

Cytotype diversity and genome size variation in *Festuca varia* complex (Poaceae) in south-eastern Europe

Ivana Rešetnik^{1*}, Marko Doboš¹, Sandro Bogdanović^{2,3}, Martina Temunović⁴, Ivica Ljubičić², Maja Mucko¹, Božo Frajman⁵

¹ Department of Biology, Faculty of Science, University of Zagreb, Zagreb, Croatia

² Department of Agricultural Botany, Faculty of Agriculture, University of Zagreb, Zagreb, Croatia

³ Centre of Excellence for Biodiversity and Molecular Plant Breeding, Zagreb, Croatia

⁴ Department of Forest Genetics, Dendrology and Botany, Faculty of Forestry and Wood Technology, University of Zagreb, Zagreb, Croatia

⁵ Department of Botany, University of Innsbruck, Innsbruck, Austria

* e-mail: ivana.resetnik@biol.pmf.hr

Introduction

The genus *Festuca* is one of the largest genera within the grass family and it dominates nearly worldwide in various types of grasslands and meadows. Within fine-leaved fescues, the earliest diverging group is *F. sect. Eския*, known also as *F. varia* complex, which includes approximately 20 species. The taxonomic complexity of the group is especially evident in SE Europe, from where several narrowly endemic taxa have been described, but their taxonomic status remains uncertain.



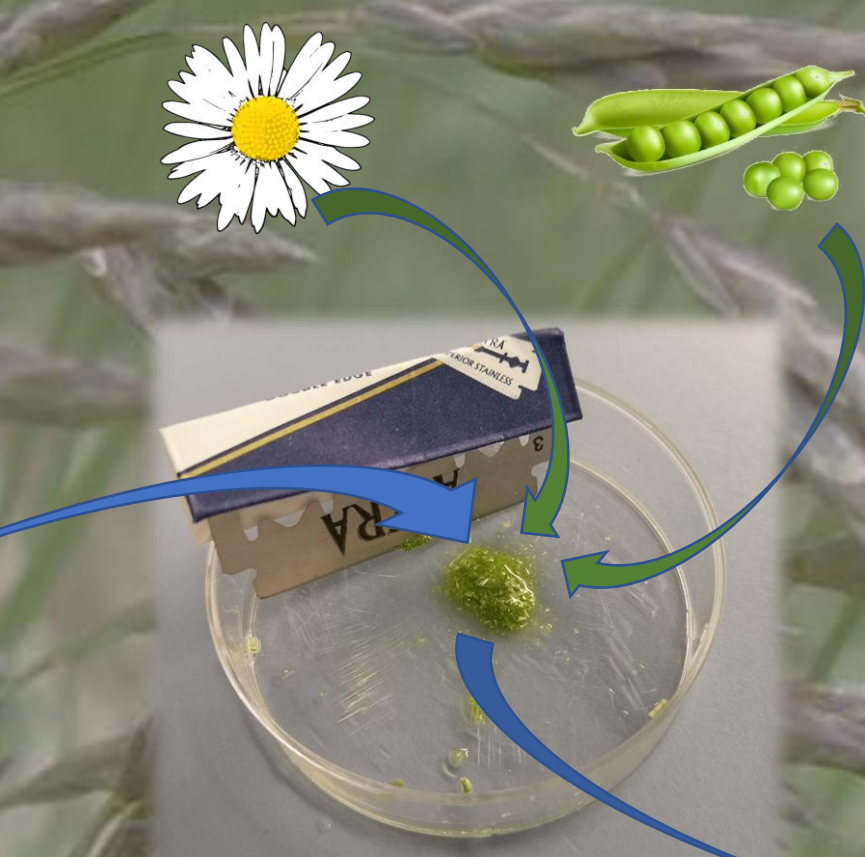
Aims

Within *F. varia* complex, the majority of taxa are reported to be diploid, but tetraploid and hexaploid species are known from the Iberian Peninsula and the Alps. The aim of the present study is to explore genome size variation and the incidence of polyploidy within the representatives of the complex on the Balkan and Apennine Peninsulas.

Material and methods



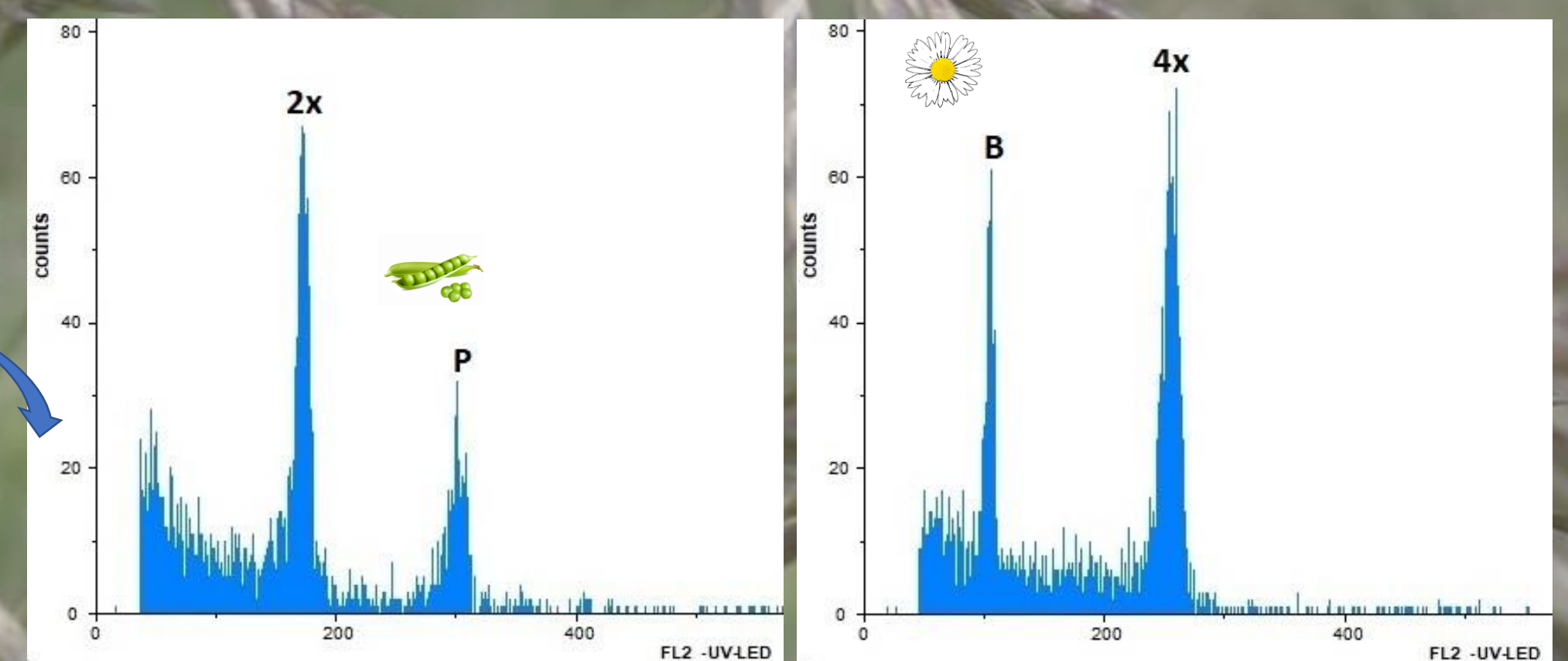
During 2018 to 2020 we sampled 77 populations of the *F. varia* complex throughout the Balkan and Apennine Peninsulas.



The material was chopped together with reference standards (*Pisum sativum* for diploid samples and *Bellis perennis* for tetraploid and hexaploid samples) and prepared for measurements.

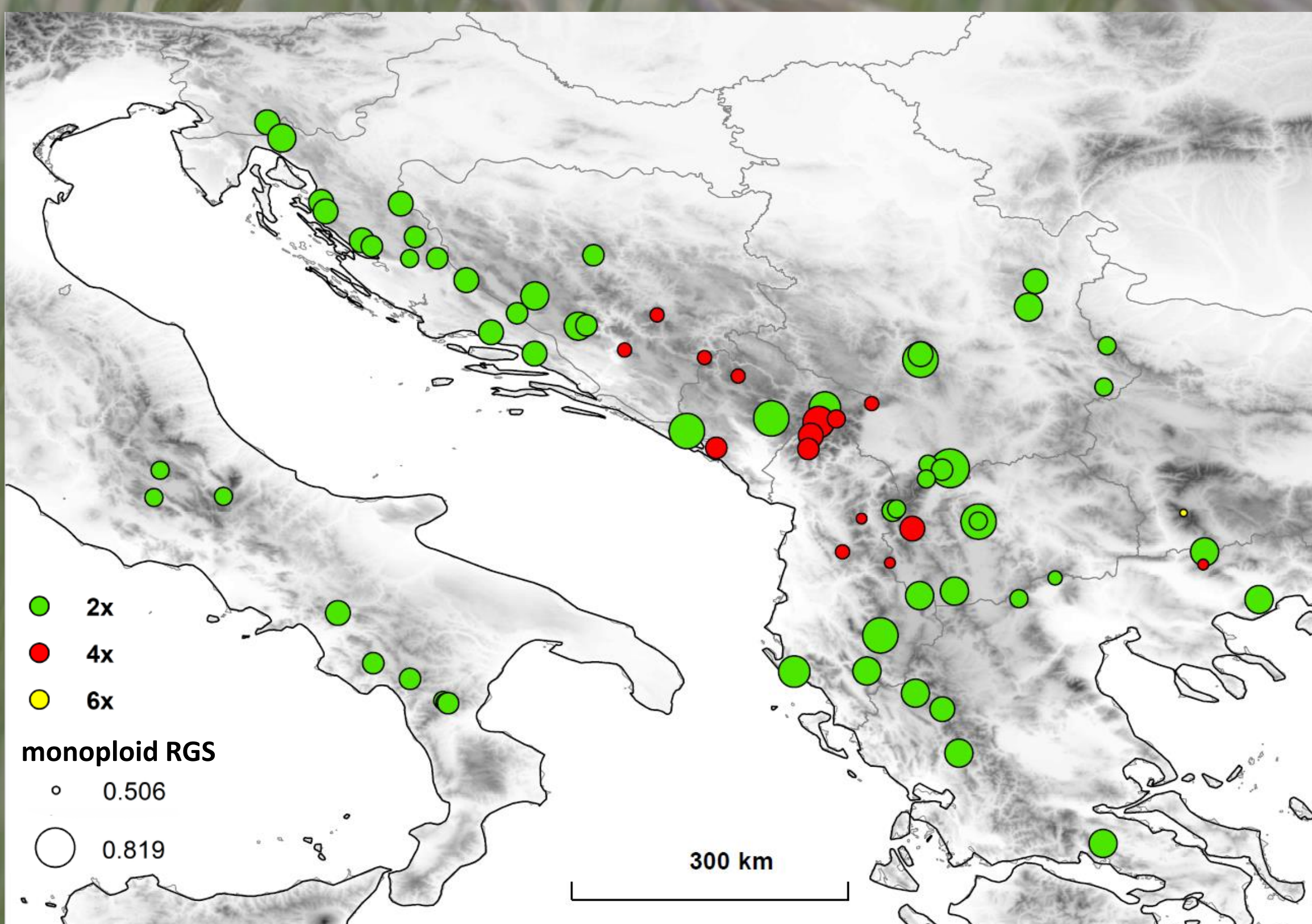


We used Partec CyFlow Space flow cytometry to measure relative genome size (RGS) and estimate ploidy level.

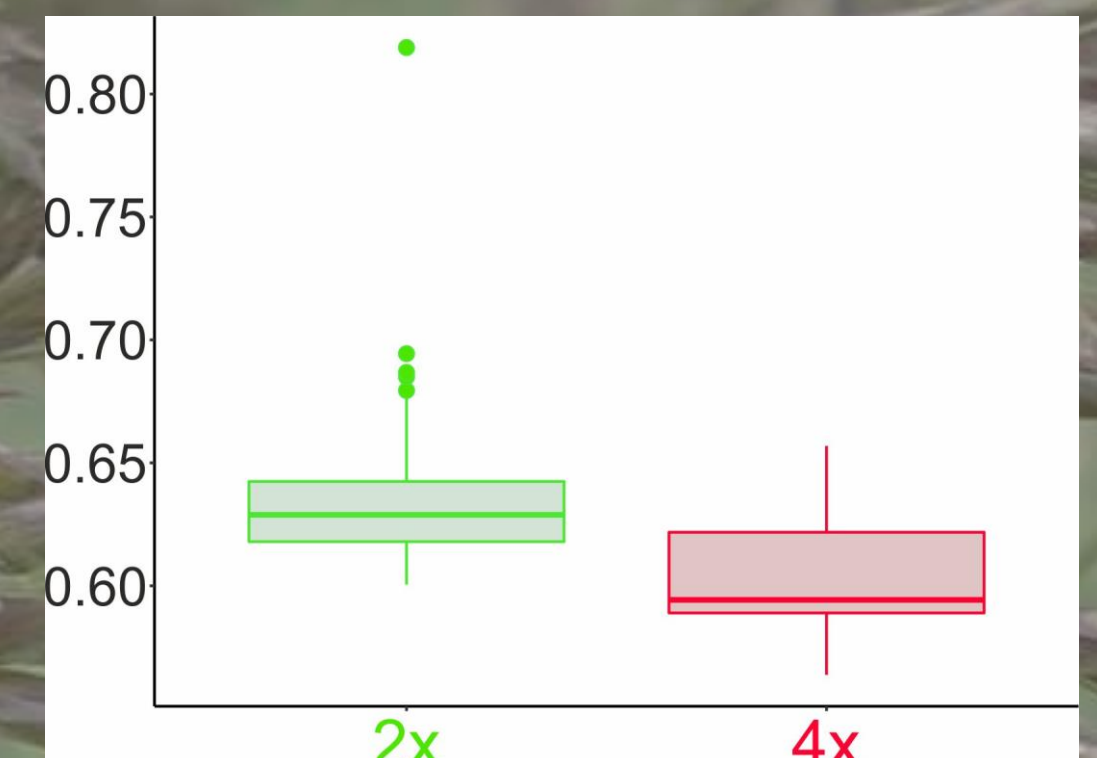


Flow cytometric fluorescence histograms of diploid (left) and tetraploid individuals (right) of *F. varia* complex compared to a reference standard (*Pisum sativum* - P and *Bellis perennis* - B).

Results



RGS measurements uncovered for the first time presence of tetraploid and hexaploid populations within some taxa of the *F. varia* complex on the Balkan Peninsula. RGS ranged from 1.201 to 1.637 for diploids, from 2.255 to 2.627 for tetraploids, and was 3.034 for hexaploid population.



Reduction to monoploid values reveals genome downsizing in higher ploidy level.

Work is not done!

Presented results are a part of the research on *F. varia* complex within our project, which also includes genetic and morphometric studies. The integrated approach will help us elucidate the evolutionary pathways and diversification within the complex.

Diploid populations are found throughout the whole Balkans and Apennines, while tetraploids are limited to the central part of the Balkans and hexaploids were found only in one population in eastern Balkans (Mt Pirin).