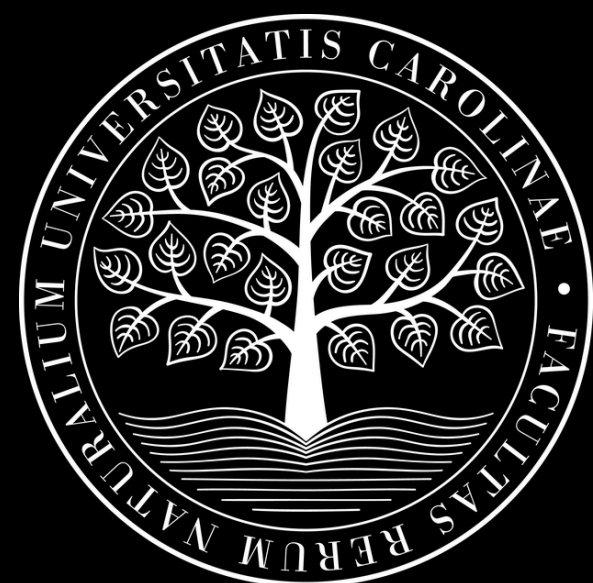


The utility of cytogenetic methods in the taxonomy of the scorpion family Euscorpiidae (Arachnida: Scorpiones)



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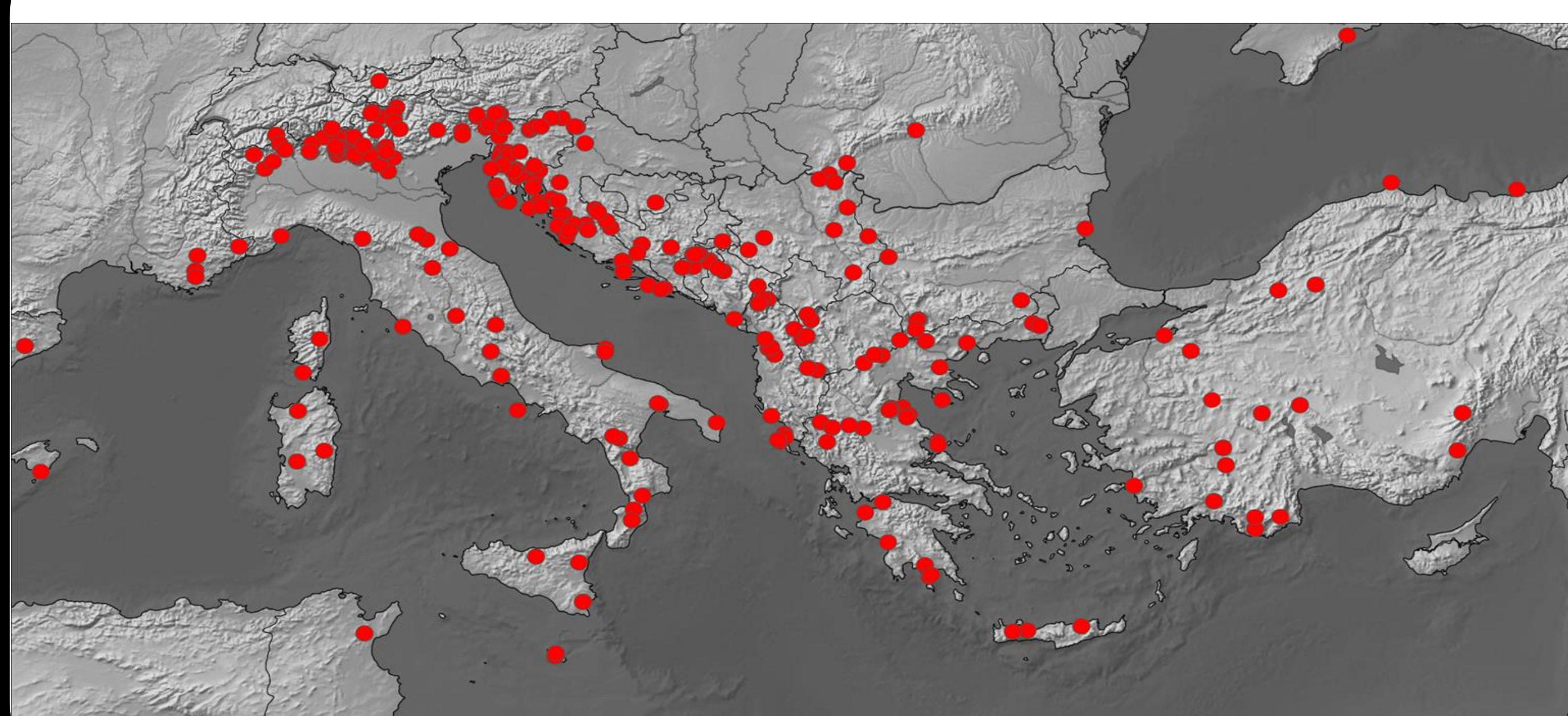
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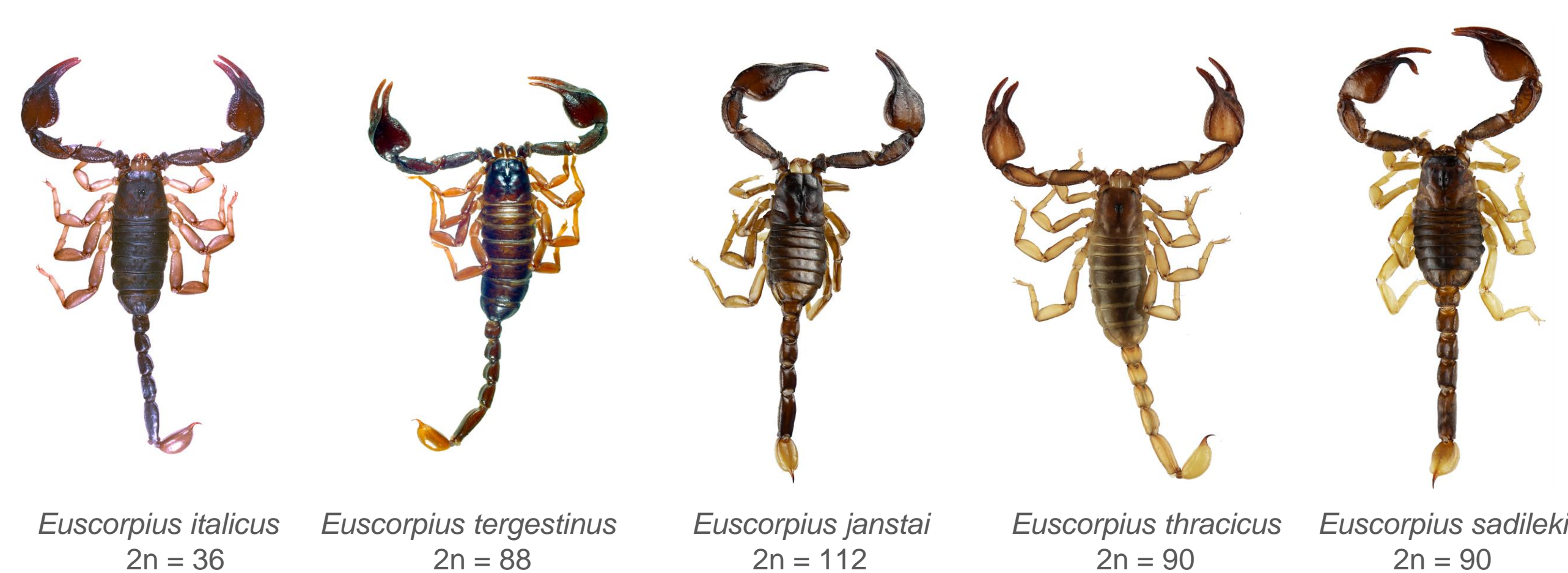
Scorpions represent an old arachnid order counting more than 2800 species. Although they are highly diverse, the group displays uniform morphology that complicates species delimitation. This problem has become sure during the last twenty years hand in hand with genetic data started to be increasingly used to species delimitation. In many cases, ambiguities were found between the results of traditional morphological taxonomy and molecular phylogenetic analyses. Today, cytogenetic data for sure can help to delimit scorpion species. Scorpions show high karyotype variability ($2n=5-175$). Even closely related species, the same based on external morphology, can differ significantly in their karyotypes. From the cytogenetic view are scorpions less discovered. So far we have karyotypes of only 16 species out of 111 described taxa published within the family Euscorpiidae.

We focused on the missing species and our cytogenetic results combined with molecular phylogenetic analyzes confirm a significant interspecific variability. We can already see the differences in the diploid number of chromosomes and in their morphology. We also used fluorescence in situ hybridization (FISH) for localization of gene clusters for 18S rRNA and the telomeric motif (TTAGG)_n, which in some cases also showed interspecific differences. Our results show the great potential of using cytogenetic markers in the delimitation of species in the studied Euscorpiidae family.

Overview of localities with our available material of scorpions of the Euscorpiidae family



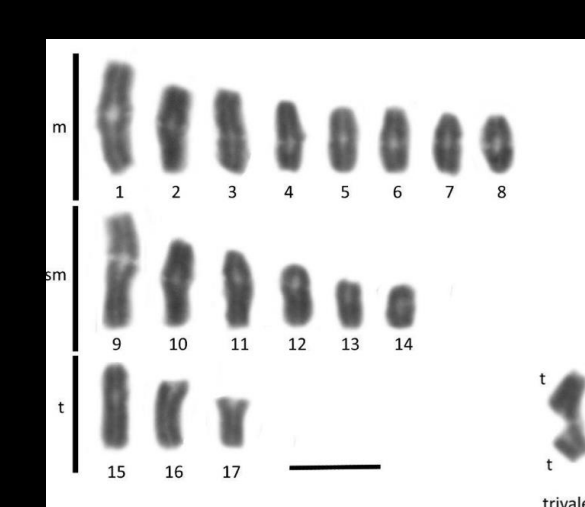
Demonstration of uniformity of morphology



What did we find out?

- The analyzed species confirm **high variability in their diploid numbers** of chromosomes. We also found fusions in the karyotype of already described species.
- Even recently diverged species show significant **differences in karyotypes**.
- Even species with the same **diploid number** can possess different chromosome morphology.
- Gene clusters for 18S rRNA also show high variability. Usually in localization on different chromosome pairs, in the position on the chromosome, but also in the number of clusters.
- Positions of repetitive sequences of telomeric motif are not variable; therefore, they are not suitable for species delimitations.

How does it look like?



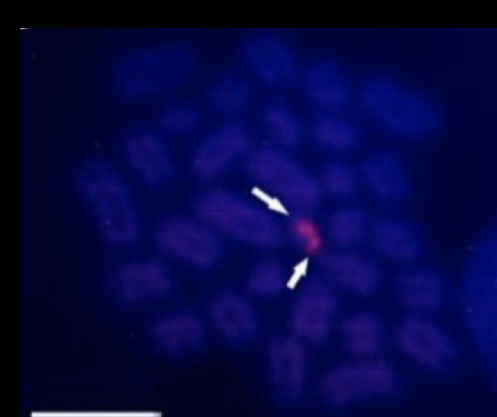
Euscorpius italicus



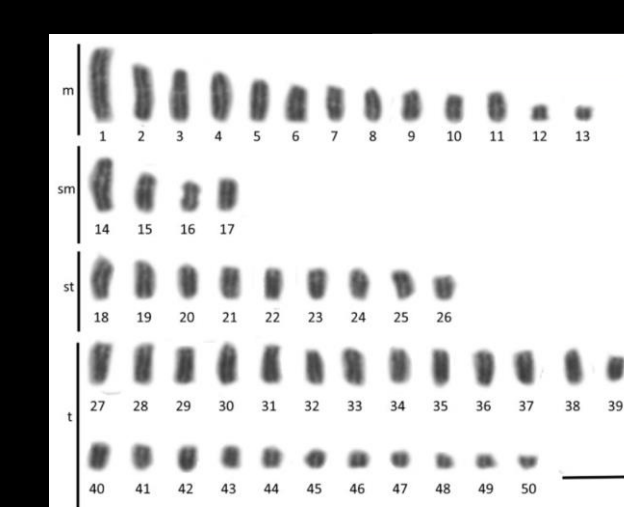
Euscorpius calabriae



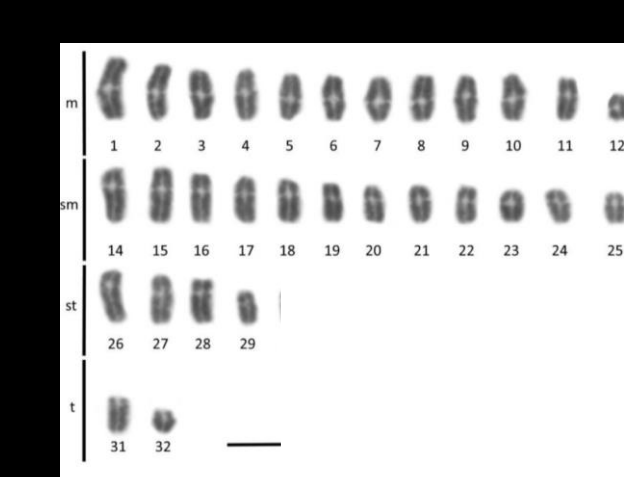
Euscorpius sicanius



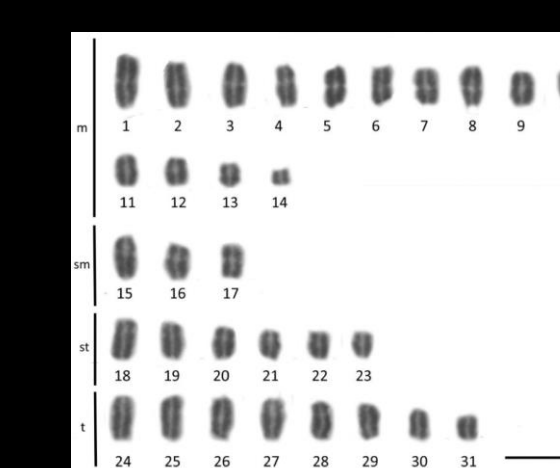
Euscorpius naupliensis



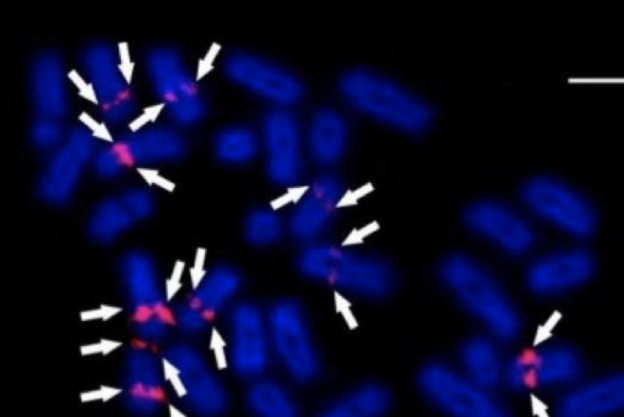
Euscorpius corcyraeus



Euscorpius gargaricus

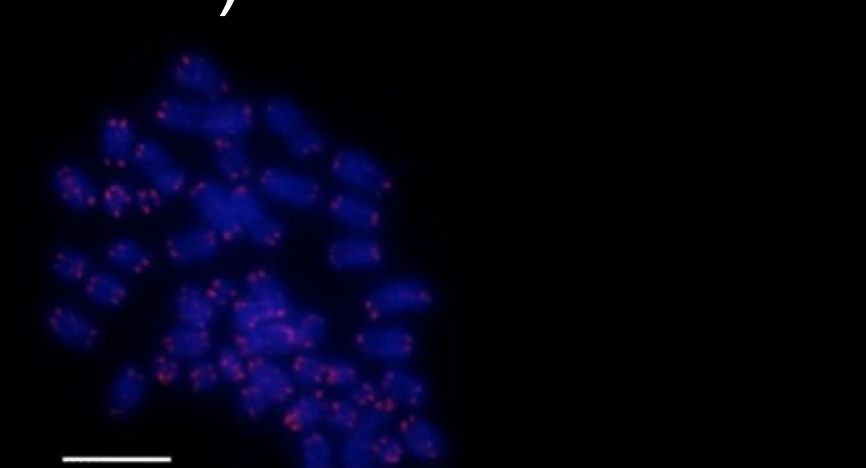


Euscorpius solegladi



Euscorpius sicanius

e)



Scale bars=10 µm

Cytogenetics seems well-suited for species delimitation in this family full of ambiguities and confusions.