2022 FLYSTRIKE RD&E TECHNICAL FORUM

Modelling of blowfly chemical resistance

Dr Trent Perry – University of Melbourne 10 August 2022

Australian Wool Innovation Limited



Modelling of Blowfly Chemical Resistance

Blowfly Genetics and Genomics

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Blowfly Genetics And Genomics





Project Team



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Blowfly genomics

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Research Funding Support

Australian Wool Innovation Limited

Australian Government **Australian Research Council**

Resources

UOM Research Focus

- 1. Blowfly genomic resources
- 2. Population genomics
- 3. Early stage myiasis
- 4. Functional genetics



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ON-00373 (2015-19) **Genetics of Blowfly Parasitism**

ON-00570 (2015-19) Development of gene knockout technology

ON-00624 (2019-22) Informed development of a flystrike vaccine





Research Facilities

- **Bio21 Molecular Science and Biotechnology Institute** ۲
 - Physical Containment Level 2 (PC2) Insectary
- Faculty of Veterinary and Agricultural Sciences •
 - Animal house with Sheep trial pens
- Office of the Gene Technology Regulator ۲
 - Gene Technology and Biosafety Committee
 - Notifiable Low Risk Dealings •
- Office of Research Ethics and Integrity ۲
 - **Animal Ethics Committee** •









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1. Blowfly Genomics

Assembly and improvement of the genetic resources available ullet



Gene Prediction Comparison	Draft 1 (14,544 genes)	Draft 2 (12,933 genes)
Genes supported by expression data	10,121 genes	10,065 genes
Single-copy orthologues (4 spp.)	4,106 genes	4,425 genes
Single-copy orthologues (1 sp.)	12,160 genes	11,142 genes
Genes unique to the blowfly	2,062 genes	572 genes

Foundational research critical for;

- Transcriptomics
- Population genomics ullet
- **Functional genetics** •









Dr Clare Anstead Dr Shilpa Kapoor

2. Population Genomics

ON-00624 Informed development of a flystrike vaccine

Objective 1: Population genetics of *L. cuprina* (2018/19, 2019/20, 2020/21)

- Understand how flies move around the country
- Examine populations for known resistance alleles and frequencies
- Identify protein variation in CSIRO vaccine development program

Can be leveraged to support current and future projects to improve fly control





Collection sites

Year	Sample collections	Number of <i>L. cuprina</i> flies
2018/2019	30	413
2019/2020	81	1235
2020/2021	49	1267
Total	160	2915

Samples collected by:

- UOM team
- Growers
- Agronomist networks









Population Structure Of Australian Sheep Blowfly



Assigned individuals to groups based \bullet

on genetic information.

- Single cluster for Eastern Australia
 - VIC, NSW, QLD and SA
- Western Australia and Tasmania form

genetically distinct clusters.





Gene Flow Between Areas

- Within cluster analysis
- 5 groupings of population samples
- Significant gene flow within the cluster proportional to geographic isolation



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Insecticide Resistance

- No resistance to <u>known</u> target site mutations were detected in our WGS samples for Spinosad Neonicotinoids Macrocyclic lactones
- Protein changes in some fly populations <u>associated</u> with resistance identified Organophosphates Organochlorines
- Caveat targets for dicyclanil or cyromazine are <u>not known</u> cannot be determined from the sequence dataset.
 Resistance has been reported (Sales et al., 2020)







Insecticide Resistance



Map of $Lc\alpha E7$ allele frequencies for OP susceptible G¹³⁷ (blue) and resistant flies *Rop-1* D¹³⁷ (orange)

Target	Protein target	Insecticide class	Resistant change detected				
GABA-gated chloride channel	RdI	organochlorines	Y				
Acetylcholinesterase	LcAce	organophosphates	Υ (LcαΕ7)				
Voltage-gated sodium channel	Kdr/para	pyrethroids	Ν				
nAChR receptor subunit α6	Lcα6	spinosyns	Ν				
nAChR receptor subunit α1	Lca1	neonicotinoids	Ν				
nAChR receptor subunit β2	Lcβ2	neonicotinoids	Ν				
nAChR receptor subunit α2	Lca2	neonicotinoids	Ν				
nAChR receptor subunit β1	Lcβ1	neonicotinoids/sulfoximines	Ν				
Glutamate-gated chloride channel	LcGlucl1α	avermectins	Ν				





Analysing Variation

Protein sequences can be compared to look for important changes

Identity		1	10	20	30	40	50 '	60 '	70	80 '	90 '	100	110	120	130	140	150	160	170	180	190	200	210	22
🖙 Lab strain		1 MKSVF	10 VCTLVLALAH	20 YAFA <mark>GVCD</mark> SN	30 VDYNSTLITP	40 CEGNDIIVEV	50	60 YKCVEFGKPQL	70 MDCPPNTYFT	80 I YYF <mark>QQCTGCE</mark>	90 NFIPAPTCEY	100 SQTTDVECV	110 P <mark>LVKPTTAAP</mark>	120 тт <mark>ск</mark> ттрѕкт	130 TPIVTTAPPST	140 IPVPSTPTT	150 NKPDPTTPKTT	160 Kppkvtttv	170 NPSPPTGTGPT	180 TTNAPSSDIPLF	190 P TAST VNT	200 KyptppGMppt		22 / QPKN
C≠ GL C≠ IM C≠ RFS C≠ STL C≠ NB C≠ NSWPOP C≠ DEF	NSW	· · · · · ·	E · · · · · · · · · · · · · · · · · · ·						· H · · · · · · · · · · · · · · · · · ·			K · · · · · · · · · · · · · · · · · · ·				IV 				A	P			· L Q · · · - L Q · · · - L Q · · - L Q · ·
GB10 GB7 GB1 GB1 GB1 GBPOP C+ JCO	QLD		F									K · · · · · · · · · · · · · · · · · · ·				S · · IV · · S · · IV · · S · · IV				A				• Q • • • Q • • • Q • •
C+ KB C+ JS C+ AG C+ K C+ SL C+ SL	SA TAS	· · · · · ·	E									K								A				· · · · · · · · · · · · · · · · · · ·
L* CA L* DL1 L* DL1 L* DL2 L* DL2 L* DL2 L* DF L* KL L* AC L* KL2 L* LK L* UK L* UK C* VICPOP L* CAPOP L* OPP L* DW L* DC L* DC LK LK LK LK LK LK LK LK LK LK	VIC																				• P • P • P • P • • P • • • P • • • P			
C* BL C* LH C* KD C* EL C* JGPOP C* TF	WA		F		· · · · · · · · · · · · · · · · · · ·				· · · · · · · · · · · · · · · · · · ·			Q			5	· · · · · · · · · · · · · · · · · · ·				a · · · · · · · · · · · · · · · · · · ·	р			

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3. Early Stage Wound Development

- ON-00624 Informed development of a flystrike vaccine ۲
- **Objective 2:** Analysis of blowfly and sheep proteins in early flystrike.
- Main aims: •
 - Identify proteins secreted by developing larvae ullet
 - Consider as new lead proteins for control strategies (Vaccine and novel targets) •
 - Provide information on proteins to CSIRO for their vaccine gene candidates
 - Profile how sheep respond to larval infection ullet





The Sheep Response To Flystrike



Enrichment analysis of functional groups for sheep proteins detected wounds AWI Flystrike RD&E Forum 2022





	- a ×
	NL: 6.99E9 X TIC MS 200609_Lumos_H ela_FAIMS_400ng _40_60
108.83	
109.23	
119.36	
110 115 120 12	5

Lucilia cuprina – Proteins Excreted During Flystrike



Enrichment scores for annotation clusters

GO enrichment scores for proteins detected in maggot implant samples.

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Functional Genetics

ON-00570 Development of gene knockout technology







Developing tools for

- Interrogating the function of genes of interest (vaccine candidates) ullet
- Identifying genes required for development and survival





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Developing tools to examine blowfly biology

To understand the importance of different genes we need to determine the effect when their function is lost or disrupted

Initial work established a CRISPR/CAS9 technique to delete specific genes in the blowfly.

Created genomic knockout of two genes;

white – A "blind" fly (POC)

Orco – A fly that cannot smell

- Validate gene function -
 - Vaccine candidate genes (MSc) -
 - **Odorant receptors (ARC DP, Hons)** -
 - Marker genes (Hons) -





Biological Validation In The Blowfly





Tested the impact of reducing the gene

expression of 10 genes of interest.

- Two led to reduced hatch rate





• Two led to mortality of larvae post hatching

Research Outcomes

- Genomic and transcriptomic resources being utilised to support current and future research efforts to enhance control of flystrike
- Identification of a Candidate genes of interest which are important for maggot development
- Technical capabilities to conduct functional genetic experiments on Australian sheep blowfly
- Expansion of research capacity
 - New projects and funding areas (Australian Research Council)
 - New training opportunities (Postdoc, PhD, MSc, Hons students)





Modelling Of Blowfly Chemical Resistance

UOM - Genetic analysis of dicyclanil and cyromazine resistance mechanisms in Australian Sheep Blowfly

- Genetic analysis will help inform modelling work by UTAS
 - Characterise resistance mechanism(s) in a field-collected strain of Australian Sheep Blowfly
 - Provide measurements of the relative fitness of the resistant strain
 - Determine the genetic basis of resistance
- Collaborate with NSW-DPI to support the identification of novel resistance mechanisms detected through NSW-DPI resistance monitoring programs.





Empirical Data For Improved Resistance Modelling

- Help to reduce the number of assumptions underlying the model ullet
 - Is one mechanism or are multiple mechanisms present? •
 - Is the same mechanism responsible for the cyromazine and ulletdicyclanil resistance?
 - Is there a fitness cost imposed on flies that are resistant?
- Potential to develop molecular assays to help monitor resistance
 - Lab based analyses •
 - On-farm diagnostic kits
- A better model will allow design of the most appropriate resistance management practices.







This publication is based on information presented at the Australian Wool Innovation Limited (AWI) Flystrike RD&E Technical Forum held on 10th August 2022. Some information in this publication has been contributed by one or more third parties and licenced to AWI, and AWI has not verified whether this information is correct. This publication should only be used as a general aid and is not a substitute for specific advice. To the extent permitted by law, we exclude all liability for loss or damage arising from the use of the information in this publication. Except to the extent permitted under Copyright Law no part of this publication may be reproduced by any process, electronic or otherwise without the specific written permission of AWI. Neither may information be stored electronically in any form whatsoever without such permission. AWI is grateful for its funding, which is primarily provided by Australian woolgrowers through a wool levy and by the Australian Government which provides a matching contribution for eligible R&D activities. © 2022 Australian Wool Innovation Limited. All rights reserved.