

PAPACLIMA: MARKER ASSISTED SELECTION FOR POTATO GERMLASM ADAPTED TO BIOTIC AND ABIOTIC STRESSES CAUSED BY GLOBAL CLIMATE CHANGE

Partner: NEIKER

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Specific Objective 5: Dissemination and Transfer of Project results and Products

A 5.1 Establishment of a Knowledge Base on Analysis and Evaluation of Resistance / Tolerance to stresses in potato

Period: First 6 Months

Available external resources of Potato on stress tolerance such as sequences, publications and others were compiled and all project results including sequences, markers and primers were integrated into a large database.

The POTATO Knowledge Database for Stress Tolerance has been established in form of the PATVIEW browser Software. Fig 5.1 in the Annex shows a partial view of the Software.

The PATVIEW browser pretends to integrate all results obtained within the PAPACLIMA project with relevant external information and data which are available elsewhere.

The Main Menu of PATVIEW has currently the following options:

- PROJECT - Displays the Workplan of the Project and all Project Results
- DATABASES - Displays several Databases used in the PAPACLIMA Project
 - CG Database displays the Database of Candidate genes for Stress Tolerance which are being detected
 - AM-Results will display the upcoming Results of Association Mapping in the future.

SEQUENCES - For retrieving Information on molecular resources of PAPACLIMA, and viewing internal and external sequences with the following options and sub-options:

- Internal Sequences
 - Sequence DB Feed able Sequence Database of genes of interest for the user
 - FASTA File (The corresponding FASTA file)
- External Sequences
 - Mol. Resources of *Solanum tuberosum*

BROWSE-Libs

You can browse and process public available sequences in Solanum spec.

Currently we have implemented *S. tuberosum* Nucleotides, EST and GSS, as well as the sequences of the Potato chromosomes and unassembled Contigs. Moreover sequences of the *S. phureja* chloroplast and mitochondrium can be viewed.

The integrated Support Database is useful to organize your tasks and research activities.

LIBRARIES

Several Databases are associated which contain information about “Useful Literature”, “Useful Links” and “external and internal Sequences” of useful genes and transcripts. These databases can be fed with additional data within the PATVIEW program.

OTHER - Contains options for Configuration and realizing security copies with the following options:

- Configuration
- DB Security Copies

BLAST- Contains options for performing BLAST searches in local and public Databases, with the following options:

- Local BLAST Starts the **PATblast** Program
- NCBI Blast [Link to the NCBI Blast Page](#)

Most important, it is possible to exploit the data with the coupled **PATBlaster** tool. (Fig. 5.1 and see User manual for details)

The aim of this program is to provide a simple tool for integrating the PAPA CLIMA Sequence Resources and for performing local Blast searches using a WINDOWS interface.

This program allows to make BLAST Databases, to perform any BLAST search, to Browse the available molecular resources as mentioned above and contains several utilities for merging tables, converting formats and others.

Tis program was mainly used to process the detected candidate genes.

Period: Month 7 to 16

The knowledge base **PATVIEW** has been updated with all relevant new results. This include particularly this report, the results of Library construction and RNA-Seq (PATLib.xlsx), the updated CG Stress database and the analyses results of the CG Amplicon Sequencing: (PAB1-AM.xlsx).

Period: Month 17 to 24

The knowledge base **PATVIEW** has been updated with all new results mentioned above. This include particularly this report, the update in Library construction (PATLib.xlsx), the updated CG Stress database and the analyses results of the CG Amplicon Sequencing using CG driven approach, as well as the first results in Association mapping and Model building for the available trait data.

Period: Month 25 to 30

The knowledge base **PATVIEW** has been further enhanced with all new results mentioned above. This include particularly this report, the specific AL/AC expression analyses in Library construction (PATLib.xlsx), the updated CG Stress database, the sequence analyses and Association mapping results of CG Amplicon Sequencing using CG (PAS4) and RAD markers (PATR), as well as the Model building results in the updated PATX and PATRX projects with the updated phenotypic trait data.

Period: Month 31 to 39

The knowledge base **PATVIEW** has been further enhanced with all new results mentioned above. This include particularly the updated CG Stress database, the sequence analyses and Association mapping results of CG Amplicon Sequencing using PATF, as well as the Model building results in the updated PATXf and PATRf projects with the updated phenotypic trait data and AM and Model building analyses with the new SNP projects PATXS and PATRS.

A 5.2: Establishment of a Project WEB Page

Period: First 6 Months

Initially the domain: <http://www.papaclima.com> has been acquired.

An informative project WEB page has been established which contains information about the PPAKLIMA project and its participants. Fig. 5.2 in the Annex shows an image of the web page.

Several sections are implemented which will be extended when appropriate. The main menu of the WEB page has the topics: General which will contain the WORKPLAN and all upcoming results.

The topic “Plant Materials & Assays” contains information about the plant material used and the planned assays by each partner.

The “Methodology” topic contains some general information about agronomic evaluations, specific protocols on how to evaluate abiotic stresses (drought, cold, others) and how to evaluate resistance levels to *Phytophthora infestans*. Moreover the ICG field book and evaluation sheet can be downloaded here.

Under “Breeding” the different breeding activities of the partners will be shown when scheduled.

The “Molecular Marker” topic contains several sub-topics such as “CG detection” with molecular markers for *P. infestans* resistance and the CG database for abiotic stresses which has been mentioned above.

In the future we will implement here also information and results of Association Mapping and Model Building.

In the “Dissemination” section all upcoming publications presentations and dissemination events will be shown.

Finally the “Link” topic presents currently useful links to PGSC, SPUD, PlantGDB and SOLCAP and will be further enhanced with additional links in the future.

Period: Month 7 to 16

The WEB page has been updated with the results of Library construction and RNA-Seq, the updated CG Stress database and the analyses results of the CG Amplicon Sequencing. In addition, information of the different dissemination actions by all partners has been integrated, together with several photos.

Period: Month 17 to 24

The WEB page has been updated with all new relevant results from this reporting period. This includes the update in Library construction (PATLib.xlsx), the updated CG Stress database and all analyses results of the CG Amplicon Sequencing using CG and Random approach, as well

as the first results in Association mapping and Model building. In addition, information of the different dissemination actions by all partners has been integrated, together with several photos.

Period: Month 25 to 30

The WEB page has been updated with all new relevant results from this reporting period. This includes particularly the updates in Library analyses, Association mapping and Model building results. In addition, information of the different dissemination actions by all partners has been integrated, together with several photos.

Period: Month 31 to 39

The WEB page has been updated with all new relevant results from this reporting period. This includes particularly the CG Database and the updates in Library analyses, Association mapping and Model building results. In addition, information of the different dissemination actions by all partners has been integrated, together with several photos.

A5.3 Dissemination at the scientific / technical level

A 5.4 Transfer the sector (productive chain)

Period: First 6 Months

During the XXVII Congreso de la Asociación Latinoamericana de la Papa (ALAP) in Panama City, August 22 to 26, 2016, an informative Poster was presented about the PAPA CLIMA project entitled: SELECCIÓN ASISTIDA POR MARCADORES DE GERMOPLASMA ÚTIL DE PATATA ADAPTADO A LOS ESTRESSES BIÓTICOS Y ABIÓTICOS CAUSADOS POR EL CAMBIO CLIMÁTICO GLOBAL. The authors were: Enrique Ritter, Leire Barandalla, Jose Ignacio Ruiz de Galarreta, Xavier Cuesta, Antonio Leon, Enrique Fernandez Northcote.

Period: Month 7 to 16

- NEIKER launched a Press note about CLIMAPAPA in 2017

- The partners participated in the congress: "VII CONGRESO ECUATORIANO DE LA PAPA, June 29 – July 1st, 2017, TULCAN

. - At his occasion NEIKER gave an invited Keynote with the Title: "Mapeo por asociación para detectar genes candidatos de tolerancia a estreses abióticos en Papa".

- Part of this event was la "Feria de la Papa" where also farmers and stakeholders of the potato chain from the region participated. Dr. E. Ritter gave a television interview at this occasion, promoting the Papaclima Project.

- An internal PAPA CLIMA Project meeting was realized July, 3rd, 1017 at INIAP, Sta Catalina, Ecuador. NEIKER presented the achieved progress.

- From July 4 to July 7 also a Technology Transfer course (TT) was realised at INIAP. Around 20 scientists from the region participated In the TT course.

In the TT course initially several software packages were transferred and installed (PATVIEW/ PATBLAST, ASPAM and others) and some installation problems were solved.

- Then the features and possibilities of the PATVIEW/PATBLAST Software described above were explained in detail and for each option exercises were made interactively with the participants of the workshop.

- An intensive session about “CG Detection & Primer Design” followed, also accompanied by interactive exercises with the participants. The contents of the large resources of NCBI were shown and used and different other, public bioinformatics tools were demonstrated and applied at this occasion.

- Finally, Exercises and Analyses with Sample Project EG1 including phenotypic data (since no Potato Data were yet available) were performed. The topics covered amplicon sequence processing and analyses as well as Association mapping using SAS software.

Period: Month 17 to 24

- The partners participated in the combined congress: “**World Potato Congress 2018 / ALAP 2018**”, **May 27 to 31, 2018, Cuzco (Peru)**.

- At his occasion NEIKER presented a poster with the Title: “**Construction of a cDNA library and amplicon sequencing for the detection of candidate genes for abiotic stress in potato**, L Barandalla, A Álvarez, J-I. Ruiz de Galarreta, E Ritter” and an oral presentation “**Candidate Gene Detection for abiotic and biotic stresses and Association Mapping for marker assisted selection of useful potato germplasm adapted to the stresses caused by climate change**, E Ritter’, A Alvarez’, J-I R. de Galarreta, E F. Northcote, X Cuesta, A León, L Barandalla”

- An **internal PAPA CLIMA Project meeting** was realized June, 3rd, 2018 in Cuzco.. NEIKER presented the achieved progress so far..

- From June 4 to 9 also a **Technology Transfer course (TT)** was realised in Cuzco. Around 20 scientists from the region participated In the TT course.

In the TT course initially several updated software packages were transferred and installed (PATVIEW/ PATBLAST, ASPAM and others) and some installation problems were solved.

- Then the features and possibilities of the PATVIEW/PATBLAST Software described above were explained in detail and for each option exercises were made interactively with the participants of the workshop.

- An intensive session about “CG Detection & Primer Design” followed, also accompanied by interactive exercises with the participants.

- Finally, Exercises and Analyses with Sample Project PAS1 including phenotypic data were performed. The topics covered amplicon sequence processing and analyses as well as Association mapping and Model building.

Period: Month 25 to 30

A Poster was presented at the “IX Congreso de Genética de Plantas” in Murcia in September 2018 (National Plant Genetics Congress) which is entitled: **Construcción de una librería de cDNA para la identificación de genes candidatos relacionados con estreses abióticos en patata (*Solanum tuberosum* L.)**; Alba Álvarez, Leire Barandalla, Jose I. Ruiz de Galarreta, Enrique Ritter

A Poster was presented at the “19th Joint Meeting of the *Section 'Breeding & Varietal Assessment'* of the European Association for Potato Research (*EAPR*) and the *EUCARPIA Section* in Rostock-Warnemünde, Germany. December 2018” which is entitled: **Candidate Gene Detection for Abiotic and Biotic Stresses and Association Mapping for Marker Assisted Selection of Useful Potato Germplasm Adapted to the Stresses Caused by Climate Change**, *Álvarez, Alba, Barandalla, Leire, Ruiz de Galarreta, Jose Ignacio, Northcote, Enrique F., Cuesta, Xavier, León, Antonio; Ritter, Enrique*

A publication has been realized in: “Revista Latinoamericana de la Papa 21 (2): 33 - 38 ISSN: 1853-4961” entitled: **Identification of candidate genes involved in the response to different abiotic stresses in potato (*Solanum tuberosum* L.); L. Barandalla, A. Álvarez, J. I. Ruiz de Galarreta, E. Ritter**

Further presentations are planned for the **VIII Congreso Ecuatoriano de la Papa**, end of June 2019, Ambato Ecuador. In the frame of this event also a **Technology Transfer Course** of Project results and Analyses methods is foreseen.

Period: Month 31 to 39

During the VIII Congreso Ecuatoriano de la Papa, end of June 2019 in Ambato Ecuador the partners presented updated project results. NEIKER gave an invited presentation with the Title: “Ventajas de la Mejora Genética Molecular en papa.” Also a Project coordination Meeting was held, were all partners presented and discussed the updated project results.

- From July 2 to 5 also a **Technology Transfer course (TT)** was realised at USFQ (Cumbaya, EC). Around 20 scientists from the region participated In the TT course. **The course was similar to previous courses, since mostly new trainees participated.** In the TT course initially several updated software packages were transferred and installed (PATVIEW/PATBLAST, ASPAM and others) and some installation problems were solved. Then the features and possibilities of the PATVIEW/PATBLAST Software described above were explained in detail and for each option exercises were made interactively with the participants of the workshop.

- An intensive session about “CG Detection & Primer Design” followed, also accompanied by interactive exercises with the participants.

- Finally, Exercises and Analyses with Sample Project PAS1 including phenotypic data were performed. The topics covered amplicon sequence processing and analyses as well as Association mapping and Model building.

A final “wrap up” Project Meeting was held in the frame of the IV Congreso peruano de mejoramiento genético de plantas y biotecnología agrícola, in October in LIMA Peru. The partners presented updated project results and the activities for the finalization of the project were coordinated.

Also an official closing event of the PAPA CLIMA project was realized, where all partners presented the project results to local officials.

In the congress NEIKER gave an invited presentation with the Title: “Aplicaciones de la Mejora Genética Molecular en papa.”

IV Publications, posters, presentations)

Period: First 6 Months

Enrique Ritter, Leire Barandalla, Jose Ignacio Ruiz de Galarreta, Xavier Cuesta, Gustavo Fermin, Enrique Fernandez Northcote. SELECCIÓN ASISTIDA POR MARCADORES DE GERMOPLASMA ÚTIL DE PATATA ADAPTADO A LOS ESTRESSES BIÓTICOS Y ABIÓTICOS CAUSADOS POR EL CAMBIO CLIMÁTICO GLOBAL. Proceedings of the XXVII Congreso de la Asociación Latinoamericana de la Papa (ALAP) in Panama City, August 22 to 26, 2016. Poster.

Period: Month 7 to 16

- A press note about the PAPA CLIMA Project has been released in 2017.
- Invited Keynote: “**Mapeo por asociación para detectar genes candidatos de tolerancia a estreses abióticos en Papa**”, “VII CONGRESO ECUATORIANO DE LA PAPA, June 29 – July 1st, 2017, TULCAN.

Period: Month 17 to 24

Construction of a cDNA library and amplicon sequencing for the detection of candidate genes for abiotic stress in potato, L Barandalla, A Álvarez, J-I. Ruiz de Galarreta, E Ritter” (Poster), WPC/ALAP 2018, May 2018, Cuzco (Peru)

Candidate Gene Detection for abiotic and biotic stresses and Association Mapping for marker assisted selection of useful potato germplasm adapted to the stresses caused by climate change, E Ritter, A Alvarez, J-I R. de Galarreta, E F. Northcote, X Cuesta, A León, L Barandalla (**Oral**) WPC/ALAP 2018, May 2018, Cuzco (Peru)

Period: Month 25 to 30

Construcción de una librería de cDNA para la identificación de genes candidatos relacionados con estreses abióticos en patata (*Solanum tuberosum* L.). Alba Álvarez, Leire Barandalla, Jose I. Ruiz de Galarreta, Enrique Ritter, Poster presentation. “IX Congreso de Genética de Plantas” in Murcia in September 2018 (National Plant Genetics Congress)

Candidate Gene Detection for Abiotic and Biotic Stresses and Association Mapping for Marker Assisted Selection of Useful Potato Germplasm Adapted to the Stresses Caused by Climate Change, Álvarez, Alba, Barandalla, Leire, Ruiz de Galarreta, Jose Ignacio, Northcote, Enrique F., Cuesta, Xavier, León, Antonio; Ritter, Enrique. Poster presentation, 19th Joint Meeting of the Section 'Breeding & Varietal Assessment' of the European Association for Potato Research (EAPR) and the EUCARPIA Section, Rostock-Warnemünde, Germany, December 2018

Identification of candidate genes involved in the response to different abiotic stresses in potato (*Solanum tuberosum* L.), L. Barandalla¹, A. Álvarez¹, J. I. Ruiz de Galarreta^{1/*}, E. Ritter, **Publication**, Revista Latinoamericana de la Papa 21 (2): 33 - 38 ISSN: 1853-4961

Period: Month 31 to 39

Invited Keynote: **Ventajas de la Mejora Genética Molecular en papa.** E. Ritter at **VIII Congreso Ecuatoriano de la Papa**, end of June 2019 in Ambato Ecuador.

Invited Keynote: **Aplicaciones de la Mejora Genética Molecular en papa.** E. Ritter at **IV Congreso peruano de mejoramiento genético de plantas y biotecnología agrícola**, in **October in LIMA Peru.**