

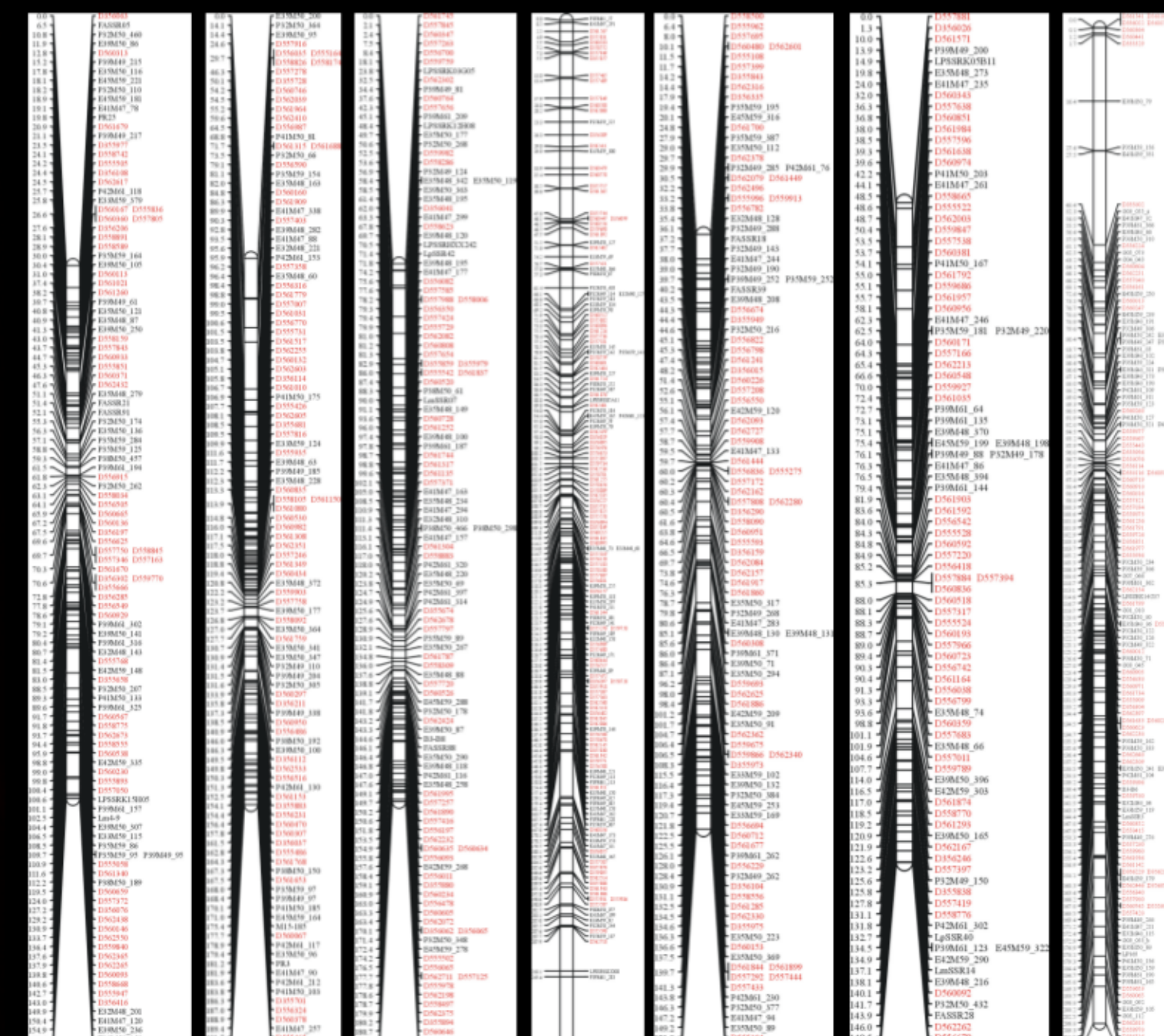
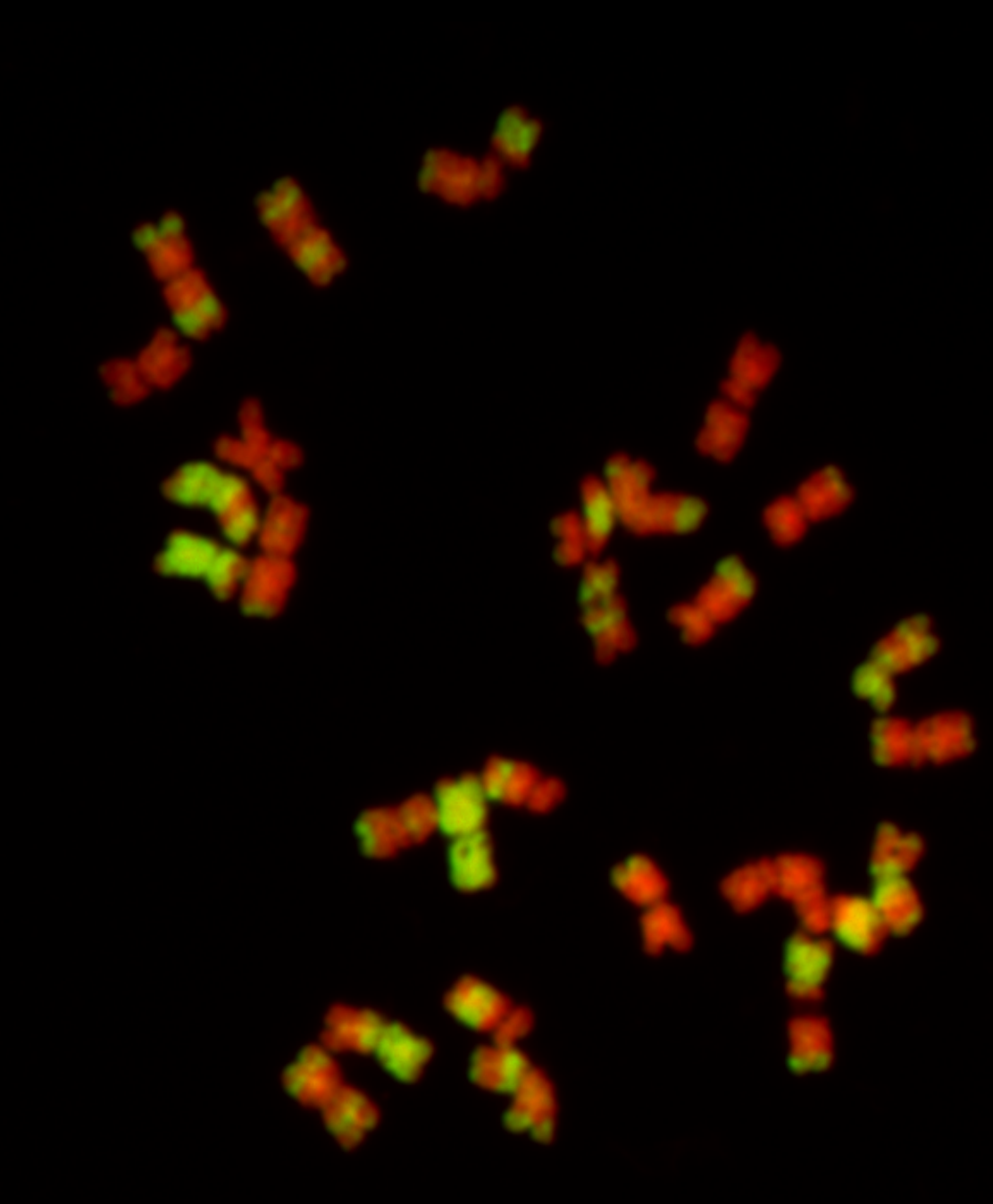


# GENOME STRUCTURE AND EVOLUTION IN FORAGE AND TURF GRASSES

Species of ryegrass, especially Italian ryegrass (*Lolium multiflorum* Lam.) and perennial ryegrass (*L. perenne* L.) are widely used in agriculture. They provide high quality fodder and are used in temporary and permanent pastures. However, their use is limited by susceptibility to abiotic stresses (summer drought and winter freezing). On the other hand, fescues (namely *Festuca pratensis* Huds. and *F. arundinacea* Schreb.) display complementary attributes to those of ryegrasses. Thus, interspecific hybrids were developed in frame of several breeding programs over the world. These hybrids became widely used by farmers for their superiority over parental species. This poster summarizes the grass research in our laboratory during the last decade.

## GENOMIC CONSTITUTION

We screened a large set of cultivars for genomic constitution using GISH and revealed enormous variation ranging from amphiploid forms to genotypes with small introgressions. In several cultivars, no visible chromatin of one of the parents was detected.

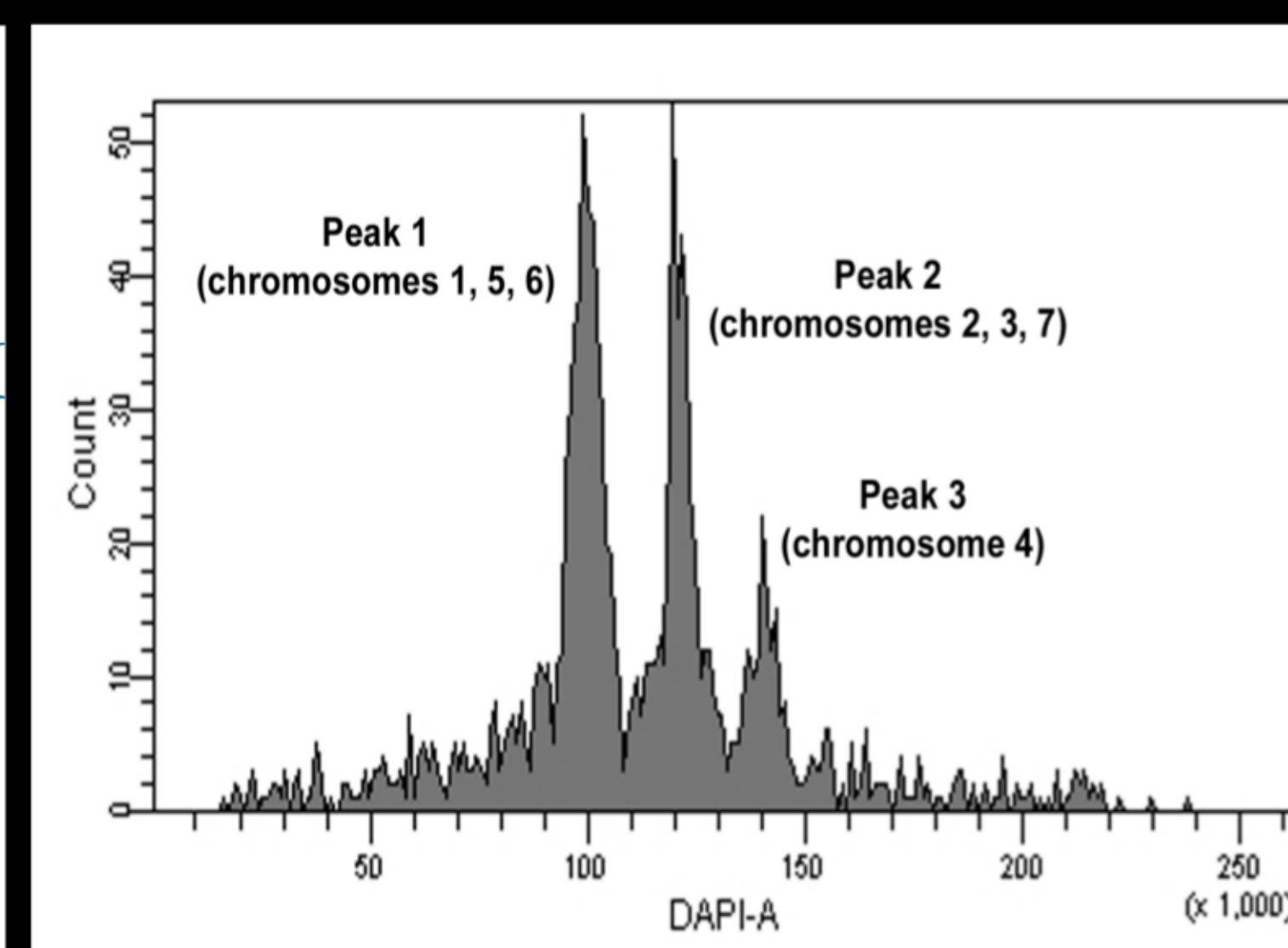
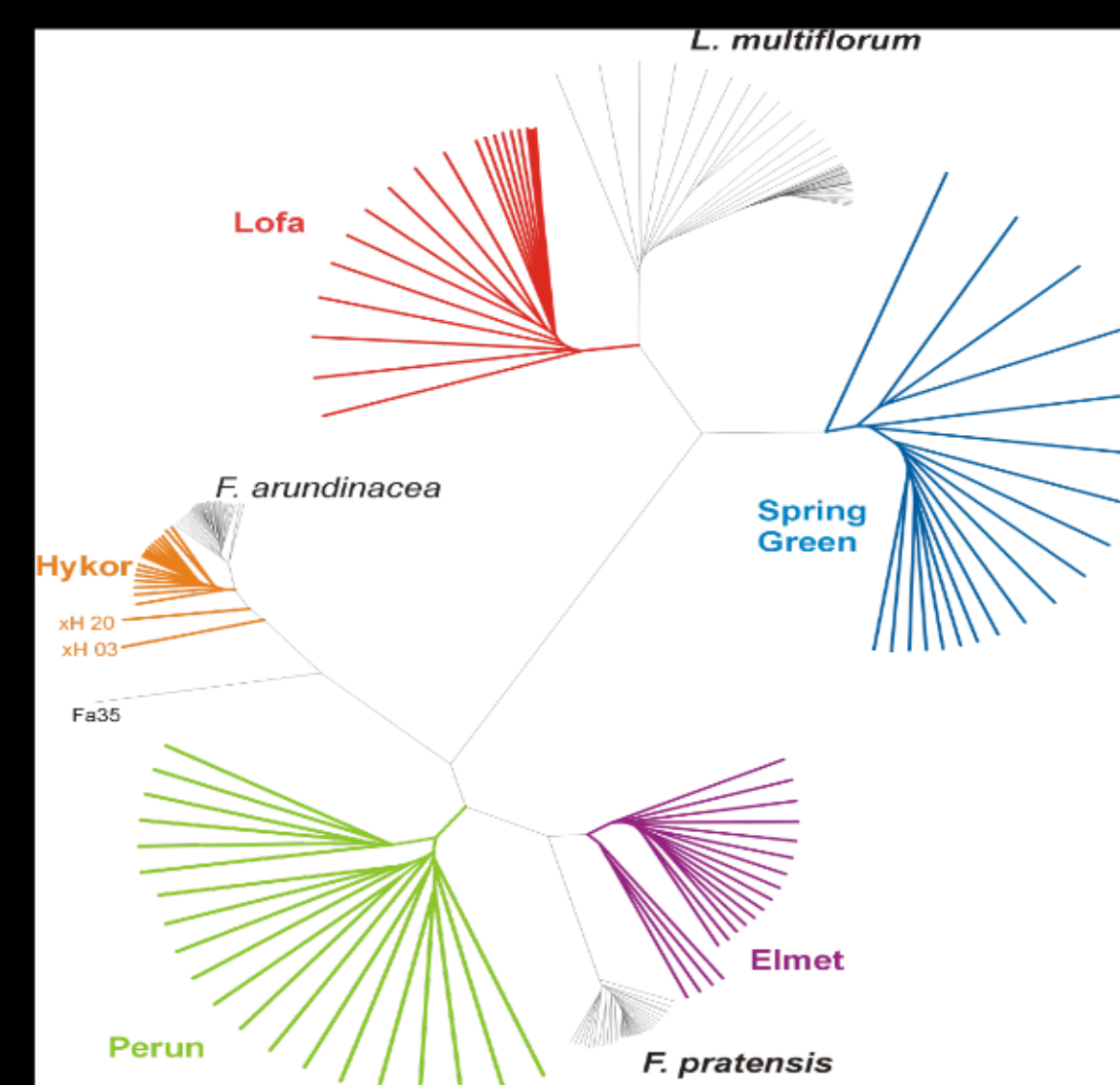


## NUCLEAR GENOME SIZE AND MOLECULAR SIZE OF INDIVIDUAL CHROMOSOMES

We estimated genome size of species of *Festuca - Lolium* complex using flow cytometry. Based on the karyotyping data, we have established molecular size of individual chromosomes and their arms.

## DEVELOPMENT OF CYTOGENETIC STOCKS

We have developed unique plant materials, including various F1 and successive hybrids and introgression lines. We have the genotypes of tetraploid *L. multiflorum* with one or two (homologous) chromosomes of *F. pratensis* for all 7 chromosomes. Moreover, we developed series of recombinant lines for all seven chromosomes by backcross to *Lolium*.

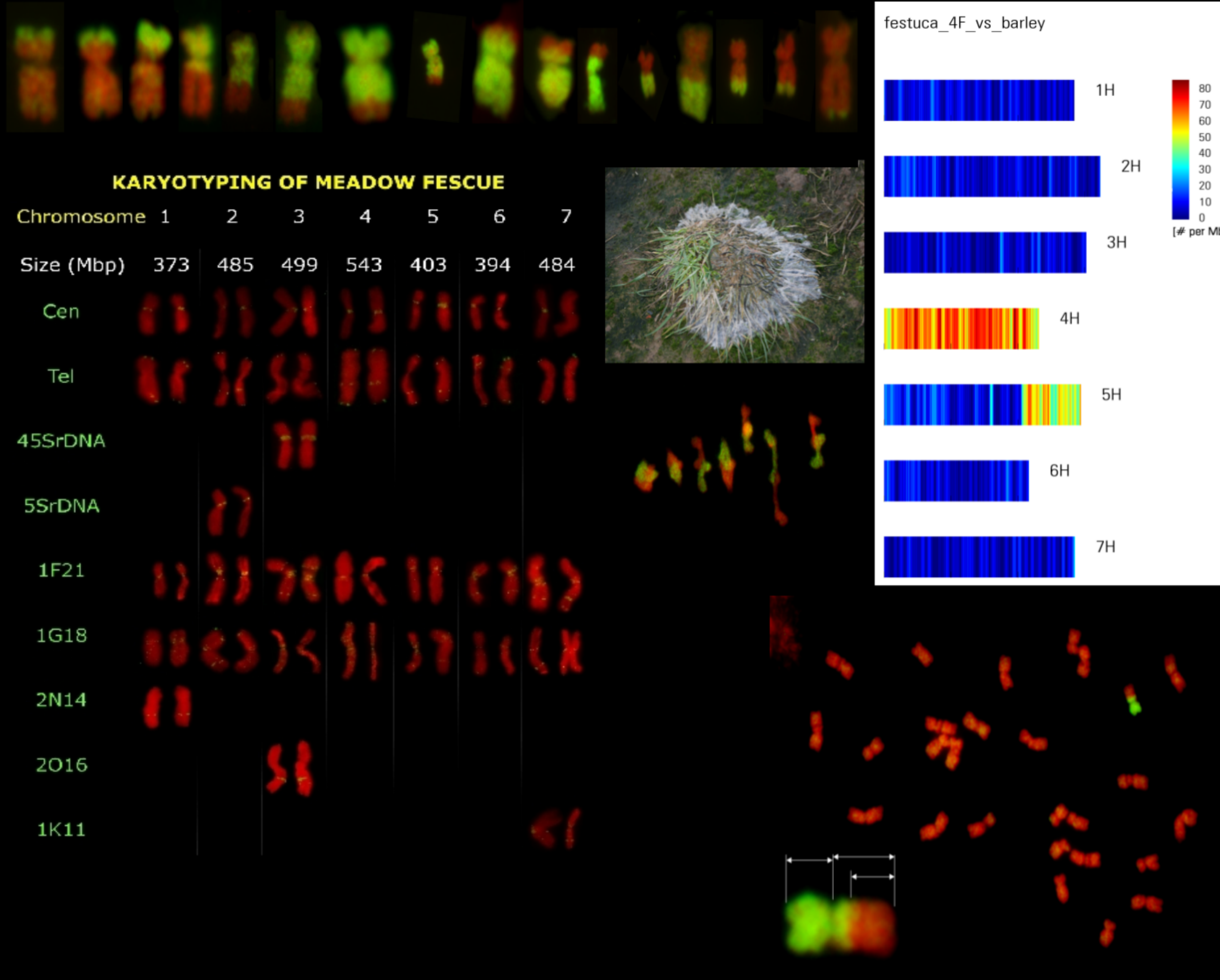


## DArTFest ARRAY

We have developed a Diversity Arrays Technology (DArT) array for five important species of *Festuca* and *Lolium*. The DArTFest array contains 7680 probes derived from methyl-filtered genomic representations. It is widely used for studies on genetic diversity and genomic constitution of hybrids, for genetic and physical mapping and marker assisted selection.

## MEIOTIC STUDIES

We studied behavior of individual chromosomes during meiosis in introgression lines. We also studied meiosis in various F1 hybrids.



## GENE EXPRESSION ANALYSIS OF F1 AND SUCCESSIVE *FESTUCA* x *LOLIUM* HYBRIDS

Using Illumina, we sequenced transcriptomes of *Lolium* and *Festuca*. Currently we are optimizing sequence assembly with the aim to identify species-specific SNPs. Subsequently, we will sequence transcriptomes of reciprocal F1 and successive hybrids to determine their genomic constitution and assess contribution of parental genomes to gene expression.

## KARYOTYPING

Using cytogenetic markers, we were able to karyotype *F. pratensis*. This facilitates identification of individual chromosomes in introgression lines and other hybrids.

## SORTING AND SEQUENCING OF CHROMOSOME 4F

Using flow-cytometry, we were able to sort chromosome 4F with high purity (92.4%). Following this, we used Illumina platform to sequence this chromosome at 50x coverage.

## COLLINEARITY OF 4F CHROMOSOME WITH MODEL SPECIES

In collaboration with the team of Klaus Mayer (Munich, Germany), we applied GenomeZipper to reveal collinearity of chromosome 4F with the sequenced genomes of rice, sorghum, Brachypodium and barley.

For more info see our webpage: <http://olomouc.ueb.cas.cz>