Fungal pathogenesis in plants and crops pdf

Work off campus? Learn about our remote access options Volume 13, Issue 4 The purpose of this review was to survey all fungal pathologists with association with the journal Molecular Plant Pathology and ask them to assign which fungal pathogens they will place in the Top 10 based on scientific/economic value. The survey generated 495 votes from the international community, and resulted in the generation of the Top 10 fungal plants list of pathogens for molecular plant pathology. The top 10 list includes, in rank order, (1) Magnaporthe oryzae; (2) Botrytis cinerea; (3) Puccinia spp.; (4) Fusaarium Grammar; (5) Fusarium oxysporum; (6) Bloomeria Graminis; (7) Mikosfarella gramicol; (8) Colletotrichum spp.; (9) Ustilago Maidis; (10) Melampsora lini, with honorable mentions for mushrooms just missing out on the Top 10, including Phakopsora pachyrhizi and Rhizoctonia solani. This article presents a brief summary of each fungus in the top 10 list and its significance, with the aim of initiating discussion and discussion among the plant archaeology community, as well as laying a bench. In the future, it will be interesting to see how the performances change and which mushrooms will be included in the top 10 of the future. Recently, the journal Molecular Plant Pathology examined which viruses will appear in the Top 10 of plant viruses based on their perceived importance, scientifically or economically, in terms of opinions of the authors of the journal (Scholthof et al., 2011). This has been conducted as many documents, reviews and grant applications claim that a particular plant virus is of paramount importance, and this is probably correct. As a result of the interest generated by this exercise to plant viruses, a similar examination was initiated for plant-based fungi and with a similar virus review mechanism. All authors, reviewers, editorial board members and senior editors of Molecular Plant Pathology magazine interested in fungi were contacted and asked to appoint three plant-pathogenic fungi that they would expect to see in the list of the most scientifically/economically important fungal pathogens. The review, by its very nature, is similar in format and layout to an overview of the top 10 viruses (Scholthof et al., 2011). The poll received 495 votes from the international community, and allowed the generation of the Top 10 fungal plant list of pathogens for the journal Molecular Plant Pathology (see table 1). Table 1. Top 10 fungal plant pathogens. Rank Fungal Pathogens Author Fungal Description 1 Magnaporthe oryzae Ralph Dean 2 Botrytis cinerea Jan A. L. van Kahn 3 Puccinia spp. Sacharias A. Pretorius 4 Fusarium graminearum Kim Hammond-Kosak 5 Fusarium Oxysporum Antonio Di Pietro 6 Blumeria graminis Pietro Spanu 7 Mycosphaerella graminicola Jason J. Rudd 8 Colletotrichum spp. Marty Dickman 9 Ustilago Can 10 Melampsora lini Jeff Ellis Table is a rating list of mushrooms voted for by plant climatologists associated with the journal Molecular Plant Pathology. The fungus making the strongest appearance in the vote was Magnaporthe oryzae, in first place with almost twice as many votes Botrytis cinerea, in second place. All voters stressed the economic importance of M. Oryzae; since more than half of the world's population relies on rice as its primary source of calories, the pathogen can be devastating; however, many also highlighted how this pathogen evolved into a model system to study the interactions between plant pathogens. Botrytis cinerea, in second place, clearly has influence in many areas due to the wide host range, causing serious damage both before and after the harvest. This may be one of the few entries in the Top 10 that can claim to be of potential useful use, through its role in some aspects of wine production, with some advantages also claimed for the ninth record, Ustilago maydis, in infected cobs. Puccinia spp., with many voters grouping three rust diseases contaminated with wheat together, grouped together in third place. These fungal pathogens were already a serious threat of the disease, but have intensified in exposure since the advent of the Ug99 race, now posing a serious challenge to wheat production. On the fourth and fifth places are two types of Fusarium, but with contrasting host ranges, with F. graminearum causing significant damage predominantly to cereals and several non-metallic species, and F. oxysporum having a wide host range, with serious losses in crops as varied as tomatoes, cotton and banana. However, pathogens of cereals still have a significant presence in the Top 10 with Blumeria graminis in sixth position and Mycosphaerella graminicola in seventh. Colletotrichum spp., in eighth position, are members of an important genus of plant pathogens for which taxonomium can be described as attacking in a state of flow. The proposed number of species per genus ranges from 29 to more than 700 depending on the taxonomic interpretation. Colletotrichum spp. has long served as a model system for hemibiotrophic pathogens, with a short biotrophic stage, followed by the transition to tissue effects and necrotrophic development. Interestingly, Ustilago Maidis and Melampsora are in ninth and tenth places respectively, with many voters pointing to strong scientific rather than economic reasons for their inclusion. Both are now developed as model systems that are easily tracted, and provide a vital understanding of the molecular basis of plant immunity and infectious processes. Although This article of the review was to identify the top 10 most important plant-pathogenic fungi according to participants in molecular plant pathology, we are very well aware that the importance and priorities are priorities vary locally across continents and disciplines. We also know that not all mushrooms can get into any top 10, due to obvious numerical limits, although such mushrooms can still be considered as extremely important. Therefore, we considered it appropriate to bring honorary mentions for mushrooms just missing out on the top 10 list, including Phakopsora pachyrhizi (Goellner et al., 2010) and Rhizoctonia solani (Gonzalez et al., 2011; Vilgalys and Cubeta, 1994), both clearly important. In the future, when another Top 10 study is conducted, it will be interesting to see whether fungi such as Phakopsora pachyrhizi, a causal agent of Asian soybean rust, pretends to be a distinct disease that has only recently appeared in some parts of the world and will potentially increase in importance (Goellner et al. , 2010). This review contains one-page descriptions of the top 10 plant pathogenic fungi to introduce the reader to each of them, with illustrative figures and key references for further reading. The intention of this review is to provoke discussion and discussion among the plant archaeology community, and to lay down a bench, as it will be interesting to see how perceptions change in the future and which mushrooms enter and exit the list. Magnaporthe oryzae, a filigree fungus of accomicete, is the causal agent of the disease of the explosion of rice, the most devastating disease of rice worldwide (Ou, 1980). Its importance is underlined by the fact that about half of the world's population relies on rice for its primary calorie intake (Khush, 2005). All tissues of flora are prone to infection; However, a panic infection can lead to a complete loss of grain. Losses of 10-30% are typical, although regional epidemics can be devastating. In addition, the fungus is very subst modified to genetic and molecular genetic manipulation (Jeon et al., 2007; Talbot, 2003; Valent and Chumley, 1991). Consequently, as a result of its agronomical importance and uro-creation, M. oryzae has become a fundamental model in the study of interactions of host-fungal pathogens (Dean et al., 2005). Although host resistance is the most economically viable and environmentally sound practice to manage the disease, the fungus quickly overcomes resistance to explosions, and varieties tend to become ineffective within 2 to 3 years (Ou, 1980; Seigler et al., 1994). Magnaporthe oryzae is part of a species that can cause disease on various herbs and related species, including crops such as barley, wheat and millet (Couch et al., 2005). New varieties of wheat have emerged in South America, raising concerns that the fungus poses a serious threat to global wheat production (Urashima et al., 1993). Knowledge of the biology, genetic diversity and adaptability of this pathogen key to developing new and long-term strategies these are the devastating fungal diseases associated with them (Figure 1). The disease is the result of contamination of rice and wheat with Magnaporthe oryzae. (A) The classic symptoms of panic explosion on rice, although the fungus can cause disease on all lyolar tissues. (B) Head explosion on wheat. Symptoms on wheat are usually limited to the head and can be mistaken for wheat scabs caused by Fusarium graminearum. The discovery of Guy11, a fertile strain of Mat1-2 from French Guiana, more than 20 years ago stimulated a surge of scientific interest in the pathogen of rice explosion (Leung et al., 1988; Silue and Notegem, 1992). The ability to conduct genetic analyses led to cloning and characterizing several genes for host and variety specificity (Bryan et al., 2000; Jia et al., 2000; Orbach et al., 2000; Valent et al., 1991). Today, much effort is focused on the cloning and characterization of many of the auriulation and related rice resistance genes that have been genetically identified (Chao and Ellingboe, 1991; Scamnioti and Gurr, 2009). The development of genetic markers, such as MAGGY, MGR583 and MGR586, from repetitive elements has provided the means not only to create valuable genetic maps for M. oryzae, but also molecular tools to assess the diversity of population and the evolution of lines, valuable knowledge for the breeding and timely release of sustainable varieties (Farman et al., 1996; Hamer et al., 1989; Nitta et al., 1997; Scumnioti and Gurr, 2009). Early stages of infection have been studied at great depths in M. oryzae. Like many fungal pathogens of plants, M. oryzae develops apressory, a specialized infection (Howard and Valent, 1996). The corresponding development of this cell is necessary for infection; indeed, several effective fungicides, such as tricyclazole, which prevent the melanization of apppressoria, block the host's penetration (Woloshuk et al., 1983). The ability to call appressoria ex planta and conduct functional gene analysis through targeted gene knockout has provided powerful access to many major molecular processes (Leung et al., 1990; Oh, et al., 2008). Significant knowledge has been gained on the perception of environmental signals (Lee and Dean, 1994), famine response (Donofrio et al., 2006), cell signaling pathways (Lee and Dean, 1993; Nguyen, etc., 2008; Xi and Hamer, 1996), Turgon pressure generation (deJong et al., 1997), cell content processing (autophagy) (Veneault-Fourrey et al., 2006) and cell cycle checkpoints (Saunders et al., 2010), which regulate and regulate the development of this specialized cell (2. Infectious cycle of the rice explosion fungus. Conidia, derived from lesions, spills out on new plants, where they are firmly attached and germinate within a few hours. Subsequently, the germ stops the polar growth, the tip swells and, by forms a highly melanized dome-shaped structure, apressor. Usually within 24 hours, turgor pressure increases in the apppressoria, forcing the penetration of binding into the main tissue. Necrotic eye-shaped lesions appear only a few days after infection, from which conidis bearing condiment bearings of the conidia appear under the appropriate conditions to re-initiate the infectious cycle. (Scanning the image of an electron microscope in the bottom right corner courtesy of Nicholas Talbot and Michael Kershaw, University of Exeter, UK). The correction was added on July 5, 2012, after publication on the Internet: the lower right image was amended, and the recognition was included in the legend. Over the past six years, after the publication of the genome sequence of strain 7-15 (derived Guy11) (Dean et al., 2005), genomic resources for M. oryzae and related species have grown dramatically and now include more than 30 genome strains worldwide, as well as various data sets of transcriptoma (ESTs) and small RNA (Gowda et al . Nunes et al., 2011; Oh et al., 2008) and emerging proteome datasets. Early study of these data revealed significant differences in the content of genes and the organization of repetitive elements. Other studies have revealed a fundamental understanding of the mechanisms of master protection and gene silencing (Ikeda et al., 2002; Nguyen et al., 2008). With the advent of new sequencing technologies, population biology research and phylogenous M. oryzae analyses are poised to grow significantly in the very near future, providing a deep understanding of the evolution of phytopathogenesis. Botrytis cinerea Persoon: Fris (teleomorph Botryotinia fuckeliana (de bari) Wetzel; Figure 3, known as grey mold, can infect more than 200 plant species. , 2011). The presence of a sequence of the genome and various molecular tools the ease of transformation for the receipt of knockout mutants (van Kan et al., 1997) or to achieve a gene silencer (Patel et al., 2008, 2010) together with its economic significance contributed to the fact that B. cinerea is the most widely studied necrophic fungus pathogen. These studies have greatly advanced our understanding of B. cinerea infectious strategies, but very few absolutely necessary determinants of virulence have been identified by candidate gene approaches (Tudzynski and Kokkelink, 2009). Sexual fetal body (apothecia) teleomorphic botriotinia fuckeliana (de Bari) Whetzel. Botrytis cinerea is devastating mature or senile fabrics of wild-ateyledon hosts. This fungus sometimes stays quiet for a considerable time until tissues rot when the host's physiology changes and the environment is favorable (Williamson et al., 2007). Infection can occur all the way from seedling stage to product maturation. Serious damage can occur after the harvest of seemingly healthy crops. Collected goods can be spoiled in retail, during storage, transportation to remote markets or during retail display (Figure 4). Botrytis cinerea on raspberry fruit (from Williamson et al., 2007). The cost of damage to Botrytis is very difficult to estimate because of the wide host range. Costs are diffuse as Botrytis damage occurs at different stages of production and retail chain. There is no reliable data on Botrytis damage while growing crops, but it must be huge. Despite the increasing use of biocontrol in some cultures (Moser et al., 2008), the use of fungicides remains a common method of combating botrytis. The average cost of chemical control Botrytis (all cultures, all countries) is about 40 euros/ha (Steiger, 2007). Fungicides specifically targeted against Botrytis (botryticides) cost 540 million pounds (2001), representing 10% of the global fungicide market (UIPP, 2002). The wine and table grape segment accounts for 50% of the value of the entire botriticide market, with solanaceous vegetables, kucurbits, strawberries and decorative elements making up 5%-9% (Steiger, 2007). The costs of broad-spectrum fungicides, also effective against B. cinerea, are unknown. Resistance to fungicides is becoming an increasingly problematic problem, with a large proportion of the fungal population resistant to fungicides (Leroch et al., 2011). Multidrug resistance has been reported, mainly due to increased gene expression of the ABC transporter (Kretschmer et al., 2009). In wine and table grapes, the cost of controlling The Botrytis pile of rot is the main reason for the decline in profits in Australia (AUS $52 million per year; Sholfield and Morison, 2010), Chile ($22.4 million per year; Esterio et al., 2009) and South Africa (SA Rand 25 million per year). Estimates for other countries could not be obtained. These costs mainly include chemicals, but do not cover losses incurred as a result of lack of treatment (organic farming, low-water farming), poor treatment (resistance to fungicides) or loss of quality (fungicide levels exceeding export needs; the quality of grapes is not sufficient for high-quality wines). In 2002, about 15%-20% of pink and herbernium beams traded through Dutch flower auctions contained a detectable Botrytis infection, which led to a reduction in vases of such beams for 3 days. Revenue losses for rose producers alone were estimated at 1.3 million pounds (Vrind, 2005). These numbers Include flowers that were contaminated before the harvest and did not make it to auction, or flowers that were spoiled during transportation to retailers and became uns inhabited. Reducing shelf life (fruit) or vases (flowers) is a serious quality problem. Consumers experience economic losses when berries rot before they eat, or when roses do not last for a satisfactory period. From an economic point of view, the losses faced by consumers are often ignored because producers and retailers generate income. However, disgruntled customers may refrain from buying the product again for several weeks, an effect difficult to include in the estimates of economic losses. Therefore, the official figures for the cost of gray mold in soft fruits and decorative forms should be considered as understated. Botrytis cinerea is an exceptional pathogen, as it can sometimes be beneficial! In specific climatic conditions, B. cinerea can cause noble rot in grape berries, which are used to produce sweet wines (Souternes, Tokai). Botrytis' most prestigious wines are sold at prices of up to 500 euros per bottle. However, the overall influence of B. cinerea is negative, even in the wine industry. In total, global costs of controlling Botrytis (cultural measures, botryticides, broad-spectrum fungicides, biocontrol) are easily overcome by 1 billion euros per year. The consequences of product loss despite the fight against disease, and the loss of quality in the retail network, are likely to be much higher. Three rust diseases occur on wheat, namely the trunk (black) rust (called Puccinia graminis f. sp. tritici) (Pgt) (Figure 5), strip (yellow) rust (P. striiformis f. sp. tritici) (Pst) (Figure 6) and leafy (brown) rust (P. triticina) (P. triticina) (P. Prolific spores, effective distribution, pathogenic variability and widespread wheat cultivation, often in favourable conditions, all contribute to the destructive potential of these rusts. Historically, stem rust has been the most infamous for damaging wheat crops. The disease was feared in ancient Rome, where rituals ('Robigalia') were performed to save the crop from rust (Sadox, 1985). The stem of the rust of infected wheat is shown by the ureth and thelial spores stages. The wheat flag sheet is infected with a rust band called Puccinia striiformis f. sp. tritici. Pgt, Pst and Pt are obligatory, biotrophic basidiomyste mushrooms with macrocyclic, heteroesic life cycles (Bolton et al., 2008; Gin et al., 2010; Leonard and Szabo, 2005). Mandatory biotrophs differentiate specialized infectious structures, effectively suppress host's protective reactions and obtain nutrients by forming specialized forage structures called located inside plant cells (Voegele and Mendgen, 2011). Stem rust is often perpetuated by the repetition of the uredine stages on ordinary and durum wheat, barley and triticale. However, basidiospors can alternative hosts such as Berberis vulgaris, primary inoculum furnishing for wheat and new combinations of virulence as a result of sexual gene recalculation (Jin, 2011). The Barberry Eradication Programme between 1918 and 1980 in the United States (Roelfs, 1982) and in the United Kingdom, which also began in 1918 and continues to this day, should be considered as one of the major advances in plant pathology, both in the field and in disease management. Significant and repeated rust-related crop failures occurred in North America between 1904 and 1962 (Hodson, 2011; Rulfs, 1985). Serious epidemics have also occurred in Europe and China (Leonard and Szabo, 2005), with less frequent outbreaks in Eastern Europe, India, Australia, Mexico, Chile, Ethiopia and southern Africa (Hodson, 2011; Pretorius, etc., 2007). In many cases, there have been exotic intrusions of controversy transmitted through the wind that established new racial lines (Park, 2007; Singh et al, 2011). Recently, severe and widespread rust bands have been attributed to new and more aggressive races adapted to warmer conditions (Hovm'ller et al., 2011). Figuring out the full life cycle of Pst (Jin et al., 2010) and the genome sequence of this pathogen (Cantu et al., 2011) are important steps towards a better understanding of virulence and thus reproduction

for lasting resistance. Early stem rust epidemics initiated studies of pathogenic variability, epidemiology and genetics of host pathogens in Pgt (Loegering Review, 1984 and Roelfs, 1985). Pgt's specialization in different races has had a major impact on wheat farming and production. Numerous varieties protected by genes have become susceptible to stem rust, often with devastating boom and bust effects (e.g. Jin, 2011; Kolmer et al., 2007; Martens and, 1989; Park, 2007; Pretorius et al., 2007). The emergence of the Ug99 race from Pgt in East Africa with virulence for Sr31 (Pretorius et al., 2000), a widely used resistance gene, has resumed stem rust research (Singh et al., 2011). Seven variants of the Ug99 line were reported, varying in virulence for Sr21, Sr24, Sr31 and Sr36 (Singh et al., 2011). As a result of its adaptive ability, fitness and virulence attributes (90% of the world's wheat are susceptible), the Ug99 racial group has been recognized as a serious threat to food security (Flood, 2010; Mackintosh and Pretorius, 2011; Singh et al., 2011; Murro et al., 2010). Along with advances in detection, genetic mapping and management of genes and quantitative loci of traits (UG99) (Durable Rust Resistance in Wheat Project,), significant progress has been made in understanding the molecular basis of pathogenicity in Pgt et al., 2011). Continued surveillance and racial analysis studies, combined with pathogenic genomics, will enable characteristics and the use of sustainable management strategies for resistance. The production and adoption of widely adapted sustainable varieties are essential for the future and effective control of rust worldwide (Lowe et al., 2011; Mackintosh and Pretorius, 2011). Fusarium graminearum (teleomorph Gibberella zeae), which is found in the order of Hypocreales, is a very destructive pathogen of all types of grains ( ). Locally, F. graminearum co'exists and co'infects with other types of Fusarium. The greatest economic losses occur when floral fabrics become infected (Figure 7). This disease basically reduces the quality of grain rather than reduces grain yield, and leads to mycotoxin contaminated grain. Worldwide, all major cereal growing regions have reported a recurrence of the Fuzarium epidemics (Leonard and Bushnell, 2003). In the post-harvest period, if the contaminated grain is stored or transported with too high moisture content, the fungus increases after harvest and increases in mycotoxin levels (Magan et al., 2010). The floral tissues of hexaploid wheat are strongly contaminated with the Fusarium graminearum. This disease is often referred to as Fusarium Headache (FHB), Fusarium Ear Decline (FEB) or Head Scabies. Mycotoxin-contaminated grain is often unsafe for human consumption, animal feed or malt. In Europe, the United States and other regions, strict upper limits were introduced on specific levels of mycotoxin in grain and food (EC) 1881/2006; ». Fusarium graminearum produces several trichotetsin mycotoxins, the most important of which are deoxynivalinol (DON), acetylated derivatives of DON, nivalenol and phytoestrogen zeralene. DON binds to the protein peptiyl transferase in ribosome and inhibits the transfer of protein. Different natural isolates (term chemotypes) produce different types of mycotoxins (Alexander et al., 2011). Controlling flower fusarium infections remains problematic. In most cereals, the sources of resistance identified are only partially effective and are core based on THERs (Buerstmayr et al., 2009). Some azole fungicides are moderately effective, but spray coating and timing remain difficult. Minimizing sequential crops and plowing under any infected residues remain the best way to reduce disease pressure at the local level. Graminearum infection of non-viral species in crop rotation, such as soybeans and sugar beets, is increasingly reported. Excellent genetic, biochemical, molecular-genetic, genomic, transcriptomic and isolate collection resources currently exist for F. graminearum (, ,). The genome has no repetitive sequences and contains low levels genes, but there is a high level of polymorphism polymorphism Strains. When aligned with the genetic map, the two-speed gene is recognized with discrete areas of high recombination and high single-nucleotide polymorphisms (SNP) located near telomere and in the middle of four large chromosomes. Comparisons with the sequenced genomes of F. verticillioides and F. oxysporum f. sp. lycopersici indicate that the high diversity of sites in the F. graminearum genome was the result of events synthesis of ancestral chromosomes (Cuomo et al., 2007; Ma et al., 2010). Direct gene replacement of interest, chosen by marker using homologous recombination, is currently relatively simple. The production of mycotoxin DON contributes to the formation of diseases on wheat flower tissue (Proctor et al., 1995). In the absence of the DON, strong responses of the host defense are activated in rachis and hyphal colonization is limited to flower flowers (Jansen et al., 2005). DON synthesis is tightly regulated by at least three transcription factors: TRI6, TRI10 and TRI15. It is now recognized that another 160 pathogenic/virulence factors contribute to crop infection, most of which are post-infiltration (; Urban and Hammond-Cosak, 2012). A recent re-examination of the biology of the process of flower wheat infection showed that there is a significant phase of guileless infection, in which the gif extracellularly pass between the living host cells. High expression of TRI genes is detected on the coming front and decreases after that (Brown et al., 2010, 2011). Host cells only die in intracellular gyphool intrusion, and extensive degradation of plant cell walls is a relatively late process. These data show that F. graminearum uses a hidden approach to alleviate successful flower infections (Figure 8). Simplified three-article model of the infectious process Fusarium graminearum (Fg) through wheat rhea tissues. On the coming Hiphal front, mycotoxinol (DON) inhibits the transfer of protein, which significantly suppresses the surge of reactions of plant protection (pictured in blue). Once the gif enters the plant cells, the presence of released proteins and sugars and the high density of fungal gifs lead to a strong activation of plant protection responses. Later, at the center of the lesion (10 days), the cellular contents of fungal cells living deep in the dead cortical tissue are moved into the gif just below the epidermis of the rickish and asexual spores then occurring. Fusarium oxysporum Schlecht. is an ubiquitous pathogen transmitted through the soil that causes vascular withering on a wide range of plants. Characteristic symptoms of the disease include vascular browning, leaf epynasion, stunting, progressive withering, defoliation and plant death (Agrios, 2005). Complex F. oxysporum consists of different types of formae (f. sp.), which together total more than 100 different hosts, provoking serious losses in crops such as melon, tomatoes, cotton and banana, among others (Michielse and Rep, 2009). Fusarium oxysporum is also a new human pathogen that can cause invasive infections in immunocompromised patients (Nucci and Anaissie, 2007; O'Donnell et al, 2004). Unlike the surprisingly wide range of housewives at the species level, individual F. oxysporum isolates cause disease on only one or more plant species (Armstrong and Armstrong, 1981; Gordon and Martin, 1997). This dichotomy fascinated and puzzled generations of plant pathologists. Adding to the intrigue, phylogenetic studies show that various isolates of this form, infecting the same host plant, arose independently during evolution (O'Donnell et al., 1998). Since F. oxysporum has no known sexual cycle, the mechanism by which these new pathogenic lines appeared otherwise different genetic backgrounds has long remained elusive. Recently an analysis of the complete sequence of the tomato pathogenic genome F. oxysporum f. sp. lycopersici (Fol) has identified the presence of genomic regions of the line and LP, including four whole chromosomes that are absent in other types of Fusarium, such as grain pathogens F. graminearum and F. verticillioides (Ma et al., 2010). The transfer of two LS chromosomes from Fol to non-pathogenic isolate allowed it to cause disease in tomato plants. This suggests that horizontal transmission of small chromosomes may be a factor in the emergence of new pathogenic lines (Ma et al., 2010). Genome sequences from additional F. oxysporum isolates will provide invaluable tools for further study of this hypothesis. Dominant plant resistance genes (R) to different races of F. oxysporum have been identified in several cultures (Simons et al., 1998). The interaction between tomatoes and foul has been used to study the molecular basis of disease resistance and susceptibility (Houterman et al., 2008, 2009; Rep et al., 2004). These studies have led to the identification of a classical gene system with at least three genes of fungal auriulation, some of which can function as both projectors and R-based plant immunity suppressors (considered in Takken and Rep, 2010). The unusual ability of a single foal to isolate the disease in both tomato plants and immunosuppressive mice provides a unique model for studying the trans-kingdom pathogenicity in fungi (Ortoneda et al., 2004). Genetic analysis using targeted mutants has shown that the signaling components needed to infect tomato plants, such as mitogeneactive protein kinase (MAPK) or small Gyu protein, may be indispensable for virulence in mice (Di Pietro et al., 2001; Martinez-Rocha, et al., Ortoneda et al., 2004). Others, such as pH pH transcription factor PacC, necessary for virulence in the mouse model, but not in plants (Caracuel et al., 2003; Ortoneda et al., 2004). These results show that F. oxysporum uses fundamentally different infection strategies in plants and mammals. Further research relates to the common virulence mechanisms that are necessary for both types of host. Recent advances in understanding the genetic basis of pathogenicity in F. oxysporum include screens inserting into the width of the mutagenez genome (Lopez-Berges et al., 2009; Michelse et al., 2009a), leading, among other things, to the discovery of the main regulator of pathogenic development (Michielse et al., 2009b), the identification of the preserved pathway of nitrogen reaction, regulating invasive growth functions (Lopez Berges et al., 2010) and the characteristic of a new transembraneic sensor type of mucins (Perez-Zelion and DiPitro) , 2011). Future research in the F. oxysporum system will continue to provide new knowledge about the molecular mechanisms of fungal pathogenicity (Figure 9). (A) Fusarium oxysporum microcolidia (C) sprouting on the surface of the tomato root. Penetration occurs due to the directional growth of the infectious gif (IH) to the natural discovery between epidermal root cells (the place of penetration indicated by the arrow). (B) Fusarium oxysporum hypha grows in tomato root xylem vessel (from Di Pietro et al., 2001). Blumeria graminis is an erisifale (Takamatsu, 2004). This causes powdered mold herbs (Figure 10), including wheat and barley, which are among the leading crops worldwide (FaoStat, 2011). Grain mold infections reduce grain yields and need to be controlled to ensure an economically viable product. Control of Blumeria is achieved through the deployment of fungicides and disease-resistant plant varieties. These controls need to be constantly reviewed, updated and developed in response to fungicide resistance, changing regulatory limitations and the evolution of mold strains that can overcome host resistance. Barley leaves infected blumeria graminis f. sp hordei. Typical powdered pustules produced by mold colonies that grow on the outer surface of the host plant consist of hundreds of thousands of highly infectious asexual conids blown up by air currents to spread the disease. Epiphytic colonies feed on intracellular haustoria, which develop inside epidermal cells (see Figure 11). Erisifals have a wide range of host specificity, ranging from the broad polyphagia observed in many wild tendons (Ing, 1990) to the extremely narrow B. graminis ranges, where 'formae speciales' and hordei can only infect wheat or barley, respectively (Wyand and Brown, 2003). Other erythpoliss cause affect many other high-quality fruits and vegetables, including tomatoes, cucumbers, grapes and strawberries. Their biology, etiology and pathology are generally similar to biology, mold (Glawe, 2008). All powdered molds strictly oblige biotrophic pathogens: they are absolutely dependent on a living host plant. Epidemics are caused by a fast series of asexual cycles, which begin with the landing of air-drop conidia on the surface of the host. After a few minutes, the coneia sprouts. Blumenia, unlike other molds, produces the first short primary germ tube, designed for surface sensing (Wright et al., 2000; Yamaoka, et al., 2006). After a few hours from the conidium comes a secondary germ tube, a septum and differentiates an elongated, hooked uppressory, from which the peg penetrates through the cuticle of the host and the epidermatical cell wall. The peg develops a complex multi-hygitate haustoria, surrounded by a perigaustoric matrix and a specialized host membrane (Figure 11) (Hukelhoven and Panstruga, 2011). Like other mandatory biotrophic pathogens, the guztoria is dedicated to feeding and controlling host immunity and metabolism (Panstruga and Dodds, 2009). Plant-derived nutrients are transported to a gif growing on the surface of the plant. Within 3 days after vaccination condiidides develop from specialized cells of the foot and produce a mass of condiy: the same powder of these molds. At the end of the host growth season compatible strains mate and produce chasmothecia (Braun et al., 2002), which also act as recreational structures to survive adverse conditions. Bloomeria graminis f. sp. hordei haustorium. This haustorium was isolated by manually dissecting the epidermis of an infected sheet of barley and assimilation from the host cell wall with a protoplasting cocktail; it was spotted with a lectin (wheat agglutinin) associated with Alexa-288. The multi-digit structure is surrounded by the perigaustoric membrane of the host origin. Like other molds, this specialized membrane is continuous with the host plasma membrane, but has very different biochemical properties (Micali et al., 2011). In mold, the perihousetorial membrane is considered a gateway for nutrients and effectors. Bar, 10 microns. The genomes of barley and other powdered moulds are much larger than those of the related Ascomycota (Spanu et al., 2010). This is due to the extraordinary spread of retrotransposons. The expansion of the genome is accompanied, on the one hand, by the partial loss of genes involved in secondary metabolism, carbohydrate degradation and nitrate absorption, and on the other hand, by the mass distribution of genes that are projected to encode protein effectors. Currently, two classes of effector are recognized: ECA paralogical effectors for the Avrk1 and Avra10 genes, связанных с ретротранспонами (Ridout et al., al., Sakriston et al., 2009); and more conventional small protein secrets, which are further characterized as highly pedigree specific (Spanu et al., 2010). The importance of B. graminis, therefore, is the result of its constant and central role as a causal agent of disease of well-known cereals (Murray and Brennan, 2010), and because it is a model for the study of other mold and other mandatory biotrophic pathogens. Ascomycete Mycosphaerella graminicola (anamorph septoria tritici) is in the order of Dothideales and causes Septoria tritici blotch (STB) wheat disease (Figure 12). This is one of the major economic constraints on wheat productivity, especially in temperate growth regions (Orton et al., 2011). Mycospherella graminicular wheat infection begins with a hypnonic enlargement on the surface of the leaf and penetration through the stomat without differentiation of the apppressoria (Figure 13). A long period of non-cellless colonization (7 days) then follows, leading to the formation of necrotic leaf lesions within which mine. graminicola sporulates asexually (Kema et al., 1996; Keon et al., 2007). This last phase involves the transition to necrotrophic nutrition (Figure 13). Septoria tritici blotch (STB) is a wheat disease caused by the gramicolon Mikosfaerella. Model for wheat leaf infection Mycosphaerella graminicola. Early symptomatic colonization (7 days after the leaf vaccination, DPI) involves the release of protective and suppressive apoplastic effectors of plants (red and blue triangles) from slowly growing intercellular hyphais. After 7 days there is a death of the cells of the leaves and loss of permeability of the membrane, which allows the release of nutrients in the apoplast. Protective effects are off, although other potentially toxic effects (blue diamonds) can be produced. Extensive hypchal growth and asexual spores (pycnidia and pycnidiospore formation) are now supported in leafy lesions. Mikospheerella gramicol is an established model of the body for studying the dynamics and evolution of pathogen populations. Long-term data sets (from 1843 to 2003) have shown that STBs are affected by climate change, including those associated with the industrial revolution (Bearchell et al., 2005). It has also been reported that up to 90% of global genetic variations of this fungus may be present within a single contaminated wheat field (zhan et al., 2003). This level of genetic diversity arises from the heterothalyal reproductive system and the formation of ascosporas, which initiate epidemics every year (Chen and McDonald, 1996; Linde et al., 2002; Waalwijk et al., 2002). Most of the economic expenses incurred by My. graminicola arises indirectly from its rapid evolution in response to electoral pressures, including to wheat diseases and the sustainable use of fungicides. Examples of this the speed at which my. Graminicol populations evolved and spread a genetic mutation that was resistant to the strobilurine fungicide class (Fraaije et al., 2005), as well as the rapid evolution of the target cyp51 protein in response to the widespread use of specific fungical azoles (Cools et al., 2011). Mikosfeerella graminicola was also the subject of intensive genetics and genomics analyses. Genome sequences of isolate models, together with relatives collected from wild herbs, were published recently (Goodwin et al., 2011; Stukenbrock et al., 2011). These studies have identified the existence of 21 chromosomes, eight of which are all indispensable for plant infection and vary in number and structure between isolates (Goodwin et al., 2011; Stukenbrock et al., 2011; Wittenberg et al., 2009). This represents the largest number of dosed chromosomes so far reported in mushrooms (Wittenberg et al., 2009). Functional genomic analysis of plant infection has identified a number of genes important for signaling the transition to hygal growth and stomatal penetration (Orton et al., 2011). Subsequent post-penetration of stealth pathogenesis is supported by a reduced set of genes for cellular sten grading enzymes (Goodwin et al., 2011) and expression of high-level secret proteins, which inhibit the activation of plant defenses (Marshall et al., 2011). This initial evasion of plant protection reflects a mechanism more typical of mandatory biotrophs. However, what follows is the acute activation of plant protection involving the death of the host cell as the fungus moves to necrotrophic colonization (Keon et al., 2007; Rudd et al., 2008). This is an intriguing mechanism for future analysis (Figure 13), involving an initial ploy, followed by the subsequent hijacking of plant protection alarms (Deller et al., 2011), which can be separated by other members of the genus Mycosphaerella, which includes the largest number of plant-pathogenic fungi. Colletotrichum is one of the most common and important genera of plant-based pathogenic fungi. Virtually every crop grown around the world is subject to one or more types of colletotrichum. These fungi cause anthraconous spots and malformations of parts of air plants and rot after harvest. Members of this genus cause great losses to economically important crops, especially fruits, vegetables and ornamental crops. The damage caused by Colletotrichum spp., extends to important staple food crops, including bananas, cassava and sorghum, grown by natural farmers in developing countries in the tropics and subtropics. It is particularly successful as a post-harvest pathogen because the hidden infections that started before harvest do not become active until the fruit is preserved or Shelf. Up to 100% of stored fruit can be lost as a result of Colletotrichum disease (Prusky, 1996). Colletotrichum is an asexual genus classified in imperfect mushrooms. It belongs to the Coelomycetes, producing its conidia in acervuli. Despite significant changes, Collettotrichum's taxonom remains in a state of constant change. There are many uncertainties regarding the systematic fungal pathogens of this genus, and, depending on the criteria, the number of species can range from 29 to more than 700 (von Arx, 1957; Sutton, 1992). One of the most confusing species is C. gloeosporioides. For example, 594 types of colletorium have been reclassified by von Arks as synonyms of C. gloeosporioides (table 2). Table 2. The main view of Colletotrichum. Colletotrichum species host Lifestyle C. gloeosporioides and papaya/citrus/many other hosts of hemibiotrophy C. acutatum Strawberry/other Necrotrophy C. coccodes tomato gemibiotrophy C. graminicola Corn hemibiotrophy C. boninense Wide range host Hemibiotrophy C. trifolii Alfalfa Hemibiotrophy C. capsici Pepper/other hosts Necrotrophy C. destructivum Legumes/tobacco Hemibiotrophy C. crassipes Dryandra Hebiotrophy C. kahawae Coffee Gemibiotrophy C. orbiculare melon / cucumber Gemibiotrophy C. sublineolum Sortom Gemibiotrophy C. truncatum Legumes Hemibiotrophy C. musae Banana Hemiciotrophy C. fragariae Strawberry /other hosts C. Spinaceae Spinach Hemibiotrophy C. lindemuthianum Common As a result of its importance as a pathogen, its unique intracellular hemibiotrophic lifestyle and ease with which it can be culturally and manipulated, Colletotrichum has a long and outstanding history as an exemplary pathogen for the fundamental biochemical, physiological and genetic research. For example, the phenomenon of pathogenic variations (race/variety specificity) was first recognized in C. lindemuthianum (Barrus, 1911). The colletotrychum on beans was a model for many early studies on phytoalexins (review by Kuc, 1972). In the 1970s and 1990s, much of the work that established and characterized the phenomenon of systemic acquired/induced resistance (SAR) was done using the Colletotrichum-cucumber pathosystem (Durrant and Dong, 2004). Key genes of cyclic adenosinephate (CAMP), MAPK and RAS/small G-protein and calcium were cloned. The function of these genes, especially during conydia germination and the development of apppressoria, was characterized in several types of colletorium (Chen and Diekman review, 2004; Chen et al., 2006; Dickman and Yarden, 1999; Dickman et al., 1995; Takano et al., 2000). Most types of colletotrichums establish infection through a brief biotrophic phase associated with a large intracellular primary gif, although some species are described as subcutaneous, such as C. capsici. The fungus later switches to a destructive, necrotrophic phase associated with narrower secondary hyfams that ram throughout the host tissue (Figure 14). Molecular details that regulate the hemibiotrophic lifestyle (also known to occur in other fungal species, such as Magnaporthe) have long been of interest to phytopathologists. In particular, factors regulating the transition from biotrophy to necrotrophy are waiting to be identified. The recently completed sequence of C. graminicola (Vaillancourt et al., Department of Plant Pathology, University of Kentucky, Lexington, Kentucky), along with several other types of colletorichum in the pipeline, promises to increase our understanding of this important fungal phytopathogen. Transmission of an electronic micrograph showing hemiotrophic growth of colletothrichum destructivum during caupea infection. Notice the thick biotrophic vesicles (IV) infections after the penetration of apressoria. The host cell is still alive, and its plasma membrane can be seen around the gif. Subsequently, thinner necrophemic penetrating gif (PH) degrades tissue while growing inside the cell. A, apressory; C, conidium. Photo courtesy of Dr. Richard O'Connell (Department of Plant Microbe Interaction, Max Planck Plant Research Institute, Cologne. Corn smut is not an economically important or destructive disease. Thus, Ustilago Maydis did not get into the top 10 for this reason. Although its symptoms on corn can be quite dramatic (Figure 15, center), in most cases infections remain local, do not spread and therefore are not associated with serious losses in maize yield. On the contrary, farmers in Mexico infect corn artificially to collect infected cobs for cooking Huitlacoche, a traditional dish popular in pre-Hispanic times. The stages of development of Ustilago maydis, tools and symptoms of the disease. (A) Haploid cells show promising growth. (B) Compatible haploid strains U. maydis, express cytoplasmic red fluorescent protein (RFP) (red) and green fluorescent protein (GFP) (green) (green) under the composite mat protector and produce filament dicarion (yellow). (C) The solo-pathogenic strain, which expresses the cytoplasmic RFP from the composite promoter and the appressorial marker gene fused into triple GFP, effectively forms an apressory on the hydrophobic surface, after stimulation with hydroxy fatty acids. (D) Macroscopic symptoms of U. Maydis disease on a corn leaf 12 days after infection (left) and fungal gifs in tumor tissues 10 days after infection (right) are visualized with confocal fungal gifs painted WGA-AF488 (green); the walls of plant cells are colored with iodide propidium (red). (E) I'm not an example, an example, Gene chips allow research into the expression of the genome and width. (F) Visualization of feacin through LifeAct-YFP in beginner cells. (G) Highly effective homologous recombination is used to replace genes using hygromycin resistance (HygR), resistance to nourseottricin (NatR), carboxin resistance (CbxR) or phleomycin resistance (PhleoR) as the dominant markers chosen. (H) The Phylogenetic tree of W. Maidis and his next of kin. The figures were kindly provided by Patrick Berndt and Rolf Russer (U. Maydis Symptoms of disease in the infected corn cob, center) as at the Max Planck Institute for Ground Microbiology. Please note that their permission to use these numbers has been obtained. What are the attractions of this fungus and why it became a model for biotrophic, plant-pathogenic basidiomycetes? Ustilago maydis can be grown in culture in certain media, haploid fungus and growing budding (Figure 15A) and forms compact colonies on plates that can be replica coated. These were actually some of the reasons for choosing this fungus for seeded early studies on homologous recombination (Holliday, 2004). For host colonization and the development of symptoms, corn seedlings can be infected. Symptoms can develop on all above-ground parts of corn plants within 5-6 days (Figure 15D) and the infection cycle ends after about 2 weeks. Typical of a smut fungus is that pathogenic development equals sexual development, and mating and formation of a dikaryotic filament is absolutely necessary. These steps can be replicated in the laboratory (Figure 15B) depending on the formation of apressor on the corresponding hydrophobic surfaces (Figure 15C). The proteins that control these events are known: pheromones and pheromone receptors, as well as the hetonodimerical transcription factor formed after cell merging, which causes a regulatory cascade (Brefort et al., 2009; Heimel et al., 2010, b). This knowledge has allowed the development of haploid solopathogenic strains that cause diseases without the need for partner mating (B'lker et al., 1995; Kuemper, et al., 2006). Such strains allow forward genetic screens and significantly reduce the work in reverse approaches of genetics. Homologated recombination is surprisingly effective (Kuemper, 2004) and uses four dominant select markers (Figure 15G; Bass and Steinberg, 2004). Tools include adjustable promoters to study basic genes and various coloring techniques, to visualize fungus during biotrophic growth (Figure 15D), and fluorescent proteins for live cell imaging of gene expression and visualization of subcellular structures (Figure 15F) are available (Bemer et al., 2009; Mendoza-Mendoza et al., 2009; Steinberg and Perez Martin, Since 2006, a sequence of the genome with manual annotation and curatorial is available (K'mmper et al., 2006; 2006; The genome is skinny and contains little repetitive DNA. Transcription profiles (Figure 15E) were created for the most important stages of fungal and plant reactions (available through GeneExpressionOmnibus: . This spurred back-to-back approaches to genetics and allowed us to identify cluster genes encoding the secret effects that play a crucial role during host colonization, and determine which tissues might be infected (Doehlemann et al., 2009, 2011; Koemper, et al., 2006; Skibbe et al., 2010). It also became apparent from genome analysis that U. maydis is more closely related to humans than novice yeast, and numerous proteins are shared only by U. maydis and Homo sapiens. These include proteins involved in the basic principles of long-distance transport, mitosis, motor organization of microtubules and homologous recombination. Thus, Ustilago Maidis is the ideal place to study such processes (Banuett et al., 2008; Holloman, 2011; Steinberg and Perez Martin, 2008). Where is this system going? This will create a hierarchy of effector actions during plant colonization, give an idea of fungal nutrition during plant colonization (Eichhorn et al., 2006; Wahl et al., 2010) and serve as a plan of comparative approaches (Schirawski et al., 2010), which are likely to reveal an understanding of the evolution of the genome and the specialization of the host. Unlike most other pathogens on this Top 10 list, flax rust is better known than the infamous. Although it was originally studied as a pathogen affecting the linen and flax industry, its main influence on food and fiber production was (and comes) from its role as an exemplary system, providing insight into the molecular basis of plant immunity. Благодаря новаторским генетическим исследованиям (рис. 16) патогенности различных физиологических рас патогена и устойчивости и восприимчивости к ржавчине в лене, H.H. Flor заметил, что существует определенная связь между каждым геном, определяющим патогенность в ржавчине (Avr) генов и соответствующими генами (R) в принимающей определяющей резистентности (Flor, 1956; Лоуренс, 1988; Лоуренс и др., 2007). This became known as the gene link, which provided pathologists and plant breeders with a logical basis for harmonizing the breeding process of other crop species for resistance to pathogens. The observations also provided insights into the breeders' experience that individual resistance genes deployed in large areas are often broken by mutations of one relevant auriulation gene or genetic re-range during sexual reproduction of previously hidden recessive sexually active alleles for the production of homoygo offspring In practical terms, this classical genetic knowledge also underpins the approach to stronger resistance by pyramiding several resistance genes in a single genotype of crop species. The gene gene hypothesis has also given rise to the assumption that resistance genes encode receptor proteins that detect the presence of specific auriulation proteins in the pathogen, and the resulting recognition event, which generates host resistance, the basis for the development of modern knowledge of the basis of plant immunity. The cycle of life out of flax rust, Melampsora lini. Genetic analysis of flax rust depends on the ability to replicate all stages of the life cycle under controlled conditions for the production of independent and oververted offspring from flax rust isolates, and is complicated by rust, which is a mandatory biotrophic requiring all manipulations to be undertaken on a live plant-host. The flax rust system was among the first three systems to provide cloned resistance genes and the identification of a new class of immune receptors, cytoplasmic nucleotide binding leukine-rich proteins (NB-LRR), whose specific members ensured plant resistance to fungi, oomycetes, bacteria, viruses, nematodes, sucking insects and parasitic plants(Ellis). The same protein group was subsequently identified in animals as part of the congenital immune system. The study of alleles from L and chimeric genes between alleles expressed in transgenic flax gave the first indication that the specificity of the interactions of genes and genes was determined by the sequence of change in the LRR domain of receptor proteins, and that the likely origin of new specific features of resistance in nature is the result of point mutations, re-assortment of mutations, as well as duplication and removal of LRR receptors. , 2007). The intracellular nature of flax resistance proteins implied that Avr (effector) proteins were detected by R proteins in host cells. This was subsequently confirmed by the cloning of several Avr genes from flax rust, which encode various proteins, is released from rust and were taken into the plant's cell through the mediation of absorption signals located near the N'terminus protein Avr (Rafiqi et al., 2010). It has been shown that the molecular basis for gene recognition relies on the specific and direct interaction of flax R proteins and the corresponding Avr proteins. Only those R and Avr proteins that interacted in yeast are two-hybrid analyses of the induced reaction of plant resistance when jointly expressed in plants (Wang et al., 2007). The study of the flax rust fungus and its interaction with the host is now set for further progress after Agrobacterium conversion systems for this mandatory biotrophy (Lawrence et al, et al., (Figure 16). The authors would like to thank Dr. Diana Hurd for disseminating information on the vote and comparing the results of the vote. JALVK recognizes Marcela Estegio (University of Chile, Santiago, Chile), Erzjubet Sundor (University of Debrecen, Hungary), Jan Sukhoi (CSIRO, Urrbrae, Australia), Dirk van Eden (Terason Ltd, Wellington, South Africa), Peter Schreier (Cologne, Germany), Ernst Waltering (University of Wageningen) KECC and JJR received grants from the Research Council Agrios, G.N. (2005) Plant Pathology. St. Louis, MO: Academic press. Alexander, N.J., McCormick, S.P., Waalwijk, C., van der Lee, T. and Proctor, R.H. (2011) Genetic basis for 3-ADON and 15-ADON trichoteneken chemotypes in Fusarium. Fungal Genetic. Biol. 48, 485- 495. Amsel, D., Cuomo, C.A., van Kahn, D.A.L., Viaud, M., Benito, E.P., Kulu, A., Coutinho, P.M., De Vries, R.P., Dyer, P.S., Filler, S., Fournier, E., Podt, L., Khan, M. Lapalou, N., Plummer, K.M., Pradier, J.M., Kvevilon, E., Sharon, A., Simon, A., Ten, A., Tudchinsky, B., Tudczynski,., , M. Anthward, V. Beaver, R.E., Beffa, R., Benoit, , Chen, S., Choker, M., Collemare, J., Cotton,., Danchin, E.G., Da Silva, K. Goutier, A., Giro, K, Giro, T, Gonzalez, C. Grossetet, S., Guldener, U., Henrisat, B. Howlett, B. K, Kretschmer, M., Lappartient, A., Leroch, M., Lewis, K. Mauseli, E., Neuvelis, K., , M., Poulin, D., Pusero, N., Kesneville, H., Raskle, K., Schumacher, D., Sessions, B., Sexton, A. , Soanes, D.M., Talbot, N.J., Templeton, M., Yandava, C., Yarden, O., Tseng, S., Rollins, J.A., Lebrun, M.H. and Dickman, M. (2011) Genomic analysis of necrotrophic fungal pathogens Sclerniaoti s. PLo. 7, e1002230. Armstrong, G.M. and Armstrong, J.K. (1981) Formae specialties and races Fusarium oxyspor causes withering diseases. In: Fusarium: Diseases, Biology and Taxonomium (R. Cook, ed.), p. 391- 399. University Park, Pennsylvania: Penn State University Press Office. von Arks, J.A. (1957) Die arten der gattung Colletotrichum Cda. Phytopathology No. 29, 413- 468. van Baarlen, P., Woltering, E.J., Staats, M. and van Kahn, J.A.L. (2007) Histochemical and genetic analysis of the host and non-host interactions of Arabidopsis with three types of botites: an important role for controlling cell death. Mole. Pathol Plant. 8, 41– 54. Banuett, F., Kintanilla, R.H. Jr. and Reynaga-Pena, K.G. (2008) Cell Polarity Mechanism, Cell Morphogenesis and Cytoskkelet in Basidiomyce UsteTilago maydis - genome sequencing study. Fungal Genetic. Biol. (Supple. 1), S3- S14. Barrus, M.F. (1911) Variation of bean varieties in their susceptibility to anthrax. Phytopathology, 1, 190- 195. Bass, C.W. and Steinberg, G. (2004) Ustilago maydis, a model system for analyzing the molecular basis of fungal pathogenicity. Mole. Plant. It's Patol. 5, 83– 92. Bearchell, S.J., Fraaije, B.A., Shaw, M.W. and Fitt, B.D.L. (2005) Wheat Archive links the long-term fungal dynamics of the population pathogen to air pollution. Proc. Natl. Acad. Sci. United States, 102, 5438- 5442. Bemer, K., Rupp, K. and Bulker, M. (2009) The Germ Center of the Don3 Kinase causes a dynamic permutation of the structures of the higher order septine during cytokinesis in Ustiago Maidis. Mole. A microbiol. 74, 1484– 1496. Bulker, M., Genin, S., Lemler, K. and Kahmann, R. (1995) Genetic regulation of mating and dimorphism in Ustilago Maidis. Kang. Bot. 73, 320– 325. Bolton, M.D., Colmer, J.A. and Garvin, D.F. (2008) Wheat leaf rust caused by Puccinia triticina. Mole. Pathol Plant. 9, 563– 575. Brown, USA, Cook, R.T.A., Inman, A.J. and Sheen, H.D. (2002) Taxonomium powdered mold fungi. In: Powder Mildew: Comprehensive Treatise (R.R. Belanger, W.R. Bushnell, A.D. Dick and T.L.W. Carver, eds), p. 13-55. St Paul's, MN: APS Press. Brefort, T., Dolemann, G. Mendoza-Mendoza, A., Reissmann, S., Jamei, A. and Kahmann, R. (2009) Ustyago Maidis as a pathogen. Ana. Reverend Fitopathol. 47, 423– 445. Brown, North As, Urban, M., Van de Ming, A.M.L. and Hammond-Kosak, K.E. (2010) Infectious Biology of the Graminearum Fusarium: Determining the pathways of spikes for colonizing spikes in wheat ears. Fungal biol. 114, 535- 571. Brown, N.A., Bass, K., Baldwin, T.K., Chen, H., Massot, F., Carion, P.V.K., Urban, M., van de Ming, A. and Hammond-Cosac, K.E. (2011) Characterization of the fusarium of the gramiorum-wheat flower interaction. J. Pathogens e626345, 9 pages. Brian, G.T., Wu, C.S., Farrall, L, Jia, J., Hershey, H.P., McAdams, S.A., Faulk, K.N., Donaldson, G.K., Tancini, R. and Valent, B. (2000) One amino acid difference distinguishes resistant and sensitive cell plants, 12, 2033- 2046. Buerstmayr, H., Pan, T. and Anderson, J.A. (2009) TTL mapping and marker-assisted choice for Fusarium head decline resistance in wheat: review. Plant breed. 128, 1– 26. Kantu, D., Govindarajulu, M., Kozik, A. Wang, M., Chen, H., Kojima, K.K., Jurka, D., Michelmore, R.V. and Dubkovskiy, J. (2011) Next-generation sequencing provides quick access to the Puccinia genome striiformis f. sp. tritici causing wheat sequencing. PLoS ONE, 6, e24230. Caracuel, S., Roncero, M.I., Espeso, E.A., Gonzalez-Verdejo, H.I., Garcia-Macieira, F.I. and Di Pietro, A. (2003) The PacC pH transcription factor controls virulence in the plant pathogen Fusarium Mole. A microbiol. 48, 765– 779. Chao, C.C.T. and Ellingboe, A.H. (1991) Choice for mating competence in Magnaporthe grisea pathogenic rice. Kang. Bot. 69, 2130– 2134. Chen, C. and Dickman, M.B. (2004) Dominant Active Rac and dominant negative Rac return the dominant active Ras phenotype in colletotrichum trifolii on separate signaling pathways. Mole. A microbiol. 51, 1493– 1507. Chen, C., Ha, Y., Ming, J., Memmott, S.D. and Dickman, M.B. (2006) Cdc42 is required for proper growth and development in the fungal pathogen Collettotrichum trifolii. Eukaryotes. Cellular, 5, 155- 166. Chen, R.S. and MacDonald, B.A. (1996) Sexual reproduction plays an important role in the genetic structure of mycosphaerella graminicola fungus populations. Genetics, 142, 1119- 1127. Cools, HJ, Mullins, J.G.L., Fraaije, B.A., Parker, J.E., Kelly, D.E., Lucas, J.A. and Kelly, S.L. (2011) Influence of the newly emerged sterol 14 alpha-demethylase (CYP51) variants of Mycophaerella graminicola on the azoal finghaler sensitivity. Apple. Environ. A microbiol. 77, 3830– 3837. Couch, B.C., Fudal, I., Lebrun, M.H., Tarro, D., Valent, B., Van Kim,., Nottegem, J.L. and Con, LM (2005) Origin of host populations and specific populations of the explosive pathogen Magnaporthe oryzae in domestication followed by the expansion of pandemic clones. Genetics, 170, 613-630. Cuomo, C.A., Guldener, U., Xi, JR, Trail, F. F, Turgeon, B.G., Di Pietro, A., Walton, J.D., Ma, L.J., Baker, S.E., Rep, M., Adam, G., Antonio, D., Baldwin, T., Calvo, S., J.L., DeCaprio, J., Gayle, L.R., Gnerre, S., Goswami, R.S., Hammond-Kosak, C.E., Harris, L.J., Hillburn, C.C., C.C., Magnuson, J.K., Mannhaupt, G., Mouseeli, M. , R., Mulbauer, G, Munsterkotter, M., Nelson, D. O'Donnell, C. Ci, W., Kesneville, H., Roncero, M.I., Seong, K.Y., Tetko, I.V., Urban, M., Waalwijk, C., Ward, T.J., Yao, J., Birren, B.W. and Kistler, H.C. (2007) Genome Gramoor Fusar shows the connection between localized polymorphism and the pathogen. Science, 317, 1400-1402. Dean, R.A., Talbot, New Jersey, Ebbol, D.J., Farman, M.L., Mitchell, T.K., Orbach, M.J., Tone, M., Kulkarni, R., Xy, J.R., Pan, H., Reed, New Jersey, Lee, J.H., Carbon, I. D,, O, J.Y., Donofrio, N., Jeong, D.S., Soanes, D.M., Jonovic, S., Kolomiets, E., Rechmayer, K., Lee, W., Harding, , M.H., Boehner, H., Coughlan, S., Butler, D., Kalvo, , R., Purcell, S, Nusbaum, K., Galagan, J.E. and Biren, B.V. (2005) Genomic sequence of rice mushroom explosion. Nature, 434, 980- 986. Deller, S., Hammond-Kosak, C.E. and Rudd, J.J. (2011) Complex interactions between host immunity and non-biotrophic fungal pathogens of wheat leaves. J. Plant Physio. 168, 63-71. Di Pietro, A., F.I., Meglecz, E. and Roncero, M.I. (2001) Kinase of vascular withering fungus Fusarium oxysporum is essential for root penetration and pathogenesis. Mole. A microbiol. 39, 1140– 1152. Dickman, M.B. and Yarden, O. (1999) Protein kinases and phosphates in filamentous mushrooms. Fungal Genetic. Biol. 26, 99- 117. Dickman, M.B., Buhr, T.L., Warwar, V., Truesdell, G. and Huang, C. (1995) Molecular signals in the early stages of alpha anthrax. Kang. Bot. 73, 1169– 1177. Doehlemann, G., van der Linde, K., Assmann, D., Schwambach, D., Hof, A., Mohanti, A., Jackson, D. and Kahmann, R. (2009) Pep1, the secret protein effector Ustilago maydis, is required for the successful invasion of plant cells. PLoS Patog. 5, e1000290. Doehlemann, G., Reissmann, S., Assmann, D., Fleckenstein, M. and Kahmann, R. (2011) Two related genes encoding a secret effector and membrane protein are needed for tumor formation caused by Ustyalgo. Mole. A microbiol. 81, 751– 766. 2011 June 22. doi: 10.1111/j.1365-2958.2011.07728.x. Donofrio, N.M., Oh, Y., Lundy, R., Pan, H., Brown, D.E., Jeong, J.S., Coughlan, S., Mitchell, T.K. and Dean, R.A. (2006) Global gene expression during nitrogen starvation in rice explosion fungus, Magnaporthe grisea. Fungal Genetic. Biol. 43, 605- 617. Duplessis, S., Cuomo, C.A., Lin, J.K., Aerts, A., Tisserant, E., Veneo-Furry, C. K, Jolie, D.L., Hackard, S. Amsel, D., Cantarel, B.L., Chiu, R. Coutinho, P.M., Fo, N., Field, M., Frey,., Gelhay, E. Goldberg, J., Graberr, M.G., Kodira, K.D., Kohler, A., Kees, W., Lindqvist, E.A., E, Murat, K, Pangilinan, D.L., Park, R., Pearson, M., Kesneville, H., Ruhier, N., Laktikumar, S., Salamov, A.A., Shmuz, D., Selles, B. Shapiro, H., Tangui,., Tuskan, G.A.,., van de Pear, J., Rousey,., Ellis, D.G., Dodds, P.N., Shane, J.E., Jun, S., Hamelin, R.K., Grigoriev, I.V., Szabo, L.J. and Martin, F. (2011) Mandatory Biotrophy features a 10-part analysis of rust. Proc. Natl. Acad. Sci. United States, 108, 9166- 9171. DOI:10.1073/ pnas.1019315108. Durrant, W.E. and Dong, X. (2004) System gained resistance. Ana. Reverend Fitopathol. 42, 185– 209. Eichhorn, H., Persing, F., Winterberg, B, Schiravaski, D., Koemper, D., Muller,. and Kahmann, R. (2006) The ferrossidation/permeation iron absorption system is necessary for virulence in Ustylago Maidis. Cell Plant, 18, 3332- 3345. Ellis, J.G., Dodds, P.N. and Lawrence, GJ (2007) Flax Rust Resistance Gene Specificity is based on direct resistance-auriulation of protein interaction. Ana. Reverend Fitopathol. 45, 12.1– 12.18. Estegio, M. Oger, D., Ramos, C., Walker, A.S., Munoz, G. and Filler, S. (2009) Botritos en uva de mesa de exportaci'n: Sitasion actual de sensibilidad fungicidas en Chile. Reverend Akosex, 103, 16-23. FaoStat (2011) Best Productions -World (Total)-2009. Available on February 2012. Farman, M., Tosa, J., Nitta, N., Leong, S. and Leong, S. (1996) MAGGY, retrotransposon in the genome of the mushroom explosion rice, Magnaporthe grisea. Mole. General Janet. 251, 665. Flood, J.L. (2010) Importance of Plant Health for Food Security. Food Sec. 2, 215- 231. Flor, H.H. (1956) Additional gene systems in linen and flax rust. Adv. A genetics. 8, 29– 54. Fraaije, B.A., Cools, H.J., Fountaine, J., Lovell, D.J., Motteram, J., West, J.S. and Lucas, J.A. (2005) The role of ascospores in the further distribution of cytochrome alleles (G143A) in the field populations of Mikosferella. Phytopathology, 95, 933- 941. Glawe, D.A. (2008) Powdered Mold: An overview of the most famous (yet poorly known) plant pathogens in the world. Ana. Reverend Fitopathol. 46, 27– 51. Goellner, K., Loehrer, M., Langenbach, C., Conrath, U., Koch, E. and Schaffrath, U. (2010) Phakopsora pachyrhizi, causal agent of Asian soybean rust. Mole. Pathol Plant. 11, 169– 177. Gonzalez, M. Puyol, M., Me month, J.P., Gonzalez-Garcia, W., Bolton, D.J. and Borras Hidalgo, O. (2011) Tobacco Leaf Stain and Root Rot, caused by Risoctonia Solani Kuhn. Mole. Pathol Plant. 12, 209– 216. Goodwin, S.B., Ben M'Barek, S., Dillon, B. Wittenberg, A.H.J., Crane, C.F., Hahne, J.K., Foster, A.J., Van der Lee, T.J., Grimwood, J. Aerts, A., Antonio, J., Bailey, A. D, Bristow, J. van der Burgt, A., Canto-Canche, B., Churchill, A.K.L., Conde-Ferraes, L., Coolce, J.J., Coutinho, P.M., H.H.,., De Wit,., Donzelli, B. van de Gest, H.C. R.C.H.D., Hammond-Kosak, C.E., Henrissat, B., Kilian, A., Kobayashi, A.K., Kukmann, E., Kurmetiz J. Kuzniar, A., Lindqvist, E. Lombard, W., Maliepaard, K., Martins, N., Mehraby, R., Nap, J.P.H., Ponomarenko, A., Rudd, J.D., Salamov, A. Schuten, J.J., Shapiro, H., Stergiopoulos, I., Torriani, S.F.F., Tu, H., de Vries, R.P., Waalwijk, K., Ware, S.B., Wibenga, A., Tswiers, L.H., Oliver, R.P., Grigoriev, I.V. , G.H.J. (2011) The complete genome of the fungal wheat pathogen Mycosphaerella graminicola shows a dispensed structure, chromosomal plastic. PLoS Genet. 7, e1002070. doi:10.1371/journal.pgen.1002070. Gordon, T.R. and Martin, R.D. (1997) Evolutionary Biology of Oxyspor Fusarium. Ana. Reverend Fitopathol. 35, 111– 128. Gouda, M., Vienna, R.K., Ragupathia, M, Nobuta, K, Lee, H., Wing, R. Stahlberg, E, Cooglanu, S., Haudenschild, C.D., Dean, R., Nachm, B.H., Meyers, B.C. and Wang, G.L. (2006) Deep and comparative analysis of mitzelia and the apppressory transcriptomy of Magnahes grisea using MPSS BMCY Genomes, 7100. Hamer, J.E., Farrall, L., Orbach, M.J., Valent, B. and Chumley, F.G. The host of species-specific preservation of the family of repetitive DNA sequences in the genome of fungal pathogen plants. Proc. Natl. Acad. Sci. United States 86, 9981- 9985. Heimel, K., Scherer, M., Schuler, D. and Kuemper, J. (2010a) Protein Ustilago maydis Clp1 organizes pheromone and bi-dependent signaling pathways to coordinate the cell cycle and pathogenic development. Cell Plant, 22, 2908- 2922. Heimel, K., Scherer, M., Vranes, M., Val, R., Potiratana, K., Schuler, D., Wincon, W., Finkernagel, F., Flore Parra, I. and Kyo, D. (2010b) Transcription factor Rbf1 is the main regulator for the bub-brago type, controlled by the pathogen in Uppero. PLoS Patog. 6, e1001035. Hodson, D.P. (2011) Boundary Change: Problems for Rust Monitoring. Eufitic, 179, 93-104. Holliday, R. (2004) Early research of recombination and DNA repair in Ustyago Maydis. DNA repair, 3, 671- 682. Holloman, W.K. (2011) Unravelling the BRCA2 mechanism in homologous recombination. Nat Structures. Mole. Biol. 18, 748- 754. Hauterman, P.M., Cornelissen, B.J. and Rep, M. (2008) Suppression of immunity based on genetic resistance of fungus plants. PLoS Patog. 4, e1000061. Hurtman, P.M., Ma, L., Van Ooijen, G., De Vroomen, M.J., Cornelissen, B.J.C., Takken, F.L.W. and Rep, M. (2009) Effect protein Avr2 from xylem colonization of Fusar oxium fungus activates tomato protein I'2 intracell. Plant J. 58, 970- 978. Hormuller, M.S., Serenson, K.K., Walter, S. and Justesen, A.F. (2011) Variety Puccinia striiformis on cereals and herbs. Ana. Reverend Fitopathol. 49, 197– 217. DOI: 10.1146/annurev-phyto-072910-095230. Howard, RJ and Valent, B. (1996) Violation and input: host penetration of fungal rice exploding pathogen Magnaporthe grisea. Ana. Reverend Microbiol. 50, 419– 512. Hyukelhoven, R. and Panstruga, R. (2011) Cellular biology of the interaction of plant powdered mold. Carr. It's an opin. Plant Biol. 14, 738- 746. Ikeda, K.I., Nakayasiki, H., Kataoka, T., Tamba, H., Hashimoto, J., Tosa, J. and Mayama, S. (2002) Repeated turning mutation (RIP) in Magnaport grisea: effects on her sexual cycle in the context of the natural field. Mole. A microbiol. 45, 1355. Ing, B. (1990) Introduction to British Powdered Mold-2. Mycologist, 4, 88- 90. Jansen, K., von Wettstein, D., Schafer, W., Kogel, K.H., Felk, A. and Mayer, F.J. (2005) Infectious patterns in barley and wheat spikes grafted by the genome of diesel and trihodien, disrupted the fusarium graminum. Proc. Natl. Acad. Sci. United States, 102, 16,892- 16,897. Jeong, J., Park, C-Y, Chi, M.H., Choi, J., Park, D., Ro, H.S., Kim, S., Go, D., Yu, S., Choi, D., Park, J.Y., I, M., Yang, S., Kwon, M.D., Khan, S.S., Kim, B.R., Hang, Park, Park, B. Jun, K, Kong, S, Karunakaran, M, O. Park, J., Kang, S, Choi, W.B., Kang, S. and Lee, Y'H. (2007) Genome wide of functional analysis of pathogenic genes in rice explosion fungus. Nat Genet. 39, 561– 565. Jia, Y., McAdams, S.A., Brian, G.T., Hershey, H.P. and Valent, B. (2000) Direct interaction of the resistance gene and avirulence gene products lends resistance to rice explosion. EMBO J. 19, 4004- 4014. Jean, Y. (2011) The role of the Berberian spp. as alternative hosts in the creation of new races Puccinia graminis and P. striiformis. Eufitic, 179, 105- 108. Jean, Y., Szabo, LA and Carson, M. (2010) The age-old mystery of the life story of Puccinia striiformis solved with the definition of Berberis spp. as an alternative host. Phytopathology, 100, 432- 435. deJong, JC, McCormack, B.J., Smirnov, N. and Talbot, New Jersey (1997) Glycerol generates turgor in a rice blast. Nature, 389, 244- 245. Kumper, J. (2004) PCR-based system for a highly effective generation of mutant gene replacement in Ustilago maydis. Mole. A genetics. Genomics, 271, 103-110. Kjper, J. Kahmann, R, Bolker, M., Ma, L.D., Brefort, T. Saville, B.J., Banuett, F, Kronstad, J.V., Gold, S.E., Muller, O., Perlin, M.H., Vosten, H.A., de Vries, R. Ruiz-Herrera, D., Reynaga-Pena, K.G., Snetselaar, K., McCann, M., Perez Martin, D. Feldbrugge, M., Bass, K.W., Steinberg, G., J. , Farman, M., Staic, J.E., Sentandreou, R., Gonzalez-Prieto, J.M., Kennell, J.K., Molina, L. Shirawski, D., Mendoza, Mendoza, A., Graylinger, D., Munch, K., Rossel, N., Scherer, M. W, Fuchs, W., Sandrock, B. Meng, S., Ho, E.K., Cahill, M.J., Boyce, C.J., Klose, D.J., Klosterman, S.J., Deelstra, Lee, W., Sanchez Alonso,., Schreier, P.H., Hauser-Khan, I. , G., Voss, H., Schluter, T., Margolis, D., Platt, D., Swimmer, K., Gnirka, A., Chen, F., Vysotsky, W., Mannhaupt, G. Guldener, W., Munstercotter, M., Haase, D., Esterhend, M., Mews, H.W., Mauseli, E.W., DeCaprio, D. Wade, K.M., Butler, D.Y., J. and Bleiren, B.W. (2006) Research from the genome of the biotrophic fungal plant pathogen Ustylago maydis. Nature, 444, 97- 101. Kema, G.H.J., Yu, D.S., Rykenberg, F.H.J., Shaw, M.W. and Baayen, R.P. (1996) Histology pathogenesis Mikosfarella gramicol in wheat. Phytopathology, 86, 777- 786. Keon, J., Antoniw, J., Carzaniga, R., Deller, S., Ward, J.L., Baker, J.M., Beale, M.H., Hammond-Kosak, K. and Rudd, J.J. (2007) Transcription Adaptation Mycosphaerella graminicola programmed cell death of his receptive wheat host. Mole. Plant-Microbe Interaction. 20, 178– 193. Khush, G.S. (2005) What it will take to feed 5.0 billion rice consumers in 2030. Plant Mole. Biol. 59, 1- 6. Colmer, J.A., Gene, Y. and Long, D.L. (2007) leaf and rust stalk in the United States. Aust. J. Agric. Res. 58, 631- 638. Kretschmer, M., Leroch, M., Mosbach, A., Walker, A.S., Filler, S., Mernke, D., Schunwick, H., Pradieu, J.M., Leroux,., de Vaard, M.A. and Khan, M. (2009) Fungicide Evolution and The Fundamental Molecular Development of The Deep. PLoS Patog. 5, e1000696. Kuc, J. (1972) Phytoalexins. Ana. Reverend Fitopathol. 10, 207– 232. Lawrence, GJ (1988) Melampsora lini, flax and flax rust. Adv. Pathol plant. 6, 313– 331. Lawrence, GJ, Dodds, P.N. and Ellis, J.G. (2007) Profile pathogen: rust flax and linen, caused by Melampsora lini. Mole. Pathol Plant. 8, 349– 364. Lawrence, GJ, Dodds, P.N. and Ellis, J.G. (2010) Conversion of flax rust fungus, Melampsora lini: choice through silencing the gene of auriulation. Plant J. 61, 364- 369. Lee, Y. and Dean, R. (1993) CAMP regulates the formation of the structure of infection in the plant-pathogenic fungus Magnaporthe grisea. Cell Plant, 5, 693-700. Lee, Y.H. and Dean, R.A. (1994) Hydrophobic contact surface causes the formation of apressory in Magnaporthe grisea. FEMS microbiol. It's a whip. 115, 71– 75. Leonard, KJ and Bushnell, W.R. (2003) Fusarium Head Blight Wheat and Barley. Minnesota, MN: American Phytopathological Society. Leonard, KJ and Szabo, L.S. (2005) Stem rust of small grains and herbs caused by Puccinia graminis. Mole. Pathol Plant. 6, 99– 111. Leroych, M., Kretschmer, M. and Khan, M. (2011) Phenotypes of Botrytis cinerea fungicide resistance are isolated from commercial vineyards in southwest Germany. D. Fitopathol. 159, 63– 65. Leung, H., Borromeo, E.S., Bernardo, M.A. and Notteghem, J.L. (1988) Genetic analysis of virulence in the mushroom explosion of The Grill of Magnaporthe grisea. Phytopathology, 78, 1227- 1233. Leung, H., Lehtinen, USA, Karjalainen, R., Skinner, D., Tuli,., Leong, S. and Ellingbo, A. (1990) Conversion of the rice mushroom Magnaporthe grisea into hygromycin B resistance. Carr. A genetics. 17, 409. Linde, C.C., Chang, J. and MacDonald, B.A. (2002) Population structure Mycosphaerella graminicola: from defeats to continents. Phytopathology, 92, 946- 955. Loegering, W.W. (1984) Genetics Pathogen Association. In: Cereal rust, Vol. I, Origin, Specifics, Structure and Physiology (W.R. Bushnell and A.P. Roelfs, eds), 165-192. Orlando, Florida: Academic press. Lopez-Berges, M.S., Di Pietro, A., Dabussi, M.Y., Wahab, H.A., Vasnier, C., Roncero, M.I., Dufresne, M. and Hera, K. (2009) Identification of virulence genes in Fusarium oxysporum f. lycopersici large transpokers. Mole. Pathol Plant. 10, 95– 107. Lopez-Berges, M.S., Rispail, N., Prados-Rosales, R.C. and Di Pietro, A. (2010) The Path of Nitrogen Response regulates the function of virulence in Fusarium oxyporsum TOR kinase protein and MeaB BZIP protein. Cell Plant, 22, 2459- 2475. Lowe, I., Kantu, D. and Dubkowski, J. (2011) Strong resistance to wheat rust: the integration of biology systems and traditional phenotyping research methods to guide the deployment of resistance genes. Eufitic, 179, 69- 79. Ma, Los Angeles, van der Do, H.K., Borkovich, K.A., Coleman, J.J., Dabossi, M.J., Di Pietro, A., Dufresne, M., Freitag, M., Grabherr, M., Henryssat, B., Huterman, P.M., Kang, S., S. S. S. Xy, J.R., Antonio, D., Baker, S.E., Blum, B.H., Breakspair, A.R., Brown, D.W., , Coulson, R., Coutinho, P.M., Danchin, E.G., Diner, A., Gayle, L.R., Gardiner, D.M., Goff, S., Hammond-Kosak, C.E. , Gilburn, K. , Wash van, A., Jonkers, W. Kazan, K., Kodira, C.D., Kersen, M., Kumar, L. Lee, J.H., Lee, L., Manners, J.M., Miranda-Saavedra, D., Mukherjee, M., Park, Park, Park, Park, Park, D., Park, Park, D., Park, Park, Park, D., Regev, A., Ruiz-Roldan, M.K., Sain, D., Sactikumar, S., S. S., Schwartz, D.C., Turgeon, B.G., Wapinski, I., Yoder, O., Young, S., Tseng, S., Gala, S., S., , H.K. and Rep, M. (2010) Comparative Genomics shows mobile pathogenicity in Fusarium. Nature, 464, 367- 373. Magan, N., Aldred, D., Mylona, K. and Lambert, RJ.W. (2010) Limiting mycotoxins in stored wheat. Food addyst. Kontam. Ah, 27, 644- 650. Marshall, R., Combrink, A., Motteram, J., Loza-Reyes, E., Lucas, J., Hammond-Kosack, K.E., Thomma, B.P.H.J. and Rudd, J.J. (2011) Analysis 2 in planta expressed Homologs effector LysM from the fungus Mycosphaerella graminicola Plant Physics and Physio. 156, 756- 769. Martens, J.W. and, P.L. (1989) Genetics of rust resistance in cereals from a Canadian perspective. Kang. J. 11, 78– 85. Martinez-Rocha, A.L., Roncero, M.I.G., Lopez-Ramirez, A., Marine, M., Goarro, J., Martinez-Cadena, G. and Di Pietro, A. (2008) Rho1 has various functions in morphogenesa, cell wall biosynthesis and fusarium viulence. Cell. A microbiol. 10, 1339– 1351. Mackintosh, R.A. and Pretorius, WA (2011) Borlaug Global Rust Initiative provides momentum for wheat rust research. Eufitic, 179, 1- 2. Mendoza-Mendoza, A., Berndt,., Jamei, A., Weise, K., Lynn, W., Marahiel, M., Vranes, M., Camper, D. and Kahmann, R. (2009) Physical-chemical plant-derivative signals cause differentiation in Ustilago maydis. Mole. A microbiol. 71, 895– 911. Mikali, K., Neumann, USA, Grunewald, D., Panstruga, R. and O'Connell, R. (2011) Biogenesis specialized plant-fungal interface during internalization of the cells of the host Golovinomis oronty hactoria. Cell. A microbiol. 13, 210– 226. Michielse, C.B. and Rep, M. (2009) Pathogen Profile Update: Fusar oxiumysporum. Mole. Plant 10, 311– 324. Michielse, C.B., van Wijk, R., Reijnen, L., Cornelissen, B.J. and Rep, M. (2009a) Insight into the molecular pathogenic requirements of Fusarium oxysporum f. sp. lycopersici through large-scale insertion of mutagenez. General Biol. 10, R4. Michielse, C.B., van Wijk, R., Reijnen, L., Manders, E.M., Boas, S., Olivain, C., Alabouvette, C. and Rep, M. (2009b) Nuclear protein Sge1 oxyspor Fusarium is essential for parasitic growth. PLoS Patog. 5, e1000637. Moser, R., Perto, I., Elad, J. and Raffaelli, R. (2008) Farmers' attitude to the use of biocontrol agents in the production of IPM strawberries in three countries. Biol. Control. 47, 125– 132. Murray, G. and Brennan, J. (2010) Assess disease losses for the Australian barley industry. Aust. The Patol plant. 39, 85– 96. Nguyen, S.B., Kadotani, N., Kasahara, S., Tosa, J., Mayama, S. and Nakayshiki, H. (2008) Systematic functional analysis of calcium signaling proteins in the rice mushroom genome, Magnaporthe oryzae, using high RNA capacity. Mole. A microbiol. 68, 1348– 1365. Nitta, N., Farman, M.L. and Leong, S.A. (1997) Magnaporthe grisea Genome Organization: Integrating Genetic Maps, Clustering Transposable Elements, and Identifying Genome Duplication and Permutation. Theorist. Apple. A genetics. 95, 20. Nucci, M. and Anaissie, E. (2007) Fusarium infection in immunocompromised patients. Wedge, Wedge. A microbiol. Reverend 20, 695- 704. Nunez, C., Gowda, M., Sailsbery, J., Xue, M., Chen, F., Brown, D., O, J., Mitchell, T. and Dean, R. (2011) A variety of and tissue-enriched small RNA in plant pathogenic fungus, Magnaporthe oryzae. BMC Genomics, 12, 288. O'Donnell, K., Kistler, H.C., Cigelnik, E. and Ploetz, R.C. (1998) Several evolutionary origins of the fungus causing Panamanian banana disease: juicy evidence from nuclear and mitochondrial genealogy. Proc. Natl. Acad. Sci. United States, 95, 2044- 2049. O'Donnell, C., Sutton, D.A., Rinaldi, M.G., Magnon, C.K., Cox, P.A., Revancar, S.G., Sanche, S., Geiser, D.M., Dzyuba, J.H., van Burik, J.A., Padhye, A., Anaissie, E.J., Francesconi, A., Walsh, T.J. and Robinson, J.S. (2004) Genetic diversity of human pathogenic members of the Fusarium oxy complex derived from multi-cell DNA sequence : evidence of recent scattering of the widely distributed clonal line and the non-sousic origin of the toxic J. Clyne. 42, 5109– 5120. Oh, J., Donofrio, N., Pan, H., Coughlan, S., Brown, D., Meng, S., Mitchell, T. and Dean, R. (2008) Transcript analysis reveals a new understanding of the formation of apressory and function in the mushroom explosion of Magnaporthe oryzae rice. The Biol genome. 9, R85. Orbach, M.J., Farrall, L., Sweigard, J.A., Chumley, F.G. and Valent, B.

(2000) The telomere auriulation of the gene determines the effectiveness for the explosion of rice Pietha gene. Cell Factory, 12, 2019-2032. Orton, E.S., Deller, S. and Brown, J.K.M. (2011) Mikosfarella gramicol: from genomics to disease control. Mole. Pathol Plant. 12, 413– 424. Ortoneda, M., Goarro, D., Madrid, M.P., Caracuel, Z., Ronsero, M.I., Mayayo, E. and Di Pietro, A. (2004) Fusarium oxysporum as a multi-home model of genetic dissection of fungal virulence of plants and mammals. Infect. Immun. 72, 1760- 1766. Ou, S.H. (1980) Variability of pathogens and resistance to host in the disease of rice explosion. Ana. Reverend Fitopathol. 18, 167– 187. Panstruga, R. and Dodds, P.N. (2009) Stunning Protein Traffic: The Mystery of Protein Effector Delivery by Filath Plant Pathogens. Science, 324, 748- 750. Park, R.F. (2007) Wheat rust stem in Australia. Aust. J. Agric. Res. 58, 558- 566. Patel, R.M., van Kahn, J.A.L., Bailey, A.M. and Foster, G.D. (2008) RNA mediated silencing of the gene superoxide dismutase (bcsod1) in Botrytis cinerea. Phytopathology, 98, 1334- 1339. Patel, R.M., van Kahn, J.A.L., Bailey, A.M. and Foster, G.D. (2010) Unintentional silencing of the gene arginosuccinate synthase (bcass1) in Botrytis cinerea vector system pLOB1. Mole. Pathol Plant. 11, 613– 624. Perez-Nadales, E. and Di Pietro, A. (2011) Membrane Mucin Msb2 regulates invasive growth and plant infection in Fusarium oxysporum. Cell Factory, 23, 1171- 1185. Pretorius, S.A., Singh, R.P., Wagoire, V.V. and Payne, T.S. (2000) Detection of the virulence of the Sr31 wheat resistance gene in Puccinia graminis f. sp. tritici in Uganda. Plant Dis. 84, 203. Pretorius, S.A., Pakendorf, K.V., Mare, G.F., Prince, R. and Comen, J.S. (2007) Challenges for sustainable grain rust control in Southern Africa. Aust. J. Agric. Res. 58, 593- 601. Proctor, R.H., Hon, T.M. and McCormick, S.P. (1995) Gibberella zeae Virulence Decrease is caused by a violation of the trichotescenic toxin biosynthetic gene. Mole. Plant-Microbe Interaction. 8, 593– 601. Pruski, D. (1996) Pathogenic repentance in post-harvest diseases. Ana. Reverend Fitopathol. 34, 413– 434. Rafiki, M., Gan, P.H., Ravensdale, M., Lawrence, GJ, Ellis, J.G., Jones, D.A., Hardham, A.R. and Dodds, P.N. (2010) Internlization of flax rust proteins in flax and tobacco cells can occur in the absence of pathogenicity. Cell Factory, 22, 2017-2032. Rep, M. Van Der Lee, H.C., Meyer, M. Van Weik, R, Hurtman, P.M., Dekker, H.L., De Koster, K.G. and Cornelissen, B.J.C. (2004) A small, rich cystine protein, is distinguished by the oxysporus Fusarium during colonization of the quesile vessels. Mole. A microbiol. 53, 1373–1383. Ridout, CJ, Skamnioti, P., Porritt, O., Sacristan, S., Jones, J.D.G. and Brown, J.K.M. (2006) Multiple paralogies of auriulation in mushrooms of flour powdered mold can promote the suitability of parasites and the contamination of plant resistance. Cell Plant, 18, 2402- Roelfs, A.P. (1982) The effect of barberry eradication on stem rust in the United States. The Dees plant. 66, 177- 181. Roelfs, A.P. (1985) Epidemiology in North America. In: Cereal rust, Vol. II, Diseases, Distribution, Epidemiology, and Control (A. Roelfs and W.R. Bushnell, Ed.), 403-434. Orlando, Florida: Academic press. Rudd, JJ, Keon, J. and Hammond-Kosak, K.E. (2008) Wheat mitogen activated protein kinase TaMPK3 and TaMPK6 are differentiated at multiple levels during compatible disease interactions with Mycosphaerella graminicola. Plant Physics and Physio. 147, 802- 815. Sakriston, S., Viguru, M., Pedersen, K, Scamnioti,., Tordal-Christensen, J., Mikali, C., Brown, J.K.M. and Ridout, C.J. (2009) The relationship between the family of virulence effects of parasites and the retroposite class LINE.1. PLoS ONE, 4, e7463. Saunders, D.G.O., Aves, SJ and Talbot, N.J. (2010) Cell cycle mediated regulation of plant infection fungus exploding rice. Cell Plant, 22, 497-507. Shiravski, D. Mannhaupt, G. Munch, K, Brefort, T. Shipper, K. Dolemann, G. Di Stasio, M., Rossel, N. Mendoza, Mendoza, A., Pester, D., Muller, O., Winterberg, B., Meyer, E., Garib, H., Wollenberg, T., Munstercotter, M., Wong,., Walter, M., Stuckenbroke, E., Gouldener, USA and Kahmann, R. Science, 330, 1546- 1548. Scholefield, P. and Morison, J. (2010) Assess the economic costs of endemic pests and diseases in the Australian grape and wine industry. Adelaide, Australia: Grape and Wine Research corporation. Sholthof, K.B.G., Adkins, S., Tssneck, H., Palukaitis,., Dzeko, E., Hon, T., Hon, B., Saunders, K., Kandudet, T., Alquist,., Gemenway, K. and Foster, G.D. (2011) Top-10 plants in molecular pathology. Mole. Pathol Plant. 12, 938– 954. Silue, D. and Notagem, J.L. (1992) Definition of a cross between two compatible isolates of Magnaporthe grisea (Hebert) Barr and genetic analysis of rice auriulation/virulence. D. Fitopathol. 135, 77– 83. Simons, G., Groendeik, D., Weibrandi, J., Reyans, M.G.J., Diertaarde,., Van Der Lee, T. Bleecker, M., Onstenk, D., De Oba, M., Haring, M.A., Mes, J.J., Cornelissen, B.J. (1998) The autopsy of the Fusarium I2 gene cluster in tomato shows six homologies and one active gene copy. Singh, R.P., Hodson, D.P., Huerta-Espino, D., Jin, J., Bhavani, S., Njau,., Herrera-Fossel, S., Singh, P.K., Singh, S. and Govindan, W. (2011) The emergence of Ug99 races of rust-stem mushrooms poses a threat to the world's wheat production. Ana. Reverend Fitopathol. 49, 465– 481. DOI: 10.1146/annurev-phyto-072910-095423. Skamnioti, P. and Gurr, S.J. (2009) Against grain: protecting rice from the disease of rice explosion. Trends 27, 141– 150. Skibbe, D.S., Doehlemann, G., Fernandes, J. and Walbot, V. (2010) Corn tumors caused by Ustilago may require organ-specific genes in host and pathogen. Science, 328, 89- 92. Spanu, P.D., Abbott, J.C., Amsel, D. Burgis, T.A., Soanes, D.M., Stuber, C., van Temaat, E.W.L., Brown, J.K.M., Butcher, S.A., Gurr, S.J., Lebrun, M.H., Reedout, C.J., Schulze-Lefert,., Talbot, New Jersey, Ahmadinejad, N., Ametz, K., Barton, G.R., Benji, M. Bidzinsky,., Bindschedler, L.V., Both, M., Brewer, M.T., Kadle-Davidson, L. Collemare, D., Kramer, R., Frankel, O, Year J, J Garriman, J., Hide, K., King, B.K., Clages, S., Klemann, D., Knoll, D., Coty, P.S., Kreplak, D. Lopez-Ruiz, F.J., Lu, H., Maekawa, T., Maannil, S., Mikali, K. Milgrum, M.G., Montana, G, Noir, S., O'Connell, R.J., Oberhaensley, S., Parlange, F. , Pedersen, C. R, Rott, M., Sakristan, S., Schmidt, S.M., Shen, M., Skamnioti,., Sommer, H. Stevens, A., Takahara, H., Tordal Christensen, H., Viguru, M., Wessling, R., Wicker, T. and Panstruga, R. (2010) genes in powdered soft mushrooms. Science, 330, 1543- 1546. Steiger, D. (2007) Global Economic Value protection Botrytis. In: Book of Abstracts, 14th Botrytis International Symposium, Cape Town, South Africa, October 21-26, 2007 (P. Fourie and M. Vivier, eds.), Cape Town, South Africa: AFRICAN SUN MEDIA Pty (Ltd.). Steinberg, G. and Perez-Martin, J. (2008) Ustilago Maydis, a new fungal system model for cellular biology. Trends Cell Biol. 18, 61-67. Stukenbrock, E.H., Jorgensen, F.G., Halla, M., Hansen, T.T., McDonald, B.A. and Schierup, M.H. (2011) Evolution of the entire genome and chromosome associated with the adaptation of the host and the species of the wheat pathogen Mycosphaerella graminicola. PLoS Genet. 6, e1001189. 10.1371/journal.pgen.1001189. Sutton, British Columbia (1992) Rod Glomerella and his colletotrichum anamorph. In: Colletotrychum: Biology, Pathology and Control (J.A. Bailey and M.J. Jaeger, eds), p. 1- 26. Wallingford: CAB International. Takamatsu, S. (2004) Phylogeny and the evolution of powdered mold fungi (Erysiphales, Ascomycota) are derived from nuclear ribosomal DNA sequences. Mikoscience, 45, 147- 157. Takano, J., Kikuchi, T., Kubo, J., Hamer, J.E., Mise, K. and Furusawa, I. (2000) Colletotrichum lagenarium MAP kinase gene CMK1 regulates various aspects of fungal pathogenesis. Mole. Plant-Microbe Interaction. 13, 374– 383. Tucken, F. and Rep, M. (2010) Arms Race between Tomatoes and Fusarium Oxysporum. Mole. Pathol Plant. 11, 309– 314. Talbot, N.J. (2003) In the footsteps of a cereal killer: an investigation into the biology of Magnaporthe grisea. Ana. Reverend Microbiol. 57, 177. Tudchinskiy. and Kokkelink, L. (2009) Botrytis Synrea: molecular aspects of necrotrophic In: Mikota. Vol.W. Plant Relationships (H. Deising, ed.), p. 29-50. Berlin, Heidelberg: Springer Verlag. UIPP (2002) Annual Report. Paris, France: Union Of Industry de la Plant Protection. Urashima, A.S., Igarashi, S. and Kato, H. (1993) Host range, type of mating and fertility pyricularity grisea from wheat in Brazil. Plant Dis. 77, 1211- 1216. Urban, M. and Hammond-Kosak, K.E. (2012) Molecular Genetics and Genomic Approaches to the Study of Fusarium Infection of Wheat Flower Tissue. In: Fusarium Of Genomics and Molecular and Cell Biology (R. H. Proctor and D. Brown, eds), Chapter 12 Norwich, Norfolk, UK: Horizon Scientific Press. Valent, B. and Chumley, F.G. (1991) Molecular Genetic Analysis of Rice Explosion Mushroom, Magnaporthe grisea. Ana. Reverend Fitopathol. 29, 443– 467. Valent, B., Farrall, L. and Chumley, F.G. (1991) Magnaporthe grisea genes of pathogenicity and virulence are identified through a number of backcrosses. Genetics, 127, 87- 101. Van Kang, J.A.L., Van't Klooster, J.W., Dees, D.C.T., Wagemakers, C.A.M. and Van der Vlugt-Bergmans, C.J.B. (1997) Cutinase A of Botrytis cinerea expressed, but is not essential, during penetration of gerberers and tomatoes. Mole. Plant-Microbe Interaction. 10, 30– 38. Veneault-Fourrey, C., Barooah, M., Egan, M., Wakley, G. and Talbot, N.J. (2006) Autophagic fungal cell death is essential for the infection of the rice explosion fungus. Science, 312, 580-583. Vilgalys, R. and Cubeta, M.A. (1994) Molecular systematics and biology of the population of Rhizoctonia. Ana. Reverend Fitopathol. 32, 135– 155. Voegele, R.T. and Mendgen, K.W. (2011) Nutrient Absorption in Rust Mushrooms: How Sweet Is Parasitic Life? Eufitic, 179, 41-55. Vrinda, T.A. (2005) Botrytis problem in numbers. Act Hortic. 669, 99– 102. Vurro, M., Bonciani, B. and Vannachi, G. (2010) New infectious diseases of agricultural plants in developing countries: impact on agriculture and socio-economic impacts. Food Sec. 2, 113- 132. Waalwijk, C., Mendes, O., Verstappen, E.C.P., de Vaard, M.A. and Kema, G.H.J. (2002) Isolation and the mating characteristics of the type of idiots from the wheat leaf septorium spots of the fungus Mycoserphaella graminicola. Fungal Genetic. Biol. 35, 277- 286. Wahl, R., Wippel, K., Goos, S., Kamper, J. and Sauer, N. (2010) A new high affinity sucrose transporter is needed for the virulence of the plant pathogen Ustilago maydis. PLoS Biol. 8, e1000303. Wang, C.A., Guncar, G., Forwood, J.K., The, T., Catanzariti, AM, Lawrence, G.D., Laughlin, F.E., McKay, J.P., Shirra, H.D., Anderson, P.A., Ellis, J.G., Dodds, P.N. and Kobe, B. (2007) Crystal Structures of Flax Rust Avrulin Protein AvrL567-A and y Cell Plant, 19, 2898- 2912. Williamson, B., Tudzinski, B., Tudzinsky,. and Van Kahn, J.A.L. (2007) Botrytis cause of gray mold disease. Mole. Pathol Plant. 8, 561– 580. Wittenberg, A.H.J., van der Lee, T.A.J., Ben M'Barek, S., Ware, S.B., Goodwin, S.B., Kylian, A., Visser, R.G.F., Kema, G.H.J. and Schuten, H.K. (2009) Mayosis leads to extraordinary genome plasticity in the haploid fungal plant pathogen Mycosphaerella. PLoS ONE, 4, e5863. Voroshuk, C.P., Sisler, H.D. and Vigil, E.L. (1983) Action of antipenetrent, tricyclazole, on the apertory of Pyricularization of anrize. A physio. Pathol Plant. 22, 245– 259. Wright, A.J., Carver, T.L.W., Thomas, B.J., Fenwick, N.I.D., Kunoh, H. and Nicholson, R.L. (2000) Rapid and accurate identification of the location of the Blumeria graminis conidia germ tube. A physio. Mole. Pathol Plant. 57, 281– 301. Wyand, R.A. and Brown, J.K.M. (2003) Genetic and forma specialized diversity in Blumeria graminis cereals and its effects on host pathogenic joint evolution. Mole. Pathol Plant. 4, 187– 198. Sui, JR and Hamer, J.E. (1996) MAP kinase and CAMP signaling regulate the formation of infection structure and pathogenic growth in the fungus exploding rice Magnaporthe grisea. Genes Of The Virgin. 10, 2696- 2706. Yamaoka, N., Matsumoto, I. and Nisiguchi, M. (2006) The role of primary germ tubes (PGT) in the life cycle of The Bloomeria gramini: stopping the lengthening of THE PHT is necessary to trigger the apprajorial germ tube (AGT). A physio. Mole. Pathol Plant. 69, 153– 159. Sadox, JC (1985) Cereal rust, dogs and stars in antiquity. Cereal. Rusts Bull. 13, 1– 10. Seigler, R.S., Leong, S.A. and Teng, P.S. (1994) Rice Blast Disease, p. 1- 626. Wallingford: CAB International. Chang, J., Pettiway, R.E. and Macdonald, British Columbia (2003) The global genetic structure of the mycosphaerella graminicola wheat pathogen is characterized by high nuclear diversity, low mitochondrial diversity, regular recombination and gene flow. Fungal Genetic. Biol. 38, 286- 297. Details of the main biotic limitations, genetically modified plants, 10.1016/B978-0-12-818564-3.09990-X, (297-300), (2021). Roger Hull, Graham Head, George T. Tsocos, Context Installation: Agriculture and Crops/Food Sustainability, Genetically Modified Plants, 10.1016/B978-0-12-818564-3.00001-9, (1-33), (2021). Ruben D. Pacheco-Cano, Ruben Salcedo-Hernandez, Luz E. Casados-Vazquez, Casemieres Wrobel, Dennis K. Bideshi, Jose E. Barbosa-Corona, Grade I of Defensine (BraDef) from broccoli seeds (Brassica oleracea var. italica) and their antimicrobial activity, World Journal of Microbiology and Biotechnology, 10.1007/s11274-020-2807-6, 36, 2, (2020). Aysun Uysal, zener Kurt, First report on fruits and leaves of anthracosis caused by Colletotrichum karstii on avocados in Turkey, crop protection, 10.1016/j.cropro.2020.105145, 133, (105145), (2020). Yin Wang, Xiaoyun Liu, Tong Chen, Yong Xi, Shiping Tian, эффекты хинокитиола на развитие Botrytis cinerea in vitro vitro in vivo, Postharvest Biology and Technology, 10.1016/j.postharvbio.2019.111038, 159, (111038), (2020). Marion O. Harris, Andrea Pitzschke, Plants make bile to accommodate foreigners: some are friends, most of them enemies, New Phytolog, 10.1111/nph.16340, 225, 5, (1852-1872), (2020). Yaowen Chang, Rong Shen, Ixue Mo, Tsiqing Li, Wei Lin, Gaoqing Yuan, Colletotrihum Siamense: new Sterkulia leaf pathogen Nobilis Smith discovered in China, Forest Pathology, 10.1111/efp.12575, 50, 1, (2020). Jose Moreno-Aores, Sebastian Michel, Thomas Miedaner, C. Friedrich H. Longin, Hermann Buerstmayr, Genomic Predictions for Fusarium Head Decline Resistance in Various Durum Wheat Panels: effective inclusion of plant height and headline dates as ova around, Euphytica, 10.1007/s10681-019-2551-x, 216, 2, 2020). Carlos Felix-Contreras, Carlos A. Alba-Fierro, Emmanuel Rios-Castro, Francisco Luna-Martinez, Mayra Cuellar-Cruz, Estela Ruiz-Baca, Proteom cell wall analysis Sporothrix schenckii shows proteins involved in an oxidative stress response induced by meadionom, microbial pathogenesis, 10.1016/j.micpath.2020.103987, (103987), (20207). Birgit Vilci, Tomislav Chernava, Alexander Dennig, Meritzell Galindo, Martina Geyer, Steffen Gruber, Marianne Habenbauer, Petra Heidinger, Enrique Herrero Asero, Regina Kracer, Christian Luli-Gedl, Cristina A. Muller, Julia Pitzer, Doris Riberic, Michael Sauer Sisen, Chung So, Kerstin Steiner, Christoph K. Winkler, Margit Winkler, Tamara Vrissnegger, Enzymes revolutionize bioproduction compounds with added value: from enzyme detection to special applications, Biotechnology Advances, 10.1016/j.biotechadv.2020.107520, (107520), (2020). An-don GON, Jun-ying Jing, Kai Chang, Tsing-Kun TAN, Go-Liang WANG, Wen-de LIU, Bioinformatics Analysis and Functional Feature of CFEM Proteins in Colletotrichum graminicola anthrax corn fungus, Journal of Integrative Agriculture, 10.1016/S2095-3119 (19)62675-4, 19, 2, (541-550), (2020). Julia Schumacher, Anna Gorbushina, light-feeling in plant and rock-associated black mushrooms, fungal biology, 10.1016/j.funbio.2020.01.004, (2020). Yaochi zhao, Shiguang Liu, Chuhua Hu, Yong Bai, Chong Shen, Xuekun Shi, Separate Degree-based Otsu and signed a similarity initiative level set for segmentation and counting anthrax spores, computers and electronics in agriculture, 10.1016/j.compag.2020.105230, 169, (105230), (2020). Shaoshuai Liu, Yi Wei, Shi-Hong Chang, C3HC-type zinc-finger protein (FC3) interacting with Lon/MAP1 is essential for regulating mitochondrial genes, developing gif infection and longevity of Magnaporthe oryzae, BMC Microbiology, 10.1186/s12866-020-1711-4, 20, 1, (2020). Irena Hillier-Rodriguez, Federico Albertazzi, Herman Rivera-Coto, Ramon Molina-Bravo, zPCR multiplex to detect fungal fungal between Trichoderma atroviride (Hypocreaceae) and Botrytis cinerea (Sclerotiniaceae) in Blackberry fruit using de novo tef1-α and probes based on IGS sequence, Biotechnology Reports, 10.1016/j.btre.2020.e00447, (e00447), (2020). Huiying Sun, Lin Sun, Yingzhe Hong, Yue Liang, First report on anthracos at Hosta ventricosa called Colletotrichum spaethianum in China, crop protection, 10.1016/j.cropro.2020.105104, (105104), (2020). Francis J. Osonga, Sanjay Kalra, Roland M. Miller, Daniel Isika, Omowunmi A. Sadiq, Synthesis, characteristics and antifungal activities of environmentally friendly palladium nanoparticles, RSC Advances, 10.1039/C9RA07800B, 10, 10, (5894-5904), (2020). Wen Liang Chen, Yi-Bing Lin, Fung-Ling Ng, Chun-You Liu, Yun-Wei Lin, RiceTalk: Rice Explosion Detection using Internet of Things and Artificial Intelligence Technologies, IEEE Internet of Things Journal, 10.1109/JIOT.2019.2947624, 7, 2, (1001-1010), (2020). Ranjit Morya, Eshvir Singh, Manisha Sinha, Kunal Singh, Pallavi Mishra, Srinivas Kumar Singh, Sandhya Verma, Kanchan Prabha, Kamal Kumar, Pravin Kumar Verma, Transcription profiling shows potential regulators for the oxidative stress response of necrotrophic chickpea pathogen Ascochyta rabiei, 3 Biotech, 10.1007/s13205-020-2107-8, 10, 3, (20205-020-2107-8, 10, 3, 3). Matthew Denton-Giles, Hannah McCarthy, Tina Serish, Yasmin Dijkwell, Karl H. Mesaric, Rosie E. Bradshaw, Murray. Cox, Paul. Dijkvel, Preservation and expansion of necrosis, causing a small secreted protein family of host-variable phytopathogens Sclerotiniaceae, Pathology of Molecular Plants, 10.1111/mpp.12913, 21, 4, (512-526), (2020). Lydia Campos-Soriano, Mireya Bundo, Marcel Bach-Pages, Su-Fen Chang, Chii-Jen Chiu, Blanca San Segundo, excess phosphate increases susceptibility to pathogenic infection in rice, molecular plant pathology, 10.1111/mpp.12916, 21, 4, (555-570), (20200). William R. Chase, Olga Jaksibayeva, Jorge Rocha, Daniel Cosgrove, Laurie R. Shapiro, Global Cellulose Biomass, horizontal gene transfers and domain fusion control the evolution of microbial expansine, New Phytologist, 10.1111/nph.16428, 226, 3, (921-938), (2020). Kaiyun Liu, Junjie Xing, Xuan Cai, Ahmed Hendy, Wenhui He, Jun Yang, Junbing Huang, Yulian Peng, Lauren Ryder, Xiao-Lin Chen, GPI7-mediated glycosilfosphatylinositol anchor regulates apppressoric penetration and immune evasion during infection, Environmental Microbiology, 10.1111/1462-2920.14941, 22, 7, (2581-2595), (2020).. A.V. Ilyina, B.Tsagdarov, A.P. Lunkova, I.S. Mysyakina, Chitina/Hitosan and its derivatives: fundamental problems and practical approaches, biochemistry (Moscow), 10.1134/S006297920140084, 85, S1, (154-176), (2020). Sachary Gorman, Sean A. Christensen, Yuanxin Yang, Yongming He, Eli Borrego, Michael W. Kolomiets, Green Sheets of Bats and acid increase susceptibility to susceptibility anthraconous diseases caused by gramicol colleotrich in corn, pathology of molecular plants, 10.1111/mpp.12924, 21, 5, (702-715), (2020). Rola El Amil, Sajid Ali, Bohra Bahri, Mark Leconte, Claude Vallavier-Pope, Kumarse Nazari, Pathotype diversification in the invasive PstS2 clonal line Puccinia striiformis f. sp. tritici causing yellow rust on durum and wheat bread in Lebanon and Syria in 2010-2011, Plant Pathology, 10.1111/ppa.13164, 69, 4, (618-630), (2020). U Xiong, Yuqi Song, Keming Yang, Yang Gu, Jun Wei, George A. Kovalchuk, Yanchun Xi, Alexander Jusset, Tsirong Shen, Stefan Geisen, Proteists of the Rizosphere are key determinants of plant health, microbiome, 10.1186/s40168-020-00799-9, 8, 1, (2020). Chuanqing, Jiang, Xinhui, Tianjie Yan, Jun Fu, Yanfeng Li, Junxiau Wu, Xiaochun Hu, Chengan Bai, Tiangan Liu, Gui Xiao, Yanbiao Chou, Liangbi Chen, Kai Wang, Yuanzhu Yang, Image caption Picl (t) from Chaling Common Wild Rice (Oryza rufipogon Griff.), Journal of Phytopathology, 10.1111/jph.12883, 168, 4, (211-219), (2020). Yichen Kang, Meixue Chou, Angela Merry, Karen Barry, Mechanisms of Powdered Resistance of Wheat Mold - Review of Molecular Breeding, Plant Pathology, 10.1111/ppa.13166, 69, 4, (601-617), (2020). Giuliana Oliveira de Carvalho, Valkyrie Broll, Anne Helen Souza Martinelli, Fernanda Cortez Lopez, endofhitic mushrooms: positive association with plants, Molecular aspects of beneficial plant microbes in agriculture, 10.1016/B978-0-12-818469-1.00026-2, (321-332), (2020). Lei Chen, Liyuan Chang, Xiang Mei, Chenyu Wang, Chuang Goo, Li Li, Baoyang Li, Yuancun Liang, Shenshen Tsou, Hansong Dong, Type II phosphosyroid 4-kinase FgLsb6 is essential for the development and virulence of Fusarium graminearum, fungal genetics and biology, 10.1016/j.fgb.2020.103443, (103443), (2020). Maria Carlota Vaz Patto, Diego Rubiales, Medicago truncatula host / nonhost bean rust interactions, Model Legume Medicago truncatula, 10.1002/97811194091444, (384-389), (2020). Paa K. Bordeaux, Asgar Ali, Matthew Dickinson, Yasmin Siddiqui, Gianfranco Romanazzi, Review for the management of old anthrax in dragon fruit caused by Colletotrichum spp., Crop Protection, 10.1016/j.cropro.2019.105067, 130, (105067), (202067). Natalia M. Albuini-Oliveira, Mayura M.M. Rubinger, Silvana Gilardi, Rafael A.K. Souza, Javier Ellen, Natalia Alvarez, Eder K. Tavares, Carlos H.K. zacchi, Antonio E.K. Vidigal, Marcelo S. Lima, Laercio Sambim, New Saltitiocarbimate: Synthesis, Structure and Antifungal Activity, Journal of Molecular Structure, 10.1016/j.molstruc.2020.128149, (128149), (2020). Margot Berenstrauh, Stefan Mann, Chloe Jakemin, Sarra Bibi, Um-Kalthum Sylla, Emmanuel Baudouin, Didier Buisson, Soizic Prado, Karolina Kunz, Molecular Cross-Talk between Paraconiotirium Paraconiotytrium and phytopathogen Fusarium oxysporum - modulation of lipoxygenase activity and the production of cosmetology during interaction, fungal genetics and biology, 10.1016/j.fgb.2020.103383, (103383), (2020). Vera Mayer, Evelina I. Basenko, J. Philippe Benz, Gerhard H. Braus, Mark H. Caddick, Michael Hscay, Ronald. de Vries, Drew Andy, Jens K. Friswad, Nina Gunde-Chimerman, Thomas Haarmann, Yitzhak Hadar, Kim Hansen, Robert E. Johnson, Nancy. Keller, Nada Krashenets, Uffe H. Mortensen, Rolando Perez, Arthur F. J. Ram, Eric Record, Phil Ross, Olga Shapaval, Charlotte Steiniger, Hans van den Brink, Jolanda van Munster, Oded Yarden, Han A.B. Wusten, Growing a circular economy with fungal biotechnology: white paper, fungal biology and biotechnology, 10. 1186/s40694-020-00095-z, 7, 1, (2020). Dolev Samir, Ortal Galsarker, Noam Alkan, Evgeny Yeltsin, Discovery of quiet mushrooms in collected fruits with the help of CMOS biosensor: proof of conceptual research, Talent, 10.1016/j.talanta.2020.120994, (120994), (2020). Mohammad Khalil Monjed, Jeffrey D. Robson, John K. Pittman, Isolation of fungal strains for biodegradation and sugarization of microalvocal biomass, biomass and bioenergy, 10.1016/j.biombioe.2020.105547, 137, (105547), (2020). Olga Kozhar, Meredith M. Larsen, Nicklaus Grunwald, Tobin L. Peever, fungal evolution in the man-made environment: Botrytis cinerea Populations Infecting Small Fruit Hosts in the Pacific Northwest quickly adapt to anthropogenic pressure selection, applied and environmental microbiology, 10.1128/AEM.02908-19, 86, 9, (2020). Ming Jae-Chang, Chen-Hao Sun, Yue Liu, Hueqiang Feng, Hao-Wu Chang, Sheng-Nan Cao, Guizhua Li, Song Yang, Jie Hou, Keyang Joo Salzman, Hao Chang, Tsing Ming Tsin, Analysis of Transcriptoma and Functional Verification show a new gene, BcCGF1, which enhances fungal virulence, contributing to the development of infection and infiltration of the host, the pathology of molecular plants, 10.1111/mpp.12934, 21, 6, (834-853), (202034). Davide Ferrigo, Massimiliano Mondin, Ladurner Edith, Fiorentini Fabio, Roberto Causin, Alessandro Raiola, Effect of seed bioprime with Trichoderma harzianum strain INAT11 on Fusarium ear rot and Gibberella diseases rot ear, biological control, 10.1016/j.biocontrol.2020.104286, (104286), (2020). Vera Hole, Philippe Vine, Rai-Ya Young, Julian Almeida Barros da Silva, Eugenia M. A. Enfissi, Marilise Nogueira, Elliott J. Price, Saleh Alzeh, Alisdair R. Fernie, Paul D. Fraser, Peter Hanson, Katie Martin, Analysis of tomato post-harvest properties: Fruit color and fungal susceptibility, Current protocols on plant biology, 10.1002/cppb.20108, 5, 2, (2020).L. F. Izquierdo-Garcia, A. Gonzalez-Almario, A. M. Cots, C.A. Moreno-Velandia, Trihoderm a virens Gl006 and Bacillus velezensis Bs006: compatible interaction, controlling the withering fusarium of gooseberry, Scientific 10.1038/s41598-020-63689-y, 10, 1, (2020). Yunlong Meng, Keiuan Jun, Chuhua Xiao, Yong Huang, You Wei, Lin Tang, Suping Chen, Huang Wu, Jinjie Ma, Sigang Cao, Xinjun Liao, Hueiqiang Lu, Exposure to pyrimethanil causes developmental toxicity and cardiotoxicity in zebra, chemosphere, 10.1016/j.chemosphere.2020.126889, (126889), (2020). Dian Wang, Hua Xu, Junyang Huang, Yingzhen Kong, Xianan AbuKamar, Diku Yu, Shengyi Liu, Gonge zhou, Gohua Chai, Arabidopsis CCCH protein C3H14 promotes basal protection against Botrytis cinerea mainly through WRKY33-dependent pathway, plant, cell and environment, 10.1111/pce.13771, 43, 7, (1792-1806), (2020). Min Xi, Yang Guo, Dong Tian, Chen Gao, Feiran Guo, Ralph T. Vugele, Juan Bao, Chenjing Li, Konguyu Jia, Hao Feng, Lily Huang, adaptive regulation of virulence genes of microRNA-like RNA in Valsa Mali, New Phytolog, 10.1111/nph.16561, 227, 3, (899-913), (20201). Huaton Lu, Baohui Wang, Iaoming Cai, Shenglong Chen, Tsongmao Chen, zhaojun Xin, tea-feeding GH19 chitinase enhances the answers of tea protection caused by the regurgitant derived from the ekroprisa grisescens, Physiologia Plantarum, 10.1111/ppl.13094, 169, 4, (529-543), (2020). Tousef Hussain, Nadeem Akthhar, Raghavendra Amenedi, Mohd. Danish, Yasar Nishat, Seema Patel, The Role of Powerful Microbial Bioagents and their new strategies for environmental management of agricultural phytopathogens, natural bioactive products in sustainable agriculture, 10.1007/978-981-15-3024-1, (45-66), (2020). Yabin Duan, Fei Lu, zehua zhou, Huhua zhao, Jie Chang, Yushuai Mao, Meixia Li, Jianxin Wang, Mingguo zhou, Kwinon out inhibitors affect the biosynthesis of DON, mitochondrial structure and toxiom formation in fusarium graminearum, Journal of Hazardous Materials, 10.1016/j.jhazmat.2020.122908, (122908), (2020). Lin Chen, Jie zhou, Tian Jieng, Ichhang Miao, Liang Mei, Guang Bo Yao, Kai Fan, Xin Fan Dong, Tao Sha, Min Ji Yang, Tao Li, Ji Wei Jao, Han Bo Chang, quantitative assessment of the exchange of lyolematic fungal pathogens by the invasive plant Ageratina adenophora and its neighbors, New Phytologist, 10.1111/nph.16624, 227, 5, (1493-1504), (2020). Syuefah Chong, Chenyu Wang, Yao Wang, Yixiao Wang, Liyuan Chang, Yuancun Liang, Lei Chen, Shensheng Tsou, Hanson Dong, Dynamin-Like GTPase FgSey1 plays an important role in fungal development and virulence in Fusarium graminearum, Applied and Environmental Microbiology, 10.1128/AEM.02720-19, 86, 11, (2020). Waiguo Hu, Xiaohui Wang, Siven Wang, Mengmeng Wang, Changyou Wang, zengrong Tian, Xinlong Liu, Wanquan Ji, Hong Chang, Gene Co-expression Network Analysis provides a new understanding of the dynamic reaction of wheat to powdered stress mold, journal Genetics, 10.1007/s12041-020-01206-w, 99, 1, (2020). Yigal Ahmon, Joshua T. Claypool, Jesus D. Fernandez-Baio, Kathy Hernandez, Dilnka G. McCurry, Duff Harold, Joey Soo, Blake A. Simmons, Steven W. Singer, Ruth M. Dahlqvist-Willard, James Stapleton, Gene S. VanderGainst, Christopher W. Simmons, Structural changes in bacterial and fungal components of the soil microbiome during biosolylization associated with the accumulation of volatile acids, applied soil ecology, 10.1016/j.apsoil.2020.103602, 153, (103602), (2020.103602, 153, (103602). Roger Antonio Sulub-Tun, Cecilia M. Rodriguez-Garcia, Leticia Perasa-Echeverria, Luis Torres-Tapia, Sergio R. Perasa-Sanchez, Daisy Perez-Brito, B. Marina Vera-Ku, antifungal wildlife activity and nursery Diospyros cuneata, native kind of dunes scrub, South African botany magazine, 10.1016/j.sajb.2020.03.029, 131, (131, 131, 131, (131, 131, 131, 131, 131, 131, 131, 131, 131, 131, 131, 131, 10.1016/j.sajb.2020.03.029, 131, 131, 131, 131 (2020). Dong Ming, Wen Ai, Jingxiang zhou, Jiaozhuo Li, Xinhua Chang, Tsilun Li, Zedong Shi, Fujun Li, Xiaoan Li, Yanying Go, contributed to the defense responses to Botritis cinerea in tomato fruits, Pest Management , 10.1002/ps.5888, 76, 9, (3292-3301), (2020). Xibo Chang, Pengcheng zhao, Peian Chang, Linjun Su, Haoran Jia, Xinke Wei, Jinggui Fang, Haifeng Jia, Integrative Transcriptomics and Metabolomics Data study of the effects of chitosan on post-harvest grape resistance Botrytis cinerea, Postharvest Biology and Technology, 10.1016/j.postharvbio.2020.11248, 167, (111248), (2020). Sajid Mehmood, Marina Sajid, Lily Huang, Cheng Kang, Alternative Hosts and their effect on the genetic diversity of Puccinia striiformis f. sp. tritici and disease epidemics, journal of plant interaction, 10.1080/17429145.2020.1771445, 15, 1, (153-165), (2020).A. Bernard, E. Dirlewanger, F. Lheureux, French Nut Improvement Program: Preliminary Investigations, Acta Horticulturae, 10.17660/ActaHortic.2020.128011.11, 128011, (77-84), (2020). Andrea Volante, Alessandro Tondelli, Francesca Desimirio, Pamela Abbruscato, Barbara Menin, Chiara Biselli, Laura Casella, Namrat Singh, Susan R. McCouch, Didier Tharreau, Eliza zampieri, Luigi Cattivelli, Giampiero Vale, Genome Broad Research Association for japonica Rice Resistance Explosion in the Field and Controlled Conditions, Rice, 10.1186/s1284-020-00431-2, 13, 1, (2020). Alejandro Hernandez, Santiago Ruiz-Moyano, Ana Isabel Galvan, Almudena V. Merjon, Francisco Perez Nevado, Emilio Aranda, Manuel Joaquin Serradilla, Maria de Gua Cordoba, Alberto Martin, antifungal activity of phenolic extract of sweet orange peel to control the fungi responsible for the breakdown of fruit after harvest, fungal biology, 10.1016/j.funbio.2020.05.005, (2020). Magdalena Cara, Annamaria Mincuzzi, Jordan Mercury, Hecuran Vrabi, Orges Kara, Antonio Ippolito, Riccardo Baroncelli, Simone Marianne Sanzani, Colletotrichum gloeosporioides sensu stricto as a causal agent of anthrax on pomegranate fruits in Albania, harvest protection, 10.1016/j.cropro.2020.105291, 137, (105291), (2020). Nukongbut, Duangporn Kantahote, Nguyen Kuok Huong, Huong, Tantirungkij, biocontrol potential acid-resistant rhododudomons palustris KTSSR54 and its exopolid substances against rice fungal pathogens to increase rice growth and yield, Biological Control, 10.1016/j.biocontrol.2020.104354, 150, (104354), (2020).S.A. Rodovikov, A.A. Churakov, N.M. Popova, S.V. Khizniak, Soil Microbial Communities as a source of strains for the biological protection of soybeans from fusary in Yenisei Siberia, Bulletin of Nizhnevartov State University, 10.36906/2311-4444/20-2/01, 2, (4-11), (2020). Afef Najari, Mohamed Bumayza, Sana Jaballah, Abdelatif Budabus, Hadda-Imene Ouzari, Application of isolated strains of Lactobacillus and Staphylococcus xylosus as a probiotic crop starter during the industrial production of Tunisian dry fermented sausages, Food Science and Nutrition, 10.1002/fsn3.1711, 8, 8, (4172-4184), (2020). Huiying Sun, Nat N.V. Kav, Yue Liang, Lin Sun, Weimin Chen, Proteome of The Phoma macdonaldii mushroom, causal agent of black sunflower stalk, proteomics magazine, 10.1016/j.jprot.2020.103878, 225, (103878), (2020). Haoran Ren, Menjuan Bai, Jingjing Sun, Jini Liu, Min Ren, Yuwei Dong, Na Wang, Guogui Ning, Changquan Wang, RcMYB84 and RcMYB123 mediate jasmonate-induced protection responses against Botrytis cinerea in rose (Rosa chinensis), Plant Magazine, 10.1111/tpj.14871, 103, 5, (1839-1849), (2020). Dionysio Fuentes-Aragon, Hilda V. Silva-Rojas, Vladimiro Guarnaccia, Jose A. Moras Aguilera, Sergio Aranda-Ocampo, Nestor Bautistash Martinez, Daniel Telliz-Ortez, colletotrichum species causing anthracosis on avocado fruits in Mexico: Current Status, Plant Pathology, 10.1111/ppa.13234, 69, 8, (1513-1528), (2020).A. Bernard, E. Dirlewanger, F. Lheureux, French walnut improvement program: preliminary studies, Acta Horticulturae, 10.17660/ActaHortic.2020.1280.11, 1280, (77-84), (2020).V. Petruccelli, E. Brailis, L. Varone, A. Valletta, G.Fun activity dime sulfoxide vs. botrytis cinerea and phytotoxicity on tomato and salad plants, Plant Biosystems - International Journal of Business with All Aspects of Plant Biology, 10.1080/11263504.2020.1779846, 154, 4, (455-462), (2020). Antonios Zambunis, Ioannis Ganopoulos, Dimitris Valasiadis, Lefkothea Karapetsi, Panagiotis Madesis, RNA sequencing based on transcriptom analysis of kiwi, infected Botrytis cinerea, physiological and molecular plant pathology, 10.1016/j.pmpp.2020.101514, 111, (101514), (202014). Fatemeh Hodadadi, Jonathan B. Gonzalez, Philippe L. Martin, Emilie Giroud, Guillaume Bilodeau, Kari A. Peter, Vinson. Doyle, Srjan G. Azimovic, identification and characterization of the types of colletorium that cause apple bitter rot in New York and the description of C. noveboracense sp. nov., Scientific Reports, 10.1038/s41598-020-66761-9, 10, 1, (2020). Christopher Biggs, Lauren A. Iger, Derek G. Bolser, Christina Bonsell, Angelina M. Dichiera, Chengsin Howe, Spencer R. Keiser, Alexis Khursigara, Kaijun Lu, Arleigh F. Mut, Benjamin Negrete, Brad E. Erisman, does functional redundancy affect environmental stability and sustainability? Review and Meta-Analysis, Ecosphere, 10.1002/ecs2.3184, 11, 7, (2020). Jeff M. Martin, Perry S. Barbosa, Thermal Biology and Bison Growth along the Great Plains: Study of Four Endotherma Body Size Theories, Ecosphere, 10.1002/ecs2.3176, 11, 7, (2020). Andrey Sokolov, Alexander Kuzov, Jeanne Buldyreva, leading spectral moments for easy pressure calculation on the rotational line, journal Roman spectroscopy, 10.1002/jrs.5923, 51, 8, (1390-1394), (2020). Joana Figueiredo, Jorge Cunha, Jose Eiras-Diaz, Marta Souza Silva, Andrei Figueiredo, related pathogens specifics of subtylasis VVISBT4.19 X1 in Vitis vinifera defense response , Ci'ncia e T'cnica Vitivin'sola, 10.1051/20203501042, 35, 1, (42-48), (20201042, 35, 1, (42-48), (2020). Stefanie Lueck, Ulrike Beukert, Dimitar Douchkov, BluVision Macro - software for automated powdery mold and rust quantify diseases on individual leaves., Open Source Software, 10.21105/joss.02259, 5, 51, (2259), (2020). Vinai Kumar, Vinakonda Rakesh Sharma, Himani Patel, Nisha Dinkar, A Look at Current Trends in The Identification of Pathogens in Plants, Phytobiois: Current Research and Future Prospects, 10.1007/978-981-15-3151-4, (127-162), (2020). Monica Borgi, Alysdair R. Ferni, Outstanding Issues in Floral Metabolism, Plant Magazine, 10.1111/tpj.14814, 103, 4, (1275-1288), (2020). Ayim B. Tleuova, Eva Vilogorska, V.S.S.L. Prasad Talluri, Frantisek Stepanek, Christopher T. Elliott, Dmitry Grigoriev, Recent achievements and remaining barriers to the production of new fungicide recipes for safe and sustainable agriculture, controlled edition journal, 10.1016/j.jconrel.2020.07.035, 326, (468-481), (2020). Tingyue Feng, Jialong Li, Mingfan Sun, Jingnan Peng, Xinhai Li, Jichiu Chi, SYAUP-CN-26 applies its antifungal activity against Botrytis cinerea, disrupting mitochondrial structure and function, Biochimie, 10.1016/j.biochi.2020.07.012, (2020). Yogita N. Sarki, Rinandahun Marwain, Sanjay Singh, Hariprasanna Dekaboruah, Dhanawantari L. Singh, Channakeshavaiah Chikkaputtaiah, Understanding the mechanism of host pathogenic interaction in the rice through genomics approaches, Rice research to improve quality: genomics and genetic engineering, 10.1007/978-981-15-5337-0, (1-33), (2020). Paige M.K. Larkin, Kathy L. Lawson, Dacey A. Contreras, Katherine S. Le, Marisol Trejo, Susan Realgegeno, Evann E. Hilt, Sucanta Chandrasekaran, Omay B. Garner, Gregory A. Fishbein, Shansin Yang, Amplicon based on the next generation of sequences for the detection of mushrooms in Formaline and Clinical Applications, Journal of Molecular Diagnostics, 10.1016/j.jmoldx.2020.06.017, (2020). Fangli Wu, Jini Chi, Xin Meng, Weibo Jin, miR319c acts as a positive tomato regulator against Botrytis cinerea infection, focusing on TCP29, Plant Science, 10.1016/j.plantsci.2020.110610, (110610), (2020). Mandeep Singh Hongjan, Jagjeet Singh Lore, Climate Change: Impact on plants pathogens, diseases and their management, protection of crops in the face of climate change, 10.1007/978-3-030-46111-9, (85-100), (2020). Claire Kanja, Kim E. Hammond-Kosak, Discovery and characteristic of the protein effector in plant filamentous pathogens, molecular plant pathology, 10.1111/mpp.12980, 21, 10, (1353-1376), (2020). Carolina Sardine Francisco, Maria Manuela zvig, Javier Palma-Guerrero, role of vegetative cell mergers in the development and asexual reproduction of the wheat fungal pathogen zimoseptory tritichi, BMC Biology, 10.1186/s12915-020-00838-9, 18, 1, (2020). Xiaoyun Liu, Dongchao Ji, Xiaomin Tsui, Chang Chang, Bokyang Li, Yong Xi, Tong Chen, Shiping Tian, r-Kumaric acid causes antioxidant ability and protective reactions of sweet cherry fruits to fungal pathogens, Postharvest Biology and Technology, 10.1016/j.postharvbio.2020.11297, 169, (111297), (2020). Mark Bardin, Maria Lodovica Gullino, fungal diseases, integrated pest control and diseases in greenhouse crops, 10.1007/978-3-030-22304-5, (55-100), (2020). Mohd. Kamran Khan, Anamika Pandey, Tabinda Athar, Saumya Choudhary, Ravi Deval, Sait Gezgin, Mehmet Hamourku, Ali Topal, Emel Atmaka, Pamela Arasen Santos, Maqboobe Rumeisa Omay, Hatis Suslu, Kamer Gulkan, Merve Inanz, Mahinur S. Akkkaya, Abdullah Kahraman, George Thomas, head of Fusarium overshadow wheat: modern status and molecular approaches, 3 Biotech, 10.1007/s13205-020-2158-x, 10, 4, (2020). Saidi R. Achari, Jatinder Kaur, Kuang Dinh, Ross Mann, Tim Sobridge, Brett A. Summerell, Jacqueline Edwards, Philogenetic Relationship between Australian Fusarium oxysporum isolates and solutions of the species complex using multi-species coal model, BMC Genomics, 10.1186/s12864-020-6640-y, 21, 1, (2020). Tao-Ho Chang, In-Chung Lu, Min Jun Yang, Jenn-Wen Huang, Pi-Fan Linda Chang, Han-yu Hsue, Multiton flower particles from environmentally friendly hydrothermal synthesis as green antimicrobials in agriculture, Journal of Clean Production, 10.1016/j.jclepro.2020.121342, (121342), (2020). Chenghui Jun, Liangyu Lin, Huakun Cheng, Jiangdong Bao, Meilian Chen, Limei Chang, Wei Tang, Daniel J. Ebbole, Tsonghua Wang, Appearance of Hybrid PKS-NRPS secondary metabolite cluster in the clonal rice population of the exploding mushroom Magnaporthe oryzae, Ecological Microbiology, 10.1111/1462-2920.14994, 22, 7, (2709-2723), (2020). Yingzi Yun, Pusheng Go, Jing Chang, Haixia You, Pinting Go, Huobin Deng, Hao, Laimei Chang, Xueyu Wang, Yakubu Yakubu Abubakar, Jie Chou, Guodong Lu, Tsongua Wang, Wenhui Cheng, Flippases play specific but different roles in the development, pathogenicity and secondary metabolism of fusarium graminearum, molecular plant pathology, 10.1111/mpp.12985, 21, 10, (1307-1321), (202). Chenyu Wang, Ishao Wang, Yao Wang, Jidong Wang, Liyuan Chang, Yuancun Liang, Lei Chen, Shenshen Tsou, Hanson Dong, ADP-ribosing factor-like small GTPase FgArl1 is involved in growth, pathogenicity and DON production in Fusar gramiuminearum, fungal biology, 10.1016/j.funbio.2020.08.004, (2020). Эухенио М. Сперандио, Таввс М. Алвес, Хельсон Марио Мартинс ду Вейл, Летия де Алмейда Гонсалвеш, Элиенай Кандия е Силва, Марта Кристина Корси де Филиппи, Сигнализация обороны ответы на авирулентных и вирулентных штаммов Magnaporthe oryzae, журнал физиологии растений, 10.1016/j. (153271), (2020.M.K. Hausbeck, B.R. Harlan, E.I. Brisco-McCann, Достижения в управлении Botrytis для цветочных культур , Acta Horticulturae, 10.17660/ActaHortic.2020.1288.35, 1288, (231-238), (2020). Розина Кабрера, Эктор Гарсия-Лопес, Энеас Агирре-фон-Вобесер, Хесус Антонио Ороско-Авития, Альдо Хирам Гутьеррес-Салданья, Amycolatopsis BX17: актинобактериальный штамм, изолированный от почвы традиционной агроэкосистемы милпа с потенциальным биоконтролем против fusarium graminearum, Biological Control, 10.1016/j.biocontrol.2020.104285, (104285), (2020). Сакет Чандра, Лопамудра Сатапатия, Ширупа Басу, Шайлендра Кумар Джа, Маниш Кумар, Кунал Мухопадхаяй, Характеристика листьев ржавчины отзывчивых генов АРФ в пшенице (Triticum aestivum L.), Отчеты о клетках растений , 10.1007/s00299-020-02591-3, (2020). Manoj K. Chitara, Chetan Keswani, Kyriakos G. Barnabas, Hareram Birla, Hager dilnashin, Surya. Singh, Viji Sarojini, Jonathan Sperry, Harikesh B. Singh, Influence of alcaloid colletotrihumin A on the pathogenic coletorium capsidi in Capsicum annum L, Rhizosphere, 10.1016/j.rhisph.2020.100247, 16, (100247), (2020.100247, 16, 16, 16, (100247). Jiehua Tsyu, Feifei Lu, Meng Xiong, Shuai Meng, Xianglin Shen, Yanjun Kou, Comparative Transcriptome Analysis shows mechanistic basis of Pib-mediated broad Spectrum Resistance vs. Magnaporthe oryzae, Functional Integrative Genomics, 10.1007/s10142-020-00752-x, (2020).