Review Article

Insights into the roles of Giant Starships of Diversity in Fungal Genomes

Abstract

Fungal genomes exhibit remarkable diversity, encompassing a wide range of ecological, morphological, and physiological traits. Among the most intriguing elements of this diversity are the "Giant Starships," large genomic regions that harbor extensive genetic variation and play crucial roles in adaptation and evolution. This review provides a comprehensive examination of the structure, function, and evolutionary significance of these genomic regions in fungi. We explore the mechanisms by which Giant Starships contribute to genetic diversity, their impact on fungal fitness and adaptation, and their potential applications in biotechnology and agriculture. By synthesizing recent research findings, this review aims to offer valuable insights into the complex dynamics of fungal genome evolution and the pivotal role of Giant Starships in shaping fungal diversity.

Keywords: Fungal genomes, genetic diversity, Giant Starships, adaptation, evolution, secondary metabolism, stress response, pathogenicity, biotechnology, agriculture

Introduction:

Fungi, a kingdom encompassing an estimated 2.2 to 3.8 million species, are fundamental to ecosystems, playing key roles in nutrient cycling, decomposition, symbiosis, and as pathogens. Their ecological versatility is matched by a remarkable diversity in life strategies, including saprophytism, parasitism, and mutualism. Fungi exhibit a wide array of

morphological forms, ranging from unicellular yeasts to complex multicellular structures like mushrooms and mold colonies. This diversity is underpinned by equally diverse genomic architectures, which provide the genetic flexibility required for survival and adaptation in varied and often hostile environments.

The genomic sizes of fungi vary dramatically, from the compact genomes of certain yeasts, which are less than 10 megabases (Mb), to the expansive genomes of some filamentous fungi and basidiomycetes, which can exceed 1 gigabase (Gb). This variation is not merely a reflection of the organism's complexity but also indicative of the evolutionary pressures and ecological niches they occupy. In particular, certain regions within these genomes, dubbed "Giant Starships," are of profound interest due to their exceptional size and the genetic variability they harbor. These Giant Starships are akin to genomic beacons, guiding our understanding of how fungi adapt and evolve.

Giant Starships are characterized by their large genomic expanses, often encompassing hundreds of kilobases to megabases of DNA. They contain a mosaic of genetic elements, including protein-coding genes, regulatory sequences, transposable elements, and repetitive DNA. The genes within these regions are frequently involved in critical biological processes such as secondary metabolism, which produces a plethora of bioactive compounds; stress response mechanisms that allow fungi to withstand environmental challenges; and pathogenicity factors that enable fungi to infect and interact with host organisms. This rich repository of genetic material provides a toolbox for rapid adaptation, offering a competitive edge in dynamic and diverse environments.

The term "Giant Starships" evokes imagery of vast, complex entities navigating the genomic

landscape, and this analogy is fitting given their roles. These regions can be seen as evolutionary engines, capable of propelling fungi through ecological challenges by fostering genetic diversity and innovation. The structure of Giant Starships is complex, with a high density of genes and regulatory elements interspersed with mobile genetic elements and repetitive sequences. This structural complexity facilitates genetic recombination and variation, driving evolution and adaptation.

Understanding the function of Giant Starships necessitates a multifaceted approach. The genes housed within these regions often encode enzymes and proteins pivotal to primary and secondary metabolism, stress tolerance, and pathogenicity. For example, secondary metabolites, which include antibiotics, mycotoxins, and pigments, are synthesized by gene clusters frequently located within Giant Starships. These metabolites can be critical for survival, providing defense mechanisms against competitors, predators, and environmental stresses. Similarly, genes involved in detoxifying reactive oxygen species, repairing DNA, and producing protective molecules are essential for stress responses.

In pathogenic fungi, Giant Starships are hotspots for genes encoding virulence factors. These genes facilitate host infection, colonization, and evasion of immune responses. The high genetic variability within Giant Starships allows pathogenic fungi to adapt rapidly to different host defenses and environmental conditions, enhancing their infectivity and survival.

From an evolutionary perspective, Giant Starships are significant because they enable rapid genetic changes and adaptations. Mechanisms such as horizontal gene transfer (HGT), gene duplication, and the activity of transposable elements contribute to the dynamic nature of these regions. HGT allows the acquisition of novel genes from other organisms, enhancing genetic

diversity and adaptive potential. Gene duplication provides raw material for the evolution of new functions, while transposable elements promote genomic rearrangements and recombination events.

The evolutionary pressures acting on Giant Starships are complex and multifaceted. Positive selection favors beneficial mutations that enhance fungal fitness, while purifying selection removes deleterious mutations. The high genetic diversity within these regions provides a reservoir of variation that can be acted upon by natural selection. Additionally, the population structure of fungi, including factors such as genetic diversity and gene flow, influences the dynamics of Giant Starships. In populations with high genetic diversity and gene flow, beneficial alleles within Giant Starships can spread rapidly, facilitating adaptation. In contrast, in structured populations with limited gene flow, genetic drift and local adaptation play more prominent roles.

The study of Giant Starships in fungal genomes has far-reaching implications beyond understanding basic fungal biology. These regions are rich sources of genes involved in the biosynthesis of secondary metabolites, which have significant applications in biotechnology and agriculture. For example, many antibiotics and other pharmaceuticals are derived from fungal secondary metabolites. Understanding the genetic basis of secondary metabolite production within Giant Starships can inform bioprospecting efforts and the development of new drugs. Additionally, insights into the genes and mechanisms underlying fungal pathogenicity can inform strategies for controlling fungal diseases in crops, animals, and humans.

Moreover, the genetic diversity within Giant Starships can be harnessed for improving

industrial fungal strains used in the production of enzymes, biofuels, and other valuable products. By engineering the expression of genes involved in metabolic pathways, it is possible to enhance the production of these compounds, increasing their commercial viability.

Giant Starships are a fascinating and crucial aspect of fungal genomics. They represent regions of high genetic diversity and innovation, driving the adaptation and evolution of fungi. Understanding the structure, function, and evolutionary dynamics of Giant Starships provides valuable insights into the complex interplay between genetic diversity and fungal fitness. Furthermore, the knowledge gained from studying these regions has important applications in biotechnology and agriculture, offering new opportunities for harnessing the genetic potential of fungi for human benefit. Continued research in this field will undoubtedly uncover new aspects of fungal genome biology and further our understanding of the intricate mechanisms that drive fungal diversity and evolution.

Diversity in Fungal Genomes

Fungal genomes exhibit remarkable diversity, reflecting the extensive adaptability and ecological roles of fungi across different environments. This diversity is seen in genome size, structure, and content, with some fungal genomes being compact and streamlined, while others are expansive with numerous repetitive elements and secondary metabolite gene clusters. The variation in genome organization and gene content allows fungi to inhabit a wide range of ecological niches, from symbiotic relationships with plants and animals to decomposing organic matter and causing diseases in plants, animals, and humans. Advances in sequencing technologies have uncovered a plethora of genetic variations and evolutionary strategies employed by fungi, highlighting their importance in biotechnology, agriculture, medicine, and ecosystem functioning. This genomic diversity not only underscores the

complexity of fungal biology but also presents opportunities for biotechnological innovations and novel therapeutic approaches.

1. Structure of Giant Starships:

Giant Starships are large genomic regions characterized by high genetic diversity and complex structural organization. These regions often contain a mix of coding and non-coding sequences, including genes, regulatory elements, transposable elements, and repetitive sequences. The structural complexity of Giant Starships is thought to facilitate rapid genetic changes, allowing fungi to adapt to new environmental challenges.

1.1 Gene Content and Organization:

The gene content of Giant Starships varies widely among different fungal species. In many cases, these regions harbor clusters of genes involved in secondary metabolism, such as the biosynthesis of antibiotics, toxins, and other bioactive compounds. The organization of these genes within Giant Starships is often modular, with distinct clusters of functionally related genes. This modular organization may facilitate the coordinated regulation of gene expression in response to environmental cues.

1.2 Regulatory Elements and Epigenetic Modifications:

Giant Starships contain numerous regulatory elements that control the expression of genes within these regions. These elements include promoters, enhancers, and insulators, which interact with transcription factors and other regulatory proteins to modulate gene expression. Epigenetic modifications, such as DNA methylation and histone modifications, also play a crucial role in regulating the activity of genes within Giant Starships. These modifications can alter chromatin structure and accessibility, thereby influencing the transcriptional landscape of these genomic regions.

2. Function of Giant Starships:

The functional significance of Giant Starships lies in their ability to generate genetic diversity and facilitate adaptation. The genes within these regions often encode proteins involved in key biological processes that are critical for fungal survival and fitness.

2.1 Metabolic Flexibility:

Giant Starships often contain genes involved in primary and secondary metabolism, enabling fungi to exploit a wide range of substrates and ecological niches. For example, the presence of multiple gene clusters for the biosynthesis of secondary metabolites allows fungi to produce a diverse array of bioactive compounds, which can be used for defense against predators, competitors, and pathogens.

2.2 Stress Response and Adaptation:

Genes within Giant Starships are frequently associated with stress response mechanisms, including the detoxification of reactive oxygen species, repair of damaged DNA, and the production of protective compounds. The ability to rapidly adapt to environmental stressors is a key factor in the success of fungi in diverse habitats.

2.3 Pathogenicity and Host Interaction:

In pathogenic fungi, Giant Starships often harbor genes involved in virulence and host interaction. These genes encode proteins that facilitate the invasion and colonization of host tissues, evasion of host immune responses, and acquisition of nutrients from the host. The high genetic variability within Giant Starships allows pathogenic fungi to adapt to different host species and evade host defenses.

3. Evolutionary Significance of Giant Starships:

Giant Starships play a pivotal role in the evolution of fungal genomes by facilitating genetic innovation and adaptation. The mechanisms underlying the evolution of these regions are complex and multifaceted.

3.1 Horizontal Gene Transfer and Gene Duplication:

Horizontal gene transfer (HGT) and gene duplication are key mechanisms driving the evolution of Giant Starships. HGT allows the acquisition of novel genes from other organisms, while gene duplication provides raw material for the evolution of new functions. The presence of transposable elements and repetitive sequences within Giant Starships can facilitate these processes by promoting genomic rearrangements and recombination events.

3.2 Adaptive Evolution and Selection:

The genes within Giant Starships are subject to strong selective pressures, which drive adaptive evolution. Positive selection acts on beneficial mutations that enhance fungal fitness, while purifying selection removes deleterious mutations. The high genetic diversity within Giant Starships provides a reservoir of genetic variation that can be exploited by natural selection.

3.3 Population Structure and Genetic Diversity:

The population structure of fungi can influence the dynamics of Giant Starships. Giant Starships can rapidly spread beneficial alleles and facilitate adaptation in populations with high levels of genetic diversity and gene flow. Conversely, in structured populations with limited gene flow, genetic drift and local adaptation can shape the evolution of these regions.

4. Applications in Biotechnology and Agriculture:

The insights gained from studying Giant Starships have important applications in biotechnology and agriculture. Understanding the genetic and functional diversity within these regions can inform the development of novel strategies for fungal disease control, bioprospecting for new bioactive compounds, and the improvement of fungal strains for industrial applications.

4.1 Fungal Disease Control:

Targeting genes within Giant Starships can provide new avenues for controlling fungal pathogens. For example, disrupting key virulence factors encoded within these regions can attenuate the pathogenicity of fungal pathogens, providing a basis for the development of new antifungal therapies.

4.2 Bioprospecting and Natural Product Discovery:

Giant Starships are rich sources of genes involved in the biosynthesis of secondary metabolites, which have potential applications as pharmaceuticals, agrochemicals, and industrial enzymes. Bioprospecting efforts can focus on these regions to identify novel bioactive compounds with commercial value.

4.3 Industrial Fungal Strain Improvement:

The genetic diversity within Giant Starships can be harnessed to improve the performance of fungal strains used in industrial processes. For example, engineering gene expression in metabolic pathways can enhance the production of enzymes, biofuels, and other valuable products.

Conclusion:

Giant Starships represent a fascinating aspect of fungal genomics, contributing to the remarkable diversity and adaptability of fungi. By facilitating genetic innovation and adaptation, these regions play a crucial role in the evolution of fungal genomes. Understanding the structure, function, and evolutionary dynamics of Giant Starships provides valuable insights into the complex interplay between genetic diversity and fungal fitness. Furthermore, the knowledge gained from studying these regions has important applications in biotechnology and agriculture, offering new opportunities for harnessing the genetic potential of fungi for human benefit. Continued research in this field will undoubtedly uncover new aspects of fungal genome biology and further our understanding of the intricate mechanisms that drive fungal diversity and evolution.

References

Aboukhaddour R, Cloutier S, Ballance G, And Lamari L. 2009, Genome

Characterization Of *Pyrenophora Tritici-Repentis* Isolates Reveals High Plasticity And Independent Chromosomal Location Of *Toxa* And *Toxb*. *Mol Plant Pathol*. **10**(2):201–12.

Aboukhaddour R, Cloutier S, Lamari L, And Strelkov S. 2011, Simple

Sequence Repeats And Diversity Of Globally Distributed Populations Of *Pyrenophora Tritici-Repentis*. *Can J Plant Pathol*. **33**(3):389–99.

Aboukhaddour R, Hafez M, Strelkov S, And Fernandez Mr. 2021. Tan Spot

Under The Lenses Of Plant Pathologists. In: Oliver Rp, Editor. Achieving Durable Resistance In Cereals. Cambridge: Burliegh Dodds;

Antipov D, Korobeynikov A, Mclean Js And Pevzner Pa. 2016, Hybrid

Spades: An Algorithm For Hybrid Assembly Of Short And Long Reads. *Bioinformatics* **32**:1009–1015.

Arkhipova Ir And Yushenova Ia. 2019, Giant Transposons In Eukaryotes: Is Bigger Better? *Genome Biol Evol.* **11**:906–918.

Baquero F. 2004, From Pieces To Patterns: Evolutionary Engineering In Bacterial Pathogens.

Nat Rev Microbiol. 2:510-518.

Bellanger X, Payot S, Leblond-Bourget N, And Guédon G. 2014,

Conjugative And Mobilizable Genomic Islands In Bacteria: Evolution And Diversity.

Fems Microbiol Rev. 38:720–760.

Benler S, Faure G, Tran H-A, Shmakov S, Zheng F, And Koonin E. 2021,

Cargo Genes Of Tn7-Like Transposons Comprise An Enormous Diversity Of Defense Systems, Mobile Genetic Elements And Antibiotic Resistance Genes. Available From: https://www.Biorxiv.Org/ Content/10.1101/2021.08.23.457393v1.

Billane K, Harrison E, Cameron D, And Brockhurst Ma. 2022, Why Do

Plasmids Manipulate The Expression Of Bacterial Phenotypes? *Philos Trans R Soc B Biol Sci.* **377**:20200461.

Brockhurst Ma, Harrison E, Hall Jpj, Richards T, Mcnally A And

Maclean C. 2019, The Ecology And Evolution Of Pangenomes. *Curr Biol.* **29**: R1094–R1103. Brown Cj, Sen D, Yano H, Bauer Ml, Rogers Lm, Van Der Auwera Ga,

And Top Em. 2013, Diverse Broad-Host-Range Plasmids From Freshwater Carry Few Accessory Genes. *Appl Environ Microbiol.* **79**: 7684–7695.

Cheeseman K, Ropars J, Renault P, Dupont J, Gouzy J, Branca A, Abraham A-L, Ceppi M, Conseiller E, And Debuchy R, Et Al. 2014,

Multiple Recent Horizontal Transfers Of A Large Genomic Region In Cheese Making Fungi.

Nat Commun. 5:2876.

- Ciuffetti Lm, Manning Va, Pandelova I, Faris Jd, Friesen Tl, And
 - Strelkov Se, Et Al. 2014, *Pyrenophora Tritici-Repentis*: A Plant Pathogenic Fungus With Global Impact. Genomics Of Plant-Associated Fungi: Monocot Pathogens. Berlin: Springer; P. 1–39.
- Dallaire A, Manley Bf, Wilkens M, Bista I, Quan C, Evangelisti E, Bradshaw Cr, Ramakrishna Nb, Schornack S, And Butter F, Et Al.
 - 2021. Transcriptional Activity And Epigenetic Regulation Of Transposable Elements In The Symbiotic Fungus *Rhizophagus Irregularis*. *Genome Res.* **31**:2290–2302.
- Dobrindt U, Hochhut B, Hentschel U And Hacker J. 2004, Genomic Islands In
 - Pathogenic And Environmental Microorganisms. Nat Rev Microbiol. 2:414–424.
- Eickbush Dg, And Eickbush Th. 1995, Vertical Transmission Of The Retrotransposable Elements R1 And R2 During The Evolution Of The *Drosophila Melanogaster* Species Subgroup. *Genetics*, **139**: 671–684.
- Espagne E, Lespinet O, Malagnac F, Da Silva C, Jaillon O, Porcel Bm, Couloux A, Aury J-M, Ségurens B, And Poulain J, Et Al. 2008, The Genome Sequence Of The Model Ascomycete Fungus *Podospora Anserina*. *Genome Biol* 9: R77. Doi:10.1186/Gb-2008-9-5-R77
- Faino L, Seidl Mf, Shi-Kunne X, Pauper M, Van Den Berg Gcm,
 - Wittenberg Ahj, And Thomma Bphj. 2016, Transposons Passively And Actively Contribute To Evolution Of The Two-Speed Genome Of A Fungal Pathogen. *Genome Res.* **26**:1091–1100.
- Fehr Wr, Caviness Ce, Burmood Dt And Pennington Js. 1971, Stage Of
- Development Descriptions For Soybeans, *Glycine Max* (L.) Merrill. *Crop Sci.* **11**:929–931. Ghinet Mg, Bordeleau E, Beaudin J, Brzezinski R, Roy S, And Burrus V.
 - 2011, Uncovering The Prevalence And Diversity Of Integrating Conjugative Elements In Actinobacteria. *Plos One*, **6**:E27846.
- Gourlie, R., Mcdonald, M., Ha Fez, M., Ortega-Polo, R., Low, K. E., Abbott, D. W., Strelkov, S. E., Daayf, F. And Aboukhaddour, R., 2022, The Pangenome Of The Wheat Pathogen *Pyrenophora Tritici-Repentis* Reveals Novel Transposons Associated With Necrotrophic Effectors Toxa And Toxb. *Bmc Biol.*, **20**(1): 1-21.
- Inoue Y, Kumagai M, Zhang X, Saga T, Wang D, Koga A, And Takeda H.
 - 2018, Fusion Of Piggybac-Like Transposons And Herpesviruses Occurs Frequently In Teleosts. *Zool Lett.* **4**:6.
- Inoue Y, Saga T, Aikawa T, Kumagai M, Shimada A, Kawaguchi Y, Naruse K, Morishita S, Koga A, And Takeda H. 2017, Complete Fusion Of
 - A Transposon And Herpesvirus Created The Teratorn Mobile Element In Medaka Fish. *Nat Commun.* **8**:551.
- Islam Ms, Haque Ms, Islam Mm, Emdad Em, Halim A, Hossen Qmm, Hossain Mz, Ahmed B, Rahim S And Rahman Ms, Et Al. 2012, Tools To Kill:
 - Genome Of One Of The Most Destructive Plant Pathogenic Fungi *Macrophomina Phaseolina*. *Bmc Genomics* **13**:493.
- Kamel S, Cherif M, Hafez M, Despins T, And Aboukhaddour R. 2019,

- Pyrenophora Tritici-Repentis In Tunisia: Race Structure And Effector Genes. Front Plant Sci. **10**:1562.
- Katoh K, Standley Dm. 2013, Mafft Multiple Sequence Alignment Software Version 7: Improvements In Performance And Usability. *Mol Biol Evol.* **30**:772–780.
- Kazazian Jr, H.H. And Moran, J.V., 1998, The Impact Of L1 Retrotransposons On The Human Genome. *Nat. Genet.*, **19**(1), Pp.19-24.
- Kazazian Jr, H.H., Wong, C., Youssoufian, H., Scott, A.F., Phillips, D.G.
 - And Antonarakis, S.E., 1988, Haemophilia A Resulting From De Novo Insertion Of L 1 Sequences Represents A Novel Mechanism For Mutation In Man. *Nature*, **332**(6160), Pp.164-166.
- Kingsley Ra, Msefula Cl, Thomson Nr, Kariuki S, Holt Ke, Gordon Ma, Harris D, Clarke L, Whitehead S, And Sangal V, Et Al. 2009, Epidemic

 Multiple Drug Resistant *Salmonella Typhimurium* Causing Invasive Disease In Sub- Saharan
- Africa Have A Distinct Genotype. *Genome Res.* **19**:2279–2287. Koga, A., Iida, A., Hori, H., Shimada, A. And Shima, A., 2006, Vertebrate Dna
 - Transposon As A Natural Mutator: The Medaka Fish Tol2 Element Contributes To Genetic Variation Without Recognizable Traces. *Mol. Biol. Evol.*, **23**(7), Pp.1414-1419.
- Lamari L, Strelkov S, Yahyaoui A, Orabi J, And Smith R (2003), The

Nature, **464**:367–373.

- Identification Of Two New Races Of *Pyrenophora Tritici-Repentis* From The Host Center Of Diversity Confirms A One-To-One Relationship In Tan Spot Of Wheat. *Phytopathol*; **93**(4):391–6.
- Ma L-J, Van Der Does Hc, Borkovich Ka, Coleman Jj, Daboussi M-J, Di Pietro A, Dufresne M, Freitag M, Grabherr M, And Henrissat B, Et Al. 2010, Comparative Genomics Reveals Mobile Pathogenicity Chromosomes In Fusarium.
- Madden Lv, Hughes G, Van Den Bosch F. 2017, The Study Of Plant Disease Epidemics. The American Phytopathological Society. Available From: https://Apsjournals.Apsnet.Org/Doi/Book/10.1094/9780890545058.
- Maistrenko Om, Mende Dr, Luetge M, Hildebrand F, Schmidt Tsb, Li Ss, Rodrigues Jfm, Von Mering C, Pedro Coelho L And Huerta-Cepas
 - J, Et Al. 2020, Disentangling The Impact Of Environmental And Phylogenetic Constraints On Prokaryotic Within-Species Diversity. *Isme J.* **14**:1247–1259
- Mcdonald Mc, Taranto Ap, Hill E, Schwessinger B, Liu Z, Simpfendorfer S, Milgate A, And Solomon Ps. 2019, Transposon-
 - Mediated Horizontal Transfer Of The Host-Specific Virulence Protein Toxa Between Three Fungal Wheat Pathogens. *Mbio* **10**: E01515–E01519.
- Melnyk Ra, Hossain Ss, And Haney Ch. 2019, Convergent Gain And Loss Of Genomic Islands Drive Lifestyle Changes In Plant-Associated *Pseudomonas*. *Isme J.* **13**:1575–1588.
- Mendiburu Fd, And Simon R. 2015, Agricolae Ten Years Of An Open Source Statistical Tool For Experiments In Breeding, Agriculture And Biology. *Peerj Inc.* **3**: E1404v1. Doi:10.7287/Peerj.Preprints. 1404v1.
- Mengistu A, Reddy Kn, Zablotowicz Rm, And Wrather Aj. 2009, Propagule
 - Densities Of Macrophomina Phaseolina In Soybean Tissue And Soil As Affected By Tillage, Cover Crop, And Herbicide. *Plant Health Prog.* **10**:28.

- Mieczkowski Pa, Lemoine Fj, And Petes Td. 2006, Recombination Between Retrotransposons As A Source Of Chromosome Rearrangements In The Yeast *Saccharomyces Cerevisiae*. *Dna Repair* (Amst) **5**: 1010–1020. Doi:10 .1016/J.Dnarep.2006.05.027
- Miki, Y., Nishisho, I., Horii, A., Miyoshi, Y., Utsunomiya, J., Kinzler, K.W.,
 - Vogelstein, B. And Nakamura, Y., 1992, Disruption Of The Apc Gene By A Retrotransposal Insertion Of L1 Sequence In A Colon Cancer. *Cancer Res*, **52**(3), Pp.643-645.
- Moniruzzaman M And Aylward F. 2021, Endogenous Giant Viruses Shape Intraspecies Genomic Variability In The Model Green Alga *Chlamydomonas Reinhardtii*. Available From: Https://Www.Biorxiv.Org/Content/10.1101/2021.11.30.470594v1.
- Pawlowski Ml, Hill Cb, And Hartman Gl. 2015, Resistance To Charcoal Rot Identified In Ancestral Soybean Germplasm. *Crop Sci.* **55**: 1230–1235.
- Rooney Ap, And Ward Tj. 2005, Evolution Of A Large Ribosomal Rna Multigene Family In Filamentous Fungi: Birth And Death Of A Concerted Evolution Paradigm. *Proc Natl Acad Sci* U S A. **102**:5084–5089.
- Sanmiguel, P., Tikhonov, A., Jin, Y.K., Motchoulskaia, N., Zakharov, D., Melake-Berhan, A., Springer, P.S., Edwards, K.J., Lee, M., Avramova, Z. And Bennetzen, J.L., 1996, Nested Retrotransposons In The Intergenic Regions Of The Maize Genome. *Science*, **274**(5288), Pp.765-768.
- Savary S, Willocquet L, Pethybridge Sj, Esker P, Mcroberts N, And
 - Nelson A. 2019, The Global Burden Of Pathogens And Pests On Major Food Crops. *Nat Ecol Evol.*, **3**(3):430–9.
- Sexton Zf, Hughes Tj, And Wise Ka. 2016, Analyzing Isolate Variability Of
 - Macrophomina Phaseolina From A Regional Perspective. Crop Prot. 81:9–13.
 - Activation, And Trafficking Of The Fet3p.Ftr1p High Affinity Iron Permease Complex In *Saccharomyces Cerevisiae*. *J Biol Chem.* **281**:13355–13364.
- Slotkin, R.K. And Martienssen, R., 2007, Transposable Elements And The Epigenetic Regulation Of The Genome. *Nat. Rev. Genet.*, **8**(4), Pp.272-285.
- Steenwyk Jl, Iii Tjb, Li Y, Shen X-X, And Rokas A. 2020, Clipkit: A Multiple
 - Sequence Alignment Trimming Software For Accurate Phylogenomic Inference. *Plos Biol.* **18**:E3001007
 - : Awanindra Kumar Tiwari (2022). Assessing The Real Productivity Of Organic Farming Systems In Contemporary Agriculture. Plant Science Archives.
- Stukenbrock Eh, And Croll D. 2014, The Evolving Fungal Genome. Fungal Biol Rev.
 - **28**:1–12.
- Sullivan Jt, Ronson Cw. 1998, Evolution Of Rhizobia By Acquisition Of A 500-Kb Symbiosis Island That Integrates Into A Phe-Trna Gene. *Proc Natl Acad* Sci U S A. **95**:5145–5149
- Te Poele Em, Bolhuis H, Dijkhuizen L. 2008, Actinomycete Integrative And Conjugative Elements. *Anton Leeuw Int J G*, **94**:127–143.
- Vidhya C. S., Priya Subramanian Kalaimani, Aniketa Sharma, Ashiq Hussain Magrey, Rajni Kant Panik (2022). Enhanced Wound Care Solutions: Harnessing Cellulose Acetate-Eusol/Polyvinyl Alcohol-Curcumin Electrospun Dressings For Diabetic Foot Ulcer Treatment. Plant Science

Archives.

Templeton Ar, Hollocher H, And Johnston Js. 1993, The Molecular Through

Ecological Genetics Of Abnormal Abdomen In *Drosophila Mercatorum*. V. Female Phenotypic Expression On Natural Genetic Backgrounds And In Natural Environments. *Genetics*, **134**:475–485.

Ter-Hovhannisyan V, Lomsadze A, Chernoff Yo, And Borodovsky M.

2008, Gene Prediction In Novel Fungal Genomes Using An Ab Initio Algorithm With Unsupervised Training. *Genome Res.* **18**:1979–1990.

Thaler, G. E., Ralston, T., Konkel, Z., Ocampos, C. G., Ganeshan, V. D., Dorrance, A. E., Niblack, T. L., Wood, C. W., Slot, J. C., Lopez-Nicora,

H. D. And Vogan, A. A., 2022, Giant Starship Elements Mobilize Accessory Genes In Fungal Genomes. *Mol. Biol. Evol.*, **39**(5): 109-126.

Rathna Kumari B. M. (2022). Exploring The Antiviral Properties Of Dietary Plant Extracts Against Sars-Cov-2: A Comprehensive Review. Plant Science Archives

Twizeyimana M, Hill Cb, Pawlowski M, Paul C, Hartman Gl. 2012, A Cut-

Stem Inoculation Technique To Evaluate Soybean For Resistance To *Macrophomina Phaseolina*. *Plant Dis*. **96**:1210–1215.

Urquhart As, Chong Nf, Yang Y, Idnurm A. 2022, A Large Transposable Element Mediates Metal Resistance In The Fungus *Paecilomyces Variotii*. *Curr Biol*. **32**:937–950.E5.

Singh A, Severance S, Kaur N, Wiltsie W, And Kosman Dj. 2006, Assembly,

Verma J, Bag S, Saha B, Kumar P, Ghosh Ts, Dayal M, Senapati T, Mehra

S, Dey P, Desigamani A, Et Al. 2019, Genomic Plasticity Associated With Antimicrobial Resistance In Vibrio Cholerae. *Proc Natl Acad* Sci U S A. **116**:6226–6231. Vogan Aa, Ament-Velásquez Sl, Bastiaans E, Wallerman O, Saupe Sj,

Suh A, And Johannesson H. 2021, The Enterprise, A Massive Transposon Carrying Spok Meiotic Drive Genes. *Genome Res.* **31**: 789–798.

Vogan Aa, Ament-Velásquez Sl, Granger-Farbos A, Svedberg J, Bastiaans E, Debets Aj, Coustou V, Yvanne H, Clavé C, And Saupe

Sj, Et Al. 2019, Combinations Of Spok Genes Create Multiple Meiotic Drivers In *Podospora. Elife* **8**: E46454.

Wang C, Milgate Aw, Solomon Ps, And Mcdonald Mc. 2021, The

Identification Of A Transposon Affecting The Asexual Reproduction Of The Wheat Pathogen *Zymoseptoria Tritici. Mol Plant Pathol.* **22**: 800–816.

: Tahir Ahmad Pattoo. Flora To Nano: Sustainable Synthesis Of Nanoparticles Via Plant-Mediated Green Chemistry. Plant Science Archives

Arshad Khayum, Ayesha Siddiqua, Sima A. Sarvade, P. Tanuja, Jige Sandipan Babasaheb (2023). Enhancing The Value Chain Of Marigold: Cultivation, Challenges, And Diverse Applications. Plant Science Archives

Wicker T, Sabot F, Hua-Van A, Bennetzen Jl, Capy P, Chalhoub B, Flavell A, Leroy P, Morgante M, And Panaud O, Et Al. 2007, A Unified

Classification System For Eukaryotic Transposable Elements. Nat Rev Genet. 8:973–982.

Viren D. Nimbark (2023) Homeopathic Management Of Lumbar Disc Herniation. Plant Science Archives. V08i01, 09 To 11.Würschum T, Boeven Phg, Langer Sm, Longin Cfh, And Leiser Wl. 2015,

Multiply To Conquer: Copy Number Variations At Ppd-B1 And Vrn-A1 Facilitate Global Adaptation In Wheat. *Bmc Genet.* **16**:96.

Yang H, Yu H, And Ma L-J. 2020, Accessory Chromosomes In Fusarium Oxysporum.

Phytopathol, 110:1488–1496.