 0.0817 0.0826 0.024 0.0129 0.0499 0.2987
0.0152 0.0288 0 0.0299 0.0916 0.0707 0.022 0.0428 0.5741 0.0619 0.1126
0.5012 0.0355 0.1584 0.1543 0.0538 0.4256 0.0224 0.0672 0.0598 0.4588 0.0712
0.0511 0.0682 0.0439 0.0255 0.0469 0.0209 0.0483 0.1073 0.0656 0.0217 0.1543
0.0308 0.0278 0.317 0.4225 0.3047 0.3412 0.0189 0.4375 0.0518 0.0374 0.1155
0.0477 0.054 0.0351 0.0374

IZBG 0.1711 0.024 0.1054 0.0635 0.0967 0.0758 0.0755 0.1922 0.0796 0.0407 0.4258
0.1025 0.0997 0.0576 0.0249 0.0935 0.0745 0.1012 0.0046 0.0156 0.0467 0.256
0.0221 0.018 0.0299 0 0.0982 0.0572 0.016 0.0315 0.6149 0.0737 0.1107
0.4572 0.0349 0.1209 0.1215 0.0264 0.3873 0.0294 0.0542 0.0335 0.4192 0.0811
0.0315 0.0616 0.0693 0.0519 0.0238 0.0351 0.0353 0.0877 0.0766 0.0335 0.1425
0.0374 0.028 0.2865 0.4037 0.2748 0.3095 0.0315 0.4172 0.0391 0.0228 0.1157
0.0661 0.0641 0.0311 0.0212

KGR 0.1563 0.072 0.1481 0.0867 0.1362 0.0898 0.093 0.1742 0.065 0.093 0.4293
0.1076 0.0886 0.1147 0.0745 0.0944 0.1137 0.0834 0.0791 0.0863 0.0489 0.3262
0.0619 0.0649 0.0916 0.0982 0 0.1153 0.106 0.0698 0.5411 0.1164 0.153
0.4604 0.1208 0.1332 0.1688 0.0765 0.3802 0.0802 0.135 0.1024 0.4132 0.1089
0.0765 0.0792 0.1208 0.1136 0.0664 0.0796 0.0753 0.1206 0.1644 0.0761 0.1774
0.1203 0.0772 0.275 0.3679 0.289 0.2817 0.064 0.3928 0.058 0.0865 0.1691
0.0963 0.0461 0.0732 0.0711

KMGR 0.1487 0.0344 0.0799 0.0901 0.0558 0.0486 0.0872 0.1702 0.0927 0.0236
0.3856 0.1066 0.0738 0.0817 0.0785 0.132 0.096 0.1102 0.0433 0.0494 0.0717
0.2756 0.0498 0.0418 0.0707 0.0572 0.1153 0 0.049 0.0499 0.5433 0.067
0.0773 0.4146 0.0615 0.1117 0.0947 0.052 0.3437 0.0383 0.0683 0.054 0.3758
0.086 0.0478 0.0939 0.0712 0.0812 0.0349 0.0565 0.0604 0.0861 0.111 0.0452
0.1569 0.0829 0.0446 0.2507 0.3426 0.2376 0.2783 0.0397 0.3824 0.0467 0.0334
0.1049 0.0954 0.0612 0.0322 0.0397

KSR 0.1622 0.0168 0.1264 0.0493 0.0832 0.0628 0.0576 0.1958 0.0818 0.0388 0.4281
0.1019 0.0955 0.0539 0.0384 0.0897 0.0701 0.0956 0.0117 0.0097 0.0466 0.2661
0.0213 0.0113 0.022 0.016 0.106 0.049 0 0.0339 0.5874 0.0635 0.1148
0.4558 0.0274 0.1354 0.1248 0.0335 0.3783 0.0201 0.0423 0.0365 0.4124 0.0652
0.0286 0.0579 0.0607 0.0361 0.0347 0.0288 0.0202 0.091 0.0512 0.0225 0.143
0.0272 0.0258 0.2848 0.3858 0.2761 0.3196 0.0282 0.4307 0.0498 0.0108 0.0959
0.05 0.0682 0.0232 0.0173

KTR 0.1599 0.0283 0.0903 0.058 0.0816 0.0706 0.088 0.1774 0.0774 0.0311 0.408
0.1069 0.0889 0.0484 0.0468 0.0955 0.086 0.0795 0.018 0.0336 0.0206 0.2561
0.0115 0.0173 0.0428 0.0315 0.0698 0.0499 0.0339 0 0.5596 0.0704 0.0835
0.4353 0.0619 0.1202 0.1123 0.0261 0.3612 0.0278 0.0642 0.0338 0.3942 0.0902
0.0338 0.0511 0.0777 0.0647 0.0427 0.0477 0.0348 0.0982 0.08 0.0142 0.1371
0.051 0.0105 0.2796 0.3687 0.2648 0.311 0.015 0.4116 0.0237 0.0186 0.101
0.0731 0.043 0.0273 0.0181

KUK 0.4509 0.5054 0.5482 0.5354 0.5749 0.4534 0.4656 0.4617 0.4721 0.5836 0.4599
0.5127 0.4505 0.5736 0.5557 0.4544 0.5313 0.4467 0.5885 0.5525 0.5397 0.5734
0.5596 0.548 0.5741 0.6149 0.5411 0.5433 0.5874 0.5596 0 0.5729 0.5927
0.4821 0.5561 0.516 0.5741 0.548 0.4041 0.5395 0.6272 0.5825 0.4334 0.4833
0.5136 0.4887 0.5182 0.5553 0.4994 0.5109 0.5432 0.4739 0.6125 0.5735 0.4893
0.6145 0.5585 0.4603 0.3778 0.4073 0.4508 0.5218 0.4268 0.5475 0.5597 0.5259
0.5369 0.4772 0.533 0.5255

LMC 0.1497 0.0447 0.1416 0.0745 0.1247 0.0688 0.1135 0.1629 0.0581 0.0739 0.3901
0.1071 0.1102 0.0913 0.0909 0.1345 0.1072 0.0841 0.0592 0.0422 0.0808 0.2417

	0.0525	0.0536	0.0619	0.0737	0.1164	0.067	0.0635	0.0704	0.5729	0	0.1354
	0.4165	0.0746	0.1824	0.1589	0.0683	0.3526	0.0371	0.1254	0.0746	0.3839	0.1255
	0.0504	0.1084	0.1206	0.0837	0.0654	0.0558	0.0775	0.1278	0.1403	0.0567	0.1336
	0.1005	0.0382	0.3048	0.3441	0.239	0.2711	0.0502	0.356	0.0757	0.0529	0.0705
	0.0891	0.0765	0.0321	0.061							
MMIT	0.1836	0.0894	0.0201	0.0974	0.0608	0.1189	0.1399	0.2039	0.1595	0.0895	0.3602
	0.1456	0.15	0.0777	0.134	0.18	0.1159	0.126	0.0897	0.1021	0.1079	0.3162
	0.0783	0.1018	0.1126	0.1107	0.153	0.0773	0.1148	0.0835	0.5927	0.1354	0
	0.3918	0.0853	0.0691	0.0407	0.1033	0.3353	0.0862	0.0776	0.1057	0.3874	0.1051
	0.1141	0.1237	0.0773	0.0854	0.0866	0.0866	0.1235	0.1605	0.1116	0.0937	0.2149
	0.0897	0.0828	0.2311	0.3504	0.2395	0.2603	0.0829	0.3271	0.1077	0.099	0.1674
	0.0855	0.115	0.0983	0.0767							
MSP	0.3678	0.3926	0.4197	0.4598	0.4096	0.3147	0.3523	0.2051	0.364	0.4562	0.0006
	0.3288	0.3359	0.4415	0.4029	0.3447	0.4104	0.3219	0.4421	0.4427	0.4078	0.5086
	0.4429	0.4235	0.5012	0.4572	0.4604	0.4146	0.4558	0.4353	0.4821	0.4165	0.3918
	0	0.3844	0.42	0.4392	0.428	0.0302	0.4403	0.4086	0.4269	0.0327	0.38
	0.4119	0.39	0.4106	0.4385	0.3651	0.4156	0.4085	0.3491	0.4417	0.4577	0.4735
	0.4758	0.4038	0.295	0.0962	0.2202	0.1913	0.406	0.0656	0.4098	0.429	0.3563
	0.3882	0.3935	0.415	0.403							
OBG	0.1701	0.0329	0.1126	0.0445	0.0576	0.0748	0.0532	0.1765	0.0918	0.0592	0.3621
	0.0916	0.1046	0.0545	0.0516	0.0896	0.0751	0.0891	0.0311	0.0174	0.0773	0.3137
	0.0424	0.0429	0.0355	0.0349	0.1208	0.0615	0.0274	0.0619	0.5561	0.0746	0.0853
	0.3844	0	0.1255	0.115	0.0581	0.3351	0.0439	0.028	0.0548	0.3836	0.0508
	0.0614	0.0909	0.0391	0.0258	0.0303	0.0091	0.0514	0.0786	0.0481	0.0584	0.1727
	0.036	0.0515	0.229	0.342	0.2343	0.2667	0.0475	0.3597	0.0681	0.0451	0.1156
	0.0348	0.0843	0.0533	0.0286							
OSA	0.1245	0.0999	0.0446	0.1235	0.1291	0.1257	0.1245	0.1934	0.1452	0.1337	0.3884
	0.144	0.1272	0.1064	0.093	0.1798	0.0977	0.1375	0.1135	0.1229	0.1059	0.3269
	0.1149	0.0954	0.1584	0.1209	0.1332	0.1117	0.1354	0.1202	0.516	0.1824	0.0691
	0.42	0.1255	0	0.0387	0.1027	0.3392	0.1131	0.1249	0.1243	0.3764	0.0933
	0.1106	0.0898	0.1111	0.1304	0.0896	0.1019	0.0988	0.147	0.1249	0.1309	0.2099
	0.1248	0.1255	0.2964	0.3333	0.2848	0.3117	0.119	0.3558	0.1204	0.1174	0.2037
	0.1039	0.1066	0.12	0.0836							
PIT	0.1566	0.1126	0.0434	0.1275	0.1187	0.1387	0.1544	0.2469	0.1772	0.1334	0.4111
	0.1825	0.167	0.0898	0.1227	0.2203	0.1022	0.1611	0.1059	0.1195	0.1416	0.317
	0.1058	0.1116	0.1543	0.1215	0.1688	0.0947	0.1248	0.1123	0.5741	0.1589	0.0407
	0.4392	0.115	0.0387	0	0.1059	0.3496	0.1038	0.1018	0.1249	0.3886	0.1082
	0.1035	0.1391	0.112	0.1185	0.1019	0.0982	0.1266	0.1776	0.1098	0.1321	0.1883
	0.111	0.122	0.2686	0.367	0.2638	0.3051	0.1275	0.3887	0.1488	0.11	0.1742
	0.1203	0.1603	0.1215	0.0804							
PMFR	0.1416	0.0221	0.1085	0.0723	0.0934	0.0693	0.0984	0.1712	0.0761	0.0403	0.3972
	0.1244	0.0859	0.0664	0.0539	0.1158	0.065	0.0955	0.0192	0.0231	0.0417	0.2331
	0.0228	0.0244	0.0538	0.0264	0.0765	0.052	0.0335	0.0261	0.548	0.0683	0.1033
	0.428	0.0581	0.1027	0.1059	0	0.359	0.0259	0.0808	0.0232	0.3909	0.1045

```
     0.0096 0.0563 0.0872 0.0678 0.0398 0.0556 0.0443 0.1069 0.0996 0.0313 0.1295
     0.0623 0.0233 0.2585 0.3731 0.2461 0.2874 0.0283 0.3893 0.0356 0.0142 0.0991
     0.0751 0.06   0.026  0.0143

PSP  0.2674 0.3248 0.3457 0.3741 0.3557 0.2482 0.2775 0.1566 0.2996 0.3863 0.0201
     0.259  0.2663 0.3656 0.3286 0.2748 0.3151 0.2501 0.3627 0.3674 0.3349 0.4295
     0.3619 0.3478 0.4256 0.3873 0.3802 0.3437 0.3783 0.3612 0.4041 0.3526 0.3353
     0.0302 0.3351 0.3392 0.3496 0.359  0      0.3636 0.3558 0.3545 0.0321 0.2948
     0.3367 0.3111 0.3296 0.3652 0.2957 0.3348 0.3326 0.2793 0.3537 0.3846 0.3848
     0.3921 0.3337 0.2269 0.0392 0.1446 0.1442 0.3379 0.047  0.3417 0.3492 0.2798
     0.3299 0.3257 0.3469 0.3227

PTR  0.1231 0.0046 0.0924 0.0246 0.0576 0.0529 0.0753 0.1698 0.0582 0.0296 0.4091
     0.1171 0.0869 0.0251 0.0508 0.1016 0.047  0.0643 0.014  0.0087 0.038  0.2604
     0.0076 0.0101 0.0224 0.0294 0.0802 0.0383 0.0201 0.0278 0.5395 0.0371 0.0862
     0.4403 0.0439 0.1131 0.1038 0.0259 0.3636 0      0.0697 0.035  0.396  0.0736
     0.0189 0.0566 0.056  0.0254 0.0359 0.0235 0.0327 0.1067 0.0713 0.0117 0.1344
     0.0406 0.0138 0.2617 0.3612 0.2505 0.2845 0.0093 0.3844 0.037  0.0083 0.0846
     0.0361 0.0445 0.0063 0.0135

PUK  0.1987 0.0661 0.1168 0.0858 0.0523 0.098  0.0801 0.2108 0.1396 0.0696 0.3853
     0.1018 0.1261 0.0634 0.067  0.1292 0.1096 0.1382 0.0484 0.0578 0.0793 0.3275
     0.0545 0.0535 0.0672 0.0542 0.135  0.0683 0.0423 0.0642 0.6272 0.1254 0.0776
     0.4086 0.028  0.1249 0.1018 0.0808 0.3558 0.0697 0      0.0738 0.4172 0.0568
     0.0825 0.0925 0.0628 0.0542 0.0537 0.0475 0.0631 0.1198 0.0675 0.0665 0.1746
     0.0592 0.0696 0.2436 0.3664 0.2668 0.2811 0.0707 0.3993 0.0913 0.0564 0.1453
     0.0554 0.1026 0.0809 0.0427

RBG  0.1627 0.0311 0.1121 0.0805 0.1012 0.0723 0.0934 0.1754 0.0832 0.0473 0.3964
     0.1253 0.0868 0.0757 0.059  0.1147 0.0751 0.0947 0.0259 0.0278 0.0448 0.244
     0.0294 0.0289 0.0598 0.0335 0.1024 0.054  0.0365 0.0338 0.5825 0.0746 0.1057
     0.4269 0.0548 0.1243 0.1249 0.0232 0.3545 0.035  0.0738 0      0.3884 0.1058
     0.0348 0.0611 0.0753 0.0788 0.0446 0.0534 0.0483 0.0861 0.0926 0.038  0.1513
     0.0714 0.0299 0.2535 0.3692 0.2421 0.2938 0.036  0.3928 0.0432 0.0139 0.0768
     0.0867 0.0658 0.0337 0.0223

RSP  0.3154 0.356  0.3809 0.4077 0.4133 0.2788 0.3102 0.206  0.3303 0.4182 0.0346
     0.296  0.2983 0.4087 0.362  0.307  0.3617 0.2826 0.3959 0.4001 0.3684 0.4878
     0.3955 0.3816 0.4588 0.4192 0.4132 0.3758 0.4124 0.3942 0.4334 0.3839 0.3874
     0.0327 0.3836 0.3764 0.3886 0.3909 0.0321 0.396  0.4172 0.3884 0      0.3292
     0.3687 0.3441 0.3626 0.41   0.3273 0.3686 0.3667 0.311  0.3909 0.4174 0.4442
     0.4268 0.3658 0.3163 0.1034 0.2174 0.2161 0.3695 0.1005 0.373  0.3825 0.3132
     0.383  0.3569 0.3782 0.3564

RUBG 0.1449 0.0618 0.1163 0.0525 0.0867 0.0931 0.0528 0.1729 0.1136 0.0964 0.3541
     0.0803 0.1012 0.0877 0.0658 0.1007 0.0968 0.0957 0.0693 0.0607 0.0734 0.3349
     0.0644 0.061  0.0712 0.0811 0.1089 0.086  0.0652 0.0902 0.4833 0.1255 0.1051
     0.38   0.0508 0.0933 0.1082 0.1045 0.2948 0.0736 0.0568 0.1058 0.3292 0
     0.1086 0.0753 0.0419 0.0518 0.0481 0.0275 0.0563 0.0934 0.066  0.0908 0.1762
```

0.0629 0.0943 0.2697 0.2938 0.2509 0.2778 0.0856 0.3377 0.0935 0.0838 0.1444
0.0443 0.0774 0.0858 0.0461

SAL 0.1092 0.0152 0.1122 0.0671 0.0888 0.0398 0.0715 0.1555 0.0514 0.0422 0.3811
0.0996 0.0686 0.0536 0.0459 0.0955 0.0479 0.0713 0.0209 0.0254 0.0502 0.2338
0.0283 0.0212 0.0511 0.0315 0.0765 0.0478 0.0286 0.0338 0.5136 0.0504 0.1141
0.4119 0.0614 0.1106 0.1035 0.0096 0.3367 0.0189 0.0825 0.0348 0.3687 0.1086
0 0.0582 0.0843 0.0618 0.0349 0.0494 0.0409 0.104 0.1009 0.0271 0.1306
0.0643 0.0201 0.2431 0.3455 0.2282 0.2638 0.0253 0.3732 0.0395 0.0124 0.0869
0.0719 0.0561 0.0181 0.0227

SBG 0.102 0.0534 0.1019 0.0562 0.1088 0.0928 0.0818 0.1482 0.0722 0.0743 0.3612
0.1023 0.0748 0.0703 0.0514 0.0939 0.0877 0.07 0.0564 0.0515 0.0214 0.2672
0.0426 0.0327 0.0682 0.0616 0.0792 0.0939 0.0579 0.0511 0.4887 0.1084 0.1237
0.39 0.0909 0.0898 0.1391 0.0563 0.3111 0.0566 0.0925 0.0611 0.3441 0.0753
0.0582 0 0.0846 0.0728 0.0653 0.0564 0.038 0.0898 0.087 0.0535 0.1733
0.0741 0.047 0.2739 0.2961 0.26 0.279 0.0532 0.3427 0.0486 0.0457 0.1093
0.0584 0.0356 0.056 0.0409

SCRO 0.1436 0.0505 0.0841 0.039 0.0484 0.08 0.0544 0.1792 0.1251 0.0591 0.3798
0.0847 0.1048 0.0549 0.0917 0.0944 0.0762 0.0721 0.0553 0.0503 0.0848 0.332
0.054 0.0663 0.0439 0.0693 0.1208 0.0712 0.0607 0.0777 0.5182 0.1206 0.0773
0.4106 0.0391 0.1111 0.112 0.0872 0.3296 0.056 0.0628 0.0753 0.3626 0.0419
0.0843 0.0846 0 0.0333 0.0487 0.0255 0.0804 0.0942 0.057 0.0641 0.2091
0.0475 0.0608 0.2325 0.3299 0.2256 0.2707 0.0496 0.3674 0.0852 0.0678 0.1171
0.0574 0.0779 0.0783 0.053

SETR 0.1333 0.0361 0.1094 0.0108 0.0401 0.0973 0.0784 0.2029 0.1084 0.062 0.4083
0.1178 0.1318 0.0248 0.0771 0.1142 0.0569 0.0834 0.035 0.0226 0.0746 0.3179
0.0299 0.0448 0.0255 0.0519 0.1136 0.0812 0.0361 0.0647 0.5553 0.0837 0.0854
0.4385 0.0258 0.1304 0.1185 0.0678 0.3652 0.0254 0.0542 0.0788 0.41 0.0518
0.0618 0.0728 0.0333 0 0.0584 0.0167 0.0609 0.1305 0.0478 0.0474 0.1797
0.0275 0.0471 0.2458 0.3653 0.2535 0.267 0.0427 0.3846 0.0775 0.0461 0.1275
0.0157 0.0833 0.0537 0.0337

SGR 0.1211 0.0127 0.0783 0.0629 0.0816 0.0195 0.024 0.1141 0.0333 0.0445 0.3356
0.0414 0.0366 0.0752 0.0199 0.0583 0.0618 0.0545 0.0175 0.0269 0.045 0.2691
0.033 0.0246 0.0469 0.0238 0.0664 0.0349 0.0347 0.0427 0.4994 0.0654 0.0866
0.3651 0.0303 0.0896 0.1019 0.0398 0.2957 0.0359 0.0537 0.0446 0.3273 0.0481
0.0349 0.0653 0.0487 0.0584 0 0.0233 0.0355 0.0572 0.0905 0.0458 0.1433
0.0556 0.0384 0.2202 0.2966 0.2044 0.238 0.0303 0.3208 0.032 0.0357 0.1222
0.0574 0.0314 0.0264 0.0215

SOBG 0.1266 0.0246 0.0918 0.0106 0.0606 0.0637 0.0442 0.1708 0.0647 0.0502 0.3904
0.077 0.0857 0.0335 0.0388 0.0754 0.0577 0.0611 0.0231 0.0085 0.0483 0.2959
0.0206 0.0266 0.0209 0.0351 0.0796 0.0565 0.0288 0.0477 0.5109 0.0558 0.0866
0.4156 0.0091 0.1019 0.0982 0.0556 0.3348 0.0235 0.0475 0.0534 0.3686 0.0275
0.0494 0.0564 0.0255 0.0167 0.0233 0 0.0391 0.0774 0.0516 0.0403 0.1514
0.0326 0.038 0.2463 0.3348 0.2392 0.2751 0.0306 0.366 0.0533 0.0352 0.1017
0.0302 0.0508 0.038 0.017

SRBG	0.1323	0.0191	0.1288	0.0551	0.0988	0.054	0.0421	0.1642	0.0539	0.0536	0.3837
	0.0842	0.0669	0.0622	0.0125	0.0728	0.0729	0.0687	0.0278	0.0302	0.0177	0.2735
	0.0336	0.0016	0.0483	0.0353	0.0753	0.0604	0.0202	0.0348	0.5432	0.0775	0.1235
	0.4085	0.0514	0.0988	0.1266	0.0443	0.3326	0.0327	0.0631	0.0483	0.3667	0.0563
	0.0409	0.038	0.0804	0.0609	0.0355	0.0391	0	0.0718	0.0713	0.0291	0.1389
	0.0512	0.0375	0.2999	0.3429	0.2909	0.3158	0.0349	0.3908	0.034	0.023	0.1094
	0.043	0.0408	0.0216	0.0204							
SRO	0.1571	0.0801	0.1425	0.1286	0.1562	0.0842	0.0552	0.1306	0.0861	0.1062	0.3211
	0.0978	0.083	0.1568	0.0665	0.0447	0.1421	0.0699	0.0834	0.0897	0.0859	0.3281
	0.0997	0.0761	0.1073	0.0877	0.1206	0.0861	0.091	0.0982	0.4739	0.1278	0.1605
	0.3491	0.0786	0.147	0.1776	0.1069	0.2793	0.1067	0.1198	0.0861	0.311	0.0934
	0.104	0.0898	0.0942	0.1305	0.0572	0.0774	0.0718	0	0.121	0.1102	0.2027
	0.1172	0.1038	0.2379	0.2646	0.2221	0.2909	0.09	0.3142	0.0756	0.093	0.0875
	0.1122	0.0756	0.0791	0.0857							
STU	0.1742	0.0753	0.1147	0.0598	0.1033	0.1345	0.0934	0.2273	0.1611	0.1042	0.4199
	0.1513	0.1726	0.0605	0.0882	0.1462	0.0939	0.117	0.0632	0.0596	0.1013	0.3582
	0.0641	0.0676	0.0656	0.0766	0.1644	0.111	0.0512	0.08	0.6125	0.1403	0.1116
	0.4417	0.0481	0.1249	0.1098	0.0996	0.3537	0.0713	0.0675	0.0926	0.3909	0.066
	0.1009	0.087	0.057	0.0478	0.0905	0.0516	0.0713	0.121	0	0.0831	0.1936
	0.0348	0.079	0.3126	0.341	0.2968	0.3438	0.0855	0.4225	0.1145	0.0709	0.1423
	0.0585	0.1273	0.0966	0.0552							
SUK	0.1551	0.013	0.1024	0.0408	0.0633	0.0544	0.0735	0.1836	0.0711	0.0144	0.4278
	0.1045	0.092	0.0354	0.0514	0.0853	0.0709	0.0726	0.0187	0.0238	0.0239	0.2714
	0.0118	0.0101	0.0217	0.0335	0.0761	0.0452	0.0225	0.0142	0.5735	0.0567	0.0937
	0.4577	0.0584	0.1309	0.1321	0.0313	0.3846	0.0117	0.0665	0.038	0.4174	0.0908
	0.0271	0.0535	0.0641	0.0474	0.0458	0.0403	0.0291	0.1102	0.0831	0	0.1514
	0.0456	0.0051	0.2949	0.3913	0.2847	0.3224	0	0.4239	0.0252	0.0131	0.104
	0.0599	0.0381	0.0146	0.0251							
TBG	0.2023	0.1437	0.2241	0.1753	0.2221	0.1803	0.1993	0.224	0.1692	0.1719	0.4465
	0.1896	0.1996	0.1757	0.1431	0.2218	0.1902	0.192	0.1272	0.1396	0.1414	0.0938
	0.1276	0.1224	0.1543	0.1425	0.1774	0.1569	0.143	0.1371	0.4893	0.1336	0.2149
	0.4735	0.1727	0.2099	0.1883	0.1295	0.3848	0.1344	0.1746	0.1513	0.4442	0.1762
	0.1306	0.1733	0.2091	0.1797	0.1433	0.1514	0.1389	0.2027	0.1936	0.1514	0
	0.1556	0.1369	0.35	0.392	0.2963	0.3175	0.1575	0.4302	0.1571	0.1344	0.1749
	0.1705	0.1678	0.1301	0.1195							
TBRU	0.1489	0.0415	0.1027	0.0371	0.0773	0.1015	0.0759	0.2139	0.1194	0.0601	0.4471
	0.1107	0.1369	0.0464	0.0622	0.106	0.073	0.0959	0.0282	0.0305	0.0681	0.2855
	0.0335	0.0388	0.0308	0.0374	0.1203	0.0829	0.0272	0.051	0.6145	0.1005	0.0897
	0.4758	0.036	0.1248	0.111	0.0623	0.3921	0.0406	0.0592	0.0714	0.4268	0.0629
	0.0643	0.0741	0.0475	0.0275	0.0556	0.0326	0.0512	0.1172	0.0348	0.0456	0.1556
	0	0.044	0.2684	0.3891	0.2621	0.3043	0.046	0.4285	0.0698	0.0453	0.1366
	0.0428	0.0906	0.0581	0.0344							
TGR	0.1397	0.0146	0.0862	0.0416	0.0649	0.0494	0.0762	0.1556	0.0626	0.0197	0.3752
	0.0814	0.0812	0.0347	0.0516	0.0854	0.0683	0.06	0.0147	0.021	0.0251	0.2344

	0.0085	0.0151	0.0278	0.028	0.0772	0.0446	0.0258	0.0105	0.5585	0.0382	0.0828
	0.4038	0.0515	0.1255	0.122	0.0233	0.3337	0.0138	0.0696	0.0299	0.3658	0.0943
	0.0201	0.047	0.0608	0.0471	0.0384	0.038	0.0375	0.1038	0.079	0.0051	0.1369
	0.044	0	0.2602	0.339	0.2275	0.2672	0.0028	0.3712	0.0221	0.0113	0.0763
	0.0613	0.0367	0.018	0.0198							
TIMO	0.1913	0.2451	0.2608	0.2845	0.226	0.2178	0.2384	0.1917	0.2614	0.2851	0.2681
	0.2493	0.2217	0.2585	0.2884	0.2297	0.2174	0.2176	0.2553	0.2634	0.2923	0.4133
	0.2625	0.2769	0.317	0.2865	0.275	0.2507	0.2848	0.2796	0.4603	0.3048	0.2311
	0.295	0.229	0.2964	0.2686	0.2585	0.2269	0.2617	0.2436	0.2535	0.3163	0.2697
	0.2431	0.2739	0.2325	0.2458	0.2202	0.2463	0.2999	0.2379	0.3126	0.2949	0.35
	0.2684	0.2602	0	0.1817	0.032	0.0822	0.2585	0.2661	0.2772	0.252	0.2384
	0.2488	0.2783	0.2682	0.2378							
TLMO	0.2119	0.3291	0.3318	0.368	0.3581	0.2478	0.2804	0.1037	0.2883	0.3955	0.0763
	0.2548	0.251	0.3706	0.3428	0.2718	0.3083	0.2402	0.3761	0.3699	0.3392	0.4509
	0.3644	0.3483	0.4225	0.4037	0.3679	0.3426	0.3858	0.3687	0.3778	0.3441	0.3504
	0.0962	0.342	0.3333	0.367	0.3731	0.0392	0.3612	0.3664	0.3692	0.1034	0.2938
	0.3455	0.2961	0.3299	0.3653	0.2966	0.3348	0.3429	0.2646	0.341	0.3913	0.392
	0.3891	0.339	0.1817	0	0.0956	0.1276	0.3313	0.0756	0.3539	0.3585	0.2619
	0.3235	0.3068	0.3481	0.3345							
TMO	0.1603	0.2319	0.2433	0.2785	0.25	0.1898	0.2292	0.1344	0.2352	0.2735	0.195
	0.1976	0.2065	0.265	0.2799	0.2156	0.2108	0.1903	0.248	0.2529	0.2799	0.3453
	0.252	0.2662	0.3047	0.2748	0.289	0.2376	0.2761	0.2648	0.4073	0.239	0.2395
	0.2202	0.2343	0.2848	0.2638	0.2461	0.1446	0.2505	0.2668	0.2421	0.2174	0.2509
	0.2282	0.26	0.2256	0.2535	0.2044	0.2392	0.2909	0.2221	0.2968	0.2847	0.2963
	0.2621	0.2275	0.032	0.0956	0	0.0681	0.2413	0.1896	0.2646	0.2449	0.1791
	0.2591	0.2589	0.2543	0.2306							
TRMO	0.194	0.262	0.2826	0.3053	0.2576	0.2178	0.2614	0.1654	0.2484	0.3125	0.1673
	0.2165	0.2285	0.2916	0.2975	0.2847	0.2509	0.2194	0.2898	0.2887	0.303	0.3595
	0.2885	0.298	0.3412	0.3095	0.2817	0.2783	0.3196	0.311	0.4508	0.2711	0.2603
	0.1913	0.2667	0.3117	0.3051	0.2874	0.1442	0.2845	0.2811	0.2938	0.2161	0.2778
	0.2638	0.279	0.2707	0.267	0.238	0.2751	0.3158	0.2909	0.3438	0.3224	0.3175
	0.3043	0.2672	0.0822	0.1276	0.0681	0	0.2843	0.16	0.2887	0.285	0.2558
	0.2569	0.2748	0.2828	0.2666							
TUK	0.1338	0.0071	0.0838	0.0342	0.0564	0.0392	0.0614	0.1405	0.0557	0.0112	0.3758
	0.0878	0.0723	0.0346	0.0495	0.0635	0.0597	0.0529	0.0169	0.0196	0.0247	0.2763
	0.0097	0.0128	0.0189	0.0315	0.064	0.0397	0.0282	0.015	0.5218	0.0502	0.0829
	0.406	0.0475	0.119	0.1275	0.0283	0.3379	0.0093	0.0707	0.036	0.3695	0.0856
	0.0253	0.0532	0.0496	0.0427	0.0303	0.0306	0.0349	0.09	0.0855	0	0.1575
	0.046	0.0028	0.2585	0.3313	0.2413	0.2843	0	0.3632	0.02	0.0167	0.0942
	0.0557	0.0257	0.0127	0.0236							
TZMO	0.3195	0.3502	0.3463	0.3983	0.3717	0.2833	0.3254	0.1597	0.3039	0.4162	0.0444
	0.2922	0.2915	0.4161	0.38	0.3051	0.366	0.2744	0.4024	0.3894	0.3696	0.4637
	0.3854	0.3903	0.4375	0.4172	0.3928	0.3824	0.4307	0.4116	0.4268	0.356	0.3271
	0.0656	0.3597	0.3558	0.3887	0.3893	0.047	0.3844	0.3993	0.3928	0.1005	0.3377

```
       0.3732 0.3427 0.3674 0.3846 0.3208 0.366  0.3908 0.3142 0.4225 0.4239 0.4302
       0.4285 0.3712 0.2661 0.0756 0.1896 0.16   0.3632 0      0.367  0.3973 0.316
       0.3257 0.3292 0.3667 0.3706

UNTR   0.1492 0.0218 0.1076 0.0633 0.0769 0.0504 0.0627 0.1482 0.0441 0.022  0.3792
       0.0802 0.0486 0.0702 0.0343 0.0677 0.0824 0.054  0.0274 0.0409 0.0164 0.2697
       0.025  0.0213 0.0518 0.0391 0.058  0.0467 0.0498 0.0237 0.5475 0.0757 0.1077
       0.4098 0.0681 0.1204 0.1488 0.0356 0.3417 0.037  0.0913 0.0432 0.373  0.0935
       0.0395 0.0486 0.0852 0.0775 0.032  0.0533 0.034  0.0756 0.1145 0.0252 0.1571
       0.0698 0.0221 0.2772 0.3539 0.2646 0.2887 0.02   0.367  0      0.0282 0.1222
       0.0691 0.0176 0.0266 0.0306

UTR    0.1424 0.0106 0.1084 0.0506 0.0685 0.0516 0.0742 0.1719 0.0661 0.0259 0.3999
       0.11   0.0725 0.0421 0.0424 0.1022 0.0623 0.0813 0.0096 0.01   0.0305 0.2407
       0.0101 0.0065 0.0374 0.0228 0.0865 0.0334 0.0108 0.0186 0.5597 0.0529 0.099
       0.429  0.0451 0.1174 0.11   0.0142 0.3492 0.0083 0.0564 0.0139 0.3825 0.0838
       0.0124 0.0457 0.0678 0.0461 0.0357 0.0352 0.023  0.093  0.0709 0.0131 0.1344
       0.0453 0.0113 0.252  0.3585 0.2449 0.285  0.0167 0.3973 0.0282 0      0.0722
       0.056  0.0505 0.0122 0.0057

YDMC          0.1687 0.0989 0.1759 0.1275 0.1565 0.1175 0.1438 0.1482 0.1248 0.1155
       0.3303 0.1526 0.1184 0.1283 0.1404 0.129  0.1555 0.1    0.1036 0.0856 0.1092
       0.2501 0.0874 0.0923 0.1155 0.1157 0.1691 0.1049 0.0959 0.101  0.5259 0.0705
       0.1674 0.3563 0.1156 0.2037 0.1742 0.0991 0.2798 0.0846 0.1453 0.0768 0.3132
       0.1444 0.0869 0.1093 0.1171 0.1275 0.1222 0.1017 0.1094 0.0875 0.1423 0.104
       0.1749 0.1366 0.0763 0.2384 0.2619 0.1791 0.2558 0.0942 0.316  0.1222 0.0722
       0      0.1313 0.1257 0.086  0.0912

YTR    0.1216 0.0362 0.1155 0.0236 0.052  0.0891 0.0638 0.1624 0.0795 0.0828 0.3596
       0.1019 0.1051 0.0405 0.0572 0.1004 0.0603 0.0615 0.0493 0.0372 0.0563 0.3145
       0.0416 0.0395 0.0477 0.0661 0.0963 0.0954 0.05   0.0731 0.5369 0.0891 0.0855
       0.3882 0.0348 0.1039 0.1203 0.0751 0.3299 0.0361 0.0554 0.0867 0.383  0.0443
       0.0719 0.0584 0.0574 0.0157 0.0574 0.0302 0.043  0.1122 0.0585 0.0599 0.1705
       0.0428 0.0613 0.2488 0.3235 0.2591 0.2569 0.0557 0.3257 0.0691 0.056  0.1313
       0      0.0655 0.0512 0.0374

YTU    0.1221 0.03   0.0993 0.0589 0.0915 0.0419 0.0495 0.1176 0.0294 0.0436 0.3631
       0.0606 0.0343 0.0858 0.0455 0.0561 0.094  0.0424 0.0516 0.0521 0.0154 0.2879
       0.0331 0.0287 0.054  0.0641 0.0461 0.0612 0.0682 0.043  0.4772 0.0765 0.115
       0.3935 0.0843 0.1066 0.1603 0.06   0.3257 0.0445 0.1026 0.0658 0.3569 0.0774
       0.0561 0.0356 0.0779 0.0833 0.0314 0.0508 0.0408 0.0756 0.1273 0.0381 0.1678
       0.0906 0.0367 0.2783 0.3068 0.2589 0.2748 0.0257 0.3292 0.0176 0.0505 0.1257
       0.0655 0      0.0338 0.0476

YUK    0.1233 0.0031 0.1027 0.0503 0.083  0.0355 0.062  0.1464 0.0361 0.033  0.3844
       0.0995 0.0651 0.0564 0.0379 0.0849 0.0627 0.0562 0.0182 0.018  0.0296 0.2485
       0.0201 0.0072 0.0351 0.0311 0.0732 0.0322 0.0232 0.0273 0.533  0.0321 0.0983
       0.415  0.0533 0.12   0.1215 0.026  0.3469 0.0063 0.0809 0.0337 0.3782 0.0858
       0.0181 0.056  0.0783 0.0537 0.0264 0.038  0.0216 0.0791 0.0966 0.0146 0.1301
```

0.0581 0.018 0.2682 0.3481 0.2543 0.2828 0.0127 0.3667 0.0266 0.0122 0.086
0.0512 0.0338 0 0.021

ZBG 0.1268 0.0121 0.0872 0.0354 0.0644 0.0573 0.0632 0.1632 0.0656 0.038 0.3759
0.094 0.0726 0.0371 0.0302 0.0967 0.0521 0.073 0.0074 0.0084 0.0265 0.252
0.0074 0.0086 0.0374 0.0212 0.0711 0.0397 0.0173 0.0181 0.5255 0.061 0.0767
0.403 0.0286 0.0836 0.0804 0.0143 0.3227 0.0135 0.0427 0.0223 0.3564 0.0461
0.0227 0.0409 0.053 0.0337 0.0215 0.017 0.0204 0.0857 0.0552 0.0251 0.1195
0.0344 0.0198 0.2378 0.3345 0.2306 0.2666 0.0236 0.3706 0.0306 0.0057 0.0912
0.0374 0.0476 0.021 0