PROFORMA FOR BIO-DATA (to be uploaded)

1. Name and full correspondence address
Dr.Raviraj VS
Silkworm breeding and Genetics
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2. Email and contact number
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3. Institution — Central Sericultural Research and training Institute
4. Date of Birth — 08-11-88
5. Gender — Male
6. Category — GM
7. Whether differently abled — No
8. Academic qualification (Undergraduate onwards)

	Degree	Year	Subject	University/Institution	% of marks
1	B.Sc.	2008	Botany, Biochemistry and Microbiology	Yuvaraja college, University of Mysore	II class
2	M.Sc.	2011	Genetics	University of Mysore	I class
3.	Ph.D.	2018	Genetics	University of Mysore	

9. **Ph.D. thesis**: *Genetic analysis of the recombination machinery in the predisposition of Down syndrome in South Indian population*.

Guide : Prof. N.B.Ramachandra
DOS in Genetics and Genomics
University of Mysore, Mysore

Year of Award : 2018

10. Work experience (in chronological order)

Sl.No.	Positions held	Name of the institute	from	to	Pay scale
1	Scientist B	Central silk board	01-11-2018	Till date	10

11. Professional recognition/award/certificate/fellowship

Sl.No.	Name of the award	Awarding agency	Year
1	Junior research fellow	UGC-BSR	2012-2014
2	Senior research fellow	UGC-BSR	2014-2017

12. Publications (List of papers published in SCI Journals)

I. **Suresh, R. V.,** Udupa, A. S., Lingaiah, K., Polapalli, S. K., & Ramachandra, N. B. (2017). Association of RFC1 A80G gene polymorphism with advanced maternal age in risk of Down syndrome. *Current Medicine Research and Practice*, *7*(1), 6-10.

II. **Suresh, R. V**., Lingaiah, K., Veerappa, A. M., & Ramachandra, N. B. (2017). Identifying the risk of producing aneuploids using meiotic recombination genes as biomarkers: A copy number variation approach. *Indian Journal of Medical Research*, *145*(1), 39-39.

III. **Suresh, R. V**, Narayanappa D, Savitha M. R & Ramachandra N. B. (2016)"Association of recombination errors and young mother age in risk of down syndrome in South Indian population"- *International Journal of Advanced Research*, **4**(8), 622-629.

IV. Prabhanjan, M., **Suresh, R. V**., Murthy, M. N., & Ramachandra, N. B. (2016). Type 2 diabetes mellitus disease risk genes identified by genome wide copy number variation scan in normal populations. *Diabetes research and clinical practice*, **113**, 160-170.

V. Veerappa, A. M., **Suresh, R. V**., Vishweswaraiah, S., Lingaiah, K., Murthy, M., Manjegowda, D. S., & Ramachandra, N. B. (2015). Global patterns of large copy number variations in the human genome reveal complexity in chromosome organization. *Genetics research*, **97**, e18.

VI. Veerappa, A. M., Vishweswaraiah, S., Lingaiah, K., Murthy, N. M., **Suresh, R. V**., Belur, K., & Ramachandra, N. B. (2014). Insertion-deletions burden in copy number polymorphisms of the Tibetan population. *Indian journal of human genetics*, **20**(2), 166.

VII. Veerappa, A. M., Murthy, M., Vishweswaraiah, S., Lingaiah, K., **Suresh, R. V**., Nachappa, S. A., & Seshachalam, K. B. (2014). Copy number variations burden on miRNA genes reveals layers of

complexities involved in the regulation of pathways and phenotypic expression. *PloS one*, **9**(2), e90391.

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VIII. Veerappa, A. M., Lingaiah, K., Vishweswaraiah, S., Murthy, M. N., **Suresh, R. V**., Manjegowda, D. S., & Ramachandra, N. B. (2014). Impact of copy number variations burden on coding genome in humans using integrated high resolution arrays. *Genetics research*, **96**, e17.

13. Details of patents

Sl.no	Patent title	Name of application	Patent No	Award date	Agency/	status
	-	-	-	-	-	-

14. Books/ Reports/Chapters/General articles

Sl.no	t title	Authors Name	Publisher	Year of publications
	-	-	-	-

15. Any other information (maximum 500 words)

Two nucleotide sequence of pyrexia gene polymorphisms has been submitted to NCBI and has been accepted for publication with accession numbers MT221438 & MT221439.