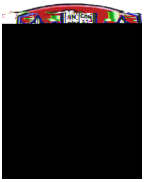
GRADUATE AND POSTDOCTORAL STUDIES

McGILL UNIVERSITY



FINAL ORAL EXAMINATION
FOR THE DEGREE OF
DOCTOR OF PHILOSOPHY

OF

UDAYKUMAR KAGE
PLANT SCIENCE

CANDIDATE GENE IDENTIFICATION FROM THE WHEAT QTL-2DL FOR RESISTANCE AGAINST FUSARIUM HEAD BLIGHT BASED ON METABOLO-GENOMICS APPROACH

August 11th 2016
9.15 A.M

Macdonald Stewart Building – Room MS2-022
McGill University, Macdonald Campus

COMMITTEE:
Dr. Ian Strachan (Pro-Dean) (Natural Resource Sciences)
Dr. J. Singh (Chair) (Plant Science)
Dr. A. Kushalappa (Supervisor) (

ABSTRACT

Wheat (L.) is the most important cereal food crop cultivated around the world. Fusarium head blight (FHB) caused by is one of the most destructive diseases of wheat. Apart from causing huge yield losses, FHB is also known to contaminate grains with mycotoxins that are harmful to human and animal health. Several quantitative trait loci (QTL) have been identified for FHB resistance in wheat, but the mechanisms of resistance and candidate genes underlying them are still unknown. Therefore, in the present study an integrated metabolomics and genomics approach was used to identify the candidate genes and mechanisms of resistance in near-isogenic lines (NILs) of QTL-2DL. The high fold-change in abundance, resistance related (RR) metabolites, identified in rachis samples of NIL-R following pathogen inoculation were, coumaroylagmatine, -coumaroylputrescine, and phosphatidic acids. The candidate gene, -coumaroylagmatine transferase ( ) is associated with the biosynthesis of coumaroylagmatine and -coumaroylputrescine. The diacylglycerol kinase ( ) and glycerol kinase ( ) are involved in the production of phosphatidic acids. The dissection of QTL based on flanking marker sequencing led to the identification of the transcription factor within the QTL-2DL region. and manual analysis of promoter sequences of , and showed the presence of WRKY binding sites, additionally luciferase assay proved their physical interaction . Further, functional validation of based on virus induced gene silencing (VIGS) in NIL-R, not only confirmed an increase in fungal biomass but also a decrease in the expression of downstream resistance genes: and ; this was associated with a decrease in abundance of RR metabolites biosynthesized by them, confirming the plausible FHB resistance mechanisms in rachis governed by this QTL. Similarly, in spikelet samples of NIL-R, we found high abundances of phenylpropanoids, glycerophospholipids and fatty acids. These are known to be involved in cutin and suberin biosynthesis. The genes involved in their biosynthetic pathway (and) were also found in the QTL-2DL region. Transcript abundance of genes in spikelets based on qRT-PCR showed higher expression in the NIL-R compared to NIL-S, confirming the potential role of QTL-2DL in spikelet resistance. However, these genes also have to be functionally validated

CURRICULUM VITAE

UNIVERSITY EDUCATION

Since 2013	Doctor of Philosophy, Plant Science
2010-2012	Master of Science - Genetics and Plant Breeding (University of Agricultural Sciences, Dharwad, India)
2006-2010	Bachelor of Science - Agriculture (University of Agricultural Sciences, Dharwad, India)

EMPLOYMENT

2012 – 2013 Research Associate – Cucurbits Breeding (Monsanto, Bangalore, India).

AWARDS

1. GREAT (Graduate research enhancement and travel) travel awards, for conference poster presentation in Kingston University (2016).
2. George H Duff Travel Bursary travel award for attending Plant Biotech-2016 meeting in Kingston, Canada.
3. Graduate excellence award Ph.D third year, Department of Plant Science, McGill University (2015-16).
4. Scherago International student travel grant award for attending Plant & Animal Genome XXIII Conference -2015, San Diego, CA, USA (2015).
5. Graduate scholarship from Réseau Innovagrains, for improving small cereal grains for PhD (2015).
6. GREAT (Graduate research enhancement and travel) travel awards, for international conference presentation. McGill University (2015).
7. Graduate excellence award – Ph.D second year, Department of Plant Science, McGill University (2014-15).
8. Differential fee waiver award for second year Ph.D (2014-2015).
9. National Overseas Scholarship from Govt. of Karnataka. India for first and second year of Ph.D (2013-2014 & 2014-2015).
10. ICAR-International Fellowship for Ph.D (2013-2016).
11. Plant Science departmental nomination for SCHULICH award for PhD (2013-2014).
12. Sir Rattan Tata travel grant award for traveling to Canada for Ph.D (2013).

13.

4. Kambe GR, **U. Kage**, H C Lohithaswa, B G Shekara and D Shobha, 2013: Combining Ability Studies in Maize (Zea Mays L.): , Vol.4, No.14, 116-127.
5. **U. Kage**, D. Madalageri, L. Malakannavar and P. Gangashetty., 2013: Genetic Diversity Studies in Newly Derived Inbred Lines of Maize (Zea Mays L.): , Vol.4, No.9, 77-83.
6. L. Malakannavar, G. Shanthakumar, T. Ontagodi, **U. Kage**, P. Gangashetty, S. Adiger.,2013: Nutritional Enhancement for Iron Content and Combining Ability Studies in Newly Derived Inbred Lines of Okra (Abelmoschus esculentus Moench L.): , Vol.4, No.3, 24-30.
7. P. Natikar., K. Madhusudan, **U. Kage**, H.L. Nadaf and B. N. Motagi., 2013: Genetic variability studies in induced mutants of Sunflower (Helianthus annuus L.): , Vol. 4, No. 16.
8. **U. Kage**, M.C. Wali and L. Malakannavar., 2012: Disease Resistance Breeding in Newly Derived Inbred Lines of Maize (Zea Mays L.): Vol. III (3rd Issue) pp. 334-338.
9. L. Malakannavar, G. Shanthkumar, T. Ontagodi and **U. Kage**, 2012: Gene Action Studies in Newly Derived Inbred Lines of Okra (Abelmoschus Esculentus Moench L.): . Vol. 3. 321- 326.
10. L. Malakannavar, G Shanthakumar, T. Ontagodi and **U. Kage**., 2012: Study of Contribution of Different Metric Traits to Fruit Yield in Newly Derived Inbred Lines of Okra for Effective Selection (Abelmoschus Esculentus Moench L.): . Vol. Vol. 3. 299-302.

Review articles

1. **U. Kage**, S. Hukkeri, D. Dhokane, A. Kumar, S. Karre, and A.C. Kushalappa, 2016, Advances in genome editing with CRISPR/Cas9 system and their application in crop improvement (Submitted).
2. A.C. Kushalappa, Yogendra Kalenhalli, Kobir Sarkar, **U. Kage** and Shailesh Karre, 2016, Gene discovery and genome editing to develop cisgenic crops with improved resistance against pathogen stress. (**Accepted**).
3. **U. Kage**, A. Kumar, D. Dhokane, S. Karre and A.C. Kushalappa. 2015, Functional molecular markers in crop improvement. , Vol. 16:1-14.

4. **U. Kage,** Y. Kalenahalli, H. Balasubramanyam and A.C. Kushalappa, 2016, Genome editing in crop plants: Plant breeding perspective and beyond. (Under preparation - Invited Review article from Theoretical and Applied Genetics Journal).

Methods, Editorial and News letters

1. **U. Kage** and A.C. Kushalappa, 2015**,** Rise of genome editing in crop improvement.
, December, 2015 issue (Commentary).
2. A. Kumar, S. Karre, D. Dhokane, **U. Kage**, S. Hukkeri and A.C. Kushalappa, 2015, Real-time quantitative PCR based method for the quantification of fungal biomass to discriminate quantitative resistance in barley and wheat genotypes to fusarium head blight.
, Vol. 62, 16-22 (Method).
3. A. Kumar, **U. Kage**, K. Mosa and D. Dhokane, 2014, Metabolomics: A Novel Tool to Bridge Phenome to Genome under Changing Climate to Ensure Food Security.
, Vol.3, 1-3. (Editorial).