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Autosomal STR Variations Reveal Genetic Heterogeneity in the Mon-Khmer Speaking Group of Northern Thailand

Antónia Völgyi[1], Jatupol Kampuansai[2]
Whibhu Kutanan[3], Daoroong Kangwanpong[2], Horolma Pamjav[1]

[1]Institute of Forensic Medicine, Network of Forensic Science Institutes, Budapest, Hungary
[2]Faculty of Science, Chiang Mai University, Chiang Mai, Thailand
[3]Faculty of Science, Khon Kaen University, Khon Kaen, Thailand

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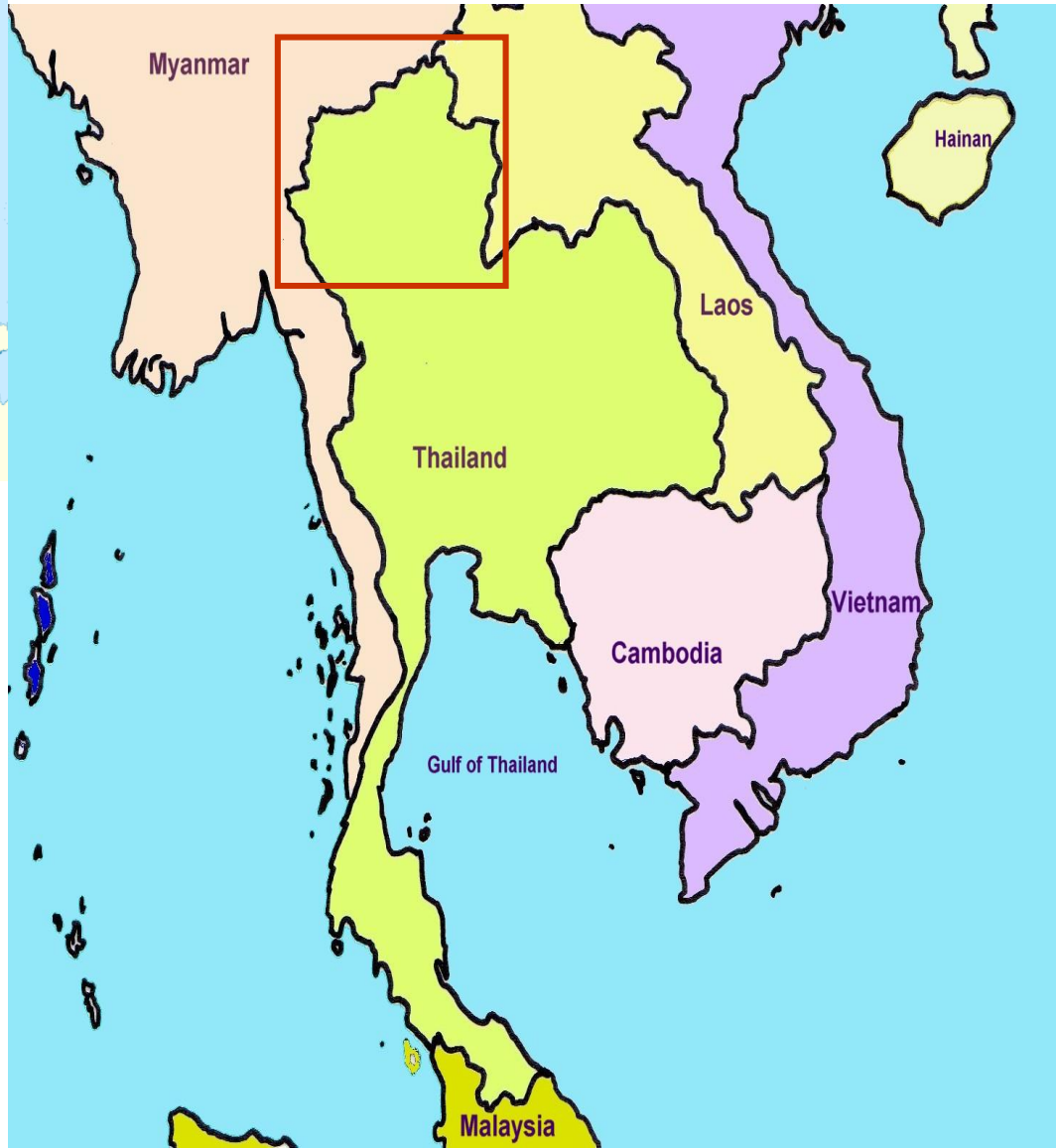
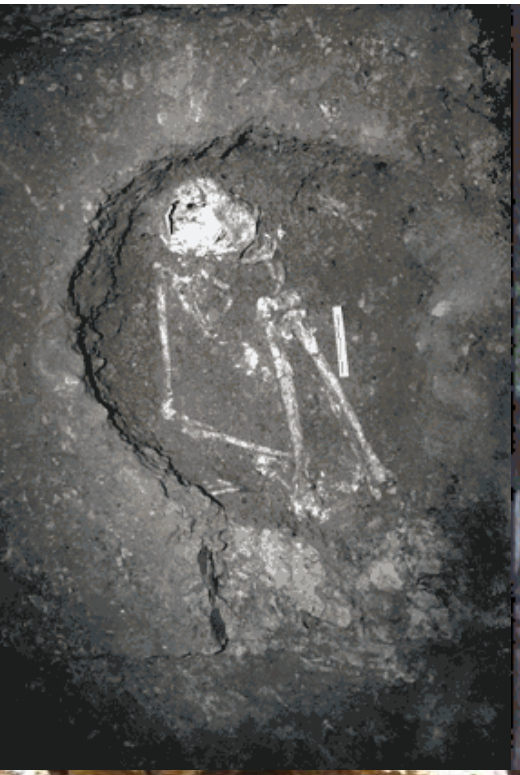
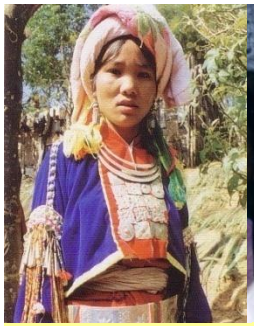

Myanmar
Hainan
Laos
Thailand
Vietnam
Cambodia
Gulf of Thailand
Malaysia

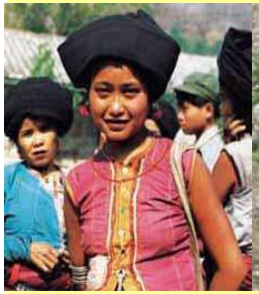
Highland Archeological Sites in Northern Thailand



Mon-Khmer


Paluang


Lawa


Blang


H'thin


Mlabri


Mon

Tai


Yuan


Yong


Lue


Khuen


Yai

Hill-tribes


Hmong


Karen


Lahu


Akha


Yao


Lisu

Aims

- To establish
  - frequencies
  - population statistic parameters of autosomal STR loci for ethnic groups of northern Thailand
  - comparative study with other populations
  - finding the optimal number of clusters in the data.

Code	Ethnic group	Linguistic group	Village/District/Province	No. of samples
KM	Khamu	Mon-Khmer	Huay Sataeng/Thung Chang/Nan	41
LA1	Lua	Mon-Khmer	Toei Klang/Pua/Nan	20
LA2	Lua	Mon-Khmer	Na Bong/Bo Klea/Nan	34
LW1	Lawa	Mon-Khmer	Pa Pae/Mae Sarieng/Mae Hong Son	40
LW2	Lawa	Mon-Khmer	Pae/Mae Sa Rieng/Mae Hong Son	29
PL	Paluang	Mon-Khmer	Nor Lae/Chiang Dao/Chiang Mai	46
TN1	Htin-Mal	Mon-Khmer	Ta Luang/Pua/Nan	38
TN2	Htin-Prai	Mon-Khmer	Nam Sod/Thung Chang/Nan	22
TN3	Htin-Prai	Mon-Khmer	Huay Kaew/Chiang Klang/Nan	42
SH1	Shan	Tai	Jong Kham/Muang/Mae Hong Son	23
SH2	Shan	Tai	Na Pu Pom/Pang Ma Pha/Mae Hong Son	30
KO	KhonMuang	Tai	Vieng Neur/Pai/Mae Hong Son	30
YO1	Yong	Tai	Pak Bong/Pa Sang/Lamphun	40
YO2	Yong	Tai	Muong Noi/Pa Sang/Lamphun	36
YO3	Yong	Tai	Pa Sang/Pa Sang/Lamphun	32
YO4	Yong	Tai	Tha Pla Duk/Mae Tha/Lamphun	46
YO5	Yong	Tai	Huay Sai/Ban Thi/Lamphun	36
YO6	Yong	Tai	Law Yaw/Ban Hong/Lamphun	50
KR1	Karen-Skaw	Karen	Mae Han/Mae Sa Rieng/Mae Hong Son	31
KR2	Karen-Skaw	Karen	Umdar Neur/Sob Mei/Mae Hong Son	14
KR3	Karen-Pwo	Karen	Dong Sangat/Mae Sa Rieng/Mae Hong Son	30
KR4	Karen-Padong	Karen	Huay Pu Kaeng/Muang/Mae Hong Son	28

Methods: done in Thailand

- Information on language, culture and village history were interviewed, informed consent form was filled.
- 5 ml of peripheral blood was collected using EDTA-Vacutainer.
- DNA extraction using standard inorganic salting out protocol (Seielstad *et al*., 1999).

Methods: done in Hungary

- Multiplex PCR amplification of 15 STR loci using commercial PowerPlex ESI16 kit (Promega, WI, USA).
- Proficiency testing programs: GEDNAP and ISFG ESWG RTW
- Accredited according to the ISO 17025 standards.



Results

171 alleles, 2 rare alleles 9.1 (0.0061) and 11.1 (0.0014) in locus D2S441

Allele	HWE	PIC	PD	MP	PE	Fis	Fis p value
D3S1358	0.8690	0.6742	0.8743	0.1257	0.4776	-0.03	0.9316
D19S433	0.5262	0.8338	0.8833	0.1167	0.4972	-0.0215	0.9062
D2S1338	0.1787	0.8517	**0.9674**	0.0326	0.7297	-0.0042	0.6393
D22S1045	0.0650	0.6960	0.8897	0.1103	0.5081	0.0108	0.3118
D16S539	0.8928	0.7554	0.9227	0.0773	0.5839	-0.0161	0.7967
D18S51	0.0007	0.8333	0.9606	0.0394	0.7028	0.0357	0.0156
D1S1656	0.0669	0.7982	0.9343	0.0657	0.6173	-0.014	0.8172
D10S1248	0.6678	0.7668	0.8916	0.1084	0.5122	0.0009	0.4761
D2S441	0.0026	0.7668	0.8620	0.1380	0.4601	0.0114	0.3060
TH01	0.0978	**0.6529**	**0.8115**	0.1885	0.3863	-0.0122	0.7058
vWA	0.1642	0.7588	0.9246	0.0754	0.5895	-0.0336	0.9658
D21S11	0.1330	0.8224	0.9241	0.0759	0.5874	0.0074	0.3177
D12S391	0.3422	0.8333	0.9602	0.0398	0.7009	-0.0072	0.6804
D8S1179	0.0022	0.8368	0.9612	0.0388	0.7041	0.0064	0.3656
FGA	0.3312	**0.8671**	0.9556	0.0444	0.6839	-0.0071	0.7048

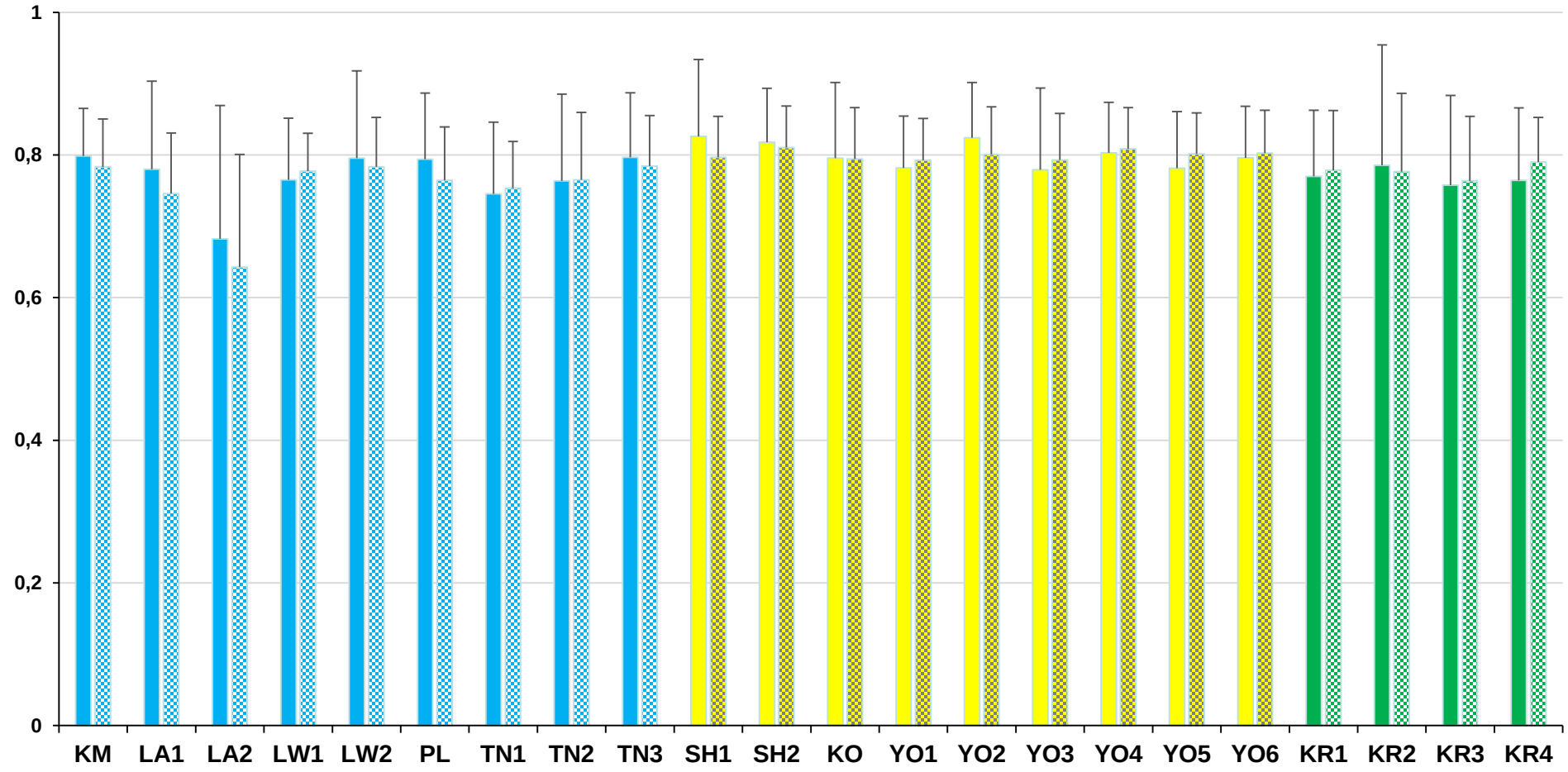
Results

_G_-tests of allelic frequencies: pooled studied ethnic samples and „general" northern Thai population.

Locus	D3S1358	D19S433	D2S1338	D16S539	TH01	vWA	D21S11	D8S1179	FGA
G	20.3197	50.1318	33.3673	24.2221	6.5112	21.8480	26.3548	10.1224	58.2207
d.f.	10	14	12	8	6	9	15	9	20
p value	0.0264	**0.0000**	**0.0008**	**0.0021**	0.3684	**0.0094**	0.0345	0.3407	**0.0000**

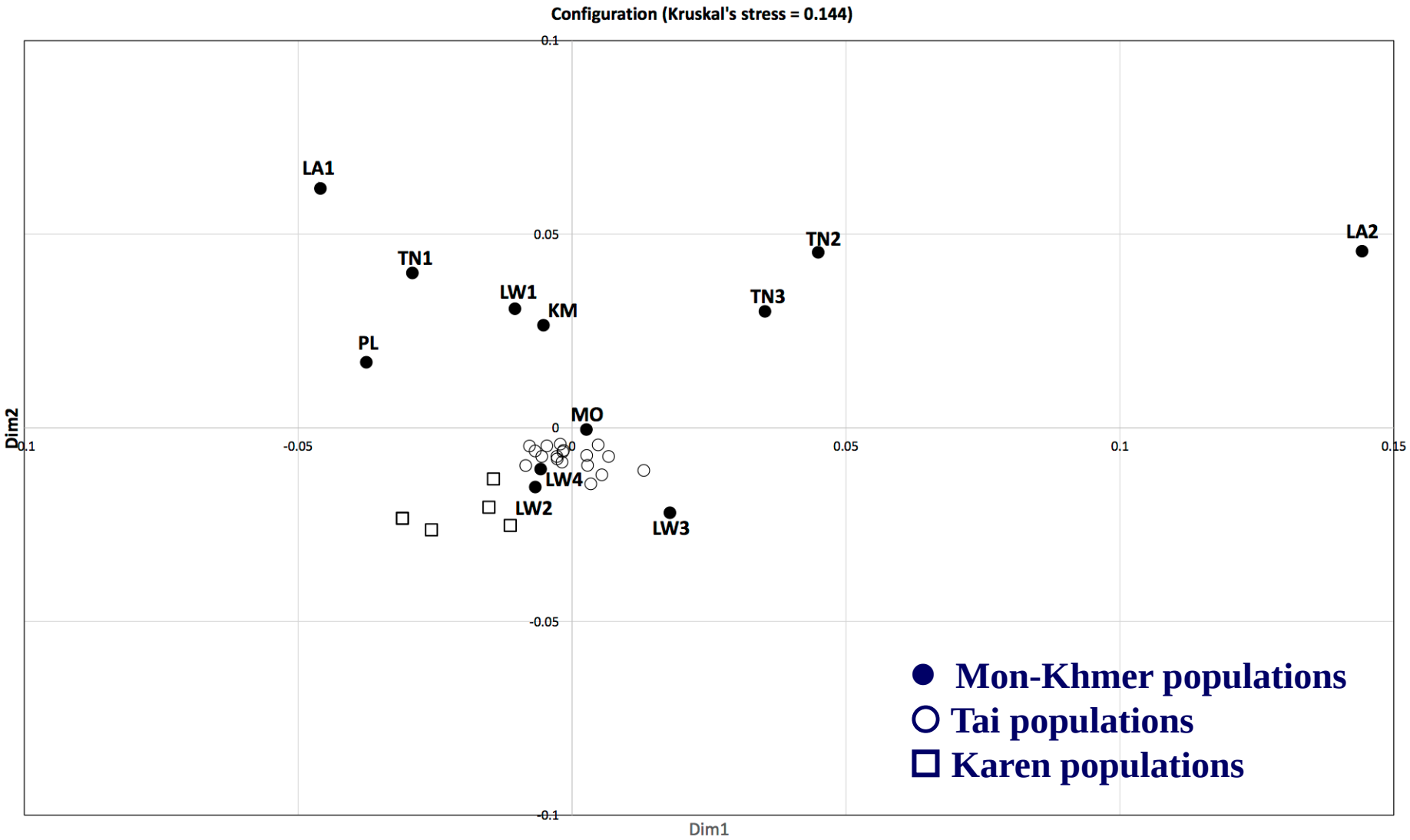
Results

Mean observed and expected heterozygosity with s.d.



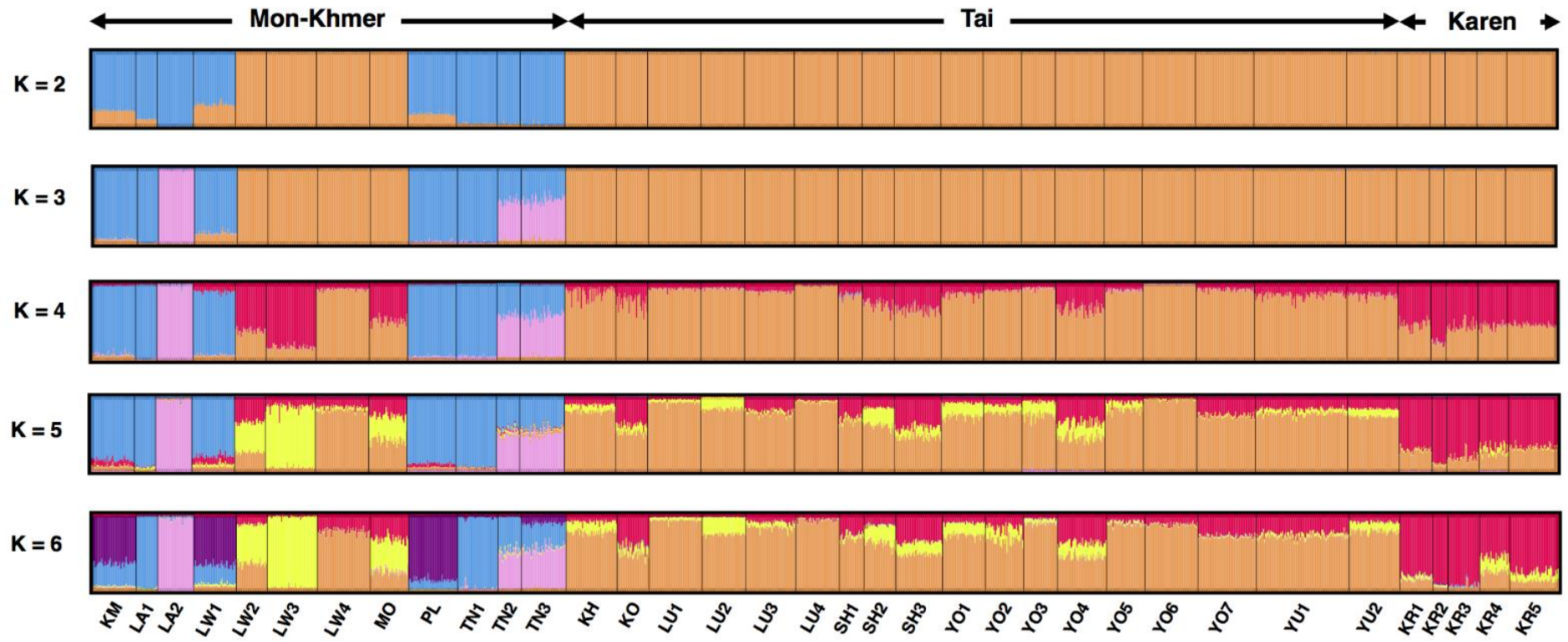
Results

Multidimensional scaling plot applied from Fst



Results

Bar plot estimation with sequential *K* values from 2 to 6



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Thank you!