*3. If data: understanding between database curator and PI as to when and how transfer will occur, who will pay for it, and long term maintenance plans and costs?* DNA data from TALEN-expressing plants will be released to NCBI HTG database as described [http://www.ncbi.nlm.nih.gov/genbank/htgs/subinfo/] and Gramene (http://www.gramene.org/). Expression data will be uploaded at GEO [http://www.ncbi.nlm.nih.gov/geo/info/seq.html#FTP]. Some expression data in completion of previous objectives will be performed using Affymetrix GeneChip microarray platform. Our experimental design has and will continue to comply with the Minimal Information About Microarray Experiment (MIAME) standards (http://www.mged.org /Workgroups/ MIAME/miame.html). Microarray hybridization data will be released to GEO and PlexDB (<http://plexdb.org>), without password-protection of access to the data immediately upon processing of the raw data. Releases are planned for all years of project (see Table IV\_1). Processing and further analyses will be posted at regular intervals, as these become available. Any changes suggested or required following review of publications will be amended at databases. Data will also be deposited in other publicly accessed databases and portals including Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo/), PlantDGB, Gramene and PlexDB once validated and analyzed for quality. Presently expression profiling data at Gramene are targeted to *Arabidopsis*, rice and maize. Gramene is also coordinating with EBI ATLAS [<http://www.ebi.ac.uk/gxa/help/AboutAtlas>] project for these species. Gramene is focused on standards to support data integration, and the data for this project will be processed and deposited in accordance with recommendations of Gramene staff. Brendel and Gramene staff will collaborate to develop a project specific webpage at Gamene. Incorporation of additional species data may be forthcoming in the future, and data from wheat, soybean, cotton and *Medicago* will be processed for Gramene as developments occur. Cost for the acquisition, processing and transfer of data to GEO, PlexDB, PlantGDB, and Gramene are borne by this project. Maintenance and any additional data processing or independent use of the project data are the responsibility to the respective databases. Letters of intent to collaborate from Drs. Ware and Wise are appended at the end of this document. All processed sequence data will be maintained on local KSU, ISU, and IU servers indefinitely.

The following table provides our intended progress and key deliverables. Scientific objectives remain as described in our original proposal. We organized milestones relative to three equally spaced time intervals of 1.0, 2.0, and 3.0 years into the project.

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| --- | --- | --- | --- |
| **Table IV\_1. Timetable, yearly goals, participant roles, and deliverables.** | | | |
| **a. Year** | **b. Goals and activities** | **c. Participant roles** | **d. Deliverables** |
| 1 | Obj. 1: TAL effector cloning from Xoo | FW and BY will have overall responsibility for Xoo TAL effector gene cloning. Graduate students in FW and BY laboratory will clone individual genes from type strains of Xoo and test in TAL effector-deficient strain. | A set of 20-25 unique naturally occurring TAL effector genes from Xoo. |
| 1 | Obj. 1: TAL effector cloning from Xoc | AB will have overall responsibility for Xoo TAL effector gene cloning. Graduate students in AB laboratory will clone individual genes from type strains of Xoo and test in TAL effector-deficient strain. | A set of 25-30 unique naturally occurring TAL effector genes from Xoc. |
| 1 | Obj. 1: RNA-seq analysis of Xoo and Xoc type strains | FW and AB will have overall responsibility for the RNAseq analyses of Xoo and Xoc type strains. Research will be conducted by graduate student and postdoc in FW and AB labs with the assistance of the technical assistant in FW lab. |  |
| 1 | Obj. 1: RNA-seq data processing and primary analysis of type strains of Xoo and Xoc | VB and graduate student will conduct RNAseq processing and primary analysis | Release of some RNA-seq data and comparison to previous expression analyses. |
| 1 | Obj. 1: Collect additional strains and characterize TAL effector complement of strains for analyses of Xanthomonas disease complexes of wheat, cotton, soybean, and Medicago | FW and BY will have overall responsibility for the assembling and analysis of additional Xanthomonas disease complexes. The research will be conducted by graduate students in the respective labs, assisted by undergraduate students. |  |
| 1 | Obj. 2: Select, acquire and genotype insertion plant lines | FW will AB will have responsibility for selection, acquisition and genotyping of candidate genes for susceptibility to Xoo (FW) and Xoc (AB). Analyses will be conducted by students and postdocs. Lines will be maintained by technical support in respective labs. |  |
| 1 | Obj. 2: Generate and analyze RNAi- and TALEN-derived transgenic plants | BY and postdoc will have overall management of Obj. 2; design of TAL effector, TALEN, and plant transformation and gene silencing vector construction. |  |
| 1 | Obj. 2: Re-sequencing of TALEN derived plant lines | BY and postdoc will have overall management of re-sequencing data generation of TALEN-derived lines. |  |
| 1 | Obj. 3. Enabling design and use of TAL effector biotechnology | AB, VB and students will update and maintain comprehensive suite of TAL effector related advances and resources | Web site dedicated to TAL effector bioinformatics and biotechnological tools and advances. Links to biological aspects of TAL effector-mediated susceptiblity |
| 1 | Obj. 4: KSU Girls researching our world (GROW) demonstration | FW will conduct summer GROW hands-on introductory demonstrations to plants and the associated microbes. |  |
| 1 | Obj. 4: ISU REU and RET after school and summer internships | BY, postdoc and student will assist in REU and RET program at ISU |  |
| 1 | Obj. 4: Undergrad. education and research at IU | VB and student will conduct undergraduate education and research in bioinformatics at IU |  |
| **a. Year** | **b. Goals and activities** | **c. Participant roles** | **d. Deliverables** |
| 2 | Obj. 1: RNA-seq analysis of host responses in other *Xanthomonas* disease complexes | FW, BY, postdoc and graduate students with assistance of technical personnel will conduct RNA-seq analysis. |  |
| 2 | Obj. 1: RNA-seq analysis of individual TAL effectors of Xoo and Xoc | FW, BY and AB will have overall responsibility for the RNAseq analyses of Xoo and Xoc type strains. Research will be conducted by graduate students and postdoc in FW, BY, and AB labs with the assistance of the technical assistant in FW lab. | Release of processed RNA-seq data from host responses to type strains and some individual TAL effectors to public and plant databases. Establish web site and links to expression analysis and functional analysis of TAL effector-mediated susceptibility |
|  | Obj. 1: RNA-seq data processing and analysis of other disease complexes | VB and graduate student will conduct RNAseq processing and primary analysis |  |
| 2 | Obj. 2: Analysis of re-sequencing of TALEN-derived lines completed | VB and graduate student will conduct RNAseq processing and primary analysis | Release o collection of nucleotide polymorphisms identified in rice lines that were subject to TALEN modification. |
| 2 | Obj. 2: Select, acquire and genotype additional insertion plant lines | FW will AB will have responsibility for selection, acquisition and genotyping of candidate genes for susceptibility to Xoo (FW) and Xoc (AB). Analyses will be conducted by students and postdocs. |  |
| 2 | Obj. 2: Generate and analyze additional RNAi- and TALEN-derived transgenic plants | BY and postdoc will have overall management of Obj. 2; design of TAL effector, TALEN, and plant transformation and gene silencing vector construction. |  |
| 2 | Obj. 2: Analysis of insertion, TALEN, and RNAi derived plant lines and susceptibility testing Xoc. | AB, graduate students, and postdoc will coordinate functional analysis of candidate genes involved in Xoc susceptibility |  |
| 2 | Obj. 2: Analysis of insertion, TALEN and RNAi derived plant lines and susceptibility testing of Xoo. | FW, BY, graduate students and postdocs will coordinate functional analysis of candidate genes involved in Xoo susceptibility |  |
| 2 | Obj. 3: Identification of shared features of functional EBEs | AB, VB, and graduate students will conduct bioinformatic approaches to TAL effector binding and prediction. |  |
| 2 | Obj. 3: Empirical and systematic testing of parameters using designer TAL effectors | AB, VB, and graduate students will conduct bioinformatic approaches to TAL effector binding and prediction. |  |
| 2 | Obj. 3. Enabling design and use of TAL effector biotechnology | AB, VB and students will update and maintain comprehensive suite of TAL effector related advances and resources | Web site dedicated to TAL effector bioinformatics and biotechnological tools and advances. Links to biological aspects of TAL effector-mediated susceptiblity |
| 2 | Obj 4: KSU GROW demonstration | FW will conduct annual summer GROW hands-on introductory demonstrations to plants and the associated microbes. |  |
| 2 | Obj 4: ISU REU and RET after school and summer internships | BY, postdoc and student will assist in REU and RET program at ISU |  |
| 2 | Obj 4: Undergrad. education and research at IU | VB and student will conduct undergraduate education and research in bioinformatics at IU |  |
| **a. Year** | **b. Goals and activities** | **c. Participant roles** | **d. Deliverables** |
| 3 | Obj. 1: Complete RNA-seq data analysis of type strains and individual TAL effectors of Xoo and Xoc | FW, AB, BY and VB and postdocs and students will collaborate for presentation of RNA-Seq analysis of host responses to Xoo, Xoc and strains with individual TAL effectors genes. | Release of processed RNA-seq data from host responses to type strains and some individual TAL effectors to public and plant databases. Establish web site and links to expression analysis and functional analysis of TAL effector-mediated susceptibility |
|  | Obj. 1: RNA-seq data processing and primary analysis of host response to other Xanthomonas disease complexes | VB and graduate student will conduct RNAseq processing and primary analysis | Release of processed RNA-seq data from host responses to type strains and some individual TAL effectors to public and plant databases. |
| 3 | Obj. 1: Completion of RNA-seq data analyses of host responses in wheat, *Medicago*, cotton, and soybean. | FW, AB, BY and VB and postdocs and students will collaborate for presentation of RNA-Seq analysis of host responses to other Xanthomonas disease complexes. | Establish web site and links to expression analysis and functional analysis of TAL effector-mediated susceptibility |
| 3 | Obj. 2: Analysis of insertion, TALEN, and RNAi derived plant lines and susceptibility testing Xoc. | AB, graduate students, and postdoc will coordinate functional analysis of candidate genes involved in Xoc susceptibility | Posting of genotyping, expression analyses, and, when available, disease functional analysis of select candidate susceptibility genes for Xoc from rice. |
| 3 | Obj. 2: Analysis of insertion, TALEN and RNAi derived plant lines and susceptibility testing of Xoo. | FW, BY, graduate students and postdocs will coordinate functional analysis of candidate genes involved in Xoo susceptibility | Posting of genotyping, expression analyses, and, when available, disease functional analysis of select candidate susceptibility genes for Xoc from rice. |
| 3 | Obj. 3: Defining final set of predictive and design | AB, VB, and graduate students will conduct bioinformatic approaches to TAL effector binding and prediction. | Update of TAL effector binding prediction to TAL effector bioinformatics and biotechnological tools website |
| 3 | Obj. 3. Enabling design and use of TAL effector biotechnology | AB, VB and students will update and maintain comprehensive suite of TAL effector related advances and resources | Web site dedicated to TAL effector bioinformatics and biotechnological tools and advances. Links to biological aspects of TAL effector-mediated susceptibility |
| 3 | Obj. 4: KSU GROW demonstration | FW will conduct annual summer GROW hands-on introductory demonstrations to plants and the associated microbes. |  |
| 3 | Obj. 4: ISU REU and RET after school and summer internships | BY, postdoc and student will assist in REU and RET program at ISU |  |
| 3 | Obj. 4: Undergrad. education and research at IU | VB and student will conduct undergraduate education and research in bioinformatics at IU |  |
| White will have overall responsibility for timely dissemination of analyses and linkage of results to participant websites. Brendel will responsible for processing and deposition of DNA re-sequencing and RNA-seq data in public repository (GEO), PlexDB\*, Plantgdb\*, and Gramene\*. Code will be deployed open source through our web sites and public repositories, and we expect instances of the code to be implemented through [iPlant Atmosphere](http://www.iplantcollaborative.org/atmosphere-preview) cyberinfrastructure. Web based TALEN resources will be maintained by Bogdanove.  \* Letters of intent from Drs. Wise and Ware are appended at the end of this document. Dr. Brendel is a participant in the Plantgdb project. | | | |