# ANAIS DO EVENTO

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XXIII Workshop de Genética

9 a 11 de Abril de 2026

Instituto de Biociências de Botucatu
Programa de Pós-Graduação em Ciências Biológicas (Genética)
Universidade Estadual Paulista "Júlio de Mesquita Filho"
Botucatu, SP

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XXIII Workshop de Genética

# SUMÁRIO


Apresentação 01

Programação 02

Palestras 03

Minicursos 04

Apresentação Oral Graduação 05

Apresentação Oral Pós-Graduação 06

Resumos: Pôster Graduação 07

Resumos: Poster Pós-Graduação 08

Resumos: Pôster Projeto de Extensão 09

## APRESENTAÇÃO

O Workshop de Genética é um evento anual idealizado e organizado pelo corpo docente e discente do Programa de Pós-Graduação em Ciências Biológicas (Genética), do Instituto de Biociências de Botucatu - IBB da Universidade Estadual Paulista “Júlio de Mesquita Filho” - UNESP. Tem como propósito criar um espaço para a discussão de temas atuais e dos grandes avanços na área de Genética.

## INSTITUIÇÃO

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# PROGRAMAÇÃO

## 9 DE ABRIL *quinta-feira*

**8h00 - 9h00:** Credenciamento
**9h00 - 9h30:** Cerimônia de abertura
**9h30 - 10h30:** "Dos Genes aos Alvos Terapêuticos em Demências: Uma Abordagem Integrativa de Biologia de Sistemas, Sequenciamento de Célula Única e Inteligência Artificial" (*Prof. Dr. Geysson Javier Fernández García*)
**10h30 - 11h00:** *Coffee Break*
**11h00 - 12h00:** "Genética da conservação aplicada à fauna silvestre: da pesquisa ao manejo" (Profª Drª Ligia Souza Lima Silveira da Mota)
**12h00 - 12h30:** Palestra técnica
**12h30 - 14h00:** Almoço
**14h00 - 16h00:** Apresentações Orais
**16h00 - 16h30:** *Coffee Break*
**16h30 - 18h00:** Apresentações Banner
**18h00 - 19h00:** Coquetel

## 10 DE ABRIL *sexta-feira*

**8h00 - 10h30:** Minicursos
**10h30 - 11h00:** *Coffee Break*
**11h00 - 12h00:** Minicursos
**12h00 - 14h00:** Almoço
**14h00 - 15h00:** "O que seus genes ouvem quando você fala Subtítulo: Epigenética, suas escolhas e a genética que você está moldando" (*Dr. Eduardo Castan*)
**15h00 - 16h00:** "O papel da biologia molecular e engenharia genética no desenvolvimento de vacinas" (*Drª Giovanna de Brito Carneiro*)
**16h00 - 16h30:** *Coffee Break*
**16h30 - 17h00:** Palestra técnica 2
**17h00 - 18h00:** "Genômica da Microbiota: Aplicações em Saúde Intestinal e Produção Animal" (*Drª Stela Virgilio*)

## 11 DE ABRIL *sábado*

**9h00 - 10h30:** Minicursos
**10h30 - 11h00:** *Coffee Break*
**11h00 - 12h00:** Minicursos
**12h00 - 14h00:** Almoço
**14h00 - 15h00:** "A Origem de um Planeta Verde: Como Microalgas Colonizaram o Ambiente Terrestre e Deram Origem às Plantas (*Embryophyta*)" (Professor Doutor Luiz Eduardo Vieira Del Bem)
**15h00 - 15h30:** *Coffee break*
**15h30 - 17h00:** "Mesa redonda Genética no Mercado: Novos Caminhos para a pós-graduação" (*Omaxlab Testes Genéticos e Medicina Personalizada, ByMyCell, CITOGEM Biotecnologia*)
**17h00 - 18h00:** Encerramento e premiações

# PALESTRAS

*palestras*

# CERIMÔNIA DE ABERTURA






**Condutora:** Me. Letícia Batista Soares

**Participantes:** Me. Pamela Cristina Ferreira de Nadai, Dr. Rafael Henrique Nóbrega, Dr. Danillo Pinhal

**Data:** 09/04/2026 **Horário:** 9h00 às 9h30

A mesa de abertura, conduzida pela Me. Letícia Batista Soares - membro da Comissão Organizadora do XXIII Workshop de Genética -, contou com a participação da Me. Pamela Cristina Ferreira de Nadai, representante discente do Programa de Pós-Graduação em Ciências Biológicas (Genética) e diretora do evento, do Dr. Rafael Henrique Nóbrega, representante docente do evento e do Dr. Danillo Pinhal, Coordenador do Programa de Pós-Graduação em Ciências Biológicas (Genética) do Instituto de Biociências de Botucatu da Universidade Estadual Paulista Júlio de Mesquita Filho (UNESP).

# PALESTRA 1

palestra 1



**Título:** “Dos Genes aos Alvos Terapêuticos em Demências: Uma Abordagem Integrativa de Biologia de Sistemas, Sequenciamento de Célula Única e Inteligência Artificial”

**Palestrante:** Dr. Geysson Javier Fernández García

**Data:** 09/04/2026 **Horário:** 9h30 às 10h30

A complexidade etiológica das doenças neurodegenerativas, particularmente as demências, impõe desafios substanciais à farmacologia convencional, que historicamente negligenciou a heterogeneidade celular do sistema nervoso central. Esta palestra propõe uma mudança de paradigma na busca por novos fármacos, fundamentada na convergência entre a Biologia de Sistemas e tecnologias de alta resolução. Central a essa abordagem está o sequenciamento de RNA de célula única (scRNA-seq), que permite a dissecação do transcriptoma em nível celular individual, revelando estados celulares patológicos específicos em neurônios e glia que permaneciam ocultos em análises de tecido total (bulk). A integração desses vastos conjuntos de dados multiômicos é viabilizada por algoritmos de Inteligência Artificial (IA) e Machine Learning, capazes de identificar redes de coexpressão gênica e nós regulatórios críticos associados à progressão da neurodegeneração. Através da modelagem de redes complexas, é possível mapear interações proteína-proteína e prever o impacto de perturbações moleculares, facilitando a identificação de alvos terapêuticos com maior potencial de eficácia e menores efeitos off-target. Ademais, a palestra discute como a biologia computacional permite o reposicionamento de fármacos (drug repurposing) e a descoberta de biomarcadores preditivos para a medicina de precisão. A transição de uma visão reducionista para uma perspectiva integrativa e sistêmica é apresentada como a via essencial para desvendar os mecanismos de resiliência e vulnerabilidade neuronal, culminando no desenvolvimento de intervenções terapêuticas mais robustas e personalizadas para o espectro das demências.

# PALESTRA 2

palestra 2



**Título:** “Genética da conservação aplicada à fauna silvestre: da pesquisa ao manejo”

**Palestrante:** Drª Ligia Souza Lima Silveira da Mota

**Data:** 09/04/2026 **Horário:** 11h00 às 12h00

A crise contemporânea da biodiversidade exige ferramentas analíticas que transcendam a ecologia clássica, posicionando a genética da conservação como um pilar indispensável para a viabilidade de populações silvestres a longo prazo. Esta palestra aborda como a aplicação de marcadores moleculares, desde microssatélites até o uso de polimorfismos de nucleotídeo único (SNPs) via sequenciamento de nova geração (NGS), permite diagnosticar a saúde genética de espécies ameaçadas. O foco central reside na quantificação da variabilidade genética, na detecção de gargalos demográficos (bottlenecks) e na mensuração dos níveis de endogamia (inbreeding), fatores que comprometem a resiliência adaptativa das populações. A discussão avança da bancada para o campo, demonstrando como dados genômicos informam decisões críticas de manejo in situ e ex situ. Serão discutidos protocolos de translocação baseados em parentesco, a definição de Unidades Evolutivas Significativas (ESUs) e a utilização do DNA ambiental (eDNA) como uma metodologia não invasiva para o monitoramento de fauna em ecossistemas complexos. A integração desses dados permite a implementação de planos de ação mais precisos, mitigando os efeitos da fragmentação de habitat e das mudanças climáticas. Por fim, a palestra ressalta a importância da translação do conhecimento científico para as esferas governamentais e órgãos de fiscalização. A utilização da genética forense no combate ao tráfico de animais silvestres e a construção de biobancos são apresentadas como estratégias vitais. Ao integrar a genômica populacional às práticas de manejo, a pesquisa deixa de ser puramente descritiva para se tornar uma ferramenta pragmática na manutenção do potencial evolutivo das espécies e na salvaguarda dos serviços ecossistêmicos.

# PALESTRA TÉCNICA 1

*palestra técnica 1*




**Título: “**Mapeando a Expressão Gênica in situ com a tecnologia Xenium”

**Palestrante:** Drª Fernanda Ferreira

**Data:** 09/04/2026 **Horário:** 12h30 às 13h00

# PALESTRA 3

palestra 3



**Título:** “O que seus genes ouvem quando você fala Subtítulo: Epigenética, suas escolhas e a genética que você está moldando”

**Palestrante:** Dr. Eduardo Castan

**Data:** 10/04/2026 **Horário:** 14h00 às 15h00

Historicamente, o dogma central da biologia molecular estabeleceu o DNA como uma matriz informacional estática, cuja hereditariedade determinaria, de forma quase determinística, o fenótipo do organismo. Todavia, a ascensão da epigenética operou uma mudança de paradigma, revelando que o genoma funciona como um sistema dinâmico, dotado de plasticidade em resposta a estímulos exógenos. Esta palestra discute como fatores ambientais e comportamentais, incluindo aporte nutricional, protocolos de exercício físico e estressores psicossociais, atuam como indutores de sinalização química capazes de modular a atividade transcricional sem alterar a sequência primária de nucleotídeos. Os mecanismos moleculares subjacentes, notadamente a metilação do DNA, as modificações pós-traducionais de histonas e a interferência por RNAs não-codificantes, permitem a sintonização fina da expressão gênica. Evidências contemporâneas sugerem que tais marcas epigenéticas transcendem a regulação celular imediata, podendo ser perpetuadas via mitose e, sob condições específicas, transmitidas por via transgeracional. Tal fenômeno implica que as exposições ambientais e escolhas de estilo de vida de um indivíduo exercem influência direta na arquitetura genômica de sua linhagem. A integração de dados oriundos da epigenômica funcional oferece uma nova perspectiva sobre a resiliência biológica e a etiologia de patologias complexas. Ao decifrar os sinais moleculares que o genoma "interpreta", a investigação científica avança na identificação de biomarcadores precoces e no desenvolvimento de intervenções terapêuticas personalizadas. Em última análise, o entendimento desses mecanismos reconfigura o papel do indivíduo, que deixa de ser um receptáculo passivo de sua herança genética para tornar-se um agente modulador de sua própria homeostase e longevidade.

# PALESTRA 4

palestra 4



**Título:** “O papel da biologia molecular e engenharia genética no desenvolvimento de vacinas”

**Palestrante:** Drª Giovanna de Brito Carneiro

**Data:** 10/04/2026 **Horário:** 15h00 às 16h00

A vacinologia moderna atravessa uma era de inovação sem precedentes, impulsionada pelo refinamento das técnicas de biologia molecular e engenharia genética. Esta palestra explora a transição das metodologias clássicas de atenuação e inativação viral para o desenvolvimento de imunizantes de precisão. O foco central recai sobre a manipulação do material genético para a construção de plataformas altamente adaptáveis, capazes de responder com celeridade a patógenos emergentes e variantes de preocupação. Serão discutidas, em profundidade, as tecnologias de DNA recombinante e a síntese in vitro de mRNA, que permitem a utilização das próprias células do hospedeiro como biorreatores para a produção de antígenos específicos. A engenharia de vetores virais, como os adenovírus não replicantes, e a estabilização de proteínas de superfície em conformações pré-fusão são apresentadas como marcos da biologia estrutural que otimizaram a imunogenicidade das formulações atuais. Adicionalmente, aborda-se o papel do sequenciamento genômico em larga escala e da bioinformática na identificação de epítopos conservados, fundamentais para o desenvolvimento de vacinas universais. A discussão encerra-se com uma análise sobre a escalabilidade e a segurança dessas novas tecnologias. A capacidade de editar genomas com ferramentas como CRISPR-Cas9 e o uso de sistemas de expressão heteróloga em células de mamíferos e insetos demonstram como a engenharia genética não apenas acelerou o cronograma de desenvolvimento vacinal, mas também elevou os padrões de eficácia e especificidade. A integração dessas ferramentas moleculares é consolidada como a estratégia mestra para a preparação contra futuras pandemias e para o avanço da imunoterapia personalizada.

# PALESTRA TÉCNICA 2

palestra técnica 2



**Título:** “Apresentação dos Laboratórios do PPG em Ciências Biológicas (Genética) do IBB”

**Palestrante:** Me. Débora Kazumi Maeda

**Data:** 09/04/2026 **Horário:** 12h30 às 13h00

# PALESTRA 5

palestra 5



**Título:** “Genômica da Microbiota: Aplicações em Saúde Intestinal e Produção Animal”

**Palestrante:** Drª Stela Virgilio

**Data:** 10/04/2026 **Horário:** 17h00 às 18h00

A compreensão dos ecossistemas microbianos evoluiu drasticamente com o advento da metagenômica e da análise de genes marcadores (16S rRNA), permitindo a caracterização de comunidades complexas que não são passíveis de cultivo in vitro. Esta palestra aborda como a genômica da microbiota redefine os conceitos de saúde e nutrição, tanto em modelos humanos quanto em sistemas de produção animal. O foco reside na análise do microbioma como um "órgão metabólico" adicional, capaz de modular a resposta imunológica, a barreira intestinal e a extração de energia a partir da dieta. No contexto da produção animal, serão discutidas as correlações entre perfis taxonômicos específicos e características de interesse econômico, como a Eficiência Alimentar (FE) e o ganho de peso. A utilização de ferramentas de bioinformática para a reconstrução de vias metabólicas microbianas permite identificar como a microbiota do rúmen ou do trato gastrointestinal inferior influencia a emissão de metano e a síntese de ácidos graxos de cadeia curta (AGCC). A palestra explora, ainda, a aplicação de probióticos de última geração e intervenções dietéticas baseadas em dados genômicos para a modulação do microbioma, visando a redução do uso de antibióticos e o aumento da resiliência frente a desafios sanitários. Na interface com a saúde humana, discute-se o eixo intestino-cérebro e o papel da disbiose na etiologia de doenças metabólicas e inflamatórias. A integração de dados de metagenômica com a transcriptômica do hospedeiro oferece uma visão holística das interações biológicas, permitindo o desenvolvimento de estratégias de precisão. Em suma, a genômica da microbiota é apresentada como uma ferramenta disruptiva para a otimização da saúde intestinal e para o estabelecimento de sistemas de produção animal mais sustentáveis e eficientes.

# PALESTRA 6



**Título:** “A Origem de um Planeta Verde: Como Microalgas Colonizaram o Ambiente Terrestre e Deram Origem às Plantas (*Embryophyta*)”

**Palestrante:** Dr. Luiz Eduardo Vieira Del Bem

**Data:** 11/04/2026 **Horário:** 14h00 às 15h00

A transição das linhagens fotossintetizantes do ambiente aquático para o terrestre, ocorrida há aproximadamente 450-500 milhões de anos, representa um dos eventos mais transformadores da biosfera. Esta palestra explora as bases moleculares e evolutivas que permitiram que ancestrais de algas verdes, especificamente do grupo das Streptophyta, superassem os desafios da dessecação, radiação ultravioleta e gravidade. Através da filogenômica comparativa, discute-se como o sequenciamento de genomas de briófitas basais e algas carófitas revelou a origem de inovações genéticas cruciais para a multicelularidade e a proteção do embrião. O foco central da discussão reside na identificação de "genes de conquista terrestre", responsáveis pela biossíntese de polímeros complexos como a esporopolenina e a cutina, fundamentais para a impermeabilização celular. Além disso, aborda-se a evolução das vias de sinalização hormonal, notadamente o papel do ácido abscísico (ABA) e da auxina, que permitiram o desenvolvimento de estruturas morfológicas complexas e a regulação hídrica em ambiente xérico. A palestra detalha como a transferência horizontal de genes de bactérias e fungos para o genoma dessas algas ancestrais pode ter acelerado a aquisição de mecanismos de resistência a estresses abióticos. A análise encerra-se correlacionando a origem das Embryophyta com as mudanças biogeoquímicas globais, como o aumento do oxigênio atmosférico e a formação dos primeiros solos. Ao integrar dados de paleobotânica com genômica funcional, a palestra oferece uma visão abrangente sobre como a plasticidade genômica de microalgas ancestrais pavimentou o caminho para a biodiversidade vegetal contemporânea, consolidando a base de todos os ecossistemas terrestres.

# MESA REDONDA







**Título:** “Mesa redonda Genética no Mercado: Novos Caminhos para a pós-graduação” (Omaxlab Testes Genéticos e Medicina Personalizada, ByMyCell, CITOGEM Biotecnologia)

**Palestrantes:** Camila Teixeira Ferreira, Drª Stela Virgílio e Me. Sayonara Ivana Santos de Assis.

**Data:** 11/04/2026 **Horário:** 15h30 às 17h00

A saturação dos modelos tradicionais de carreira acadêmica tem impulsionado uma reestruturação nas trajetórias de mestres e doutores, direcionando o capital intelectual para o setor de biotecnologia aplicada. Esta mesa-redonda reúne expoentes de empresas disruptivas, Omaxlab, ByMyCell e CITOGEM Biotecnologia, para discutir como o domínio de ferramentas genômicas e moleculares é transposto da bancada do laboratório para soluções de mercado. O foco central reside na identificação de nichos estratégicos, como a medicina personalizada, o diagnóstico molecular de precisão e a prestação de serviços biotecnológicos de alta complexidade. Através do relato da experiência da Omaxlab, discute-se a implementação de testes genéticos preditivos e o papel da farmacogenômica na clínica médica, evidenciando a crescente demanda por profissionais capazes de interpretar dados genômicos complexos. A ByMyCell contribui com a perspectiva da genômica de precisão e do suporte técnico especializado, enquanto a CITOGEM aborda as frentes de citogenética e biologia molecular voltadas ao diagnóstico. A discussão enfatiza competências além da técnica, como gestão de bioempreendimentos, propriedade intelectual e regulamentação sanitária, essenciais para a viabilidade de biotech startups. A sessão encerra-se com uma reflexão sobre a necessária integração entre universidade e empresa. A pós-graduação é apresentada não apenas como um período de formação de pesquisadores, mas como um celeiro de inovadores capazes de transformar ciência básica em produtos de alto valor agregado. Ao explorar esses novos caminhos, a mesa-redonda oferece um panorama pragmático para o jovem cientista, consolidando a genética como um pilar econômico e social que transcende os limites do ambiente acadêmico tradicional.

# MINICURSOS

*minicursos*

**Título:** Do Dado ao Resultado: Introdução à Bioinformática Aplicada

**Ministrantes:** Dr. Marcel Rodrigues Ferreira, Me. Amanda Schnepper e Me. Isabelle Mira da Silva.

**Data:** 10/04/2026 **Horário:** 8h00 às 12h00





Neste curso foram abordados os seguintes tópicos:

- Conceitos básicos de bioinformática e suas aplicações nas ciências biológicas;
- Análise de qualidade de dados biológicos;
- Uso de bancos de dados biológicos;
- Análises básicas de genomas e transcriptomas;
- Utilização de ferramentas intuitivas e plataformas online;
- Introdução a fluxos simples de análise bioinformática;
- Interpretação de dados e aplicação em pesquisas.

**Título:** Fundamentos de IA Aplicada à Biologia de Sistemas

**Ministrantes:** Dr. Ney Lemke, Ramon Hernany Martins Gomes e Me. Tainá Pereira dos Reis.

**Data:** 10/04/2026 **Horário:** 8h00 às 12h00





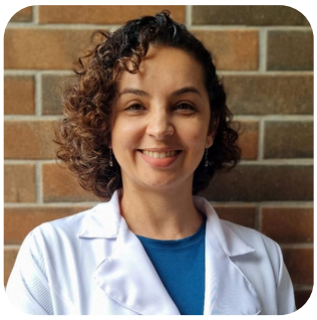
Neste curso foram abordados os seguintes tópicos:

- Inteligência artificial aplicada à análise de dados biológicos;
- IA generativa, aprendizado supervisionado e não supervisionado;
- Aplicações em proteínas, scRNA-seq e redes biológicas;
- Modelagem, identificação de padrões e organização de dados;
- Avaliação de modelos, limitações, vieses e boas práticas;
- Demonstrações no Google Colab com BioPython e métodos computacionais básicos;
- Uso da IA como suporte em biologia molecular, bioinformática e biologia de sistemas.

**Título:** Metabolômica: Conectando Genes ao Fenótipo

**Ministrantes:** Drª. Estela de Oliveira Lima

**Data:** 10/04/2026 **Horário:** 8h00 às 12h00



Neste curso foram abordados os seguintes tópicos:

- Fundamentos da metabolômica e sua aplicação no estudo do funcionamento celular;
- Mapeamento e análise de metabólitos;
- Integração de dados biológicos em diferentes níveis (abordagens ômicas);
- Princípios de espectrometria de massas;
- Identificação de biomarcadores;
- Investigação de mecanismos biológicos.

**Título:** Do DNA à Função: Análise de Sequências Regulatórias para Estudos Genéticos

**Ministrantes:** Drª. Daniela Alves Pereira

**Data:** 10/04/2026 **Horário:** 8h00 às 12h00



Neste curso foram abordados os seguintes tópicos:

- Identificação de sequências regulatórias do genoma (*enhancers*, insuladores e regiões associadas a TADs);
- Conceitos e abordagens para estudo de regulação gênica;
- Estratégias experimentais para análise funcional (ensaios de luciferase, CRISPRi e CRISPRa);
- Uso de bancos de dados públicos (RegulomeDB, ENCODE e GeneHancer);
- Análise computacional de regiões regulatórias;
- Investigação de regiões regulatórias a partir de alvos de interesse.

**Título:** Introdução ao Cultivo e a Quantificação Viral

**Ministrantes:** Agatha Mayume Silva Kubo, Dr. Leandro Moraes e Luidy Carlos de Souza Santos Quispe.





**Data:** 10/04/2026 **Horário:** 8h00 às 12h00



Neste curso foram abordados os seguintes tópicos:

- Cultivo de vírus e biossegurança;
- Culturas celulares e infecção viral;
- Ensaio de placas (plaque assay);
- Cálculo do título viral (PFU/mL).

**Título:** Ômicas na Bioprospecção de Espécies Naturais

**Ministrantes:** Drª. Paula de França

**Data:** 11/04/2026 **Horário:** 8h00 às 12h00



Neste curso foram abordados os seguintes tópicos:

- Tecnologias ômicas e bioinformática na bioprospecção;
- Prospecção de genes e identificação de proteínas;
- Metabólitos bioativos de interesse farmacêutico e industrial;
- Integração de dados genômicos e metabolômicos;
- Aplicações em espécies vegetais e microbianas.

**Título:** Sequenciamento de terceira geração via Oxford Nanopore: quando o tamanho realmente importa?

**Ministrantes:** Dr. Marcel Rodrigues Ferreira

**Data:** 11/04/2026 **Horário:** 8h00 às 12h00



Neste curso foram abordados os seguintes tópicos:

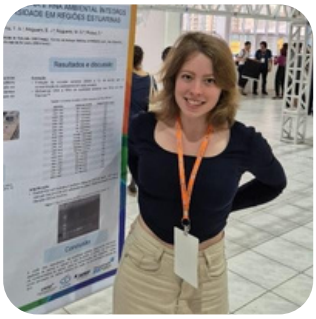
- Princípios do sequenciamento por nanoporos e tipos de dados gerados;
- Importância do tamanho das leituras;
- Aplicações: montagem de genomas, variantes estruturais, regiões repetitivas, isoformas de RNA e metilação;
- Vantagens, limitações e desafios analíticos;
- Critérios para escolha da tecnologia conforme a pergunta biológica.

**Título:** O DNA Ambiental (eDNA) no estudo da biodiversidade

**Ministrantes:** Me. Natascha Mozaner Nitzsche e Me. Gabriel Tofanelo Vanin

**Data:** 11/04/2026 **Horário:** 8h00 às 12h00





Neste curso foram abordados os seguintes tópicos:

- Conceito e aplicações do DNA ambiental (eDNA);
- Uso do eDNA no monitoramento da biodiversidade;
- Etapas de processamento de amostras;
- Aplicações na genética da conservação;
- Vantagens, limitações e desafios da técnica.

# APRESENTAÇÃO ORAL GRADUAÇÃO

*apresentação oral graduação*

**CHROMOSOMAL EVOLUTION OF THE 18S rDNA MULTIGENE FAMILY IN CICADELLIDAE (HEMIPTERA, CICADOMORPHA)**

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Cicadellidae (Hemiptera, Cicadomorpha, Membracoidea) includes over 22,000 species, mainly found in tropical and subtropical regions, commonly known as leafhoppers. They feed on plant sap, acting as agricultural pests and vectors of plant diseases. Cytogenetically, they have holocentric chromosomes, with the kinetochore region distributed along the chromosome, but the chromosome number has been described for only a few species. For the understanding of chromosomal evolution in these groups, molecular markers are applied, with the 18S ribosomal DNA being the most used in different orders of Insecta. In Hemiptera, these data are concentrated in Heteroptera, where the presence of a single terminal site in one autosomal pair is frequent. However, in Cicadellidae these data are still scarce, and chromosomal analysis can help understand the relationships among organisms in this group. In this way, we analyzed the evolutionary trajectory of five Cicadellidae species through karyotype analysis and 18S rDNA multigene detection. Five Cicadellidae species were collected at UNESP, Rio Claro campus. Males were dissected, and seminiferous tubules were fixed in ethanol:acetic acid (3:1). Slides were prepared by squashing on a heated plate with 45% acetic acid, and karyotypes were described after DAPI staining. For fluorescent in situ hybridization (FISH), we amplified and labeled the 18S DNA region of Helicoverpa zea (Lepidoptera) with digoxigenin-11-dUTP via nick translation. This probe was detected with anti-digoxigenin-rhodamine. Chromosomes were counterstained with DAPI, slides were mounted with VECTASHIELD, and images were captured using an Olympus BX51 microscope with a DP71 camera. Chromosome number ranged from 2n = 20 + X0 to 2n= 22 + X0, with only the XX/X0 sex-determination system observed. In Cicadellidae, the known variation ranges from 2n = 8 to 2n = 38, consistent with the literature. FISH results showed that 18S rDNA is located on one bivalent in all species, except in Ciminius sp., where it occurs on the sex chromosome. All species showed a terminal location for 18S rDNA. In Coreidae (Hemiptera: Heteroptera), the 18S rDNA signal was also observed on terminal of one autosomal pair, a characteristic conserved in this family. This was also observed here for Cicadellidae, suggesting structural stability and a similar evolutionary trajectory in the family, highlighting its relevance for understanding chromosomal evolution in the group.

**Keywords**: Chromosomal evolution, Cicadellidae, 18S rDNA, Fluorescent in situ hybridization

**Acknowledgments**: PROPE/UNESP

1º LUGAR NA CATEGORIA APRESENTAÇÃO ORAL GRADUAÇÃO

**INFLUENCE OF THERMAL STRESS ON THE EXPRESSION OF IMMUNITY AND DNA REPAIR GENES IN *Bombyx mori* Linnaeus, 1758**

Lourente, Maria R.R.[1]*; Dionisio, Jaqueline F.[1]; Pezenti, Larissa F.[1]; Lopez, Thayná B.F.[1]; Semprebon, Simone C.[2]; Mantovani, Mário S.[2]; Rosa, Renata[1].

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The increase in environmental temperature represents an important risk factor for animals, especially insects, affecting their physiological, immunological, and molecular processes. In lepidopterans such as the silkworm (*Bombyx mori* Linnaeus, 1758), thermal changes may compromise cellular homeostasis, animal health, productivity, and long-term survival. Therefore, this study aimed to evaluate the effect of high-temperature exposure on the expression of the DNA repair gene *Rad23* (Radiation Sensitive 23) and the immunity genes *Scav* (Scavenger Receptor), *Spz* (Spätzle-like protein), *Def* (Defensin), and *Pep* (Antimicrobial peptide) in this insect. Larvae of a commercial hybrid strain of *B. mori* (♀ Chinese × ♂ Japanese) were divided into two groups: a control group (26°C) and a high-temperature group (34°C) during the 5th instar. After exposure, three individuals were randomly selected for tissue collection, followed by total RNA extraction, cDNA synthesis, and gene expression analysis by RT-qPCR. RT-qPCR data were normalized using the reference genes *RPL3* (Ribosomal Protein L3) and Alpha-Tubulin and analyzed using REST (Relative Expression Software Tool), with a significance level set at $p < 0.05$. The results demonstrated that both immunity and DNA repair genes were downregulated in the heat-exposed group. Previous studies with *B. mori*, insects of the order Diptera, and bees of the genus *Apis* have reported similar findings under thermal stress conditions. These results support the hypothesis that thermal stress may promote metabolic reprogramming, with the redirection of energy and metabolites toward pathways essential for the immediate maintenance of cellular homeostasis. Climate change is already a global reality, and rising temperatures directly affect the well-being and survival of *B. mori*, impacting silk production. Studies evaluating the influence of thermal stress in this insect are essential to support the development of strategies to mitigate these impacts and contribute to a more sustainable and resilient sericulture.

**Keywords:** Silkworm, high temperatures, gene expression, sericulture.

**Acknowledgments:** State University of Londrina.




**2º LUGAR NA CATEGORIA APRESENTAÇÃO ORAL**
**GRADUAÇÃO**

# ASSOCIATION OF THE IL17A RS3819024 GENETIC VARIANT WITH THE DEVELOPMENT OF CERVICAL CANCER

Silva, Marie Augusta Squarca e1; Silva, P. R.1; Ramalho, N. S.1; Franco, M. L. M.1; Fernandes, C. Y. M.1; Castilha, E. P.1; Silva, M. R.1; Silva, L. M. M.1; Oliveira, Karen Brajão de1.
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Cervical cancer (CC) is the third most incident type of cancer among women in Brazil, with more than 90% of cases resulting from persistent infection with human papillomavirus (HPV). Although HPV infection is a necessary condition for the development of the disease, host genetic factors may influence viral persistence and progression to intraepithelial lesions and invasive cancer. Interleukin-17 (IL-17), produced by Th17 cells, plays a relevant role in the antiviral immune response by promoting cellular recruitment and inflammatory amplification. However, it may exhibit a dual role, as its exacerbated production can contribute to chronic inflammation and favor tumor progression. Polymorphisms in the IL17A gene may modulate its expression, and the rs3819024 (A>G) variant has been associated with different types of cancer. In this context, the aim of this study was to investigate the possible influence of this variant on CC susceptibility. The study included 415 women aged over 18 years treated by the public health system in northern Paraná, Brazil, comprising 175 HPV-negative (HPV−) and 240 HPV-positive (HPV+) individuals. The HPV+ samples were stratified into three groups: without cervical lesions (n=89), with intraepithelial lesions (n=91), and with CC (n=60). After DNA extraction, viral DNA detection was performed by conventional PCR with DNA integrity confirmed by amplification of the β-globin gene and rs3819024 genotyping was performed by qPCR using validated commercial probes. Sociodemographic and sexual health data were obtained through a structured questionnaire. Statistical analyses included Pearson's chi-square test or Fisher's exact test ($p<0.05$), with Bonferroni correction and logistic regression to control for confounding factors. A significant association was observed between HPV infection and smoking, age ≤24 years, lack of knowledge about the virus, and having more than three lifetime sexual partners. For the development of cervical lesions, income, contraceptive use, number of pregnancies, and family history of cancer showed significant associations. No association was found between the rs3819024 variant and HPV infection or intraepithelial lesions after adjustment for confounders. However, in the CC group, the GG genotype was associated with a higher likelihood of disease development under codominant ($p=0.032$) and recessive ($p=0.023$) models. It was concluded that rs3819024 does not influence susceptibility to HPV infection or lesion formation but may contribute to progression to CC, possibly due to the pro-inflammatory role of IL-17 in the tumor microenvironment.

Palavras-chave: Carcinoma cervical, Papilomavírus humano, Interleucina 17.
Agradecimentos: Agradeço ao Conselho Nacional de Desenvolvimento Científico e Tecnológico por viabilizar a reação deste projeto.




3º LUGAR NA CATEGORIA APRESENTAÇÃO ORAL GRADUAÇÃO

# APRESENTAÇÃO ORAL
*apresentação oral*

# PÓS-GRADUAÇÃO
*pós-graduação*

## Machine Learning–Based Stratification Reveals a Severity-Dependent Multi-Organ Transcriptional Landscape in Cancer Cachexia

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Cancer cachexia, a progressive wasting syndrome driven by tumor–host crosstalk that severely compromises patient survival and quality of life. While the clinical progression of cachexia—from pre-cachexia to cachexia and ultimately severe cachexia—is well established in humans, the absence of systematic stratification in preclinical models remains a critical barrier to mechanistic understanding and therapeutic translation. This study developed a machine learning–based framework to stratify cachexia stages and identify multi-organ transcriptomic programs associated with disease progression in a murine Lewis Lung Carcinoma (LLC) model. LLC tumor-bearing mice were stratified into control (n=10), pre-cachexia (n=12), cachexia (n=11), and severe cachexia (n=8) groups based on skeletal muscle and visceral adipose mass normalized to tibia length. Hierarchical clustering combined with unsupervised machine learning approaches achieved robust classification, with Random Forest model reaching accuracies above 85% and strong inter-group agreement (Cohen's Kappa > 0.8). Bulk RNA-seq was performed across five tissues gastrocnemius, heart, mesenteric adipose tissue, tumor, and liver spanning all severity stages. Likelihood ratio test (LRT) based trajectory analysis identified tissue-specific transcriptomic signatures that progressively intensified from pre- cachexia to severe cachexia, encompassing proteasomal degradation, extracellular matrix (ECM) remodelling, inflammatory and immune signalling, cytoskeletal reorganization, collagen metabolism, and calcium signalling. Ligand–receptor (LR) interaction analysis using BulkSignalR identified 69 LR pairs across samples, and integration with transcriptomic trajectories based on disease severity revealed overlapping pathways related to extracellular matrix remodelling, TGF-β signalling, inflammation, and lipid metabolism. A prominent gene group included structural ECM components (e.g., collagens such as Col1a1/Col1a2/Col6a1–3 and Fn1) and adhesion molecules (Cd44, Itgb5, Vcam1), indicating active-matrix reorganization across skeletal muscle, heart, liver, and mesenteric tissue. The presence of Tgfbr2, together with Thbs1 and Timp2, supports activation of profibrotic signalling, while metabolic regulators including Apoc3, Scarb1, and Cav1 suggest altered lipid handling, particularly in the liver and mesenteric adipose tissue. Together, these findings reveal a coordinated fibrotic–inflammatory–metabolic transcriptional program that intensifies with cachexia severity across multiple tissues. The integration of stage stratification with transcriptomic trajectories and ligand–receptor interactions highlight a severity-dependent molecular architecture of disease progression. These findings provide a foundation for identifying stage-specific biomarkers and designing temporally targeted therapeutic interventions.

**Keywords**: disease progression, cachexia mediators, multi-organ remodelling, ligand–receptor interactions

**Funding**: This work was supported by the São Paulo Research Foundation (FAPESP, Process No. 2020/03854-4 (RFC), 2022/06775-3 (APS) and 2023/15976-5 (APS)) and the Brazilian National Council for Scientific and Technological Development (CNPq, Productivity Fellowship – Level 1D, Process No. 311603/2022-0). Comité para el Desarrollo de la Investigación (CODI project number 2021-40170 (GJF and JV)




**1º LUGAR NA CATEGORIA APRESENTAÇÃO ORAL**

**PÓS-GRADUAÇÃO**

## COMPARATIVE CHROMOSOME-SCALE GENOMICS OF DYCKIA FROM RUPESTRIAN GRASSLANDS (BROMELIACEAE)

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Canga (ironstone outcrops) and quartzitic rupestrian grasslands of southeastern Brazil represent ecologically harsh and spatially fragmented environments that harbor high levels of plant endemism. In the Iron Quadrangle (Minas Gerais state), these contrasting substrates sustain diverse assemblages of narrowly distributed species, many of which occur in small and isolated populations under increasing anthropogenic pressure. The bromeliad genus Dyckia is a prominent component of these landscapes. Dyckia consimilis and Dyckia rariflora are two endangered species occurring on both canga and quartzitic outcrops, yet genomic resources for these taxa have been lacking. Here, we present chromosome-scale genome assemblies and comparative gene analyses for D. consimilis and D. rariflora, aiming to establish foundational genomic resources for conservation and evolutionary studies. High–molecular-weight DNA extracted from fresh leaf tissue was sequenced using PacBio HiFi technology, generating sequencing depths exceeding 70× for both species. Hi-C chromatin conformation data were produced using a multi-enzyme protocol and integrated during assembly. Genomes were assembled in Hi-C–aware mode using hifiasm, followed by haplotype-resolved scaffolding, manual curation, and quality assessment. Transposable elements were annotated de novo using EDTA, and gene prediction was performed with BRAKER3, supported by RNA-seq data from vegetative tissues. Functional annotation incorporated BLAST, InterProScan, and Gene Ontology assignments. Final assemblies recovered 25 chromosomes per haplotype, with more than 98% of each genome anchored into chromosome-scale scaffolds. Genome sizes ranged from 750 to 860 Mb, and repetitive elements accounted for approximately 80% of the assemblies, largely dominated by LTR retrotransposons. BUSCO analyses indicated high gene completeness, exceeding 96% in both species. Structural annotation identified approximately 20,000 protein-coding genes per genome, with conserved gene architecture and extensive functional annotation coverage. Comparative analyses based on orthogroup inference using OrthoFinder revealed a largely conserved gene repertoire, with a high proportion of single-copy orthologs shared between species. Exploratory analyses of nonsynonymous to synonymous substitution rates (Ka/Ks) across shared orthologs indicated pervasive purifying selection, alongside a limited subset of genes showing elevated Ka/Ks ratios, suggesting lineage-specific selective pressures potentially associated with adaptation to iron-rich, oligotrophic substrates. These chromosome-level genomes represent the first reference assemblies for Dyckia and provide essential tools for conservation genomics, enabling species delimitation, population monitoring, and the investigation of genomic mechanisms underlying adaptation in threatened rupestrian ecosystems.

**Keywords**: genome assembly; conservation genomics; Bromeliaceae; ironstone outcrops;
**Acknowledgements**: This study was supported by FAPESP and Agência Paulista de Tecnologia dos Agronegócios (APTA; 2022/2658)




2º LUGAR NA CATEGORIA APRESENTAÇÃO ORAL

PÓS-GRADUAÇÃO

**COMPARATIVE GENOMIC INVESTIGATION OF SEXUAL SYSTEM IN Semaprochilodus insignis (TELEOSTEI, CHARACIFORMES)**

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Sex determination is a process commonly influenced by genetic factors and may be driven by a linkage group whose loci are located within sex chromosomes. Although the sexual system in mammals is highly conserved, in several genera, including fish, there is great diversity in sex-determination patterns, highlighting the existence of both monofactorial and multifactorial systems. Advances in genomics have enabled the study of species lacking heteromorphic sex chromosomes, which were previously limited by the scarcity of specialized tools. In the present study, two species of the same genus, popularly known as jaraqui in the Northern region, were selected to investigate aspects of sex determination in this group. Semaprochilodus taeniurus presents heteromorphic sex chromosomes, whereas S. insignis lacks this feature. Thus, comparing species with different systems may improve our understanding of sex chromosome evolution. To identify the probable sexual system of S. insignis, we performed several steps, ranging from the use of publicly available data to refined tools for sex-specific analyses. We used the chromosome-level assembled genome of S. insignis from GenBank, with high quality, to identify regions with a higher density of SNPs associated with sex-specific regions. For this purpose, we collected samples from 20 males and 20 females of each species and sequenced short reads to construct sex-specific libraries (pool-seq). The PSASS pipeline was used to compare the assembled genome with the pool-seq from both species to identify regions with higher divergence rates between males and females. To further investigate these divergent regions, IGV software was used to determine whether the species exhibits male (XY) or female (ZW) heterogametic. Our results revealed an interesting finding: the S. insignis genome did not present significant peaks in any region when analyzed with its own pool-seq that could be associated with sex-specific regions. However, when the pool-seq from S. taeniurus were mapped onto the S. insignis genome, we observed a high SNP peak on chromosome pair 9 in females, indicating a ZZ/ZW system. Therefore, these findings may shed light on the sexual system of S. insignis in an unprecedented way and reinforce the importance of comparative analyses in the study of sex chromosome evolution.

**Keywords**: Genomic, sex determination, evolution

**Acknowledgments**: FAPESP, CAPES and CNPq




3º LUGAR NA CATEGORIA APRESENTAÇÃO ORAL PÓS-GRADUAÇÃO

# RESUMOS: PÔSTERES GRADUAÇÃO

*resumos: pôsteres graduação*

## ANALYSIS OF THE EXPRESSION PROFILE OF PLASMATIC EXTRACELLULAR VESICLES FROM PREGNANT WOMEN WITH GESTATIONAL DIABETES MELLITUS AND NORMOGLYCEMIA

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Gestational diabetes mellitus (GDM) is a metabolic condition characterized by hyperglycemia diagnosed during pregnancy, adversely affecting maternal and fetal health. In this scenario, extracellular vesicles (EVs) emerge as promising biomarkers, offering diagnostic, prognostic, and therapeutic potential, especially exosomes (with a size comprised between 30–150 nm), which during pregnancy participate in fetomaternal communication and in the regulation of processes such as angiogenesis and metabolism. Thus, the main objective of this project is to analyze the expression profile of EVs in pregnant women with and without GDM, as well as their morphological and structural characterization. Samples from 20 pregnant women (n=20), 10 normoglycemic and 10 with GDM, were evaluated between 24 and 28 weeks (GDM diagnosis period) and 36 and 40 weeks of gestation (delivery). The groups were matched for age, gestational age, BMI, and glycemic index. EVs were isolated from plasma by size exclusion chromatography (SEC) and subsequently concentrated using centrifugal filters. Nano tracking analyses (NTA) were performed to determine size and distribution in solution, and Zeta potential was analyzed to determine the surface charge of EVs. The results show that women with GDM have a higher concentration of EVs (8.1111 ± 2.12e+10 SD), mainly in the period from 36 to 40 weeks (p= >0,0001). In contrast, non-GDM women have lower concentration of exosomes (157.8 ± 2.8 SD) in both periods when compared to those with GDM (p= >0,0001). Similarly, the surface charge was identified as being between −10 mV and −30 mV, which is normally found in exosomes in the literature. Our results revealed that GDM can affect the expression profile of circulating EVs, reinforcing their potential as a source of biomarkers and highlighting their role in causing functional changes, suggesting its importance in maternal-fetal communication during pregnancy. Additionally, it demonstrates that EVs are mediators of cellular plasticity; in addition to transporting bioactive molecules, they can modify the behavior and functional properties of recipient cells, influencing cellular communication and the interaction of these cells with the microenvironment. The results of this project are expected to contribute to the identification of biomarkers based in circulating EVs with diagnostic and therapeutic potential in GDM, promoting advances in early detection and the development of innovative strategies to improve maternal-fetal health.

**Keywords**: Extracellular Vesicles, Biomarkers, Gestational Diabetes Mellitus, Maternal-Fetal Health.

**Acknowledgments**: FAPESP.




1º LUGAR NA CATEGORIA APRESENTAÇÃO PÔSTER GRADUAÇÃO

## ASSOCIATION OF THE APAI POLYMORPHISM IN THE VITAMIN D RECEPTOR (VDR) WITH HYPERTENSION IN SOUTHWESTERN BAHIA

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Systemic arterial hypertension (SAH) is a multifactorial disease responsible for high mortality rates in Brazil. This condition is closely associated with vitamin D, which is considered a pre-hormone precursor of several physiological processes in the human body and can be obtained through diet or cutaneous synthesis induced by sun exposure. The literature reports that vitamin D deficiency affects a large number of individuals and may contribute to the development of several diseases, such as type 2 diabetes mellitus, obesity, and cardiovascular diseases, including systemic arterial hypertension. Vitamin D deficiency is also related to SAH through the regulation of the renin–angiotensin–aldosterone system. Genetic alterations, such as the substitution of cytosine by adenine in intron 8 of the VDR gene, may influence the affinity of the active form of vitamin D, $1,25(OH)_2D$, which acts as a ligand for the nuclear vitamin D receptor (VDR). This receptor functions as a transcription factor and can be expressed in several target tissues, such as the prostate and the juxtaglomerular apparatus, participating in the regulation of physiological processes relevant to blood pressure control through gene transcription.Therefore, the present study aimed to investigate the association between the ApaI polymorphism in the VDR gene and the risk of systemic arterial hypertension. The analyzed sample consisted of a total of 190 individuals, divided into two groups: cases (n = 100) and controls (n = 90). To amplify the region of interest, the Polymerase Chain Reaction (PCR) technique combined with Restriction Fragment Length Polymorphism (RFLP) was used, employing the restriction enzyme ApaI, which is able to cleave the PCR product when the polymorphism is present. After genotyping, statistical analyses were performed using the JASP software through chi-square ($\chi^2$) tests, as well as dominant and recessive models. The frequencies of the *C and *A, alleles were 0.614 and 0.386 in the cases and 0.541 and 0.459 in the controls, respectively. The case and control samples did not show genetic or genotypic differentiation ($p > 0.05$). Similarly, no significant result was observed in the dominant model. Interestingly, a statistically significant association was observed in the recessive model ($p = 0.019$), with an Odds Ratio of 0.34 (95% CI: 0.11–0.93), indicating a protective effect for carriers of the A allele, who showed a 66% reduction in the likelihood of hypertension.

**Palavras-chave:**SNP'S, Hipertensão, Deficiência,1,25(OH) 2D

**Agradecimentos**:UESB




2º LUGAR NA CATEGORIA APRESENTAÇÃO PÔSTER GRADUAÇÃO

## INTEGRATIVE ANALYSIS OF *KIR2DL4* COPY NUMBER AND ALLELIC DIVERSITY: INSIGHTS FROM WORLDWIRE SAMPLES

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KIR2DL4 is an atypical member of the Killer-cell Immunoglobulin-like Receptor (KIR) family that combines inhibitory and activating features, depending on the ligand interacting with it. Although it was previously assumed that the *KIR2DL4* gene is present in two copies in most individuals (one per chromosome 19), it exhibits copy number variation and allelic diversity, including insertions and deletions that can generate null alleles whose protein products are potentially non-functional, resulting in absent or functionally altered receptors across populations. *KIR2DL4* genetic diversity remains understudied in real population samples, particularly admixed ones. Therefore, we aimed to characterize copy number variation and allelic diversity of *KIR2DL4* across populations and to evaluate the frequency of alleles associated with the absence of functional KIR2DL4. We analyzed whole-genome sequencing data from 4,459 unrelated individuals representing 78 populations from the 1000 Genomes Project, HGDP, and the Brazilian SABE dataset using kir-mapper. Populations were grouped into 7 biogeographic regions based on ancestral background. Most individuals worldwide carry two copies of *KIR2DL4* (87.9–97.4%). However, chromosome 19 lacking *KIR2DL4* was detected in 10% of individuals in Africa, 7.5% in the Americas, 4% in Brazil, 11% in South Asia, 3.1% in East Asia, and 2.5% in Europe. The cases with *KIR2DL4* gene deletion were associated with a larger deletion within the *KIR* complex, involving more than one *KIR* gene. Regarding alleles encoding potentially truncated forms, a higher frequency of *KIR2DL4*008* (which produces a truncated KIR2DL4) was observed in Europe (35.42%) and the Middle East (39.8%) compared to other regions. Overall, our results show that a functional *KIR2DL4* is not always present, and that other mechanisms may modulate NK function. Although two copies are predominant worldwide, copy number changes and functionally distinct alleles contribute to variation in receptor status across populations. Considering both structural variation and allelic composition provides a more accurate view of *KIR2DL4* variability and its potential functional impact.

**Keywords:** *KIR2DL4*; copy number variation; allelic diversity; NK cell receptors; population genetics.

**Acknowledgments:** FAPESP (2025/04343-7)




3º LUGAR NA CATEGORIA APRESENTAÇÃO PÔSTER GRADUAÇÃO

**ANALYSIS OF TYPE III COLLAGEN IN TUMOR RECURRENCES OF PATIENTS WITH UROTHELIAL BLADDER CANCER AS A POTENTIAL PROGNOSTIC INDICATOR**

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Urothelial bladder cancer (UBC) is the most common malignancy of the urinary tract and one of the most prevalent worldwide. The extracellular matrix (ECM) is a three-dimensional network that surrounds organs, tissues and body cells. In addition to stabilizing tissue structure, it is involved in several physiological processes, such as protection against invasion, immune suppression and tumor growth through cell-cell interactions. Its main structural component is the collagen, which is responsible for preserving its function. The tumor microenvironment, composed of the ECM and other components, may determine tumor morphology and prognosis. Within this context, the present study aimed to analyse the immunostaining profile of type III collagen in samples from recurrences from nine patients diagnosed with UBC at Cancer Hospital of Londrina (HCL), in order to understand its role in tissue composition and to evaluate its potential as a biomarker for UBC recurrences. Tissue samples (n=26) were obtained (CAAE: 47092521.2.1001.523), and prognostic parameters (tumor grade, staging, and muscle invasion) were collected. Indirect immunohistochemistry was performed using an anti–type III collagen antibody. Subsequently, photomicrographs of each sample were captured and analyzed using ImageJ Fiji software. Statistical analysis was conducted using SPSS software (version 26.0), applying Friedman's ANOVA to assess differences in type III collagen expression among recurrence samples from the same patient, and Kendall's Tau-b correlation test to evaluate the association between collagen deposition and prognostic factors. As a result, significant differences in type III collagen deposition were observed among recurrences in some of the evaluated patients. In patient 1, the third recurrence differed from the first (p=0,037) and second (p=0,001). In patient 2, the fourth recurrence differed from the first (p=0,003), second (p=0,003) and third (p=0,003). The patient 3 showed a difference between the first and second recurrence (p=0,011). Similar results were observed in patients 4 and 5, where the first recurrence differed from the second (p=0,002 for both). In patient 9, a difference was found between the third and fourth recurrences (p=0,003). In patients 6, 7, and 8, collagen deposition remained stable across all recurrences. No significant associations were observed with any of the evaluated prognostic parameters. Despite the observed results, no consistent pattern was identified across patients, suggesting that this ECM component does not appear to be suitable for investigation as a prognostic biomarker for UBC recurrence.

**Palavras-chave**: prognosis, immunohistochemistry, extracellular matrix.

**Agradecimentos**: CNPq, UEL, CAPES.

## ANNEXIN A EXPRESSION DYNAMICS IN LIPOPOLYSACCHARIDE-INDUCED EPIDIDYMITIS IN MICE

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Introduction: The epididymis provides a specialized environment for sperm maturation, storage, and protection. Epididymitis, a frequent cause of male infertility, is mostly triggered by retrograde bacterial infections and may cause permanent tissue damage depending on the magnitude of the inflammatory response. Thus, preventing excessive epididymal inflammation is crucial to mitigate tissue dysfunction. Resolution of inflammation and restoration of tissue homeostasis involve multiple mediators, including the Annexin A family. Annexin A family comprises 12 calcium-dependent phospholipid-binding proteins (AnxA1-AnxA11, AnxA13), known for diverse functions, notably anti-inflammatory and pro-resolutory activities. Here, we tested the hypothesis that annexin A family members are downstream regulators of epididymal inflammatory responses. Objective: This study aimed to evaluate whether annexin A transcripts are regulated in a mouse model of lipopolysaccharide (LPS)-induced epididymitis. Methods: Epididymitis was induced in C57BL/6 mice (90-120 days old; CEUA nº 6272050320) by retrograde intraluminal injection of either sterile saline (control) or ultrapure LPS from E. coli (50 µg) into the vas deferens towards the cauda epididymidis. Mice were euthanized at 2, 6, 24, and 72 h post-injection, and their cauda epididymis were processed for RT-qPCR to evaluate the expression of annexin A transcripts. A group of naïve mice was euthanized, and their testis and epididymides were processed for RT-PCR to evaluate the basal annexin A transcripts expression. Additionally, in silico analyses using data from the Mammalian Reproductive Genetics Database were conducted to evaluate the expression of these transcripts in mouse and human epididymides. Results: All members of the annexin A family were constitutively expressed in the mouse testis and epididymis, showing a higher abundance in the corpus and cauda regions. A similar expression pattern was observed in the human epididymis. LPS challenge up-regulated Anxa1 and Anxa2 transcripts at 2 h. LPS further down-regulated Anxa2 and Anxa5 transcripts at 6 h, followed by an up-regulation of Anxa5 transcript at 24 and 72 h. Discussion: Annexin A family members are likely to contribute to immune microenvironment regulation in the epididymis. Anxa1, Anxa2, and Anxa5 genes may play roles as anti-inflammatory and pro-resolutory mediators during epididymitis, thus limiting inflammation-induced damage. Conclusion: Our results show that members of the annexin A family are dynamic downstream mediators during epididymitis, likely protecting the tissue from excessive inflammation. This study provides a framework for future investigations evaluating the potential of annexin A1, A2, and A5 as potential adjuvant therapeutic targets to preserve male fertility in epididymitis cases.

**Keywords**: Annexins, Epididymitis, Inflammation
**Acknowledgments**: CNPq (PIBIC), FAPESP

## DETERMINATION OF THE OPTIMAL MMS EXPOSURE WINDOW FOR GENETIC VARIABILITY INDUCTION IN MILTONIA FLAVESCENS

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Generating genetic variability is a fundamental strategy for the breeding of ornamental plants, particularly in species such as Miltonia flavescens, which exhibit slow natural propagation and limited genetic diversity. Chemical mutagenesis using methyl methanesulfonate (MMS), an alkylating agent capable of inducing point mutations through DNA alkylation, represents a practical approach to increase variability under controlled in vitro conditions. This study aimed to evaluate the effects of different MMS exposure times on the survival and physiological integrity of M. flavescens protocorms, identifying the most promising interval for inducing genetic variability while preserving explant viability. Protocorms previously established in vitro were distributed into five experimental groups: control (0 minutes) and treatments with 5% MMS for 15, 20, 30, and 45 minutes. After mutagen exposure, explants were thoroughly washed and transferred to fresh Murashige and Skoog medium supplemented with sucrose and solidified with agar, maintained at 25 ± 2°C under a 16 h photoperiod and controlled light intensity. Viability was assessed through morphological parameters, including tissue coloration, onset of oxidative browning, and structural integrity, classifying protocorms as viable (green), presenting oxidative stress (initial browning), or necrotic (complete browning). The control group showed 100% survival. The 15-minute treatment resulted in apparent partial lethality, with 33.3% viable and 66.7% necrotic protocorms; however, given the limited sample size, these results should be interpreted cautiously and require validationwith a larger experimental population. At 20 minutes, most protocorms remained viable, although one exhibited early oxidative signs. Notably, the 30-minute exposure maintained complete survival, with all protocorms exhibiting preserved morphology and green coloration. In contrast, 45 minutes of exposure led to 100% necrosis. These findings suggest that intermediate exposure times, particularly between 20 and 30 minutes, balance mutagenic stress and cellular tolerance, potentially enabling DNA modification without inducing irreversible oxidative damage. The establishment of an optimized mutagenic exposure window is particularly relevant for M. flavescens, as increasing genetic variability in this species may support the development of novel ornamental phenotypes and enhance breeding strategies aimed at improving its commercial and genetic potential.

**Keywords**: Mutagenesis; Genetic variability; In vitro culture.
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**DIFFERENT BIOINFORMATICS APPROACHES IMPACTING MICROBIAL ECOLOGY STUDIES: ANALYSIS OF THE MICROBIOTA OF Atta sexdens AND SOIL**

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Leaf-cutting ants of the genus Atta play an important role in Neotropical ecosystems. In addition to their relationship with the cultivated fungus, the associated bacterial microbiota is involved in nutrition, defense, and nutrient cycling, influencing the functioning of the system. To characterize and understand the composition of this microbiota, appropriate bioinformatics tools are required, as they are capable of estimating its diversity and ecological metrics. Metabarcoding of the 16S rRNA gene has been widely used in the analysis of microbial communities, and different pipelines have been developed for processing these data. However, the choice of analytical tools can influence the results and, consequently, the ecological interpretation of the studied communities. Therefore, this study compared the approaches of Kraken2 and DADA2, evaluating their impact on taxonomic classification and diversity metrics of the microbiota of Atta sexdens and the associated soil samples. For this purpose, ant and soil samples were analyzed through sequencing of the V3-V4 region of the 16S rRNA gene using the Illumina® NextSeq 2000 platform (2 × 300 bp). Two workflows were employed: Kraken2, with quality control (FastQC), filtering (Trimmomatic), and classification using the SILVA 138.1 database (confidence threshold 0.05); and DADA2 in the R environment, including filtering, ASV inference, chimera removal, and classification using the same database. The ecological analyses performed included observed richness, Shannon and Simpson indices, Bray-Curtis dissimilarity, PCoA ordination, PERMANOVA, and ANOVA to compare richness. Kraken2 indicated higher genus richness in ants (ANOVA, $p = 0.043$), with no differences for Shannon ($p = 0.471$) and Simpson ($p = 0.102$). PERMANOVA did not detect significant separation between groups ($R2 = 0.384$; $p = 0.1$). In contrast, DADA2 revealed a trend toward higher richness in soil ($p = 0.064$), also with no differences for Shannon ($p = 0.699$) and Simpson ($p = 0.314$), and a non-significant PERMANOVA ($R2 = 0.376$; $p = 0.1$). Although the overall patterns of diversity structure remained similar between the methods, the abundance of taxa such as Tsukamurella in ants and Acidothermus, Bradyrhizobium, and Paenibacillus in soil differed. Regarding richness, only Kraken2 detected a statistical difference by ANOVA, whereas DADA2 did not. These results support the hypothesis that different bioinformatics approaches influence ecological interpretation. Thus, the choice of tool is decisive for interpretations regarding the microbiota of leaf-cutting ants and soil, and it should be carefully considered in microbial ecology studies.

**Keywords**: leaf-cutting ants; microbial ecology; 16S rRNA; bioinformatics.
**Acknowledgements**: This study was supported by FAPESP (grants 2021/10639-5 and 2024/21504-1).

## GENETIC EVALUATION OF AGE AT FIRST CALVING AND STAYABILITY IN BRAZILIAN HEREFORD CATTLE

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The Hereford is a British beef breed widely used in purebred systems in southern Brazil. Genetic progress in Brazilian Hereford populations has been driven by conventional evaluations targeting growth, maternal ability, reproduction, meat quality, and adaptability. Reproductive efficiency is crucial for herd profitability, as unproductive cows increase production costs. Among reproductive traits, age at first calving (AFC) reflects sexual precocity, whereas stayability (STAY) measures the ability of females to remain productive in the herd, directly influencing replacement rates and lifetime performance. This study estimated heritability and genetic correlations for AFC and STAY to assess their potential use in the Hereford breeding program. A performance database of approximately 15,000 cows was subjected to quality control in R software and contemporary groups (GCs) were defined by the significant ($p<0.05$) effects of herd-year-month of birth. A total of 335 and 272 GCs were considered in the analysis of AFC and STAY, respectively. Stayability was defined as the occurrence of at least three calvings by 76 months of age; cows meeting this criterion received a score of 2 (success), and the others a score of 1 (failure). Genetic parameters were estimated using BLUPF90+ under an animal model in single- and two-trait Bayesian analyses. Heritability estimates were 0.21 ± 0.02 for AFC and 0.06 ± 0.02 for STAY. The moderate heritability for AFC indicates sufficient additive genetic variation for effective direct selection, supporting its use to improve sexual precocity and reduce generation intervals. In contrast, the low heritability for STAY suggests a stronger influence of environmental and non-additive effects, which may limit response to direct selection. The genetic correlation between AFC and STAY was high and negative (−0.83 ± 0.08), indicating that genetically earlier-calving females are more likely to remain longer in the herd. Phenotypic (−0.36 ± 0.01) and environmental (−0.28 ± 0.02) correlations were also negative, suggesting that management and environmental conditions contribute to this association. Therefore, the results indicate that selection for reduced AFC can indirectly improve STAY. Given the low heritability of STAY and its strong genetic association with AFC, emphasizing AFC in selection programs appears to be a practical and efficient strategy to enhance reproductive longevity and overall herd profitability.

**Keywords**: Animal breeding, *Bos taurus*, Genetic parameters, Heritability, Selection

## HERITABILITY ESTIMATES AND GENETIC CORRELATIONS FOR DIFFERENT DEFINITIONS OF STAYABILITY IN LARGE WHITE SOWS

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Herd longevity is a constant concern in swine production, particularly from both animal welfare and economic perspectives. The retention of females in the herd can be improved through direct selection for length of productive life or through traits that present favorable genetic correlations with longevity. Among the reproductive traits important for swine production, stayability (STAY) stands out because it measures the permanence of the female in the herd up to a given parity. The objective of this study was to estimate heritabilities and genetic correlations among different definitions of stayability in Large White sows to identify the definition that best represents reproductive longevity and shows the greatest potential for application in breeding programs. Thus, multiple definitions of stayability were established, defined as the probability that a female remains in the herd from the first to the second, third, fourth, and fifth parity (STAY1_2, STAY1_3, STAY1_4, and STAY1_5), as well as definitions based on ordered scores of retention up to different parities (STAY1_2_3; STAY1_2_3_4; and STAY1_2_3_4_5). The number of animals evaluated was 18,097; 18,097; 15,740; 15,740; 18,097; 15,740; and 15,740 for each definition, respectively. Variance components were estimated using an animal model under the single-step approach (ssGBLUP), considering genomic (44,467 molecular markers) and pedigree (25,676 animals) data. Estimated heritabilities ranged from 0.10 (STAY1_2_3_4_5) to 0.18 (STAY1_2). Genetic correlations were predominantly high and positive. The highest genetic correlation was observed between STAY1_2_3_4_5 and the other definitions (1.00 ± 0.00), whereas the lowest was found between Stay1_5 and STAY1_2_3 (0.54 ± 0.38). Based on these results, selection for STAY1_2_3_4_5 would generate a strong correlated response in the other definitions due to the high genetic correlations. However, its lower heritability (0.10), compared with STAY1_2 (0.18), suggests lower efficiency of direct response to selection, greater environmental influence, and the need for later evaluation, which may limit its practical usefulness as a selection criterion. STAY1_2 stood out for presenting higher heritability and strong genetic correlations with all other evaluated definitions, ranging from 0.62 ± 0.06 to 0.99 ± 0.01, indicating an important genetic association with STAY1_3, STAY1_4, and STAY1_5. In conclusion, among the evaluated definitions, STAY1_2 shows the greatest potential as a selection criterion for reproductive longevity in breeding programs, combining higher heritability with strong genetic correlations with the other stayability traits, promoting correlated response to selection and enabling earlier selection decisions, thereby reducing economic impact.

**Keywords**: Animal Model, Genetic parameter, Longevity, Selection, Swine

**IS THE CHROMOSOMAL VARIATION ATTRIBUTED TO Epidendrum secundum REAL? A CYTOGENETIC REVIEW**

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Epidendrum L. (Orchidaceae: Laeliinae) is one of the largest genera in the family, currently comprising 1800 described species, with variations in morphological and cytogenetic characters (chromosome number and genome size), colonizing diverse environments ranging from tropical forests to the mountainous regions of the Andes. Potentially, cytogenetic and ecological diversity has driven the diversification of the genus. Among the species, E. secundum shows a wide distribution, spreading from southern Brazil to Central America; the species also exhibits variation in cytogenetic characters, with 13 different chromosome numbers reported in the literature, ranging from 2n=28 to 2n=84. Considering that chromosomal variation can act as a reproductive barrier, this intraspecific cytogenetic variation is peculiar and is not widely accepted. Among the possible causes of the differing chromosome number records are the morphological similarity with other species of the genus, which complicates the correct identification of E. secundum, and the high potential for hybridization among Epidendrum species. Both hypotheses may lead to misdelimitation of the species and consequently affect biodiversity records. Thus, the present study aims to determine whether the various karyotypic descriptions reported in the literature for E. secundum can be attributed to the species itself or represent misidentified specimens, and what the actual chromosome number(s) and genome size(s) of the species are. For this purpose, 50 isolated populations from South America were collected and identified as E. secundum, of which 42 individuals from 16 populations are maintained in cultivation. For chromosome number analysis, roots were collected and pretreated with the antimitotic 8HQ at 8°C for 24 hours and subsequently fixed in Carnoy's solution 3:1 (ethanol:acetic acid, v:v) for 2 hours, then stored at -20°C. Preliminary results indicate a constant chromosome number of 2n=56 observed in three populations. Preliminary genome size analysis also shows constancy, indicating 2C ≅ 3.8 pg for 35 populations from 11 Brazilian states. These results suggest that the cytogenetic variation attributed to E. secundum in the literature is a consequence of misidentified specimens, possibly associated with morphological similarity to other species of the genus, such as E. denticulatum, and the high potential for interspecific hybridization. Such errors compromise the correct delimitation and distribution of the species, potentially causing confusion between threatened and widely distributed populations, which may have environmental implications for native flora conservation plans.

**Keywords**: Epidendrum, Orchidaceae, chromosome number, genome size
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**SATELLITE DNA DISTRIBUITION IN Triatoma sordida (HETEROPTERA: TRIATOMINAE)**

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Triatomines (Heteroptera: Reduviidae), commonly known as kissing bugs, are the vectors of Trypanosoma cruzi, etiological agent of Chagas disease. Approximately 150 species of triatomines have been described to date. This group exhibits remarkable conservation in chromosome numbers, contrasting with considerable diversity in heterochromatin composition and distribution patterns. At the molecular level, these regions constitute reservoirs of satellite DNAs. Therefore, these sequences represent promising markers for investigating chromosomal evolution within the group. In this context, we performed the physical mapping of satellite DNA (satDNA) families in Triatoma sordida in order to characterize and better understand the chromosomal evolution of this species. The insects were provided by the Coordenadoria de Controle de Doenças, Instituto Pasteur (Mogi Guaçu, SP, Brazil). In the laboratory, the insects were anesthetized and dissected, and the testes were fixed in ethanol:acetic acid (3:1). Cytological preparations were obtained by macerating and spreading testes in 50% acetic acid, followed by evaporation on a heated plate. Probe amplification was carried out by polymerase chain reaction (PCR), using specific primers. After confirmation of PCR products on a 1% agarose gel, the probes were labeled by nick translation with biotin (TsoSat03, TsoSat04, TsoSat06, and TsoSat08) or digoxigenin (TsoSat01, TsoSat02, TsoSat05, and TsoSat07). Subsequently, the probes were hybridized onto the slides and detected using anti-digoxigenin–rhodamine and avidin–Alexa Fluor 488. Chromosomes were counterstained with DAPI (4′,6-diamidino-2-phenylindole) and visualized using an Olympus BX51 fluorescence microscope. Among the eight satellite DNAs analyzed, four (TsoSat04, TsoSat06, TsoSat07, and TsoSat08) did not exhibit detectable hybridization signals, indicating a non-clustered distribution pattern. TsoSat03 showed hybridization signals restricted to the terminal regions of the autosomes. In contrast, probes corresponding to TsoSat01, TsoSat02, and TsoSat05 produced distinct bands located on the autosomes and on one of the sex chromosomes. Notably, signals for TsoSat02 and TsoSat05 were detected on the Y chromosome, whereas TsoSat01 was localized on the X chromosome. Although the chromosomal distribution of satDNAs in T. sordida was generally consistent with the pattern described for four other triatomine species, some discrepancies were observed, particularly regarding the sex chromosomes. In triatomines, the X chromosome typically harbors a greater number of satDNA families than the Y chromosome. The latter is generally characterized by the predominance of microsatellites, with the only reported exception being Tinf01-33 in Triatoma infestans. However, this pattern was not observed in T. sordida, suggesting a distinct evolutionary trajectory for the sex chromosomes in this species.

**Keywords**: satellite DNA; Heteroptera; Sex chromosomes
**Acknowledgments**: PROPE/UNESP

**Karyotypic Diversity of the Lambari *Psalidodon fasciatus* Collected from the Batalha River**

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*Psalidodon fasciatus* (Characidae), popularly known as the "red-tailed lambari", is a Neotropic fish notable for its wide distribution and cytogenetic diversity. This species is part of a complex of morphologically similar species with distinct genomic characteristics, reflecting differentiated evolutionary processes. A particularly interesting aspect of *P. fasciatus* is the occurrence of B chromosomes supranumerary elements predominantly composed of repetitive DNA. These chromosomes are generally considered dispensable, as they do not encode essential genes and are typically regarded as intragenomic parasites. In light of this, the objective of this study was to cytogenetically characterize *P. fasciatus*, with an emphasis on the detection and intraspecific variation of B chromosomes using classical cytogenetic analysis. To this end, five individuals of *P. fasciatus* were analyzed from the Batalha River, a tributary of the Tietê River located in the municipality of Bauru (SP). Taxonomic identification was confirmed via the DNA barcoding technique, utilizing the mitochondrial cytochrome oxidase I (COI) gene. Cytogenetic analyses were performed on metaphase preparations obtained from the anterior kidney and stained with Giemsa. All specimens exhibited a basic diploid number of 2n = 46. However, in one of the individuals, the presence of three supranumerary chromosomes, characterized as B chromosomes, was observed. These findings reinforce the intraspecific genomic variability of *P. fasciatus* and highlight the importance of cytogenetic studies in natural populations of this species, especially in poorly explored hydrographic basins.

**Keywords:** Characidae, B chromosome, Cytogenetics

**Acknowledgments:** This study was supported by the National Council for Scientific and Technological Development (CNPq) and the São Paulo Research Foundation (FAPESP).

**MOLECULAR DELIMITATION OF FRESHWATER STRINGRAY SPECIES OF THE GENUS PLESIOTRYGON (CHONDRITHYES: MYLIOBATIFORMES) BASED ON THE COI GENE.**

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The subfamily Potamotrygoninae, composed of freshwater stingrays, comprises four genera, Heliotrygon, Paratrygon, Plesiotrygon and Potamotrygon, distributed in rivers of the Amazon basin. In this context, the cytochrome c oxidase subunit I (COI) gene is widely used in the molecular identification of species through the DNA barcoding technique. Molecular delimitation studies are important for recognizing evolutionary lineages and understanding biological diversity. Thus, the present study aimed to investigate and recognize the taxonomic boundaries of species of the genus Plesiotrygon based on species delimitation analyses. Initially, the morphological identification of the analyzed specimens was performed, which are deposited in the biological collection of the Fish Biology and Genetics Laboratory (LBGP), Unesp – Botucatu. Subsequently, three specimens of Plesiotrygon iwamae were subjected to total DNA extraction and polymerase chain reaction (PCR) for amplification of the COI gene, and were later sequenced using the Sanger method. In addition, 10 sequences of the COI gene (P. nana = 4, P. iwamae = 6) obtained from GenBank were included. For sequence editing and species delimitation analyses, the programs Geneious v7.1.3 and MEGA X were used. The phylogenetic tree reconstructed using the Maximum Likelihood (ML) method recovered a single clade grouping the two analyzed species. The Assemble Species by Automatic Partitioning (ASAP) and Poisson Tree Processes (PTP) analyses corroborated these results. The DNA barcoding approach indicated that the analyzed gene did not show sufficient resolution to discriminate the evaluated species, highlighting the limitation of this marker for the taxonomic resolution of this group of fishes. Therefore, the investigation of other, more informative genetic regions is necessary to expand the understanding of genetic diversity within the genus and contribute to advancing knowledge about the biodiversity present in this group of stingrays.

**Keywords**: Amazon Basin, DNA barcoding, biodiversity, phylogenetic relationships.

## GENETIC PARAMETER ESTIMATION FOR STAYABILITY IN LARGE WHITE SOWS

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Longevity is an economically relevant trait in pig production, as it is associated with reproductive efficiency and sow retention in the herd. Female retention can be enhanced either through direct selection for productive lifespan or by selecting traits that are favorably genetically correlated with longevity. Among the reproductive traits relevant to swine production, stayability (STAY) is particularly informative, as it represents the probability that a female remains in the herd until a specified parity. This study aimed to estimate genetic parameters for different STAY definitions in Large White pigs. Phenotypic records were used to define STAY as the probability that a sow remained in the herd from first to second farrowing (STAY1_2), from first to third (STAY1_3), from first to fourth (STAY1_4), and from first to fifth farrowing (STAY1_5). The number of evaluated animals was 18,097 (STAY1_2 and STAY1_3) and 15,740 (STAY1_4 and STAY1_5). Variance components were estimated using an animal model under the single-step genomic BLUP (ssGBLUP) approach, integrating genomic information (44,467 molecular markers) and pedigree records (25,676 animals). A threshold model was fitted, and the residual variance was fixed at 1.0. Additive genetic variance ranged from 0.1159 (STAY1_4) to 0.2237 (STAY1_2). Heritability estimates for STAY1_2, STAY1_3, STAY1_4, and STAY1_5 were equal to 0.18 ± 0.02, 0.15 ± 0.02, 0.10 ± 0.02, and 0.16 ± 0.02, respectively. The highest heritability was observed for STAY1_2, suggesting greater potential response to selection for early stayability compared with later definitions. Because STAY1_2 is assessed at early parities, early culling may reduce the influence of environmental effects on the trait. The lower heritability estimates for STAY1_3, STAY1_4, and STAY1_5 indicate a greater influence of non-genetic factors as the required number of parities increases. These estimates may also reflect prior selection and culling processes, since only sows with adequate reproductive performance and adaptability remain in the herd for longer periods. Despite the low heritability estimates, the results indicate the presence of additive genetic variability for stayability in Large White pigs, supporting its potential inclusion in breeding programs.

**Keywords**: Animal Model, Heritability, Longevity, Pig breeding, Selection

## GENOME-WIDE ASSOCIATION STUDY FOR TEMPERAMENT TRAITS IN A COMPOSITE BEEF CATTLE BREED

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Beef cattle temperament is an important trait in modern production systems due to its direct impact on animal welfare, handling safety, and productive efficiency. In Brazil, composite breeds like Canchim (5/8 Charolais, 3/8 Nelore) were developed to combine productivity with adaptability to the tropical environment. However, selecting behavioral traits requires a deep understanding of their polygenic nature. This study aimed to perform a genome-wide association study to identify genomic regions and candidate genes associated with two specific temperament measures: movement (MOV) and tension (TEN). Phenotypic data were collected from approximately 2,790 Canchim animals born between 2013 and 2025. The MOV trait was scored on a scale from 1 (no movement) to 5 (jumping), while TEN was evaluated from 1 (relaxed) to 4 (paralyzed/freezing). Genotypic data from 2,551 individuals were obtained using the high-density BovineHD BeadChip. A single-step approach was utilized to estimate molecular marker effects by integrating pedigree and genomic data through a threshold model. The analysis focused on genomic windows explaining at least 0.40% of the genetic variance, specifically targeting markers located within genes. A total of 14 (CGAS, EPAS1, SRBD1, KCNQ5, CD109, EXOC4, EEF1A1, LRGUK, MTO1, OOEP, PRKCE, DDX43, KHDC3L, and SLC17A5) and 13 (EPAS1, AKIRIN2, SRBD1, CFAP206, SLC35A1, CGA, RARS2, ORC3, C9H6orf163, PRKCE, SMIM8, HTR1E, and ZNF292) genes were identified for MOV and TEN, respectively, with an overlap of three (EPAS1, PRKCE, and SRBD1) genes between both traits. Functional analyses using the STRING database were carried out to retrieve biological processes and molecular functions of the genes. The genes HTR1E, KCNQ5, PRKCE, SLC17A5, and EXOC4 perform molecular functions related to the encoding of serotonin receptors, regulation of neuronal excitability, synaptic signaling, myelin sheath maintenance, and exocytosis of synaptic vesicles, respectively. The HTR1E gene was associated with the regulation of aggressive behavior in a study conducted with Golden Retriever dogs. In a study with Brahman cattle, the EXOC4 gene was associated with exit velocity. Therefore, these two genes can be considered candidates for the selection of animals with adequate behavior. The remaining genes, as they have not been linked to temperament in previous studies, may be considered novel candidate genes. These findings contribute to the understanding of the genetic architecture of temperament in Canchim cattle and provide a scientific basis for incorporating MOV and TEN into breeding programs.

**Keywords**: Animal welfare, Beef cattle, Candidate genes, Single-step GWAS, SNP markers

**DETECTION AND FREQUENCY OF FOUR KNOCKDOWN RESISTANCE MUTATIONS IN AN *Aedes aegypti* POPULATION COLLECTED IN LONDRINA, PARANÁ, BRAZIL**

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The mosquito Aedes (Stegomyia) aegypti (Linnaeus, 1762) is a culicid species native to the African continent and currently widely distributed across tropical and subtropical regions worldwide. This mosquito is the primary vector of several arboviral diseases, including dengue, chikungunya, Zika, and urban yellow fever, representing a significant public health concern. In Brazil, more than 1.6 million suspected dengue cases and approximately 1,793 deaths were reported in 2025 alone. Among the strategies used for vector control, chemical insecticides are widely used, particularly those belonging to the pyrethroid group, extensively employed in vector control programs and commonly found in household insecticides. However, the intensive use of these compounds has favored the selection of resistant populations of Ae. aegypti, frequently associated with mutations in the gene encoding the voltage-gated sodium channel (VGSC), resulting in the phenomenon known as kdr (knockdown resistance). In this context, the present study aimed to determine the genotypic and allelic frequencies of four kdr mutations (Phe1534Cys, Val1016Ile, Val410Leu, and Ile1010Met) in a population of Ae. aegypti collected at the Historical Museum of Londrina, located in the central region of Londrina, Paraná, Brazil. A total of 25 adult mosquitoes were collected using a Nasci aspirator, subsequently identified and stored at −80 °C until analysis. After DNA extraction, the analysis of kdr mutations was performed using allele-specific PCR, followed by visualization of the amplified fragments by electrophoresis in a 2% agarose gel. The results indicated a high frequency of the Phe1534Cys mutation, with 96% of individuals presenting the mutant genotype. For the Val1016Ile mutation, the mutant genotype was not detected, with 96% of individuals being heterozygous. Regarding the Val410Leu mutation, 96% of individuals presented the mutant genotype, while for the Ile1010Met mutation all analyzed individuals (100%) exhibited the mutant genotype. High mutant allele frequencies were observed, particularly for Metkdr (100%), Cyskdr (98%), and Leukdr (98%), whereas the Ilekdr allele showed a frequency of 52%. Among the 25 individuals analyzed, 92% presented three mutations and 8% at least two mutations. The accumulation of kdr mutations may increase pyrethroid resistance in the insect. These results demonstrate a high frequency of mutations associated with pyrethroid resistance in the analyzed population, highlighting the importance of genetic monitoring of Ae. aegypti populations to evaluate the effectiveness of control strategies and support the development of more efficient approaches aimed at reducing vector infestation and consequently reducing the transmission of arboviral diseases.

**Keywords**: Molecular entomology; pyrethroids; insecticide resistance.

**Acknowledgements**: Fundação Araucária.

**GENOMIC ARCHITECTURE OF FACIAL HAIR WHORLS IN CANCHIM CATTLE**

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The Brazilian beef cattle industry utilizes composite breeds to optimize productivity in tropical environments. The Canchim breed was developed to combine the productive potential of Charolais with the adaptability of Nelore. While selection traditionally prioritizes growth, morphological traits, such as facial hair whorls, are studied as indirect indicators of temperament due to their shared embryological origin with the nervous system. This study performed a genome-wide association study to identify genomic regions and candidate genes associated with the presence/absence (WHORL) and height (WH) of facial hair whorls. Phenotypic data from 1,260 Canchim animals and genotypic information from 2,551 individuals (BovineHD BeadChip) were analyzed. The trait WHORL identified the presence or absence of hair whorls, while WH defined their vertical position relative to the eye line (low, middle, high, or very high). A single-step approach was employed, integrating pedigree and genomic data through a threshold model to estimate molecular marker effects. Genomic windows approach was considered and those explaining at least 0.40% of the genetic variance were studied, focusing on markers located within genes. Results identified 194 genes for WHORL and 136 for WH, with 40 genes in common. Functional analysis via the STRING database revealed that the biological mechanisms underlying these traits are governed by complex genomic pathways. Key genes including *CREB3L3*, *TBXA2R*, *MAP2K2*, *EEF2*, *SEMA6B*, and *MATK*, participate in pathways highlighting the link between neural development and morphological traits. Dopaminergic and Cholinergic synapses, along with Neuroactive ligand-receptor interactions, are fundamental for regulating motivation and fear responses. Additionally, the Oxytocin signaling pathway modulates social bonding, while Cortisol synthesis and secretion manage the physiological "fight or flight" response. These pathways provide a framework for understanding the relationship between whorl traits and behavior. The association between hair whorls and temperament stems from their shared ectodermal origin. The Axon guidance and Neurotrophin signaling pathways are critical for neuronal growth; since the nervous system and skin develop simultaneously, genetic signals directing nerve fibers also influence hair follicle orientation. Furthermore, the Regulation of actin cytoskeleton is essential for cell migration during development, influencing specific whorl patterns. In summary, these genomic pathways suggest that facial hair whorls are external markers of the underlying neural architecture shaping an animal's behavioral profile. These findings demonstrate the polygenic nature of hair whorls in Canchim cattle, providing a basis for incorporating these morphological traits into breeding programs to improve management and animal welfare through genomic selection.

**Keywords**: Animal welfare, Candidate genes, Composite breed, Single-step GWAS, SNP markers

**GENOMIC CHARACTERIZATION AND PHYLOGENETIC ANALYSIS OF DENGUE VIRUSES (DENV-1, DENV-2 and DENV-3) IN ARARAQUARA-SP**

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The recent increase in dengue cases reinforces the relevance of effective genomic epidemiological surveillance. Araraquara, one of the most industrialized cities in São Paulo state, with 242,228 inhabitants, located 270 km from the state capital, is a suitable location to monitor emerging variants due to its demographic and epidemiological profile. The monitoring included 145 dengue-positive samples collected between 2024 and 2025 sequenced in the laboratory where this study was conducted, using NGS technology and the Illumina COVIDSeq protocol for library preparation and the Illumina MiSeq system for data generation. Analysis was performed with the DRAGEN Microbial Amplicon pipeline. Subsequently, a phylogenetic analysis was conducted using the Nextclade platform, incorporating all 145 sequences. The phylogeny of the Araraquara samples showed patterns very similar to those observed in the rest of the country. All mutations found had been previously described. Genomic distribution revealed the co-circulation of three serotypes: DENV-2 (55.7%), DENV-1 (33.3%), and DENV-3 (11%). For DENV-1, the main clades were 1V_E.1 (96.30%) and 1V_D.1.1 (3.70%). In DENV-2, 100% prevalence of clade 2II_F.1.1.2 was observed, while for DENV-3, clade 3III_B.3.2 (100%) was identified. These findings highlight the importance of surveillance for timely public health interventions, strengthening global genomic monitoring of arboviruses.

**Keywords**: Genomic Surveillance; Dengue; NGS.

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**BALANCED TRANSLOCATION t(5;9)(p11;p11) IDENTIFIED BY FISH IN A COUPLE WITH RECURRENT CHROMOSOMAL ABNORMALITIES IN OFFSPRING**

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Balanced translocation is a relatively common type of chromosomal anomaly that does not involve gain or loss of genetic material; therefore, carriers are generally phenotypically normal. However, during meiosis, the quadrivalent formed may segregate abnormally, generating unbalanced gametes and leading to reproductive complications such as spontaneous abortion, stillbirths, or offspring with chromosomal syndromes. A phenotypically normal couple was referred to the Genetic Counseling Service (SAG) of the State University of Londrina (UEL) following the recurrence of chromosome 5 abnormalities in two of their children. The first child died at nine months of age, and the second newborn also presented clinical suspicion of a chromosomal anomaly. Karyotyping of both children revealed structural rearrangements involving chromosome 5, described as 46,XX,?inv(5)(p15.2p14) and 46,XY,add(5)(p14), respectively, according to the International System for Human Cytogenomic Nomenclature (ISCN). This study aimed to investigate the cytogenetic basis underlying the recurrence of chromosome 5 alterations within the same family through the combined use of conventional and molecular cytogenetic techniques. Both parents underwent cytogenetic analysis from peripheral blood lymphocyte cultures. After 72 hours of incubation, cells were treated with 0.0017% colchicine, followed by hypotonic treatment with 0.0175 M KCl, fixation, and slide preparation. GTG-banding was performed; however, this technique proved insufficient for a definitive diagnosis in the mother, revealing only a possible alteration in the size of bands at 5p. Given the inconclusive maternal karyotype, complementary analysis by Fluorescence In Situ Hybridization (FISH) was performed. FISH analysis identified a maternal balanced translocation, characterized as 46,XX,t(5;9)(p11;p11). During meiosis, adjacent segregation of the quadrivalent formed by the derivative chromosomes generates unbalanced gametes, which — alongside abnormal crossing-over events — may account for the altered karyotypes observed in the offspring. Nevertheless, determining the exact karyotype of each child would require additional molecular techniques, such as FISH. Understanding the origin of the chromosomal rearrangement enables accurate reproductive risk stratification for the couple. This case highlights the importance of integrating conventional cytogenetics with molecular techniques to elucidate structural chromosomal rearrangements. Furthermore, it underscores the clinical value of parental karyotyping when structural anomalies are identified in a child, providing the couple with a more informed basis for reproductive decision-making.

**Keywords**: balanced translocation; FISH; chromosome 5; genetic counseling; cytogenetics.

## EXTRACELLULAR VESICLE PROTEINS ALTERATIONS IN GESTATIONAL DIABETES MELLITUS: POTENTIAL BIOMARKERS

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Gestational Diabetes Mellitus (GDM) is characterized by any degree of hyperglycemia first diagnosed during pregnancy and is associated with short and long-term maternal and fetal complications. Recent evidence indicates that extracellular vesicles (EVs), membrane-bound nanoparticles released by different cell types and responsible for contact-independent intercellular communication, present quantitative and qualitative alterations in pregnancies complicated by GDM. These vesicles transport proteins, RNAs, and other bioactive molecules capable of modulating metabolic and epigenetic processes, reflecting the maternal pathophysiological state. The present project aims to analyze the proteomic profile of EVs isolated from the plasma of pregnant women with GDM and normoglycemic pregnancies in order to investigate their potential as biomarkers and to understand possible mechanisms involved in maternal–fetal metabolic programming. A total of 20 pregnant women (n=20) were included, 10 normoglycemic and 10 with GDM, evaluated between 24–28 weeks (period of GDM diagnosis) and 36–40 weeks of gestation (last gestational trimester). The groups were matched by age, gestational age, BMI, and glycemic index. EVs were isolated from plasma by size-exclusion chromatography (SEC) and subsequently concentrated using centrifugal filters. Total protein quantification was performed using the MicroBCA™ protein assay kit. The results demonstrated that the total protein concentration in EVs from women with GDM was higher (2000–3000 µg/mL) than that observed in the normoglycemic group (1000–2000 µg/mL). A reduction in protein concentration was observed between 36–40 weeks in the control group, while levels remained relatively constant in the GDM group. These differences suggest alterations in the composition or release of EVs associated with the hyperglycemic state. The findings indicate that GDM may impact the proteomic content of circulating EVs, reinforcing their potential as a source of biomarkers and as mediators of epigenetic mechanisms involved in maternal–fetal communication. Future studies will be essential to identify differentially expressed proteins and to understand their role in the pathophysiology of GDM and in the metabolic programming of the offspring.

**Keywords**: Extracellular Vesicles, Gestational Diabetes Melittus, Targettings, Proteins, MicroBCA.

**Acknowledgement**: FAPESP.

**IMPACT OF DAPAGLIFLOZIN ON SIRTUIN GENE EXPRESSION IN THE MYOCARDIUM OF RATS WITH TYPE 1 DIABETES MELLITUS**

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Introduction: Type 1 diabetes mellitus (T1DM) is a chronic metabolic disorder associated with myocardial dysfunction, oxidative stress, and cardiac remodeling. Sirtuins (SIRTs) play a central role in metabolic regulation, mitochondrial homeostasis, and cellular stress responses. Although sodium–glucose cotransporter 2 (SGLT2) inhibitors have demonstrated cardiovascular benefits in type 2 diabetes, their molecular effects in T1DM remain poorly understood. Objective: This study aimed to evaluate the impact of dapagliflozin on the gene expression of Sirt1, Sirt3, Sirt5, Sirt6, and Sirt7 in the myocardium of rats with streptozotocin-induced T1DM. Methods: Male Wistar rats (90 days old) were divided into four groups: control (C), control treated with dapagliflozin (C-Dapa), diabetic (DM), and diabetic treated with dapagliflozin (DM-Dapa) (n=20/group). T1DM was induced by streptozotocin (50 mg/kg, i.p.) and confirmed by blood glucose >220 mg/dL. Dapagliflozin (10 mg/kg/day) was administered via chow for 16 weeks. At the end of the protocol, cardiac tissue was collected for quantitative real-time PCR (qPCR) analysis. Relative gene expression was calculated using the EndoGeneAnalyze and normalized to validated reference genes (Ppia, Gapdh, Rpl32, Actb, Rpl18a, and Hprt1). Statistical analysis was performed using ANOVA followed by Tukey's test or Kruskal–Wallis followed by Dunn's test ($p<0.05$). Results: Body weight and initial blood glucose did not differ between groups. The DM group showed a significant reduction in Sirt1 and Sirt5 gene expression compared to controls. No significant differences were observed in Sirt3, Sirt6, or Sirt7 expression among groups. Dapagliflozin treatment did not significantly restore the reduced expression of sirtuins in diabetic animals. Conclusion: These findings demonstrate that T1DM promotes selective downregulation of Sirt1 and Sirt5 in the myocardium, suggesting impairment of pathways related to energy metabolism and oxidative stress response. Under the experimental conditions evaluated, dapagliflozin did not modulate the expression of these sirtuins, indicating that its potential cardioprotective effects in T1DM may involve mechanisms independent of sirtuin gene regulation.

**Keywords**: type 1 diabetes mellitus, dapagliflozin, sirtuins, myocardium, qPCR.

**Acknowledgments**: São Paulo Research Foundation (FAPESP).

**ANALYSIS OF THE ORGANIZATION OF REPETITIVE DNAS AND THE EVOLUTION OF SEX CHROMOSOME SYSTEMS IN CERAMBYCID BEETLES (LAMIINAE)**

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Coleoptera is one of the most diverse orders of Insecta, comprising 400,000 species. The family Cerambycidae is the fourth most numerous; however, knowledge about its cytogenetics and genomics is still scarce. An example of this is the availability of karyotypic descriptions for only 176 species. The presumed ancestral chromosome number for Cerambycidae is 2n = 20, XY, with the lowest known number being 2n = 10 in *Plocaederus obesus* and the highest in *Vesperus xatarti* (2n = 53). Regarding repetitive DNAs, data are lacking. We used *Steirastoma marmorata* (Xyp) and *Cipriscola fasciata* (Xyp) to understand the composition, organization, and differentiation patterns of satellite DNAs (satDNAs) in Cerambycidae. The insects were collected at UNESP Rio Claro campus and stored in 100% ethanol for DNA extraction. Genome sequencing was performed by Novogene (Illumina MiSeq). The reads were processed, filtered, and paired using tools from the Galaxy/RepeatExplorer platform. Identification and characterization of the satellitome (satellite DNAs) were carried out using TAREAN/RepeatExplorer2 from a sample of 12,000,000 reads, followed by curation in Geneious (11.1.5). The TAREAN/RepeatExplorer2 output identified 49 and 64 putative satDNAs in *C. fasciata* and *S. marmorata*, respectively. After curation, 20 satDNAs were confirmed in *C. fasciata* and 29 satDNAs in *S. marmorata*. Molecular characterization of satDNAs in *C. fasciata* showed monomer sizes ranging from 22 base pairs (bp) to 404 bp, with an average of 146 bp. The AT base pair content ranged from 46.8% to 73.10%, with an average of 62.14%. The abundance of satDNAs relative to the input sample used in TAREAN/RepeatExplorer2 was 0.678%, with a gradual decrease in abundance observed among the different satDNA families. In *S. marmorata*, satDNA monomer sizes ranged from 90 bp to 5,035 bp, with an average of 314.06 bp. The AT content ranged from 46.8% to 75.4%, with an average of 61.7%. The total abundance of satDNAs within the sample analyzed was 2.348%. Notably, two satDNAs showed higher proportions, while the others exhibited a gradual decrease in abundance. Both species showed high AT base pair content, which is characteristic of satDNAs. However, the number of satDNA families, monomer size, and abundance displayed marked differences. This highlights distinct evolutionary pathways in the organization and composition of satDNAs in these species of the subfamily Lamiinae (Cerambycidae).

**Keywords**: satellite DNA; Coleoptera; Genome
**Acknowledgments**: PIBIC (Edital 8/2025, processo nº19393), FAPESP

# RESUMOS: PÔSTERES PÓS-GRADUAÇÃO

*resumos: pôsteres pós-graduação*

**SELENOP GENE RS3877899 POLYMORPHISM AS A PREDICTOR OF RECURRENCE IN UROTHELIAL BLADDER CANCER: ROLE OF DIABETES MELLITUS AND ALCOHOLISM**

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Urothelial bladder cancer (UBC) is the 10th most frequent cancer in Brazil and the 9th in the world. Single nucleotide polymorphisms (SNPs) in antioxidant response genes can influence the expression of distinct protein isoforms, thereby influencing cancer susceptibility and prognosis. Selenoprotein P (SELENOP) transports selenium (Se) to tissues and has two isoforms: a 50 kDa and a 60 kDa form, the latter being associated with a reduced risk of colorectal cancer. In this context, the present study investigated the impact of the rs3877899 (C>T) variant of the SELENOP gene on the prognosis of UBC. Blood samples were collected from 350 patients diagnosed with UBC at the Cancer Hospital of Londrina. All participants provided written informed consent and completed a structured questionnaire to obtain sociodemographic data (sex and age), clinical information (hypertension, diabetes, and family history of cancer), and exposure history (smoking, alcohol consumption, and pesticide exposure). Clinicopathological data were obtained from anatomopathological reports, including tumor grade (low or high), muscle layer invasion status (non–muscle-invasive bladder cancer [NMIBC] or muscle-invasive bladder cancer [MIBC]), and recurrence at six months, one year, two years, five years, as well as multiple recurrences. DNA was extracted using a commercial kit and genotyped by qPCR using a TaqMan® probe. The allelic frequencies found for this SNP were 0.72 (C) and 0.28 (T), and the genotypic frequencies were 53%, 38%, and 9% for CC, CT, and TT, respectively. An increase in 5-year relapse risk was observed i) among diabetic patients carrying the C allele, in the genotypic and dominant ($p = 0.018$; OR = 4.529; CI = 1.546-12.097) and in the recessive model ($p = 0.005$; OR = 4.324; CI = 1.038-16.311), and ii) for alcoholic patients in the recessive model ($p = 0.044$; OR = 4.114; CI = 1.038-16.311). Previous studies have demonstrated that the C allele favors the synthesis of the 60 kDa SELENOP isoform, which appears to enhance selenium availability for the synthesis and maintenance of intracellular antioxidant enzymes. This mechanism could theoretically mitigate oxidative stress and contribute to a better prognosis in CUB. However, patients with diabetes and/or chronic alcohol consumption are often exposed to excessive reactive oxygen species production driven by chronic hyperglycemia and ethanol metabolism. This persistent pro-oxidative state may overwhelm endogenous antioxidant defenses, potentially offsetting the protective effect associated with the C allele and contributing to a less favorable prognosis in these patients.

**Keywords**: bladder cancer, SNPs, oxidative stress, selenoproteins, tumor recurrence.

**Acknowledgements**: CNPq, CAPES, and Londrina Cancer Hospital.




1º LUGAR NA CATEGORIA APRESENTAÇÃO PÔSTER
PÓS-GRADUAÇÃO

## WORLDWIDE PATTERNS OF KIR–HLA-C DIVERSITY REVEAL REGIONAL DIFFERENCES IN NK REGULATION

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The interaction between KIR (Killer-cell Immunoglobulin-like Receptors) on NK cells and their HLA ligands on nucleated cells is central to immune regulation, regulating the Natural Killer (NK) cell cytotoxicity. KIR and HLA genes are among the most polymorphic in the human genome and, although located on different chromosomes, have coevolved under selective pressures driven by pathogens and reproductive fitness. KIR2DL2 and KIR2DL3 are two genes that mark the main KIR haplotype groups, as they segregate mutually exclusively within different haplotypes. The primary ligands of the inhibitory receptors KIR2DL2, KIR2DL3, and KIR2DL1 are the HLA-C molecules, classified into two functional groups, C1 and C2. KIR2DL2 and KIR2DL3 preferentially recognize HLA-C1, whereas KIR2DL1 binds HLA-C2; KIR2DL2–C1 interactions are stronger than KIR2DL3–C1, while KIR2DL1-C2 exhibits intermediate inhibitory potential. KIR polymorphisms and copy numbers interfere with NK regulation. However, KIR–HLA diversity remains underrepresented in several populations, especially admixed ones. We applied kir-mapper to estimate copy-number variation in KIR genes and hla-mapper to estimate HLA-C allele genotype from whole-genome sequencing data in 4,459 unrelated individuals from 78 worldwide populations. KIR haplotypes were grouped as AA, AB, or BB based on the presence of KIR2DL3 (A haplogroup) and KIR2DL2 (B haplogroup). HLA-C genotypes were classified as C1C1, C1C2, or C2C2. Associations between KIR and HLA-C were evaluated by biogeographic regions. KIR haplotypic diversity showed strong population structure, with significant differences in AA, AB, and BB frequencies across regions ($\chi 2$ $p \approx 3.8 \times 10-51$). Globally, AA was the most frequent genotype. Haplogroup A was more frequent among East Asians, whereas haplogroup B was relatively more common in South Asia. The C2C2 genotype was less frequent in East Asia than in other regions, resulting in a lower proportion of individuals carrying the C2 ligand. The reduction of the C2 ligand in East Asia might alter the distribution of potential KIR2DL1-mediated interactions, reshaping the receptor–ligand landscape in this region. Integrating KIR copy number and HLA-C groups allowed estimation of the number of potential receptor–ligand pairs per individual, summarized as a receptor-ligand pair index. This index differed significantly among regions (Kruskal-Wallis $H = 70.7$, $p < 10-12$), with East Asia showing lower mean values. Overall, our results demonstrate that KIR haplotypic architecture and HLA-C ligand distribution vary across human populations and jointly shape both the inhibitory interaction potential of NK cells and the gestational risk landscape.

**Keywords**: KIR Haplotypes; copy number variation; HLA-C, NK cell receptors; population genetics.
**Acknowledgments**: CAPES, FAPESP, CNPq




2º LUGAR NA CATEGORIA APRESENTAÇÃO PÔSTER
PÓS-GRADUAÇÃO

## CHROMOSOME-SCALE PRELIMINARY GENOME ASSEMBLY OF THE CRITICALLY ENDANGERED VRIESEA LONGISTAMINEA (BROMELIACEAE)

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Brazil harbors the highest diversity of Bromeliaceae worldwide, with a substantial proportion of endemic and threatened species associated with specialized habitats. Vriesea longistaminea C.C. Paula & Leme is a critically endangered bromeliad with ocurrence on ferruginous rocky outcrops (canga) of the Iron Quadrangle, Minas Gerais, southeastern Brazil. The species has an extremely restricted distribution and occurs in small, fragmented populations, frequently located near active iron mining areas. Habitat loss, population isolation, and microclimatic alteration represent major threats, highlighting the need for genomic resources focused on this narrowly endemic taxon. Here, we present a chromosome-scale preliminary genome assembly for V. longistaminea, generated to provide a foundational genomic reference for this species. High–molecular-weight DNA extracted from young leaf tissue was sequenced using PacBio HiFi technology, and chromatin conformation capture (Hi-C) data were produced using a multi-enzyme protocol. Genome assembly was performed using a HiFi + Hi-C–assisted strategy, followed by contamination screening, Hi-C–based scaffolding, and manual curation of chromosomal structures. The curated assembly recovered 25 chromosomes per haplotype, with more than 98% of the assembled sequence anchored into chromosome-scale scaffolds, indicating high structural continuity and successful chromosomal reconstruction. Assembly quality assessments revealed high completeness of conserved embryophyte genes. Analysis of repetitive elements showed that the genome is dominated by transposable elements, accounting for approximately two-thirds of the assembly. Long terminal repeat retrotransposons constitute the most abundant class, with Gypsy elements representing the primary contributors to genome composition and chromosomal architecture. This chromosome-level genome assembly represents the first genomic reference for Vriesea longistaminea, providing a structurally resolved view of its genome organization, repetitive landscape, and chromosomal architecture. The recovery of complete chromosome sets and the high proportion of sequence anchored into chromosome-scale scaffolds establish a solid genomic baseline for subsequent analyses of gene content, genome evolution, and structural variation in ferruginous rupestrian grassland bromeliads.

**Keywords**: HiFi sequencing, Hi-C scaffolding, transposable elements, Bromeliaceae
**Acknowledgements**: This study was supported by Agência Paulista de Tecnologia dos Agronegócios (APTA; 2022/2658)




3º LUGAR NA CATEGORIA APRESENTAÇÃO PÔSTER
PÓS-GRADUAÇÃO

**ASSEMBLY AND ANNOTATION OF THE Atta robusta MITOGENOME: A COMPARATIVE EVALUATION OF RNA-seq AND UCE APPROACHES**

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The ants of the subtribe Attina (Formicidae: Myrmicinae) cultivate symbiotic fungi that degrade plant material and constitute their main food source. Atta robusta Borgmeier, 1939 is a leaf-cutting ant endemic to the restinga ecosystems of Espírito Santo and Rio de Janeiro, and has been classified as threatened with extinction since 2003. Phylogenomic analyses indicate that this species represents the most recently diverged lineage of the genus Atta, highlighting its evolutionary and conservation significance. In this context, sequencing mitochondrial DNA (mitogenome) provides important molecular markers for phylogenetic studies and for understanding the evolution of leaf-cutting ants. Thus, this study aimed to assemble and annotate the mitogenome of A. robusta using two distinct approaches: transcriptomic data (RNA-Seq) and sequences of ultraconserved elements (UCEs). The transcriptome was generated and made available by the Molecular Evolution Laboratory (LEM, UNESP – Rio Claro). UCE data were obtained from public databases (SRA: SRR15342868). The reads were subjected to preprocessing to remove adapters and filter low-quality sequences using Seqyclean and Trimmomatic, while the FASTX-Toolkit was used to remove initial bases and correct GC-content bias. Sequence quality was assessed using FastQC. Mitogenome assembly was performed using the programs MITGARD and MitoFinder, using the mitogenome of A. laevigata as a reference. Gene annotation was conducted in MITOS2, and data visualization and organization were carried out using RStudio and OGDRAW. Although mitochondrial reads are often present in transcriptomic data due to high gene expression, we observed low coverage in the assembly generated from RNA-Seq compared with the UCE data. RNA-Seq produced a fragmented assembly with the absence of tRNAs and protein-coding genes. In contrast, using UCE data we obtained a complete mitogenome assembly and greater consistency in the recovery of protein-oding genes, as well as transfer and ribosomal RNAs. The limitations of the transcriptomic approach likely reflect variations in mitochondrial expression among tissues and possible RNA degradation processes, although more conserved genes were successfully recovered. The comparison between approaches showed that, although RNA-Seq can provide mitochondrial information, its efficiency for reconstructing complete mitogenomes is limited, whereas UCE data showed greater robustness in the final assembly. These preliminary results highlight the importance of method selection in phylogenomic studies and contribute to improving protocols applied to non-model organisms.

**Palavras-chave:** Bioinformatics, Mitochondrial DNA, Leaf-Cutting Ants, Transcriptomics.
**Agradecimentos:** Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES) e CEPID CBioClima 2021/10639–5.

**TAP1 allelic diversity and ancestry-based frequency variation in the Brazilian population**

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The transporter associated with antigen processing genes, TAP1 and TAP2, are located within the major histocompatibility complex (MHC) region and encode the two subunits of the TAP heterodimer. TAP is essential for antigen presentation via MHC class I, mediating the transport of peptides containing 8 to 12 amino acids to the lumen of the endoplasmic reticulum (ER). Genetic polymorphisms in the TAP1 gene may influence repertoire selection, immune response efficiency, and disease susceptibility. However, little is known about TAP1 allelic diversity across populations. Objective: To describe the allelic diversity of the TAP1 gene in Brazilian individuals from the SABE cohort, and evaluate whether allele frequencies differ according to the ancestry background. Methods: We processed whole-genome sequencing (WGS) data using the hla-mapper workflow, focusing on the TAP1 gene. Allele frequencies were estimated for the overall cohort and stratified by the ancestry backgrounds, using a ≥70% ancestry proportion threshold for group classification. Results: A total of 1,171 samples were analyzed and divided into four groups: Admixed (n = 370), major African (n = 46), major East Asian (n = 33), and major European (n = 722) ancestry. The allelic frequencies of the TAP1 gene showed that the TAP1*01:01:01 allele has a high prevalence across all evaluated groups, ranging from 72,83% (AFR), among 72,84% (admixed) to 80,58% (EUR) among 81,82% (EAS). The uncommon allele TAP1*01:05 was also identified, with its highest frequency in the African-Brazilian group (3.26%), and absent among the individuals with higher Asian ancestry. Discussion: Our data indicate that, in an admixed population such as Brazilians, ancestry might influence TAP1 allele frequencies. Although TAP1*01:01 is the prevalent allele in all subgroups, there are major frequency differences among groups for alleles encoding different TAP1 isoforms. These frequency differences are likely to occur across African, European, and Asian populations, potentially modifying the patterns of antigens presented in each population. Conclusion: This study contributes to the characterization of TAP1 genetic diversity in an admixed population and provides insights into how variation in antigen-processing genes may influence immune responses at the population level, demonstrating that allelic diversity differs across subgroups stratified by genetic ancestry.

**Keywords**: TAP1; alleles; Ancestry; Brazilian Population; MHC Class I.

**Acknowledgments**: This study was supported by the National Council for Scientific and Technological Development (CNPq).

**GENETIC DIVERSITY ASSESSMENT OF THE "DOURADA" (*Brachyplatystoma rousseauxii*, SILURIFORMES: PIMELODIDAE) BASED ON MICROSATELLITE MARKERS**

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The dourada (*Brachyplatystoma rousseauxii*) is a migratory catfish widely distributed in the Amazon basin and holds significant socioeconomic relevance. However, intense fishing pressure and a lack of genetic data highlight the urgent need for studies focused on its conservation. This study aimed to evaluate the genetic diversity of natural populations of B. rousseauxii using previously developed microsatellite markers. Samples were collected from the area of influence of the hydroelectric power plant installed on the Madeira River. The methodology involved DNA extraction, PCR amplification, and genotyping using an automated sequencer. The results revealed concerning levels of genetic imbalance in the Madeira River population, with observed heterozygosity (Ho) ranging from 0 to 0.97 (mean 0.49) and expected heterozygosity (He) ranging from 0.71 to 0.95 (mean 0.84). These values were compared to data recorded in 2010 (Ho = 0.14–0.91, mean 0.636; He = 0.21–0.93, mean 0.706). Discussion of these findings indicates that while the studied population maintains a wide range of alleles and high potential diversity, the observed heterozygosity is drastically lower for most loci compared to populations described in the literature. In conclusion, this discrepancy is a strong indicator that the population is suffering from inbreeding, which may severely impact its fitness and long-term survival capacity.

**Keywords**: Amazon Basin, Catfish, Population Analysis.

**Acknowledgements**: This work was funded by the Coordination for the Improvement of Higher Education Personnel (CAPES) and the Foundation for the Development of Unesp (FUNDUNESP).

**IDENTIFICATION OF SEX-ASSOCIATED REGIONS IN DRAFT GENOME ASSEMBLIES OF CURIMATIDAE (TELEOSTEI, CHARACIFORMES) SUGGESTS SEX SYSTEM TURNOVER**

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Teleost fish display remarkable diversity in sex determination systems, ranging from simple monofactorial mechanisms with males (XX/XY) or female (ZZ/ZW) heterogamety to complex multifactorial systems involving multiple sex chromosomes. Within Characiformes, only about half of the 27 recognized families have been investigated for sex determination, and even fewer have had their sex systems properly characterized. Given this knowledge gap and the high diversity of the group, investigating sex chromosome evolution in these fishes is highly relevant. Here, we investigated two Curimatidae species Cyphocharax modestus and Steindachnerina insculpta, aiming to identify their sex determination systems and infer their evolutionary trajectories. PacBio HiFi reads were generated for both species to produce female draft genome assemblies at the contig level. Pools of male and female paired-end reads were mapped onto the respective assemblies and analyzed using a bioinformatic pipeline designed to detect sex-linked genomic signals based on SNP density and male-to-female coverage differences. Candidate sex-associated contigs were identified through comparative analyses and further inspected in IGV to manually evaluate coverage patterns and sex-specific variants. In C. modestus, a few contigs highlighted significant differences in male-associated SNPs, but depth ratio analysis provided clearer signals. Twelve candidate contigs were examined in detail; two were identified as putative Z-specific regions, displaying approximately double coverage in males relative to females and containing part of a pseudoautosomal region, consistent with a ZZ/ZW system. On the other hand, in S. insculpta, male-associated SNPs were more prevalent. Thirteen contigs were analyzed, and the three with the highest male SNP density were identified as putative X-specific regions, exhibiting sex-specific SNP patterns and approximately double coverage in females and supporting a XX/XY system. These findings indicate the presence of two distinct sex systems in Curimatidae. This is notable because most families within Curimatoidea, such as Cynodontidae, Prochilodontidae, Anostomidae, and Parodontidae, exhibit a ZZ/ZW system. The occurrence of an XX/XY system in S. insculpta indicates a turnover event in sex-determination system during the evolutionary history of this clade. As Curimatoidea predominantly exhibits a ZZ/ZW system, the occurrence of an XX/XY system, as found in Serrasalmidae species Colossoma macropomum may indicate either multiple independent turnover events within the superfamily or a lineage-specific turnover within Curimatidae family.

**Palavras-chave:** evolution, fish, sex genomics.

**Agradecimentos:** CAPES, FAPESP (2025/04823-9), Proex, CNPq.

**LANDSCAPE GENOMICS OF *Acrocomia intumescens*: THE ROLE OF CLIMATIC GRADIENTSIN GENETIC DIFFERENTIATION UNDER THE CAATINGA BIOME.**

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Landscape genomics provides a powerful framework to examine how environmental gradients shape genetic variation in natural populations by jointly considering neutral processes and adaptive responses. In the Brazilian semiarid region, historical cycles of forest expansion and retraction led to the fragmentation of humid vegetation into isolated upland refuges known as Brejos de Altitude, forming an archipelago of mesic enclaves subjected to intense selective pressures. Within this scenario, Acrocomia intumescens—an oil-rich palm endemic to northeastern Brazil and strongly associated with mesophytic habitats—emerges as an informative system for assessing how montane isolation and climatic heterogeneity contribute to genetic structuring and adaptive divergence among plant populations persisting in Caatinga refugial landscapes.In this study, we evaluated genetic diversity, population structure, and the association between genomic variation and environmental variables in natural populations of A. intumescens. We analyzed 139 individuals from ten populations distributed along the Sertaneja Depression, using genomic data generated through ddGBS. After filtering, 3,466 high-quality SNPs were retained for population genetic and landscape genomic analyses. DAPC and sNMF analyses revealed the presence of two well-defined genomic groups corresponding to the northern and southern portions of the Sertaneja Depression, with high genetic differentiation between groups (FST = 0.79–0.86) and restricted connectivity mainly at a local scale. Redundancy analysis (RDA) indicated that genetic variation is strongly associated with environmental gradients, with precipitation seasonality (BIO15) emerging as the main explanatory variable, that influence 60% of the genetic structure, followed by precipitation in the driest month (BIO14) and edaphic characteristics. The findings indicate that the genetic configuration of A. intumescens is shaped by both biogeographic discontinuities and selective pressures linked to water limitation, highlighting signatures of local adaptation within mesophytic refugia. The pronounced genetic divergence observed among populations suggests that each highland enclave functions as a distinct reservoir of genetic diversity. Consequently, safeguarding the Brejos de Altitude within the Caatinga domain is both strategic and urgent: beyond ensuring the long-term survival of this palm species, such protection also preserves numerous co-occurring endemic taxa and maintains irreplaceable evolutionary processes in the face of ongoing global climate change.

**Keywords**: Genetic structure, Population Genomics, Macaúba, SNPs.
**Acknowledgment**: CAPES, FAPESP.

## LEISHMANIA INFANTUM INFECTION MODULATES ALTERNATIVE SPLICING WITH DIFFERENTIAL ISOFORM USAGE IN HUMAN NEUTROPHILS

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Alternative splicing (AS) is a common co-transcriptional mechanism in eukaryotes that allows the generation of multiple mRNA isoforms from a single gene through the differential selection of splicing sites in pre-mRNA. This process is crucial in the regulation of gene expression, since the different isoforms generated can be translated into proteins with distinct structural and functional characteristics, increasing the complexity of the transcriptome and the proteome, being an important mechanism of molecular plasticity. Visceral leishmaniasis is a severe systemic infectious disease caused, in the Americas, by the zoonotic species Leishmania infantum, and which mainly affects vulnerable populations, being considered a zoonosis of great importance for public health in endemic regions. During the course of infection, the parasite establishes a complex interaction with the host, being able to modulate molecular mechanisms when establishing itself in cells of the immune system, including neutrophils, which constitute one of the first cells to come into contact with the parasite after its inoculation, as a strategy to favor its survival and dissemination. In this context, we aimed to analyze possible alterations in AS and in isoform usage in human neutrophils obtained from five healthy individuals, before and after in vitro exposure to L. infantum. RNA-Seq data from ten paired samples (5 infected and 5 controls) were analyzed for the identification of differentially regulated events and isoforms, using the SUPPA2 tool. Differential transcript expression analysis was also conducted seeking to integrate the results of the differentially regulated isoforms with quantitative alterations in transcript expression, as well as in silico analyses of protein domains and structural prediction of the selected isoforms using AlphaFold2 Colab. Six splicing events were significantly different between control and infected samples (Skipping Exon=3, Alternative 5′ Splice Sites=2, Alternative 3′ Splice Sites=1; $|\Delta PSI| \geq 0.1$; $p \leq 0.05$), and 10 differentially regulated isoforms ($|\Delta PSI| \geq 0.1$; $p \leq 0.05$). The associated annotated genes include coding transcripts (CCM2L, ZNF273, NPIPB11, MACO1, SLC25A52) and non-coding transcripts (LINC01150, MORC2-AS1), some with potential functions in signaling and inflammatory response. Integration of the differential transcript expression analysis with the isoform results revealed two key genes that presented isoform switching after infection, highlighting CCM2L and SLC25A52, which also presented differences in domain composition and in structural prediction between the isoforms. We conclude that infection by L. infantum results in alterations in isoform expression in human neutrophils, which may reveal new regulatory targets for disease control.

**Palavras-chave:** RNA-Seq, isoforms, visceral leishmaniasis, splicing

**Agradecimentos:** FAPESP, CAPES.

## REVEALING A HETEROMORPHIC XX/XY SYSTEM IN *Psalidodon paranae* (CHARACIFORMES, ACESTRORHAMPHIDAE) USING HIGH-RESOLUTION OLIGOPAINT PROBES

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The eukaryotic genome contains essential genes, as well as additional elements that do not follow the Mendelian pattern of segregation. Among them are the B chromosomes, defined as supernumerary and traditionally considered dispensable because they do not have a well-defined function. In a species of tetra fish called *Psalidodon paranae*, previous studies have shown a significant difference in the frequency of B chromosomes between females (57.1%) and males (8.7%), suggesting a strong association between these elements and female gonadal development. Preliminary genomic analyses indicated the presence of an XX/XY sex determination system with a highly differentiated Y chromosome. However, classical cytogenetic approaches were not able to clearly identify or physically validate this sex chromosome system, as no conspicuous heteromorphism or diagnostic chromosomal markers could be consistently detected using conventional staining and banding techniques. Thus, the chromosomal basis of sex determination in the species remained unresolved. The objective of this study was to develop and apply high-specificity oligonucleotide-based probes (Oligopaint) to physically validate the sex determination system and directly visualize structural differences between the sex chromosomes. Additionally, the influence of B chromosomes on sex differentiation was investigated. Specimens were collected from the Cascatinha stream (Botucatu-SP), and metaphase chromosomes were obtained. Oligopaint probes were designed using the Chorus2 pipeline based on single-copy genomic regions and applied through fluorescence *in situ* hybridization (FISH). DNA was extracted and sex-specific primers were developed for genotyping analyses. The application of Oligopaint probes enabled high-resolution physical mapping of sex-associated sequences, allowing clear visualization of structural differences between the sex chromosomes and confirming, for the first time in the species, a heteromorphic XX/XY system. The X chromosome was identified as subtelocentric, whereas the Y chromosome was submetacentric. Notably, these differences were not detectable using classical cytogenetic techniques, highlighting the essential role of Oligopaint-based FISH in uncovering the species' sex chromosome architecture. Molecular analyses corroborated the presence of an XX/XY system: females without B chromosomes presented a single band (XX), while males presented two bands (XY). Interestingly, some females carrying B chromosomes exhibited the male genotype, indicating that the presence of this element influences the process of sex reversal. Males and females carrying B chromosomes with a YY constitution were also identified, possibly resulting from crosses between 0B males and 1B females. Together, these findings confirm the existence of an XX/XY sex determination system and demonstrate the significant influence of B chromosomes on sexual differentiation. Moreover, they underscore that classical cytogenetics alone was insufficient to resolve the sex system, whereas Oligopaint-based FISH proved to be a decisive and highly effective tool for the physical validation of the species' chromosomal architecture

**Keywords:** Oligonucleotide Probes; Sex chromosomes; Sex reversal
**Acknowledgments:** FAPESP, CAPES and CNPq

**LANDSCAPE GENOMICS OF Acrocomia intumescens: THE ROLE OF CLIMATIC GRADIENTSIN GENETIC DIFFERENTIATION UNDER THE CAATINGA BIOME.**

Roncaglia, Laura M.1*; Morales-Marroquín, Jonathan A.2,3; Francisconi, Ana F.3; Vianna, Suelen A.4; Zucchi, Maria I5.
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Landscape genomics provides a powerful framework to examine how environmental gradients shape genetic variation in natural populations by jointly considering neutral processes and adaptive responses. In the Brazilian semiarid region, historical cycles of forest expansion and retraction led to the fragmentation of humid vegetation into isolated upland refuges known as Brejos de Altitude, forming an archipelago of mesic enclaves subjected to intense selective pressures. Within this scenario, Acrocomia intumescens—an oil-rich palm endemic to northeastern Brazil and strongly associated with mesophytic habitats—emerges as an informative system for assessing how montane isolation and climatic heterogeneity contribute to genetic structuring and adaptive divergence among plant populations persisting in Caatinga refugial landscapes.In this study, we evaluated genetic diversity, population structure, and the association between genomic variation and environmental variables in natural populations of A. intumescens. We analyzed 139 individuals from ten populations distributed along the Sertaneja Depression, using genomic data generated through ddGBS. After filtering, 3,466 high-quality SNPs were retained for population genetic and landscape genomic analyses. DAPC and sNMF analyses revealed the presence of two well-defined genomic groups corresponding to the northern and southern portions of the Sertaneja Depression, with high genetic differentiation between groups (FST = 0.79–0.86) and restricted connectivity mainly at a local scale. Redundancy analysis (RDA) indicated that genetic variation is strongly associated with environmental gradients, with precipitation seasonality (BIO15) emerging as the main explanatory variable, that influence 60% of the genetic structure, followed by precipitation in the driest month (BIO14) and edaphic characteristics. The findings indicate that the genetic configuration of A. intumescens is shaped by both biogeographic discontinuities and selective pressures linked to water limitation, highlighting signatures of local adaptation within mesophytic refugia. The pronounced genetic divergence observed among populations suggests that each highland enclave functions as a distinct reservoir of genetic diversity. Consequently, safeguarding the Brejos de Altitude within the Caatinga domain is both strategic and urgent: beyond ensuring the long-term survival of this palm species, such protection also preserves numerous co-occurring endemic taxa and maintains irreplaceable evolutionary processes in the face of ongoing global climate change.

**Keywords**: Genetic structure, Population Genomics, Macaúba,

## THE FIRST ORCHID GENOME FROM BRAZIL: A GENOMIC RESOURCE FOR CONSERVATION AND FLORAL PIGMENT BIOLOGY

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The family Orchidaceae, the second largest among angiosperms, exhibits genomes of high structural complexity and elevated repetitive content, which has historically limited the generation of high-quality reference assemblies. Here, we present the first reference genome of an orchid species from Brazil, addressing a critical gap in genomic resources for Neotropical orchids. Most available orchid genomes are concentrated in Asian species, highlighting the lack of genomic data for Neotropical lineages, particularly the genus Cattleya, which is of ornamental and evolutionary importance. We present the genome of Cattleya milleri, the first genome for the genus Cattleya and for a rupicolous, microendemic, and critically endangered species from the Quadrilátero Ferrífero, Minas Gerais, Brazil. High-molecular-weight DNA extraction, optimized in Brazil, enabled Oxford Nanopore Technologies® (ONT) sequencing and PacBio® HiFi sequencing, processed at the Arizona Genomics Institute. This hybrid strategy resulted in a 2.02 Gb assembly with an N50 of 27.1 Mb, 481 contigs, and 94.8% BUSCO completeness, placing this genome among the most contiguous assemblies published for Orchidaceae. Genomes based solely on short-read sequencing showed high fragmentation, whereas approaches integrating PacBio HiFi and ONT long reads yielded gains in continuity and structural accuracy. The C. milleri genome further stands out because critical experimental steps were conducted domestically, strengthening Brazil's scientific autonomy in plant genomics. We also performed structural and functional annotation, identifying approximately 49.7 thousand genes and 53.5 thousand proteins, while maintaining 90% BUSCO completeness after filtering false predictions and short transcripts. Functional annotation, based on the integration of PANNZER2, InterProScan, and EggNOG-mapper, enabled the assignment of functional descriptions, KEGG categories, and Gene Ontology (GO) terms to approximately 43% of the predicted genes. Key genes involved in floral pigment biosynthesis pathways and members of the CCD family were identified, confirming the conservation of flavonoid/anthocyanin and carotenoid pathways in C. milleri. This genome provides a reference for functional and gene expression studies aimed at understanding and manipulating floral coloration in ornamental orchids. It also supports comparative transcriptomic analyses, gene-editing applications in Cattleya, and investigations of symbiotic interactions with mycorrhizal and endophytic fungi essential for orchid germination and survival. Furthermore, the assembly fills a reference gap for the genus, enabling SNP discovery and improving studies of species delimitation and evolution. Overall, the C. milleri genome provides a platform for evolutionary and applied research in Neotropical Orchidaceae.

**Keywords**: Cattleya milleri; Orchidaceae; genome assembly; Brazilian biodiversity.
**Acknowledgements**: Agência Paulista de Tecnologia dos Agronegócios (APTA; grant no. 2022.2658)

**KARYOTYPIC DIVERGENCE IN Psalidodon anisitsi POPULATIONS OF TWO LOCATIONS OF UPPER PARANÁ RIVER BASIN (Teleostei; Characiformes).**

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Fish of the genus Psalidodon are model organisms for cytogenetic and cytogenomic studies due to remarkable characteristics, such as high karyotypic diversity and the presence of supernumerary (B) chromosomes. Furthermore, the intricate hydrographic grid of the Neotropical region is composed of geographical features that result in a variety of environments with large rivers and many small tributaries, providing an ideal setting for studying the evolution and diversification of fish lineages, especially fast generation species like Psalidodon. Given this context, the aim of this study was to characterize and compare the karyotype of two previously unstudied populations of Psalidodon anisitsi. For this purpose, 20 individuals of P. anisitsi were collected in an artificial lake near the Cascatas stream (a tributary of the Tietê River) (22°54’04”S 48°27’44”W), and six were collected from the Batalha River (22°23'40.9"S 49°06'34.3"W). The sex of the individuals was identified through gonadal observation under an optical microscope. Cell suspensions containing metaphase chromosomes were obtained from kidney cells. Under optical microscopy, the diploid numbers were obtained, and the karyotypes were arranged and compared. The results indicated a diploid number of 2n=50 for both populations and the absence of B chromosomes, while the karyotypic formulas were (2M+14SM+18ST+16A) and (4M+14SM+12ST+20A) for the Cascatas and Batalha populations, respectively. These results support previous data present in the literature regarding the diploid number, as well as the absence of B chromosomes in P. anisitsi. Such divergences in karyotypic formula may be explained by the accumulation of structural mutations under a geographic isolation setting. Moreover, tributary rivers like the Batalha are more susceptible to environmental changes, while lakes tend to be more stable. As some cytogenetical studies in fish have demonstrated, geographically isolated populations are more susceptible to the fixation of chromosomal alterations, as observed in Psalidodon scabripinnis, P. bockmanni and P. fasciatus. Although these results may suggest the initial stages of karyotypic divergence, additional cytogenetic analyses are needed to confirm this hypothesis.

**Keywords**: Fish cytogenetics; Psalidodon.

**Agradecimentos**: CNPq, FAPESP, Proex, CAPES.

**ADVANCES AND TRENDS IN GENETIC STUDIES OF *Manihot esculenta Crantz***

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Introduction: Cassava (Manihot esculenta Crantz) is one of the most important crops for food security in tropical regions. In recent decades, advances in molecular tools and omics approaches have significantly expanded genetic research on this species, enabling deeper investigation of genetic diversity, breeding strategies, and conservation efforts. Objective: To investigate the evolutionary dynamics of genetic research in Manihot esculenta through the development of a quantitative analytical framework integrating indicators of technological transition, methodological diversity, and scientific collaboration networks. Methods: Scientific records related to cassava genetics published between 1960 and 2022 were analyzed. Bibliographic and scientific parameters were extracted from the selected articles, including publication year, authorship, institutional affiliations, thematic classification, and methodological tools employed. Based on these data, the Genomic Evolution Analytical Framework (GEAF) was proposed, integrating three quantitative indicators. The genomic transition index (GTI) models the temporal adoption of genomic approaches using a logistic function describing the transition from classical genetic methodologies to molecular and omics-based approaches. Methodological diversity was estimated using the methodological diversity index (MDI), and calculated from the relative frequency of genetic tools used in the studies. In addition, scientific collaboration networks were evaluated using connectivity metrics and clustering coefficient to characterize structural patterns of scientific production. Results: A total of 3246 records were initially identified, of which 654 met the inclusion criteria. A significant increase in scientific production was observed throughout the analyzed period, with a pronounced expansion beginning in the 1990s. Brazil presented the highest number of publications, followed by China and the United States. The application of the GTI indicated a gradual transition from classical genetics to molecular and genomic approaches. The MDI revealed an increase in methodological diversity over time, reflecting the incorporation of increasingly complex genetic tools. Scientific collaboration network analysis showed institutional concentration of research production in agricultural research centers and universities specialized in plant genetics. Discussion: The integration of indicators within the GEAF framework allows the identification of structural patterns in the evolution of cassava genetic research, highlighting the relationship between technological advances, diversification of methodologies, and the organization of scientific collaboration networks. Conclusion: Genetic research on Manihot esculenta has shown consistent growth and increasing methodological complexity over recent decades. The GEAF framework provides an integrated analytical approach capable of quantifying the technological evolution of research in this field and may be applied to comparative studies of scientific development in other crop species.

**Keywords**: Manihot esculenta; plant genetics; genomics; scientific analysis; methodological evolution.
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**MINIMAL CHROMATIN MODELS IN GENOME ORGANIZATION: EXTRACHROMOSOMAL DNA IN GLIOBLASTOMA**

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Introduction: The three-dimensional organization of chromatin is essential to understand genetic functions and mechanisms of chromosomal instability. Computational models such as MiChroM enable the simulation of genomic interactions and the integration of experimental data. Objective: To investigate chromatin dynamics in glioblastoma, focusing on the region of chromosome 7 that tends to circularize, generating extrachromosomal DNA (ecDNA) and genomic instability. Methods: Contact maps derived from Hi-C experiments of a glioblastoma patient were combined with super-resolution microscopy images. Simulations were adapted to observed conformations to reproduce nuclear trajectories and structural features. Results: The analysis revealed pronounced structural plasticity in chromosome 7, associated with recurrent formation of ecDNA. Simulations reproduced contact patterns consistent with experimental data, suggesting that circularization of this region directly contributes to the chromosomal instability characteristic of glioblastoma. Discussion: These findings reinforce the hypothesis that chromosome 7 circularization is a central mechanism in tumor progression, expanding the understanding of nuclear architecture in glioblastoma. The integration of simulations and experimental data validates MiChroM as a powerful tool to investigate genomic instability. Conclusion: This study establishes a solid basis for future applications of MiChroM in genome organization research, offering new perspectives for innovative strategies in oncology.

**Keywords**: Chromatin; Extrachromosomal DNA; Glioblastoma; Hi-C; Super-resolution microscopy

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## NATURAL HDAC INHIBITORS PROMOTE EPIGENETIC PRIMING AND SENSITIZE COLORECTAL CANCER CELLS TO SN-38

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Colorectal cancer (CRC) exhibits high prevalence and mortality rates worldwide. Epigenetic deregulation is a hallmark of cancer and contributes to disease progression, including the acquisition of chemotherapy resistance. Epigenetic priming is a strategy in which pretreatment with epigenetic modulators sensitize cancer cells to subsequent chemotherapeutic agents. Histone deacetylase inhibitors (HDACi), such as suberoylanilide hydroxamic acid (SAHA), promote chromatin relaxation and transcriptional activation, potentially enhancing the efficacy of DNA-targeting drugs such as irinotecan, an inhibitor of topoisomerase I. Previous studies from our group indicate that the royal jelly (RJ)-derived medium-chain fatty acids 10-hydroxy-2-decenoic acid (10-HDA) and 10-hydroxydecanoic acid (10-HDAA) act as HDACi. Based on this evidence, we hypothesized that these natural compounds could function as epigenetic priming agents capable of increasing CRC cells sensitivity to SN-38, the active metabolite of irinotecan. To test this hypothesis, we investigated the effects of these fatty acids on HCT116 cells. Non-cytotoxic doses were then selected to prime the cells (continuous treatment with 50μM for 7, 14, or 21 days) before challenging them with SN-38 at 10, 50, and 100nM. SAHA (0.1μM) was used as a reference HDACi. In parallel, metabolic alterations were evaluated using untargeted mass spectrometry-based metabolomics after 24 hours of exposure. Single-dose exposure experiments revealed time- and dose-dependent effects of 10-HDA on cell viability, including a transient increase at intermediate concentrations (100-150μM) after 24h, followed by a consistent reduction in viability at concentrations above 50μM after 48h. In contrast, 10-HDAA induced a stronger and more sustained cytotoxic effect, with significant reductions in cell viability observed within 24h at 150μM and further decreases after 48 and 72h. Nonlinear regression analysis indicated an approximately two-fold reduction in the $IC_{50}$ of SN-38 after 7 days of priming with 10-HDA and 10-HDAA ($IC_{50}$ values of 10.43, 12.57, and 9.20nM for 10-HDA, 10-HDAA, and SAHA, respectively), compared with unprimed cells ($IC_{50}$=22.52nM). Dose-response curves differed significantly according to an extra sum-of-squares F test ($p = 0.0417$). These findings are consistent with a possible epigenetic or metabolic modulation effect that increases cellular susceptibility to SN-38, although this effect was not observed after prolonged priming periods. Untargeted metabolomics analysis identified differentially expressed metabolites but did not reveal significant enrichment of specific metabolic pathways. These results demonstrate that RJ-derived fatty acids function as natural HDACi significantly enhancing the sensitivity of HCT116 cells to SN-38. This study highlights the potential of epigenetic priming strategies as adjuvants to improve irinotecan efficacy in CRC.

**Keywords:** histone deacetylase inhibitors; royal jelly fatty acids; epigenetic priming; colorectal cancer; chemotherapy sensitization.

**Acknowledgment:** CAPES

# RESUMOS: PÔSTERES PROJETO DE EXTENSÃO

*resumos: pôsteres projeto de extensão*

## “RAROS EM CENA”: INTEGRATING THEORY AND PRACTICE IN THE DISSEMINATION AND AWARENESS OF RARE GENETIC DISEASES AND INTELLECTUAL DISABILITY

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In Brazil, Rare Diseases (RDs) are conditions that affect up to 65 individuals per 100,000 people. These pathologies may present in a chronic or progressive form and often have a significant impact on the quality of life of affected individuals. RDs also include conditions in which Intellectual Disability is present, characterized by significant limitations in intellectual functioning and adaptive behavior, with onset before the age of 18. It is estimated that a genetic origin is present in approximately 80% of RDs and in 25–50% of cases of moderate or severe intellectual disability. These conditions affect a significant portion of the population and constitute an important public health issue. The dissemination of knowledge about rare diseases associated with intellectual disability is essential to reduce misinformation, train healthcare professionals, and raise public awareness. In this context, undergraduate and graduate students, under the supervision of professors affiliated with the Institute of Biosciences of Botucatu and the Botucatu School of Medicine, conduct extension projects and activities aimed at promoting scientific discussions within the university and in the broader community. These initiatives are directed toward the general public and healthcare professionals who work directly with individuals with intellectual disabilities and genetically based rare diseases, with the goal of improving communication with patients and increasing social awareness about these conditions.The “Raros em Cena” team visited the APAE of Botucatu to identify the needs of healthcare and support professionals. This step ensured that the actions and materials produced were aligned with the real demands of the field. As a result, three science communication booklets were developed for distribution at APAE and to the general population, along with the creation of a social media profile dedicated to producing informative content and promoting the group’s activities. Based on the recent publication “Treating rare diseases with the cinema: Can popular movies enhance public understanding of rare diseases?” (Domaradzki, 2022), we also organized the event “CineMundo”, which included the screening of the documentary “Na Minha Pele”. The event featured specialists in the field who discussed the focus of the short film—Generalized Pustular Psoriasis—and was attended by 68 participants, most of whom were undergraduate students. The event promoted important reflections on the impact of rare diseases on the lives of affected individuals and their families, as well as a deeper scientific and conceptual discussion. The group will continue to promote education and awareness among different audiences in order to reduce prejudice and expand access to information about rare diseases.

**Keywords**: Rare diseases, awareness, dissemination.
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**REDE PROPAGAR: INTEGRATING GENOMICS AND EX SITU CONSERVATION OF ENDEMIC PLANTS**

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Effective conservation of plant species restricted to highly specialized habitats requires the integration of biological data with applied propagation strategies. In rupestrian grasslands of the Quadrilátero Ferrífero, southeastern Brazil, extreme edaphic conditions and spatial fragmentation promote microendemism while simultaneously constraining natural regeneration and ex situ cultivation. As a consequence, conservation initiatives are frequently limited by the scarcity of genomic resources and by the absence of reliable propagation protocols for threatened taxa. REDE PROPAGAR operates as an extension-based scientific initiative structured as a collaborative partnership among public research institutions (ESALQ–USP and APTA) and the mining sector (Vale S.A.), enabling the integration of genomic research, applied plant propagation, and conservation-oriented actions. Within this framework, chromosome-scale nuclear genomes and chloroplast genomes have been generated for multiple microendemic taxa, including Dyckia consimilis, Dyckia rariflora, Vriesea longistaminea, Vriesea minarum, Hoplocryptanthus schwackeanus, Hoplocryptanthus ferrarius, and Cattleya milleri. In parallel, ddRADseq datasets were produced to characterize population structure and genetic diversity in selected lineages of Dyckia and Cattleya. Molecular identification using DNA barcoding was applied across several plant families, including Bromeliaceae, Orchidaceae, Asteraceae, Cactaceae, and Eriocaulaceae, supporting accurate taxonomic assignment in conservation and restoration contexts. Ex situ conservation actions resulted in the production of more than 2,000 seedlings derived from seed germination, currently allocated to species translocation and restoration programs involving threatened plants. For several taxa, successful propagation under controlled conditions was only achieved after the development of species-specific germination protocols and in vitro cultivation methods, overcoming limitations observed under conventional cultivation approaches. The integration of genomic information with propagation outcomes enabled the selection of genetically representative individuals for ex situ cultivation and downstream conservation actions. This extension-based initiative demonstrates that coupling genomic approaches with applied plant propagation can deliver measurable biological outputs while directly informing conservation strategies for microendemic species in one of Brazil's most threatened ecosystems.

Keywords: Conservation genomics; ex situ propagation; microendemism; ferruginous rupestrian grasslands;

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XXIII
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