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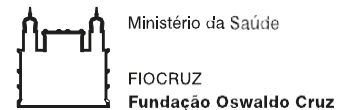
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## Content

1. WELCOME TO THE WORLDDLEISH7.....	7
2. GENERAL SCHEDULE.....	9
3. SYMPOSIUMS .....	11
S1. ROLE OF ASYMPTOMATICS IN THE TRANSMISSION OF LEISHMANIASIS, SLEEPING SICKNESS AND CHAGAS DISEASE .....	12
S2. NEW VACCINES AND IMMUNOTHERAPIES FOR CANINE LEISHMANIASIS.....	16
S3. EMERGING FOCI AND CHANGING EPIDEMIOLOGY OF LEISHMANIASIS .....	21
S4. ELIMINATING VL AS A PUBLIC HEALTH PROBLEM IN THE WHO SOUTH-EAST ASIA REGION: THE LAST MILE CHALLENGES AND OPPORTUNITIES THROUGH THE NEW REGIONAL STRATEGY .....	28
S5. INFLAMASOMES AND Leishmania .....	38
S6. PATHOGENESIS OF KALA-AZAR.....	44
S7. INNOVATION IN R&D TO CONTRIBUTE TO VL ELIMINATION .....	54
S8. SAND FLY SALIVA AND IMMUNE RESPONSE OF BITTEN HOSTS .....	59
S9. ELIMINATING VL IN INDIA: THE LAST MILE CHALLENGES AND OPPORTUNITIES	66
S10. NEW TRENDS IN THE DIAGNOSIS OF CHAGAS DISEASE.....	75
S11. NEW INSIGHTS IN POSTTRANSCRIPTIONAL REGULATION IN Leishmania: IMPLICATIONS IN THE PARASITE DEVELOPMENT AND DISEASE CONTROL .....	84
S12. VL-HIV COINFECTION .....	94
S13. "ATYPICAL" CUTANEOUS LEISHMANIASIS .....	99
S14. EPIDEMIOLOGY OF LEISHMANIASIS IN AMERICA.....	109
S15. ANIMAL MODELS FOR VISCERAL LEISHMANIASIS: SUITABILITY AND APPLICATIONS .....	120
S16. DRUG RESISTANCE AND TREATMENT FAILURE IN LEISHMANIASIS: A 21ST CENTURY CHALLENGE .....	129
S17. VL ELIMINATION AS A PUBLIC HEALTH PROBLEM IN INDIA .....	136



# WORLD LEISH7

S18. VECTOR COMPETENCE AND Leishmania-SAND FLY INTERACTIONS.....	142
S19. DRUG TARGET IDENTIFICATION.....	150
S20. LEISHMANIASIS VACCINE: PAST, PRESENT AND FUTURE .....	158
S21. NEW GUIDELINE FOR THE TREATMENT OF LEISHMANIASIS IN THE AMERICAS: WHAT HAS CHANGED? .....	169
S22. MOLECULAR PATHOLOGY AND STRATIFICATION OF LEISHMANIASIS.....	172
S23. FUTURE PROSPECTS IN THE TREATMENT OF CUTANEOUS LEISHMANIASIS FORM.....	179
S24. LEISHMANIASIS AND MOVEMENT: IMPORTED LEISHMANIASIS BY TRAVELERS AND MIGRANTS.....	187
S25. BIOMARKERS FOR DIAGNOSIS OF LEISHMANIASIS.....	193
S26. CELL BIOLOGY AND Leishmania INFECTION .....	198
S27. Leishmania EXTRACELLULAR VESICLES: IMPACT ON DISEASE PROGRESSION	204
S28. VECTOR SURVEILLANCE AND CONTROL FOR VISCERAL LEISHMANIASIS ELIMINATION.....	211
S29. A GLOBAL VISCERAL LEISHMANIASIS DATA PLATFORM .....	222
S30. IMMUNOPATHOGENESIS AND HOST-DIRECTED THERAPIES IN LEISHMANIASIS .....	228
S31. RESERVOIRS OF LEISHMANIASIS.....	234
S32. GENOMICS AND EPIDEMIOLOGICAL SURVEILLANCE.....	241
S33. EXPERIENCE WITH mHEALTH AND LEISHMANIASIS.....	251
S34. EMPOWERING PEOPLE WITH CUTANEOUS LEISHMANIASIS THROUGH INTERDISCIPLINARY RESEARCH AND COMMUNITY-BASED INTERVENTIONS (ECLIPSE) .....	254
S35. DATA FOR DECISION MAKING FOR VL ELIMINATION .....	265
S36. LEISHMANIASIS AND IMMUNOSUPPRESSION .....	273
S37. LEISHVET: ANIMAL LEISHMANIOSIS: IS A CHANGE OF MIND NEEDED? .....	282
S38. THE CUTANEOUS LEISHMANIASIS IN THE MAGHREB REGION .....	291



# WORLD LEISH7

S39. DRUG RESISTANCE & QUIESCENCE: UNRAVELLING MECHANISMS AND EXPLOITATION FOR BETTER/NEW DRUGS .....	296
S40. IMMUNOLOGICAL PERSPECTIVES OF LEISHMANIASIS: BEYOND THE TH1/TH2 PARADIGM .....	302
S41. WHAT CAN SOCIAL SCIENCES CONTRIBUTE TO UNDERSTANDING AND ADDRESSING LEISHMANIASIS?: EXAMPLES FROM THE FIELD.....	307
S42. MUCOCUTANEOUS LEISHMANIASIS .....	315
S43. BRASILEISH. ANIMAL LEISHMANIOSIS: IS A CHANGE OF MIND NEEDED? .....	325
S44 NEW HOPE FOR LEISHMANIASIS: HOW TO COMMUNICATE TO A BROADER NON-SCIENTIFIC AUDIENCE.....	334
4. ORAL COMMUNICATION .....	336
4.1 CANINE LEISHMANIASIS .....	337
4.2 DIAGNOSIS - TREATMENT AND RESISTANCE - CLINIC .....	359
4.3 DRUG DISCOVERY & DEVELOPMENT.....	418
4.4 EPIDEMIOLOGY/ECOEPIDEMIOLOGY/MOLECULAR EPIDEMIOLOGY/PREVENTION AND CONTROL.....	478
4.5 IMMUNOLOGY - CELL BIOLOGY – PATHOGENESIS - VACCINES.....	547
4.6 OMICS - MOLECULAR BIOLOGY – BIOCHEMISTRY - OTHERS.....	633
4.7 SOCIAL INNOVATION - IMPLEMENTATION RESEARCH - OPERATIVE RESEARCH .....	701
4.8 VECTORS & RESERVOIRS.....	727
5. POSTER .....	753
5.1 CANINE LEISHMANIASIS .....	754
5.2. DIAGNOSIS-TREATMENT AND RESISTANCE-CLINIC.....	827
5.3. DRUG DISCOVERY & DEVELOPMENT.....	962
5.4. EPIDEMIOLOGY – ECOEPIDEMIOLOGY - MOLECULAR EPIDEMIOLOGY - PREVENTION AND CONTROL.....	1035
5.5. IMMUNOLOGY - CELL BIOLOGY – PATHOGENESIS - VACCINES.....	1088

The logo for 'World Leish7' features the word 'WORLD' in blue, with a globe icon integrated into the letter 'O'. Below it is a blue fly icon, and the word 'LEISH7' is written in red and green. The page is decorated with colorful abstract shapes: concentric circles in blue, red, and green, and solid circles in blue, red, and green, scattered around the text.

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5.6 OMICS - MOLECULAR BIOLOGY – BIOCHEMISTRY - OTHERS.....	1207
5.7. SOCIAL INNOVATION - IMPLEMENTATION RESEARCH - OPERATIVE RESEARCH .....	1367
5.8 VECTORS & RESERVOIRS.....	1392
6. LIST OF CHAIR, CO-CHAIR & SPEAKERS.....	1470
7. LIST OF PARTICIPANTS .....	1480





## **1. WELCOME TO THE WORLDDLEISH7**

The logo for WorldLeish7 features the word "WORLD" in blue, with a globe icon integrated into the letter "O". Below "WORLD" is a blue sandfly icon. To the right of the sandfly is the word "LEISH7" in red, with the number "7" in green. The background of the page is decorated with colorful abstract shapes, including concentric circles and irregular shapes in shades of blue, red, green, and yellow.

Every four years, leishmaniacs from around the world gather in WorldLeish to discuss the latest advancements around these neglected tropical diseases and the seventh version was not an exception. In 2022, we had the participation of around 700 people, from 47 countries. Also, we had a great response from 536 students and professionals from around the world who sent us their abstracts to be part of the event as a poster or oral communications presentation and we are glad to say that we counted 195 oral presentations and 341 posters.

The experience and knowledge of the 210 speakers enriched the 44 Symposia, 8 Round Tables, 4 Special Meetings, 5 Plenary talks and 4 Successful stories that took place in those 6 days.

For Colombia and specifically the University of Antioquia, it was an honor to be the host of this Congress. And, for PECET, is a recognition for its almost 40 years of effort, research and hard work to treat leishmaniasis.

I would like to express my gratitude for your participation in this seventh version of the congress. Thanks to the knowledge and contributions, of all participants, it has been a complete success.

We know that it was not easy at all, however seeing all of you in Cartagena filled us with deep pride for the great challenge undertaken and the achievement reached.

May these events strengthen our "leishmaniac" spirit and recharge us to continue working in favor of this NTD.

Thank you very much.

With the expression of my admiration and respect.

A handwritten signature in black ink, appearing to read "Ivan Dario Vélez".

Ivan Dario Vélez  
Chair WorldLeish7



## **2. GENERAL SCHEDULE**

# WORLD LEISH7

MONDAY August 1st	Time	TUESDAY August 2nd	WEDNESDAY August 3rd	THURSDAY August 4th	FRIDAY 27 August 5th	Time	SATURDAY August 6th	
		REGISTRATION	REGISTRATION	REGISTRATION	REGISTRATION		REGISTRATION	
	7:00 - 8:00	REGISTRATION	REGISTRATION	REGISTRATION	REGISTRATION			
	8:00 - 9:00	PLENARY TALK #1	PLENARY TALK #2	PLENARY TALK#3	PLENARY TALK #4	8:30 - 9:30	PLENARY TALK #5	
	9:00 - 9:30	SUCCESSFUL STORY #1	SUCCESSFUL STORY #2	SUCCESSFUL STORY #3	SUCCESSFUL STORY #4	9:30 - 10:00	COFFEE BREAK	
	9:30 - 10:00	COFFEE BREAK					10:00 - 11:30	SPECIAL MEETING #4
	10:00 - 11:30	SATELITE SYMPOSIUMS (sessions 1 - 5)	SATELITE SYMPOSIUMS (sessions 12-16)	SATELITE SYMPOSIUMS (sessions 23-27)	SATELITE SYMPOSIUMS (sessions 33 -38)		AWARDS	
	11:30 - 13:00	SATELITE SYMPOSIUMS (sessions 6 -11)	SATELITE SYMPOSIUMS (sessions 17 - 22)	SATELITE SYMPOSIUMS (sessions 28 - 44) SPECIAL MEETING #2	SATELITE SYMPOSIUMS (sessions 39 - 44)	11:30 - 12:00.		
	13:00 - 14:00	LUNCH	LUNCH	POSTER PRESENTATION Session 3	LUNCH	12:00 - 13:10	CLOSING LECTURE	
	14:00 - 15:30	SPECIAL MEETING #1	ROUND TABLE (1 - 4)	LUNCH/ FREE AFTERNOON			ROUND TABLE (5 - 8)	
REGISTRATION	15:30 - 16:30	ORAL COMMUNICATIONS (sessions 1 - 7)	ORAL COMMUNICATIONS (sessions 15 - 21)				ORAL COMMUNICATIONS (sessions 29 - 35)	
	16:30 - 17:30	POSTER PRESENTATION Session 1	POSTER PRESENTATION Session 2				POSTER PRESENTATION Session 4	
OPENING SESSION	17:30 - 18:00	COFFEE BREAK		CLOSING REMARKS			COFFEE BREAK	
INAUGURAL LECTURE	18:00 - 19:00	ORAL COMMUNICATIONS (sessions 8 - 14)	ORAL COMMUNICATIONS (sessions 22 - 28)				ORAL COMMUNICATIONS (sessions 36 - 41)	
WELCOME RECEPTION	19:00 - 20:30							



## **4. ORAL COMMUNICATION**



## 4.6 OMICS - MOLECULAR BIOLOGY & BIOCHEMISTRY - OTHERS

### 06-01: THE SKIN MICROBIOME ENHANCES TRANSCRIPTIONAL INFLAMMATORY SIGNATURES AND DELAYS CLINICAL RESOLUTION IN CUTANEOUS LEISHMANIASIS

**Camila Farias Amorim<sup>1</sup>, Victoria Lovins<sup>2</sup>, Fernanda O. Novais<sup>3</sup>, Jordan Harris<sup>2</sup>, Lucas P. Carvalho<sup>4</sup>, Edgar M Carvalho<sup>4</sup>, Daniel P. Beiting<sup>1</sup>, Elizabeth Grice<sup>2</sup>, Phillip Scott<sup>1</sup>**

<sup>1</sup>Department of Pathobiology, School of Veterinary Medicine, University of Pennsylvania, Philadelphia, United States; <sup>2</sup>Department of Dermatology, Perelman School of Medicine, University of Pennsylvania, Philadelphia, United States; <sup>3</sup>Department of Microbial Infection and Immunity, College of Medicine, The Ohio State University, Philadelphia, United States; <sup>4</sup>Laboratório de Pesquisas Clínicas do Instituto de Pesquisas Gonçalo Muniz & Fiocruz/Bahia, Brazil

Cutaneous leishmaniasis (CL) caused by *Leishmania braziliensis* is associated with chronic lesions that are often difficult to drug treat. We previously found that treatment failure is associated with increased expression of cytolytic genes, including GZMB, GNLY and PRF1, as well as IL1B. Here we investigate how the skin microbiome influences host gene expression in lesions and treatment outcome. We carried out an integrative multi-omics study from 64 *L. braziliensis* patients including RNA-seq from lesion biopsies, 16 seq from skin swabs collection of bacterial isolates prior to treatment. We first assessed the total bacterial burden in lesions by qPCR of the 16S ribosomal subunit and found that patients with higher bacterial burdens exhibited delayed healing. To identify the bacteria, we performed 16S sequencing of lesion swabs and found that *Staphylococcus* was the most frequent dysbiosis observed in patients and was associated with delayed

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lesion resolution. Since 50% of the *Staphylococcus* isolates, we collected were *S. aureus*, and *S. aureus* can be associated with severe infections, we asked whether lesions with high levels of *S. aureus* might be associated with inflammatory gene expression. We generated an in-house *Staphylococcus aureus* pangenome from our clinical isolates and known public references to quantify *S. aureus* transcript abundances through dual RNA-seq mapping analysis. We found that lesions with increased *S. aureus* transcripts exhibited high expression of inflammatory-related genes, such as CXCL5/8, CCL3/4, IL1A, IFNG, as well as genes we previously reported as biomarkers for treatment failure including PRF1, GNLY, GZMB and IL1B. Together, these results suggest that the skin microbiome influences immune responses in lesions of CL patients, affecting how patients respond to therapy with antimony leading to a delay in healing. These studies suggest that antibiotics or probiotic therapies given in conjunction with anti-parasitic drugs might augment healing.

**Keywords** BIOMARKERS; MICROBIOME; TRANSCRIPTS; TREATMENT; FAILURE

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