producing filamentous fungi). They cause invasive infections in immunsupressed patients, but they are also able to cause local infections through external injuries (first of all on eye and on skin) in immuncompetent patients (Pfaller et al. 2004). Identification and discrimination of *Bipolaris* species and members of some closely related genera using morphological markers are really difficult, because of the great similarity of their conidia. The present taxonomy, which is based on the morphology of the conidia, is fuzzy, incoherent and it does not fit the real phylogenetical relationships.

Our work had three major aims: (i) phylogenetic analysis of the genus *Bipolaris* to clarify their taxonomical relationships using molecular, physiological and biological methods; (ii) to elaborate a reliable molecular methodology for the detection of the human pathogenic strains; and (iii) to examine the biological activity of the sesterterpene-type secondary metabolites produced by the members of this fungal group.

Twenty-five strains isolated from human keratomycosis and 15 isolates obtained from international strain collections were involved in the study. The ITS region of the ribosomal DNA and fragments of the calmodulin, the β-tubulin and the transcriptional elongation factor-1α genes were sequenced and compared to infer phylogenies and investigate the taxonomic position of the involved strains.

Currently, identification of *Bipolaris* strains isolated from clinical samples is carried out by the examination of the conidial morphology (*i.e.* determining the numbers of the conidial septa). Our preliminary examinations suggested that the three human pathogenic species cannot be distinguished merely on the basis of their conidial septation. In the molecular phylogenies inferred from the analysis of the abovementioned genes and also from RAPD-PCR data, only *B. hawaiiensis* could be clearly distinguished from *B. australiensis* and *B. spicifera*, while these two species formed a more or less uniform group in each resulting trees suggesting that they may belong to the same species. Carbon source assimilation tests (utilization of 68 compounds as a single carbon source was tested in the study) and morphological examinations also confirmed the results of the phylogenetic studies.

Sequence data were analysed to test their applicability as markers for molecular identification. As a result, an effective and rapid PCR-based method was developed to identify the members of the two human pathogenic groups (*i.e. B. hawaiiensis* and *B. australiensis* - *spicifera*).

Sensitivity of the clinical isolates against several generally used antifungal agents was also investigated. Itraconazole, clotrimazole and ketoconazole proved to be the most effective against the *Bipolaris* species. Interestingly, all of the investigated strains were resistant to amphotericin B, one of the most frequently used antifungal agents against filamentous fungi.

Bipolaris species often produce ophiobolins, secondary metabolite compounds of the family of sesterterpens. The phytotoxic, antimicrobial and nematocide effects of these compounds are well-known (Li et al. 1995; Au et al 2000) . In our study, effect of different ophiobolins against opportunistic pathogen Zygomycetes fungi was investigated in a broth microdilution assay. We also started to study the background of this antifungal effect in the case of ophiobolin A. This compound induced apoptotic-like changes in *Mucor* and *Rhizopus* strains presumably through the inhibition of the calmodulin. Further investigations are in progress to prove this hypothesis.

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Identification of fusarium resistance QTLs in the Ságvári/Nobeoka Bozu//Mini Manó/Sumai3 prebreeded wheat population

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Fusarium head blight (FHB) is one of the most serious diseases of wheat worldwide, caused by *Fusarium* species complex. Epidemics of FHB can cause severe yield losses and decreasing quality. During pathogenesis harmful levels of mycotoxins can be accumulated, jeopardizing food and feed safety. The most cost-effective way to control the disease is breeding and cultivation of genetically resistant cultivars.

The FHB resistance in wheat is inherited by quantitative trait locus (QTLs). Many QTLs, with different effectiveness, are found on all wheat chromosomes except 7D from different resistant genotypes (Buerstmayr et al. 2009) Identification, effectiveness, inheritance, usage (marker assisted selection, MAS) and pyramiding of different QTLs is a powerful tool to help breeding varieties with enhanced Fusarium resistance.

105 recombinant inbred lines (RIL) of a double cross population (Ságvári/Nobeoka Bozu//Mini Manó/Sumai3) which contains two resistance sources from Asia – *Nobeoka Bouzu* (NB) a Japanese landrace and *Sumai 3* (Sum3) a Chinese variety - and two Hungarian genotypes - *GK Sagvari* (Sgv) and *GK Mini Mano* (MM) - were tested for *Fusarium* resistance.

Phenotyping was made in field trials during 2008 and 2009. Wheat ears were inoculated artificially with two isolates (one *Fusarium graminearum* and one *F. culmorum*) in 2008 and with four isolates (three *F. graminearum* and one *F. culmorum*) in 2009. Suspension of the

fungus was sprayed directly onto a bunch of ears in full flowering stage. Afterwards 48 hours polyethylene bag coverage was maintained to allow moisture condition for growing fungus. Head blight symptoms were evaluated visually as the percentage of scabby spikelets from 10 days after inoculation (dai) on every 4th day till the 26 dai. Inoculated ears are harvested and trashed so as to evaluate the percentage of Fusarium damaged kernels (FDK) and deoxynivalenol content (DON) by HPLC. Flowering time, plant height, ear type, present of awns, thousand kernel weight (TKW) was evaluated also during the experiment. Analysis of the data was made by two-way ANOVA and Pearson's-correlation.

Genotyping was carried out with microsatellite (SSR) markers, linked to FHB resistance QTLs, collected from literature. At the present time four QTL regions, located on the 2D, 3BS, 5A and the 6B chromosomes was mapped with 40 SSR markers. Since in resistant genotypes Sumai3 alleles dominated the tested regions, alleles were scored as derived from Sumai3 and others non-Sumai3. Linkage analysis and QTL mapping were done with JoinMap and MapQTL. Reduced hegiht (Rht) genes Rht-B1b, Rht-D1b and Rht8 were also detected.

Significant (P = 0,1%) positive correlations were found between FHB, FDK, DON, and TKW data. Plant height was in significant (P = 10%) negative correlation with disease traits. This means that taller plant and plants with lower TKW had lower disease level. Highly effective QTL, originated from Sumai3, found on the 3BS chromosome, explained the 60% of the phenotypic variance (p.v.) of FHB with 21 LOD value and the 45% of p.v. of FDK with 14 LOD value. It is flanked by 3 SSR markers on a 3 cM distance. A Sumai3 originated medium effective QTL found on the 5A (LOD 6-8), and small or medium effective QTL on 2D (LOD 3-7) and 6B (LOD 4-6) chromosomes. The mapped regions had significant effect on TKW also. Sumai3 alleles are linked to lower TKW mainly on 5A and 6B chromosomes which is a negative effect in breeding. The distribution of QTLs according to head type showed significant differences. The ratio of QTL carrying genotypes in the group of tapered and spindle headed plants was larger than in the group of square or semi-butt headed plants.

Fusarium resistance QTLs are identified and their effectiveness and agronomic relation are investigated in this study. However this research program wasn't finished, members of this population with good agronomic characters and Fusarium resistance (supported by known QTLs) are able to start to do marker assisted selection.

Buerstmayr H, Ban T, Anderson JA (2009) QTL mapping and marker-assisted selection for Fusarium head blight resistance in wheat: a review. Plant Breeding 128:1-26.

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The role of the *Drosophila* DAAM in the development of the Indirect Flight Muscle

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In the past few years our group has working on to study of a new *Drosophila* formin protein called DAAM (Dishevelled associated activator of morphogenesis). This protein has many interesting tissue-specific functions. For instance, it regulates the tracheal cuticle pattern (Matusek et al. 2006), plays a role during axon growth (Matusek and Gombos et al. 2008), and participates in the process of genitalia rotation.

In collaboration with a research group from the University of York (UK) we showed that the *Drosophila* DAAM (dDAAM) is localized in the Indirect Flight Muscle (IFM) of both the pupae and adult flies.

In non-muscle cells, generally there are two major actin nucleating-polymerizing systems, the formins and the Arp2/3 complex. Formins are producing long straight actin filaments and the Arp2/3 complex is producing branched actin network (Pollard 2007; Chhabra and Higgs 2007).

Because unbranched straight actin filament is the major form in striated muscle cells, it is possible that a formin family protein serves as the key regulator of actin dynamics in myofibrils (Taniguchi et al. 2009). These straight actin filaments are organized into the contractile unit called sarcomere but little is known about the regulation of actin assembly in muscle cells.

Our aim was to reveal the function of *Drosophila* DAAM insight the striated muscle's sarcomere.

With the use of different approaches, like muscle functional tests, immunohistochemistry, biophysical essays, we confirmed that dDAAM plays role in the nucleation of actin filaments and sarcomere assembly.

In the 6% of the dDAAM loss of function hypomorph mutants, called Ex1, about 16% reduction in the sarcomere length was observed compared to the wild type. These flightless mutants carrying the full length protein construct could rescue the phenotype at 100% both in sarcomere level and functionally as well.

With the overexpression of the tagged full length protein, we found that it is partially localized in the expected region, namely in the M-line of the sarcomere.

The RNA interference-mediated depletion of dDAAM resulted in a marked reduction in sarcomere length and disruption of the sarcomeric structure.

These findings suggested that actin dynamics regulated by dDAAM are critical for sarcomere organization in striated muscle cells.