LANGELIN - LANguages Genes LINeages
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Historical Bio-Linguistics.

A biostatistic approach to the study of linguistic phylogenies and the correlation of genetic, linguistic and geographical data.

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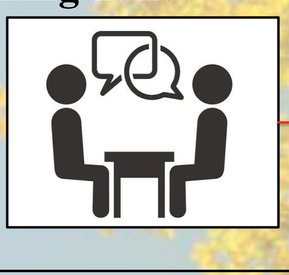
Background

Demographic events often leave traces in languages and genes: this prompted Darwin's prediction that the evolutionary tree of human populations would provide the best possible phylogeny of language relationships. We tested Darwin's expectation through long-distance genome-language comparisons across Eurasia, relying on independently assessed quantitative tools on both sides. To do so, we had to resort to a linguistic method able to compare across different families, based on abstract syntactic characters, which proved more apt for long-term historical reconstruction than phonemic ones.

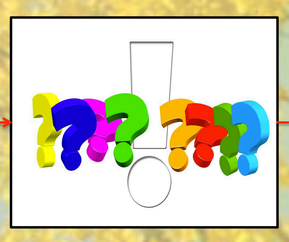
Materials and Methods

Data collection

Linguistics:



Interviews with native speakers (collection of actual grammaticality judgments)

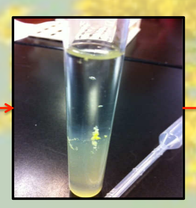


Manifestations

Binary strings for each language

Genetics:

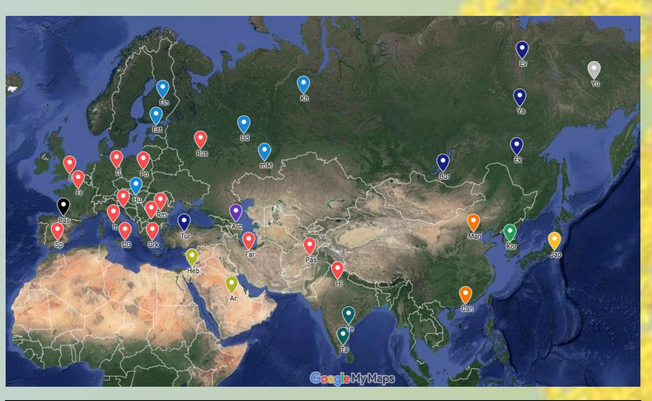
Sample collection



DNA extraction

Binary strings for each DNA collected

Geography



Three types of geographic distances were calculated: Great Circle Distance (GCD), Least Cost Distance (LCD) and CircuitScape Distance (CSD)

Phylogenetic analysis

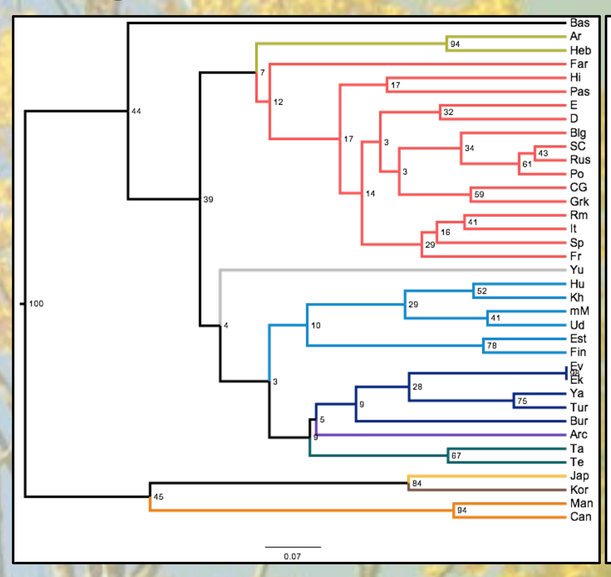
1) **Linguistic data**
   - Distance based method (Jaccard-UPGMA) for syntactic and phonetic data (the latter found in literature: Creanza et al., 2015).
   - Character based methods (Bayesian).
2) **Genetic data**
   - Distance based method (Fixation Index (FST)-UPGMA).

Correlations

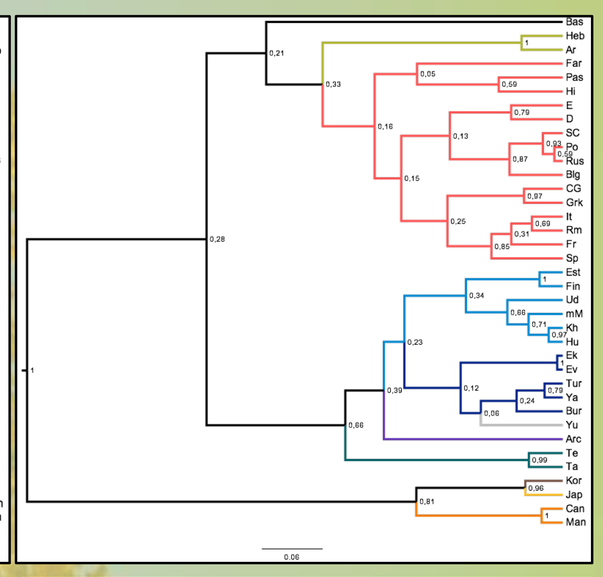
Relationships between syntactic, phonetic, genetic and geographic distances were assessed by using Mantel tests and partial Mantel tests

Results

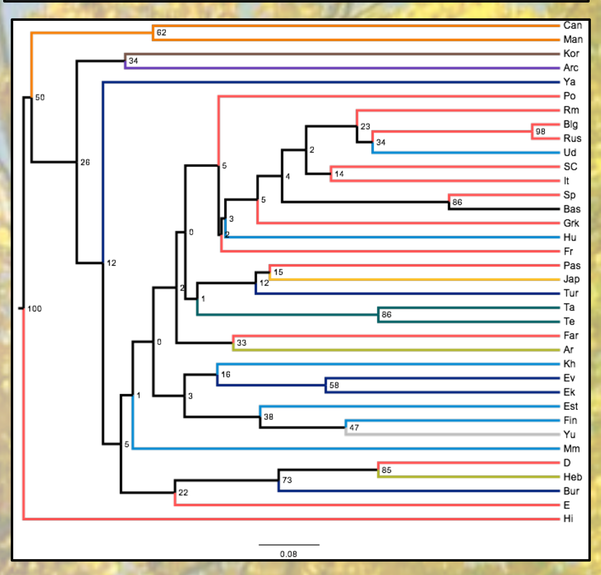
Linguistics



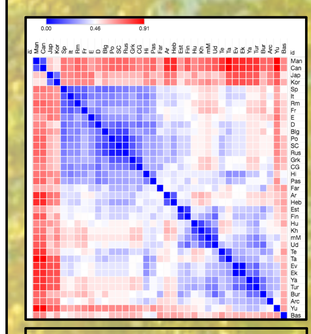
Distance-based tree from syntactic data



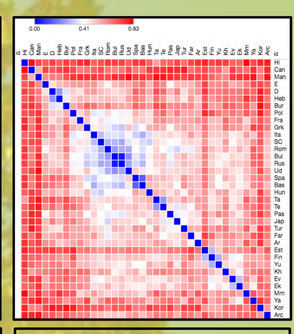
Character- based tree from syntactic data



Distance-based tree from phonemic data

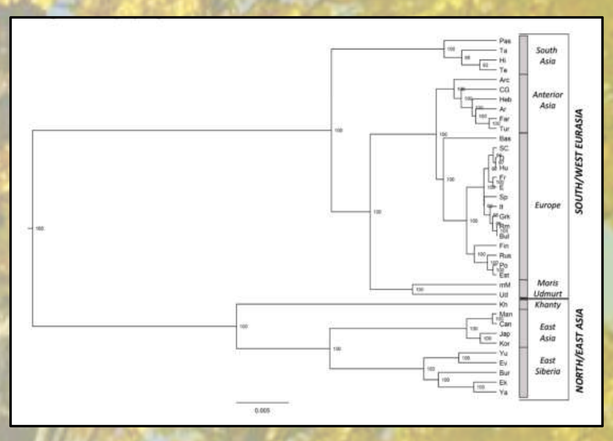


Heat map from syntactic data

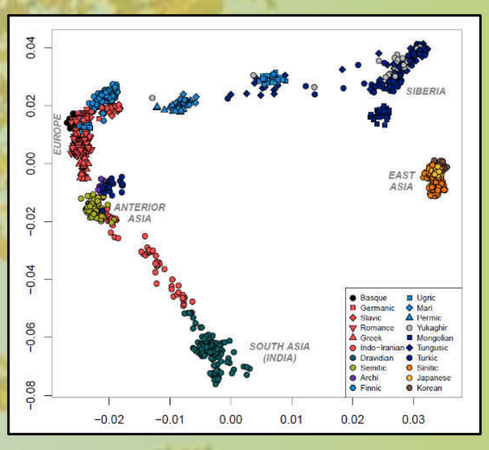


Heat map from phonemic data

Genetics



Distance based tree of genetic data



PCA of genetic data

Mantel correlations

The Mantel correlation for the full dataset of syntactic data:

Dsyn-Dgen: r=0.53 p=0.001
Dsyn-Dgeo: r=0.47 p=0.001
Dgen-Dgeo: r=0.88 p=0.001

Dsyn/Dgen-Dgeo: r=0.28 p=0.004
Dsyn/Dgeo-Dgen: r=0.01 p=0.380
Dgen/Dgeo-Dsyn: r=0.84 p=0.001

The Mantel correlation for the full dataset of phonemic data:

Dphon-Dgen: r=0.33 p=0.001
Dphon-Dgeo: r=0.27 p=0.002
Dphon-Dsyn: r=0.35 p=0.001

Dphon/Dsyn-Dgeo: r=0.26 p=0.01
Dphon/Dgen-Dgeo: r=0.20 p=0.02
Dphon/Dgeo-Dgen: r=-0.04 p=0.65

These correlations data were confirmed in strategically chosen subsets and performing an analysis on 9604 randomly chosen subsets of cardinality n=15 (Confidence value= 99% ±1).

Conclusions

We discovered significant congruence between biological and linguistic traits, not fully accounted for by any of the three types of geographic distances: this suggests that in the Old World the grammatical structure of most languages was largely transmitted along with the ancestral speakers' genes. Indeed, we found that language history is much more vertical and independent of geography than genes, and correlates with geography only as a byproduct of its correlating with genes. Few exceptions to the congruence emerged, and were analyzed into differently motivated types, based on plausible conditions on language diffusion and on gene-language combinations. The patterns observed were summarized into a set of foundational generalizations for a science of long-term glottogenetic history, as emerging from the Eurasian domain.

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