***April 2016***

# CURRICULUM VITAE

## BACKGROUND AND PERSONAL DATA


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|---|---|
| **NAME:** | Jean Denis Jonathan Labonne |
| **CURRENT ADDRESS**: | 1001 Greene Street APT 3<br>Augusta, Georgia 30901 United States |
| **HOME ADDRESS:** | Gandhi Rd Pont-Lardier Bel-Air R/S<br>Mauritius |
| **Phone no.:** | 1-706-691-1205 (current) and (230) 419 82 95 |
| **Email:** | molgenetics_and_epigenetics@hotmail.com |
| **BIRTH DATE AND PLACE:** | September 12, 1980; Bel-Air, Mauritius |
| **CITIZENSHIP:** | Mauritius |


**LANGUAGE PROFICIENCY:**

**English**: Excellent in writing and speaking.
**French**: Very good in writing and speaking.

## ACADEMIC QUALIFICATION and EDUCATION:

### Postdoctoral position:

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|---|---|---|---|
| Apr 2014-current | Postdoctoral Fellow | Human Genetics | Medical college of Georgia at Georgia Regents University, UNITED STATES |
| Jul 2013 to | Postdoctoral Fellow | Priming & stress | King Abdullah University of Science & |

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|---|---|---|---|
| Jan 2014 | | tolerance | Technology, SAUDI ARABIA |
| Jan 2011 to Dec 2012 | Postdoctoral Associate | Epigenetics | Florida State University UNITED STATES |

**Education**:

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|---|---|---|---|
| 2005-2010 | Ph.D | Molecular Genetics | York University, CANADA |
| 2005 | Transferred to Ph.D | Molecular Genetics | York University |
| 2003-2005 | Master's candidate | Molecular Genetics | York University |
| 1999-2002 | B.Sc | Biology with environmental science | University of Mauritius |
| 1992-1998 | High School | - | Sir Leckraz Teelock State Secondary School, Mauritius |

**<u>Previous Positions</u>:**

2003-2010 Teaching Assistant York University

List of courses I've been appointed as a teaching assistant:

| | | |
|---|---|---|
| 2003 | Natural Science – Evolution | Nats 1690 |
| 2004 | Cell Biology and Biochemistry I | BIO 2020 |
| 2004 | Processes of Evolution (marker) | BIO 3200 |
| 2005 | Cell Biology and Biochemistry II | BIO 2021 |
| 2005 | Processes of Evolution (marker) | BIO 3200 |
| 2005 | Natural Science - The Living Body | Nats1610 |
| 2006 | Genetics | BIO 2040 |
| 2006 | Processes of Evolution (marker) | BIO 3200 |
| 2007 | Natural Science – Evolution | Nats 1610 |
| 2007 | Processes of Evolution (marker) | BIO 3200 |
| 2008 | Genetics | BIO 2040 |
| 2009 | Cell Biology and Biochemistry II | BIO 2021 |
| 2009 | Genetics | BIO 2040 |
| 2010 | Genetics | BIO 2040 |

| | | |
|---|---|---|
| Jan 2003-Aug 2003 | Biology Education Officer | Sebastopol State Secondary School, Mauritius<br>Bon Accueil State Secondary School, Mauritius |
| Aug 2002-Sept 2002 | Teacher<br>*(To effect a replacement)* | Loreto College Rose-Hill, Mauritius |

Work Experience as a trainee

| | | |
|---|---|---|
| Jul 2002-Aug 2002 | Data analysis<br>*Research and Development Dept* | Deep River- Beau Champs Sugar Estate, Mauritius |
| Jun 2001-Aug 2001 | Plant pathology Assistant researcher | Mauritius Sugar Industry Research Institute<br>*Plant Pathology and Microbiology Dept* |

**Ph.D DISSERTATION :**

Genetic mapping and positional cloning of the *S*-locus of distylous *Turnera subulata* (Turneraceae).
*York University 2010*

**Honours thesis**

Polyclonal antibody Production against Sugarcane yellow leaf virus
*University of Mauritius 2002*

**AWARDS:**

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|---|---|
| 2011 | Nomination for the prestigious Governor General's Gold medal for Academic Achievement – nominated by the chair of biology department, York University |
| 2011 | Nomination for the distinguished Council of Graduate Schools/UMI dissertation prize (Canada-wide dissertation prize) – nominated by the Faculty of Graduate Studies York University |
| 2010 | Doctoral degree – Pass with distinction and thesis-prize nomination for top 5% dissertation at York University |

2008 Research Cost Fund Award ($600)

2003 York Entrance Scholarship ($3000)

2003 Canadian Commonwealth Scholarship ($54,000)

2002 B.Sc Biology with First Class

**CO-SUPERVISORY EXPERIENCE:**

I have trained and co-supervised 8 students during the 7 years I spent at York University as a PhD candidate. I've also trained and co-supervised one student as a postdoctoral associate at FSU and four students as a postdoctoral fellow at Georgia Regents University. I also provided some training to one graduate student at FSU on how to isolate chromatin. All students were new to research and their lab experiences were limited to the lab component of undergraduate courses.

While I was a PhD candidate at York University, I taught the students how to perform molecular techniques such as PCR, DNA and RNA extractions, polyacrylamide gel electrophoresis and Single strand conformation polymorphism analysis. I also helped them in data analysis and interpretation. For one of the students (Alina G), I co-supervised her throughout her honours thesis. Furthermore, two of the students namely, Alina G and Alon V are both authors on two of the nine research articles published so far.

As a postdoctoral associate at FSU, I have trained one student on performing PCR, agarose gel electrophoresis, and RT-qPCR. I also helped her in data analysis and interpretation. At GRU, I have trained four students so far on cell culture work, PCR and agarose gel electrophoresis. Among the four students, I taught two of them how to perform genomic DNA extraction from human blood samples.

**Honours BSc. Students co-supervised**:

| | | |
|---|---|---|
| 2007-2008 | Alina Goultiaeva | York University |

**NSERC Summer Bursary Students co-supervised**:

| | | |
|---|---|---|
| 2005 | Alon Vaisman | York University |
| 2005 | Sukvinder Johal | York University |
| 2006 | Alon Vaisman | York University |
| 2007 | Akansha Tiwari | York University |

| | | |
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| 2008 | Ruth Haile-Meskale, Jessica Tavone | York University |

**Work-Study Students co-supervised**:

| | | |
|---|---|---|
| 2005 | Alon Vaisman | York University |
| 2006 | Alon Vaisman | York University |
| 2007 | Mohammad Mokhtari | York University |
| 2008 | Alina Goultiaeva | York University |
| 2009 | Alina Goultiaeva, Lusine Zakharyan | York University |
| 2010 | Lusine Zakharyan | York University |

**Directed individual study (DIS) student co-supervised**:

| | | |
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| 2011 | Loury Migliorelli | Florida State University |
| 2012 | Loury Migliorelli | Florida State University |

**Graduate student trained on nuclei extractions and micrococcocal nuclease (MNase) digest.**

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|---|---|---|
| 2012 | Zadarreyal J Wiggins (student from Florida A&M University ) | Trained at Florida State University |

**Volunteer students co-supervised:**

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|---|---|---|
| 2014 | Tyler Graves | Georgia Regents University |
| 2014 | Vinh Nguyen | Georgia Regents University |
| 2015 | Tyler Graves | Georgia Regents University |
| 2015 | Akosua Sarfo | Georgia Regents University |
| 2016 | Tyler Graves | Georgia Regents University |
| 2016 | Evadne Beshiri | Georgia Regents University |

**Other Activities**

2005-2008 Organized weekly soccer matches in the Biology Dept during the summer at York University.

## PUBLICATIONS IN REFEREED JOURNALS:

1. **Labonne JDJ**, Lee KH, Iwase S, Diamond, MP, Layman LC, Kim CH, Kim HG. 2016. An atypical 12q24.31 microdeletion implicates six genes including a histone demethylase KDM2B and a histone methyltransferase SETD1B in syndromic intellectual disability. **Human Genetics** (ahead of print - *doi:10.1007/s00439-016-1668-4*)

2. **Labonne JDJ**, Graves TD, Shen Y, Diamond MP, Layman L, Kim HG. 2016. Comparative deletion mapping implies *NFIA* for intellectual disability coupled with macrocephaly and the presence of several genes for syndromic intellectual disability at 1p31.3-p32.2. **Molecular cytogenetics** 9:24

3. **Labonne JDJ**, Chung MJ, Jones JR, Anand P, Wenzel W, Iacoboni D, Layman LC, Kim HG. 2016.Concomitant partial exon skipping by a unique missense mutation of RPS6KA3 causes Coffin-Lowry syndrome. **Gene** 575: 42-47

4. **Labonne JDJ**, Vogt J, Reali L, Kong IK, Layman LC, Kim HG. 2015. A microdeletion encompassing PHF21A in an individual with global developmental delay and craniofacial anomalies. **Am J Med Genet A**. 167: 3011-3018.

5. Vera DL, Madzima TF, **Labonne JD**, Alam MP, Hoffman GG, Girimurugan SB, Zhang J, McGinnis KM, Dennis JH, Bass HW. 2014. Differential nuclease sensitivity profiling of chromatin reveals biochemical footprints coupled to gene expression and functional DNA elements in maize. **Plant Cell** 26: 3883-93

6. **Labonne, JDJ**., Dorweiler JE, and McGinnis KM. 2013. Changes in nucleosome position at transcriptional start sites of specific genes in *Zea mays mediator of paramutation1* mutants. **Epigenetics** 8:398-408

7. **Labonne, J.D.J** and Shore J.S. 2011. Positional cloning of the *s* haplotype determining the floral and incompatibility phenotype of the long-styled morph in distylous *Turnera subulata*. **Molecular Genetics and Genomics** 285: 101-111.

8. **Labonne, J.D.J**., F. Tamari, and J.S. Shore. 2010. Characterization of X-ray-generated floral mutants carrying deletions at the *S*-locus of distylous *Turnera subulata*. **Heredity** 105: 235-243

9. **Labonne, J.D.J**., A. Goultiaeva, and J.S. Shore. 2009. High resolution mapping of the *S*-locus in *Turnera* leads to the discovery of three genes tightly associated with the *S*-alleles. **Molecular Genetics and Genomics** 281: 673-685

10. **Labonne, J.D.J**., A. Vaisman, and J.S. Shore. 2008. Construction of a first genetic map of

distylous *Turnera* and a fine-scale map of the *S*-locus region. **Genome** 51: 471- 478.

11. **Labonne, J.D.J**., A.J. Hilliker, and J.S. Shore. 2007. Meiotic recombination in *Turnera* (Turneraceae): Extreme sexual difference in rates, but no evidence for recombination suppression associated with the distyly (*S*) locus. **Heredity** 98: 411-418.

## Submitted manuscript:

*1.* **Labonne JDJ**., Layman LC, Kim HG. 2016. A microdeletion encompassing *GLRA4* at Xq22.2 in a patient with severe learning disability and behavioral problems, submitted in *BMC Neurology*

2. Ha K., Anand P., Lee JA., Jones JR., Kim CA., Bertola DR., **Labonne JDJ**., Wenzel W., Layman LC., Kim HG. 2016. Steric clas in SET domain of histone methyltransferase NSD1 as a cause of sotos syndrome and its genetic heterogeneity in Brazilian cohort. submitted in *GENE*

**MANUSCRIPT IN PREPARATION**

1. **Labonne JDJ**., Il-Keun Kong, Layman LC, Kim HG. 2016. Two pathogenic microdeletions which segregate independently in a family implicate *LRRK2* for autism and motor delay at 12q12 and HDHD1 and PNPLA4 for X-linked intellectual disability at Xp22.31

2. **Labonne JDJ**., Layman LC, Kim HG. 2016. Loss-of-function mutations of PTPRD cause syndromic intellectual disability and autism in 9p23 microdeletion syndrome

3. **Labonne JDJ**, Layman LC, Kim HG. 2016. A rare exonic point mutation (c. 1955delC) within *PHF21A* in a female patient with developmental delay, learning disability and craniofacial anomalies

4. **Labonne JDJ**, Layman LC, Kim HG. 2016. Microdeletions encompassing *MERTK*, *ANAPC1*, *ZC3H6* and *ZC3H8* at 2q13 are associated with learning disability, speech delay, and seizures.

5. **Labonne JDJ** and Shore JS. 2016. Identification of genes associated with the *S* and *s* haplotypes of *T. subulata*.

**Large-scale pilot study on priming at King Abdullah University of Science and Technology, Saudi Arabia**

Scientific report in manuscript format

1. Labonne JDJ., Sharkhuu A., Fedoroff NV and Mahfouz MM. 2014. Investigating the effects of salt priming in inducing drought stress tolerance in Arabidopsis epigenetic mutants and wild-type accessions.

## Papers selected and recommended for reading by the prestigious Faculty of 1000 biology (http://f1000.com)

## 1st paper selected and recommended for reading by the Faculty of 1000.

Labonne, J.D.J., A. Goultiaeva, and J.S. Shore. 2009. High resolution mapping of the *S*-locus in *Turnera* leads to the discovery of three genes tightly associated with the *S*-alleles. **Molecular Genetics and Genomics** 281: 673-685

***Evaluation:***

Faculty Comments & Author Responses
Faculty Member Comments
Deborah Charlesworth
University of Edinburgh, United Kingdom
Plant Biology

"This genetic study has discovered the closest gene yet found to the incompatibility region in any plant with distyly (a flower morphology polymorphism in which each of two hermaphrodite morphs can mate only with the other). Because there are several flower developmental differences between the two morphs, and also because of the difference in their compatibility, it has long been thought likely that several tightly linked genes must be involved to explain how only the two distinct morphs are seen in plants with this system. This 'supergene hypothesis' should clearly be tested by mapping the distyly locus or region (the S-locus), and then fine-mapping to determine whether there is a non-recombining region containing several (or perhaps many) genes, rather like a small sex-chromosome-like region. Using a large segregating family, genetic markers have now been found in a distylous species of Turnera, a plant genus in a family most of whose members are distylous.

The high-resolution map of the S-locus region of Turnera includes three sequences that are probably genes, and tight linkage was tested further by examining whether any sequences are found only in one morph or the other (just as Y-linked sequences are found in males but not females). A non-LTR retroelement was found to be associated with the dominant allele in two species in addition to the one in which linkage was tested, which indicates a long-lasting association (i.e. very little recombination). The other sequence that did not recombine in the family is a putative sulfotransferase. Its expression level differs between the two morphs. However, the genomic DNA sequences obtained from individuals homozygous for the dominant and recessive S alleles did not differ, which is puzzling if the region has been maintained with two different alleles, but without recombination, since early in the evolution of the Turnera genus, or its family. Although these results do not yet test the supergene

hypothesis, it is likely that this system will soon yield to testing, now that very closely linked markers have been found, and approaches including chromosome walking are feasible."

*Evaluated 9 Jul 2009*

## 2nd paper selected and recommended for reading by the Faculty of 1000.

Labonne, J.D.J., F. Tamari, and J.S. Shore. 2010. Characterization of X-ray-generated floral mutants carrying deletions at the *S*-locus of distylous *Turnera subulata*. **Heredity** 105: 235-243

***Evaluation:***
Faculty Comments & Author Responses
Faculty Member Comments
Deborah Charlesworth
University of Edinburgh, United Kingdom
Plant Biology

"Unlike homomorphic, multi-allele self-incompatibility systems in plants, which are now well understood at the molecular level, heterostyly remains mysterious. It is important to study the distylous kind of incompatibility system (in which there are two flower morphs, each with a different incompatibility type) because it is thought to be controlled by a supergene -- a tightly linked complex of several genes whose alleles determine different aspects of the flower morphology and the pollen incompatibility type. The supergene hypothesis is based on homostyle mutants that combine some long-style morph characters with some short-styled ones, and are inherited as alleles at the same genetic locus as the normal long- and short-styled morphs. The size of the genome region involved, and the number of genes, is, however, unknown. This paper describes deletion mutants in plants of a Turnera species that have lost alleles at loci previously shown to be tightly linked to the S allele (for short-styled flowers) or the s allele (long-styled).

The mutants are mostly homostyled, and they support the previously inferred gene order in the genome region (though this was inferred in Primula, a distantly related plant). Interestingly, some mutants had some intermediate phenotypes, so it is possible that the region contains more genes than has been thought. This progress in identifying the region should lead to the ability to investigate it in detail. Most of the mutants appear likely to have defects in pollen function, as they transmitted their mutations poorly to progeny when used as male parents in crosses. This hints that the region may contain many genes and it may soon be possible to get direct evidence on this point."

*Evaluated 10 May 2010*

## 3rd paper selected and recommended for reading by the Faculty of 1000.

Labonne, J.D.J and Shore J.S. 2011. Positional cloning of the *s* haplotype determining the floral and incompatibility phenotype of the long-styled morph in distylous *Turnera subulata*. **Molecular Genetics and Genomics** 285: 101-111.

***Evaluation:***
Faculty Comments & Author Responses
Faculty Member Comments
Deborah Charlesworth
University of Edinburgh, United Kingdom
Plant Biology

"This study has made a big stride in the progress towards discovering the gene or genes involved in flower dimorphism and associated self-incompatibility in a distylous plant (called the self-incompatibility locus, or S-locus).

No molecular details are yet available from any distylous plant, and so it remains unclear what kind of genetic differences are involved in controlling the positions of flower parts and the two different incompatibility types that are associated with the two flower morphs. It is not even clear whether these differences are all the effects of alleles at a single gene or whether, as has long been thought more likely, the S-locus includes several distinct but tightly linked genes (a supergene). Now the distyly locus (or tightly linked gene cluster) of one of the two morphs seems to have been localized to within a single bacterial artificial chromosome (BAC) clone.

The other allelic version of this genome region has not been pinned down, and it may be larger, as current information suggests that it is found in parts of two BACs. More mapping is necessary to clarify the arrangement of this 'S-allele'.

The limited analyses that can be done do not suggest that recombination is suppressed in the region (though this will need to be tested further). If these findings are true, they lead to surprising conclusions. Perhaps this genome region includes genes with the ability to control the disparate phenotypic characters involved in distyly, despite its small extent; in this case, suppressed recombination would not need to evolve in the region because recombination events would be rare, simply because the region is physically small. Even more surprising is the idea that the long-standing supergene hypothesis could be incorrect (perhaps a single gene can control these disparate characters). A third possible alternative is that genes controlling these characters have been collected together in this genome region, having arrived from different initial locations. Any of these possibilities are very interesting."

*Evaluated February 2011*

## Paper appearing in the "*News and Commentary*" section of Heredity.

Labonne, J.D.J., F. Tamari, and J.S. Shore. 2010. Characterization of X-ray-generated floral mutants carrying deletions at the *S*-locus of distylous *Turnera subulata*. **Heredity** 105: 235-243

**Evaluation**

Gilmartin PM and Li J
School of Biological and Biomedical Sciences,
University of Durham, Durham, DH1 3LE, UK
Correspondence: Professor PM Gilmartin,
e-mail: philip.gilmartin@durham.ac.uk

*Heredity* 105: 161-162 (2010)

## - *Delineation of the S locus in Turnera subulata*

## *Homing in on heterostyly-*

**"**The majority of plants are hermaphrodite and produce both male and female gametes. In addition to the various contrivances by which plants facilitate outcrossing—using wind, insects and other animals—an elaborate range of mechanisms has evolved to prevent self-fertilization. One such mechanism, known as floral heteromorphy,results in the development of different forms of self-incompatible flowers on different individual plants (Darwin, 1877). Development of the distinct floral morphs with different anther height and style lengths is orchestrated by the *S* locus (see Richards, 1997). In species such as *Turnera subulata* (white alder), *Fagopyrum esculentum* (buckwheat) and *Primula vulgaris* (primrose), which produce two forms of flower with long and short styles, this phenomenon is also known as distyly and is coordinated by two alleles of the *S* locus (see for example Matsui et al., 2004; Li et al., 2007; Labonne et al., 2009). In contrast, most self-incompatibility (SI) systems, in which self-pollination is prevented by rejection of pollen following molecular self-recognition, occur in otherwise indistinguishable homomorphic flowers (see for example Hiscock and McInnis, 2003). To date, much greater progress has been made toward a detailed molecular understanding of homomorphic SI in a range of species than SI associated with floral heteromorphy. However, the recent study by Labonne et al. (this issue) provides a key step forward toward the identification of genes located at the *S* locus that control floral heteromorphy in distylous *T. subulata*. In this species, long-styled plants are homozygous recessive (*ss*) and short-styled plants are heterozygous (*Ss*) with respect to the two *S* locus alleles.

In their paper, Labonne et al. (this issue) present an X-ray deletion mutagenesis screen of *T. subulata*. Although mutagenesis has been successfully used in studies of homomorphic SI systems, this is the first published systematic screen in a heterostyled plant aimed at defining the *S* locus. This study focused on the identification of mutants that affect heteromorphic flower development, whereas previous studies in *F. esculentum* have focused on the identification of self-fertile mutants (see for example Matsui et al., 2004 and the references therein). In *Primula*, self-fertile and homostyle plants

resulting from recombination within the *S* locus have defined different genetic functions at the *Primula S* locus responsible for style length (G), anther position (A), pollen size (P) and both pollen (IP) and style (IS) incompatibility phenotypes demonstrating the presence of a co-adapted linkage group of genes rather than the presence of a single master regulator (Dowrick, 1956; Richards, 1997). The existence of a similar co-adapted linkage group has been proposed in *F. esculentum* (see Matsui et al., 2004 and the references therein).

The Shore laboratory has pioneered the development of *T. subulata* as a model for the study of heteromorphy, and the scale and scope of this current study is impressive. The data presented are an accumulation of nearly a decade of study starting with the generation of genetically defined parental lines, an unusual homozygous (*SS*) short-styled plant, which provided the pollen for X-irradiation, and the long-styled (*ss*) pollen recipient, through to the analysis of 3982 progeny plants. All progeny from this cross should have been short styled with genotype *Ss*, but 10 longstyled mutants were obtained, suggesting deletion of the dominant *S* allele, together with a short-homostyle and a long-homostyle plant. In parallel to the mutagenesis studies, the Shore laboratory have painstakingly identified a number of *S* locus-linked genes and DNA markers (Labonne et al., 2009), together with morph-specific proteins (Athanasiou and Shore, 1997), which were used to delimit the extent of the *S* locus deletions within these 12 mutants. As would be predicted by analogy to the known architecture of the *Primula S* locus (Dowrick, 1956; Richards, 1997), the long-styled plants seem to be derived from pollen in which the entire dominant *S* allele has been deleted. Subsequent analysis of the short homostyle did not reveal a simple explanation, but analysis of the long homostyle indicates that the dominant alleles responsible for development of a short style (*G*) and large pollen grains (*P*), but not that which determines high anthers (*A*), have been lost. These data provide evidence of a co-adapted linkage group in *Turnera*, often referred to as a 'supergene', as previously proposed in *Fagypyrum* and *Primula* (see for example Richards, 1997 and Matsui et al., 2004).

Although the mutant screen could have been extended to identify mutants showing the expected short-styled phenotype that were rendered self-fertile following mutagenesis, the large deletions defined in those plants analyzed suggest that it is unlikely that such self-fertile short-styled plants would have been identified, as this would have required deletion of genes responsible for pollen or stigma SI functions ($I^P$ or $I^S$) within the *S* locus without loss of the genes (*G*, *P* or *A*) responsible for heteromorphic architecture (Dowrick, 1956; Richards, 1997). What is remarkable, however, is that in the three heteromorphic species currently under investigation, *P. vulgaris*, *F. esculentum* and *T. subulata*, which fall within three distinct orders, namely, Ericales, Caryophyllales and Malpighiales, in different clades of the core Eudicots, independent evolution has resulted in similar predicted S locus architectures.

The identification of morph-specific genes and proteins in *Primula* (McCubbin et al., 2006) and *Turnera* (Athanasiou and Shore, 1997) that are not associated with the *S* locus provide an opportunity to characterize the regulatory functions of the *S* locus controlling heteromorphy in different species. Indeed, a further key observation from Labonne et al. (2010) is the finding that expression of the two morph-specific *Turnera* proteins known to be encoded by genes not associated with the *S* locus is absent in the long-styled and long-homostyle deletion mutants. This observation defines a regulatory role of the *S* locus in the modulation of unlinked genes that encode morph-specific characteristics.

A number of unknowns remain to be elucidated in *Turnera* and other heteromorphic models, such as the relationship between genetic map distance and physical map distance in each species, and

the extent of recombination suppression within the *S* locus. Some of the *S* locus deletions presented in Labonne et al. (2010) span up to 7 Mb, others are smaller but result in the loss of only one DNA marker and so the size cannot be estimated. However, a previous study suggested that the locus could be as compact as 32 kb (Labonne et al., 2009). Knowledge of the physical size of the *S* locus in *Primula* and *Fagopyrum* also remains elusive, but with rapid progress being made in the analysis of the *S* locus-linked genes, generation of genetic maps and screening of BAC libraries (Li et al., 2007, 2010; Labonne et al., 2008, 2009; McCubbin, 2008; Yasui et al., 2008), it is only a matter of time before sequences corresponding to each *S*
locus are available for comparison of gene organization, function and genetic architecture. The current paper by Labonne et al. (this issue) takes us a step closer to homing in on the genes that control floral heteromorphy; one of the most remarkable mechanisms for preventing self-pollination and promoting outbreeding in plants.**"**

**PAPERS PRESENTED AT SCIENTIFIC MEETINGS**:

1. Labonne, JDJ. Layman LC., Kim HG. 2015. Two microdeletions that segregate independently in a family, suggesting three candidate genes for autism and motor delay at 12q12 and two candidate genes for cerebral palsy at Xp22.31. American Society of Human Genetics, 65th Annual Meeting. Baltimore, MD (poster presentation).

2. Labonne, JDJ., Vogt J., Reali L., Layman LC., Kim HG. 2014. A microdeletion encompassing only three genes within the Potocki-Shaffer syndrome interval at 11p11.2 associated with intellectual disability and craniofacial anomalies. American Society of Human Genetics, 64th Annual Meeting. San Diego, CA (poster presentation).

3. Labonne, J.D.J. and J.S. Shore. 2009. A Quest to find the genes determining Distyly. 36th Annual Biology Symposium, York University, Toronto, ON (oral presentation).

4. Labonne, J.D.J. and J.S. Shore. 2008. High-resolution mapping of the *S*-locus in distylous *Turnera* (Turneraceae). Botanical Society of America/Canadian Botanical Association Meeting, University of British Columbia, Vancouver BC (oral presentation).

5. Labonne, J.D.J. and J.S. Shore. 2007. Fine-scale mapping and Chromosome walking in distylous *Turnera* (Turneraceae). Genetics Society of Canada Meeting, McGill University, Montreal. (poster presentation).

6. Labonne, J.D.J. and J.S. Shore. 2006. Fine-scale mapping in distylous *Turnera* (Turneraceae). Canadian Botanical Association Meeting, Concordia University, Montreal (oral presentation).

**CONTRIBUTION TO POSTERS:**

1. HW Bass*, DL Vera , TF Madzima, **JDJ Labonne**, P Alam, GG Hoffman, JH Dennis, KM McGinnis. (TALK) MNase Profiling of Chromatin Landscapes in Maize. Society for Experimental Biology Meeting, SEB 2013, Valencia, SPAIN; July 2 – 6, 2013.

2. **Labonne, JDJ**., Vera, DL , Alam MP., Madzima, TF., Hoffmann, G., Dennis JH., McGinnis, KM., Bass, HW. 2012. Development of a Robust Buffer System for Microscopic and Molecular Assays of Nuclear Architecture and Chromatin Structure in Maize. Maize Genetics meeting 2012.

3. Bass, HW., Vera, DL., Hugues, DD., Fincher, JA., Alam, MP, **Labonne JDJ**., Madzima, TM., Wiggins, ZJ., Onokpise, OU., Moose, SP., McGinnis, KM, Dennis, JH . 2012. Tissue-specific nucleosome occupancy in the promoter/TSS region of 400 classical maize genes. Maize Genetics meeting 2012. Poster presentation.

4. HW Bass, DL Vera, DD Hughes, JA Fincher, AM Parwez, **JDJ Labonne**, TF Madzima, ZJ Wiggins, OU Onokpise, GH Hoffman, KM McGinnis, & JH Dennis. (POSTER) Chromatin Structure and Genome Response in Maize. NSF Plant Genome Research Program Awardee Meeting. Arlington, VA. 2012.

5. Bass, HW., Dennis, JH., McGinnis, KM., Onokpise, OU., Justin A. Fincher, JA., Vera, DL., **Labonne, JDJ**., Alam, P., Madzima, T and Hoffman, G. 2011. Nucleosome Mapping and Chromatin Structure in Maize, a Novel Platform for Genome Response Assays. NSF Plant Genome Program (PGRP) Awardee meeting, Arlington Virginia.

## Meetings attended.

1. Maize Genetics Conference 2011. St Charles, Illinois, USA

## Seminar/Presentation

### Center for Desert Agriculture – King Abdullah University of Science and Technology

**2013**

Paper presented:

An *Arabidopsis* Soil-Salinity–Tolerance Mutation Confers Ethylene-Mediated Enhancement of Sodium/Potassium Homeostasis

Plant Cell 2013 **25**: 3535-3562

Authors: Caifu Jiang., Eric J. Belfield, Yi Cao, J. Andrew C. Smith and Nicholas P. Harberd

**Green group seminar series (Biology department - Botany) – Florida State University**

**2012**

Paper presented:

A packing mechanism for nucleosome organization reconstituted across a eukaryotic genome

**Science 2011 vol. 332**

Authors: Zhenhai Zhang, Christian J. Wippo, Megha Wal, Elissa Ward, Philipp Korber, B. Franklin Pugh

**2011**

Paper presented:

Control of Flowering and Cell Fate by LIF2, an RNA Binding Partner of the Polycomb Complex Component LHP1

**PLoS ONE. 2011. Vol 6 issue 1.**

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**INVITED SEMINAR**

1. Labonne J.D.J. 2012. Genetic mapping and chromosome walking in *Turnera* & Epigenetics research in *Zea mays*. University of Chicago, IL, USA (invited by Dr Gilad Yoav).

2. Labonne J.D.J. 2010. Genetic mapping and positional cloning of the *S*-locus of distylous *Turnera subulata* (Turneraceae). University of California, San Diego, CA, USA (invited by Dr Yunde Zhao).

3. Labonne J.D.J. 2010. Genetic mapping and positional cloning of the *S*-locus of distylous *Turnera subulata* (Turneraceae). University of Minnesota, St Paul, MN, USA (invited by Dr William Gray).

4. Labonne J.D.J. 2010. Genetic mapping and positional cloning of the *S*-locus of distylous *Turnera subulata* (Turneraceae). Florida State University, Tallahassee, FL, USA (invited by Dr Karen McGinnis).