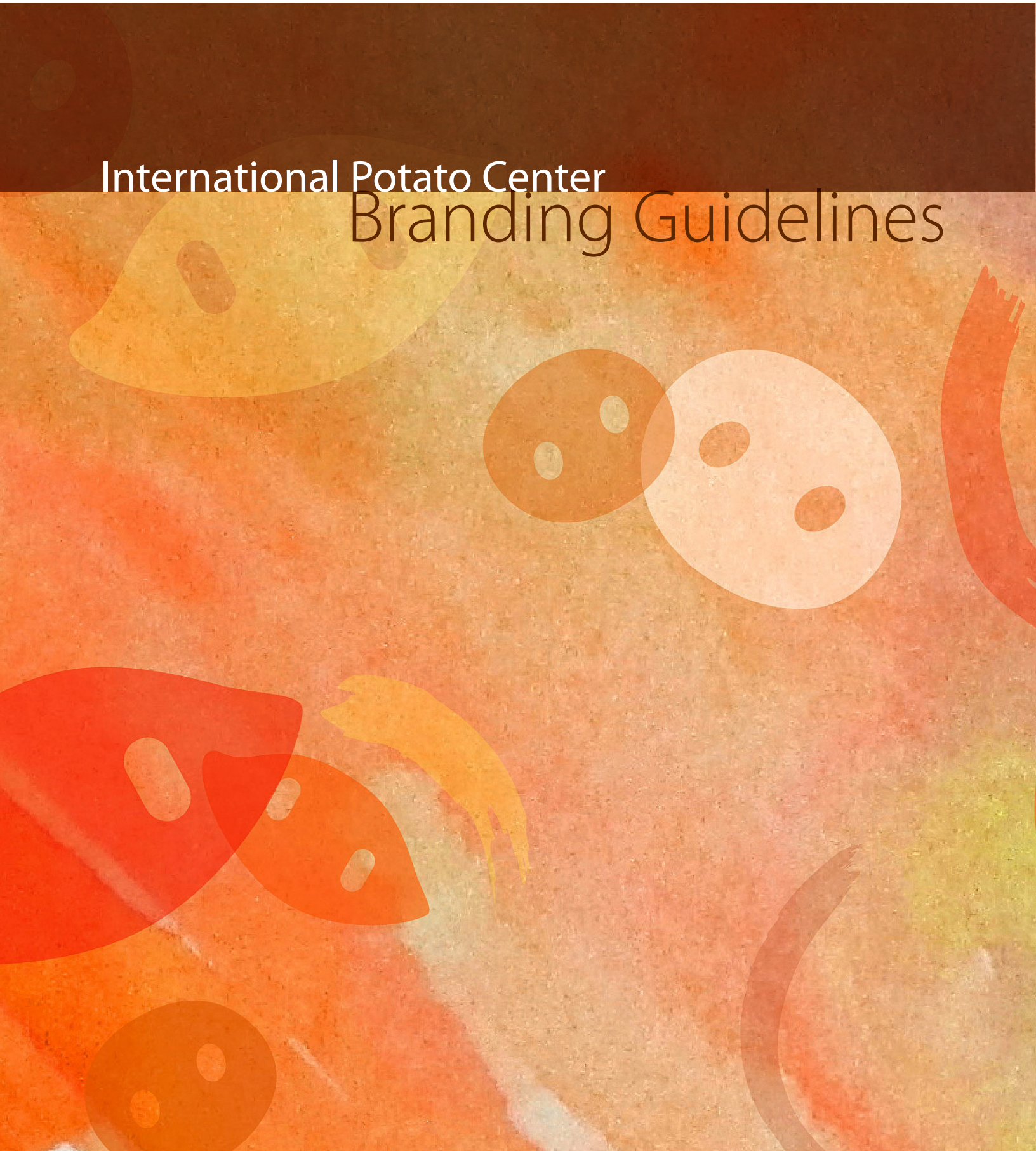
CIP
INTERNATIONAL POTATO CENTER

CGIAR

International Potato Center
Branding Guidelines



Contents

4 Introduction

6 CIP mission & vision

7 Logo

8 Logo variant

9 Logo guidelines in use

10 Correct usage
11 Minimum clear space
11 Minimum print size
12 Typography
13 Color palette
15 Modular grid

16 Correct logo placement

18 Applications:

18 Stationery
19 Posters
21 Power point presentations
23 Name tags
24 Email signature
25 Publications
27 Social media

Introduction

Welcome to the International Potato Center (CIP) Branding and Style Guide. Here you will find information to help you properly apply elements of the International Potato Center brand. By following these standards, you can ensure the clarity and strength of the International Potato Center brand throughout all communications. These guidelines should be used in conjunction with any other partner organizations and their branding guidelines.

CIP is a more than 50 year-old organization that has pioneered major advances in agriculture research for development. It is a CGIAR Research Center. Unified branding throughout CIP will help elevate the name of the organization to the level it deserves. This is as an overarching global brand that expresses our shared vision and enables us to be seen as more than the sum of our parts.

The International Potato Center (CIP) was founded in 1971 as a research-for-development organization with a focus on potato, sweetpotato and andean roots and tubers. It delivers innovative science-based solutions to enhance access to affordable nutritious food, foster inclusive sustainable business and employment growth, and drive the climate resilience of root and tuber agri-food systems. Headquartered in Lima, Peru, CIP has a research presence in more than 20 countries in Africa, Asia and Latin America. www.cipotato.org

CIP is a CGIAR research center, a global research partnership for a food-secure future. CGIAR science is dedicated to transforming food, land and water systems in a climate crisis. Its research is carried out by 13 CGIAR Centers/Alliances in close collaboration with hundreds of partners, including national and regional research institutes, civil society organizations, academia, development organizations and the private sector. www.cgiar.org

Our Vision

A healthy, inclusive and resilient world through root and tuber systems.

Our Mission

CIP delivers innovative science-based solutions to enhance access to affordable nutritious food, foster inclusive sustainable business and employment growth, and drive climate resilience of root and tuber agri-food systems.

Logo

The CIP official logo is in English. It includes a graphic design depicting the importance of root and tuber crops.

The base color of the logo is orange and brown, to represent potato and sweetpotato.

The logo for the International Potato Center is comprised of the following elements:

- **The Symbol:** A square with corner elements, containing the figure of the potato guardian Papa Arariwa, holding both a potato and a sweetpotato.
- **The Logotype:** is the text International Potato Center and the Spanish acronym CIP
- **The Tagline:** A CGIAR Research Center

Symbol

Logotype

Logo variant

For Spanish use only

Logo guidelines in use

CIP logo and name are registered trademarks in Peru and other countries. Furthermore, CIP's symbol is protected by copyright worldwide. Therefore any alteration, distortion, recreation, translation, or misuse is strictly prohibited.

A number of digital file formats are available for download at **www.cipotato.org/branding**. Each of the files available is optimized for a variety of applications, for both print and on-screen communications, to ensure easy adherence to these guidelines. Do not re-create the logo under any circumstances.

Correct usage

Here are some examples of proper logo use.

The official logo must always appear in full color.

The black logo can be used when necessary.

The logo can be used in white on top of any color.

If you need advice or assistance on logo use, please contact the Communications Department CIP-CPAD@cgiar.org

Minimum clear space

To maximize the impact of the logo there must always be a minimum amount of clear space surrounding the logo. This clear space protects the image from being obscured by nearby text or pictures. The minimum clear space required is the 'C' in International Potato Center.

Minimum print size

A minimum print size has been established to ensure legibility.

Minimum height = 1.7 cm

Minimum width = 4 cm

Example: used for business cards.

Typography

CIP logo type

CIP has typography standards to ensure brand consistency across all printed materials. Typography is an extremely important design element not to be overlooked. The font family, Square and Myriad Pro, have been established as the CIP logo standard.

Primary font for print

As a general rule, Square and Myriad Pro should be used for headlines. For subheads and body text Myriad Pro is recommended. If the Myriad Pro font family is not available Arial is an acceptable and commonly available substitute.

Square BT

Square BT Roman	A B C D E F G H I J K L M N O P Q R S T U V W X Y Z 1 2 3 4 5 6 7 8 9
Square BT Bold	**A B C D E F G H I J K L M N O P Q R S T U V W X Y Z 1 2 3 4 5 6 7 8 9**

Myriad Pro

Myriad Pro Light Condensed	A B C D E F G H I J K L M N O P Q R S T U V W X Y Z 1 2 3 4 5 6 7 8 9
Myriad Pro Condensed	A B C D E F G H I J K L M N O P Q R S T U V W X Y Z 1 2 3 4 5 6 7 8 9
Myriad Pro SemiboldCondensed	**A B C D E F G H I J K L M N O P Q R S T U V W X Y Z 1 2 3 4 5 6 7 8 9**
Myriad Pro BoldCondensed	**A B C D E F G H I J K L M N O P Q R S T U V W X Y Z 1 2 3 4 5 6 7 8 9**
Myriad Pro BlackCondensed	**A B C D E F G H I J K L M N O P Q R S T U V W X Y Z 1 2 3 4 5 6 7 8 9**
Myriad Pro Light	A B C D E F G H I J K L M N O P Q R S T U V W X Y Z 1 2 3 4 5 6 7 8 9
Myriad Pro Regular	A B C D E F G H I J K L M N O P Q R S T U V W X Y Z 1 2 3 4 5 6 7 8 9
Myriad Pro Semibold	**A B C D E F G H I J K L M N O P Q R S T U V W X Y Z 1 2 3 4 5 6 7 8 9**
Myriad Pro Bold	**A B C D E F G H I J K L M N O P Q R S T U V W X Y Z 1 2 3 4 5 6 7 8 9**
Myriad Pro Black	**A B C D E F G H I J K L M N O P Q R S T U V W X Y Z 1 2 3 4 5 6 7 8 9**

Color palette

The CIP logo should be reproduced in full color. These colors serve as the source for our standard color palette. These colors should be employed throughout CIP communications and are equivalent to the PANTONE® numbers listed in the table below.

For **four-color process** printing refer to the CMYK values shown.

For **desktop publishing**, such as Word or PowerPoint®, refer to RGB (print/on-screen).

For **web applications**, refer to Hexadecimal Web values.

Primary color palette

PANTONE: 1505 C

C:00 | M:65 | Y:100 | K:00

R:238 | G:114 | B:3

HEX: #EE7203

PANTONE: 1545 C

C:00 | M:65 | Y:100 | K:75

R:93 | G:46 | B:0

HEX: #5D2E00

Secondary color palette

Used for publications and other applications

PANTONE: 364 C

C:73 | M:09 | Y:94 | K:39
R:52 | G:117 | B:45
HEX: #34752D

PANTONE: 1795 C

C:00 | M:90 | Y:100 | K:00
R:230 | G:51 | B:18
HEX: #E53212

PANTONE: 2607 C

C:80 | M:100 | Y:00 | K:10
R:86 | G:33 | B:122
HEX: #56217A

PANTONE: 354 C

C:80 | M:00 | Y:100 | K:00
R:19 | G:165 | B:56
HEX: #12A537

PANTONE: 1665 C

C:00 | M:75 | Y:100 | K:00
R:234 | G:91 | B:12
HEX: #EA5A0B

PANTONE: 192 C

C:00 | M:100 | Y:70 | K:00
R:228 | G:00 | B:58
HEX: #E4003A

PANTONE: 369 C

C:60 | M:00 | Y:100 | K:00
R:118 | G:184 | B:42
HEX: #76B82A

PANTONE: 152 C

C:00 | M:50 | Y:100 | K:00
R:243 | G:146 | B:00
HEX: #F39200

PANTONE: Pro. Mag. C

C:00 | M:100 | Y:00 | K:00
R:230 | G:00 | B:126
HEX: #E6007E

PANTONE: 376 C

C:40 | M:00 | Y:100 | K:00
R:175 | G:202 | B:11
HEX: #AFCA0A

PANTONE: 137 C

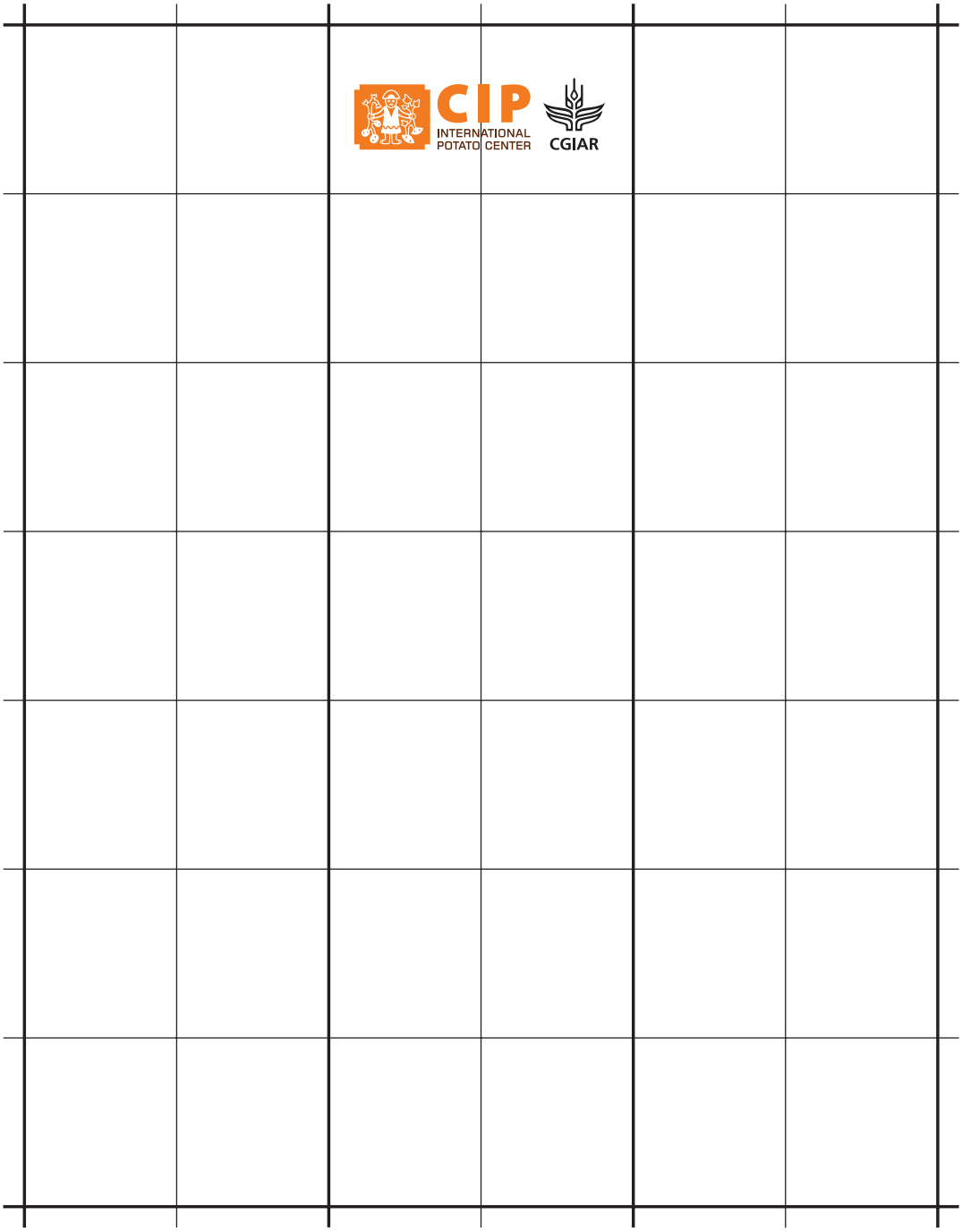
C:00 | M:30 | Y:100 | K:00
R:251 | G:186 | B:00
HEX: #FBBA00

PANTONE: Pro. Cyan C

C:100 | M:00 | Y:00 | K:00
R:00 | G:159 | B:227
HEX: #009FE3

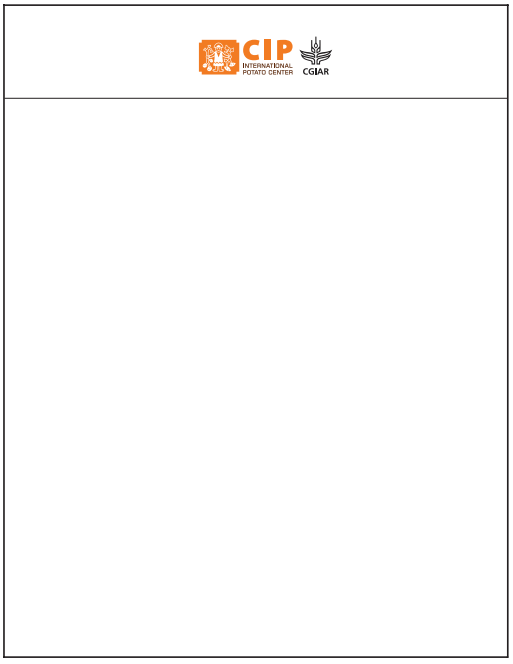
Modular grid

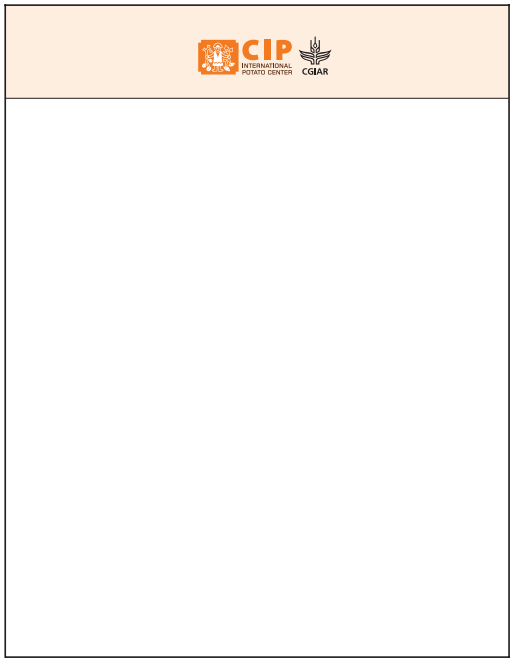
The modular grid should be divided horizontally into seven rows and vertically into six columns futher subdivided in three main columns.

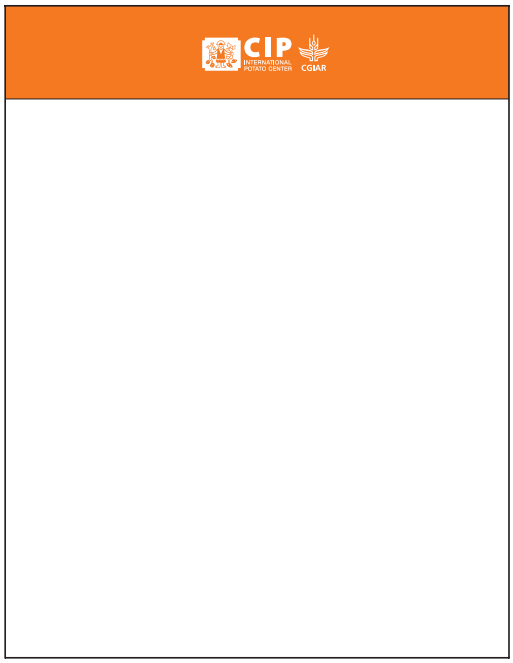


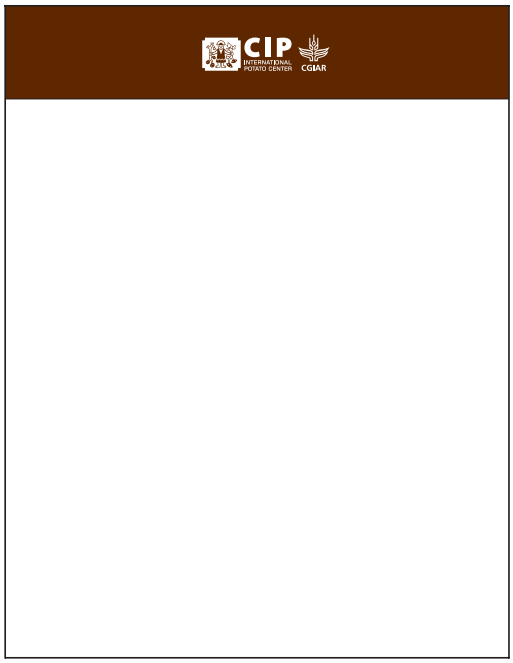
Correct Logo placement

The CIP logo must be placed in the upper center, in a white, orange or brown field. It may also be placed in 10% of any color.









Applications:

Stationery

Letterhead

CIP INTERNATIONAL POTATO CENTER CGIAR

CIP is supported by the Consultative Group on International Agricultural Research
El CIP es apoyado por el Grupo Consultivo para la Investigación Agrícola Internacional
Street Address/Dirección:
Av. La Molina 1895, La Molina, Lima, Perú

Lima 24 de Enero de 2016

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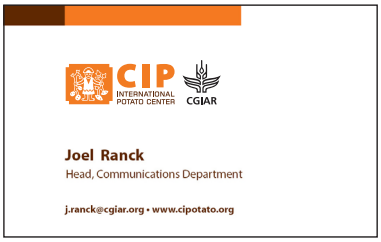
Atentamente

Lorem ipsum dolor sit amet

Business card



CIP INTERNATIONAL POTATO CENTER CGIAR

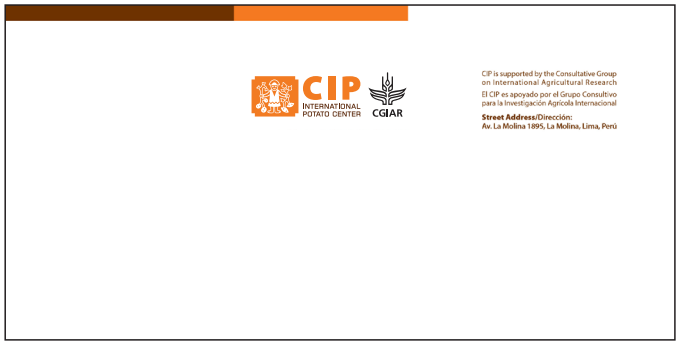
Joel Ranck
Head, Communications Department

j.ranck@cgiar.org • www.cipotato.org

Mailing Address: Apartado 1558, Lima 12, Perú
Tel: +51 1 349 6017 ext 3011• **Direct:** +51 1 317 5334
Fax: +51 1 317 5348

Street Address: Av. La Molina 1895, La Molina, Lima, Perú

Envelope



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Posters

CIP Poster (36x48 inches)

CIP INTERNATIONAL POTATO CENTER CGIAR

Respuesta de tres variedades de papa en un sistema Aeropónico novedoso para la producción

Carlos Chuquillanqui[1] • Ian Barker[1]

[1] International Potato Center (CIP). Germplasm Enhancement and Crop Improvement-Crop Management Division • Av. La Molina 1895. La Molina. Lima 12. Perú

Background

WRKY proteins are a superfamily of transcription factors involved in various physiologial processes in plants, including pathogen defence. WRKY transciption factors have been shown to act as both negative and positive regulators of defence, suggesting that they may operate through different regulatory complexes. The different roles can be partly determined by the topological features of the proteins.

The WRKY domain is defined by the conserved amino acid sequence WRKYGQK at the N-terminal end followed by a zinc-finger-like motif. WRKY proteins are classified based on the number of WRKY domains and the structure of the zinc-finger-like motif.

The data presented here is the first step towards unveiling the role of WRKY transcription factors in regulating pathogen defence responses in CIP's potato germplasm.

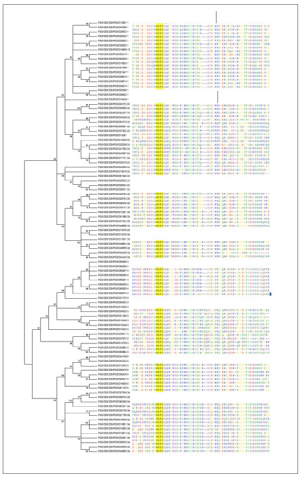

Figure 1. Evolutionary relationships of 96 WRKY proteins.

supported phylogenetic groups. Group 4 is new as compared to Arabidopsis and is clearly distinguished by a a different type of zinc finger motif with the C-X4-C motif typical to Group 2 but with a H-X-C motif typical for group 3. Groups 2d and 2e each form well supported phylogenetic groups. Group 4 is new as compared to Arabidopsis and is clearly distinguished by a a different type of zinc finger motif supported phylogenetic groups. Group 4 is new as compared to Arabidopsis and is clearly distinguished by a a different type of zinc finger motif with the C-X4-C motif typical to Group 2 but with a H-X-C motif typical to Group 2 but with a H-X-C motif typical for group 3.

The evolutionary history was inferred using the Neighbor-Joining method [2]. The bootstrap consensus tree inferred from 1000 replicates [3] is taken to represent the evolutionary history of the taxa analyzed [3]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [3]. The evolutionary distances were computed using the Poisson correction method [4] and are in the units of the number of amino acid substitutions per site. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 61 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 [5]. Sequence alignment of each group with each groups characteristic motifs are shown on the right.

Methods

WRKY Pfam profile PF03106 consisting of the alignment of 34 WRKY type sequences was used to mine the PGSC DM peptides with HMMER algorithm and 135 sequences were obtained. After alignment the proteins lacking either the WRKY motif or part of the zinc finger motif were removed. WRKY domains (75 amino acids) of 96 proteins were subjected to phylogenetic analysis by MEGA4 and NJ consensus tree was computed (Figure 1). Potential leucine zippers, leucine repeats and coiled coil domains were predicted in full length WRKY proteins using 2ZIP server at http://2zip.molgen.mpg.de/.

Potato WRKY protein Phylogeny

The groups previously classified in Arabidopsis [1] were identified: Group 1 proteins contain 2 WRKY domains and based on the C-terminal WRKY domain alone do not form a clearly supported group in phylogenetic tree. Part of the group 2b proteins cluster together with group 2a proteins. However, these groups can be differentiated on the N-terminal region of the protein before the WRKY domain. Only group 2a proteins were found to contain a predicted leucine zipper (LZ) whereas some of the group 2b proteins contain a coiled coil (CC) domain.

Groups 2d and 2e each form well supported phylogenetic groups. Group 4 is new as compared to Arabidopsis and is clearly distinguished by a a different type of zinc finger motif with the C-X4-C motif typical to Group 2 but with a H-X-C motif typical for group 3. Groups 2d and 2e each form well supported phylogenetic groups. Group 4 is new as compared to Arabidopsis and is clearly distinguished by a a different type of zinc finger motif with the C-X4-C motif typical to Group 2 but with a H-X-C motif typical for group 3. Groups 2d and 2e each form well supported phylogenetic groups. Group 4 is new as compared to Arabidopsis and is clearly distinguished by a a different type of zinc finger motif with the C-X4-C motif typical to Group 2 but with a H-X-C motif different type of zinc finger motif with the C-X4-C motif typical

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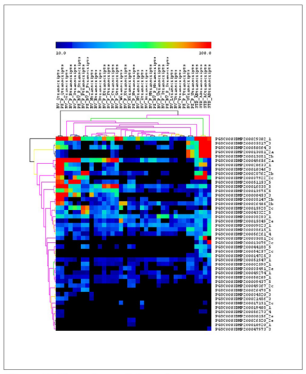

Figure 2. Comparison of transcript accumulation in different tissues and in response to abiotic and biotic stimuli. Expression in DM is determined by FPKM (Fragments Per Kilobase of exon per Million fragments mapped) values (PGSC).

Transcript profiles

For 77 of the WRKY peptides transcripts were detected among the RNA sequence libraries. Most of the transcripts had a low abundancy suggesting low level of expression, but there are also transcripts that accumulate in large amounts in certain tissues or after biotic or abiotic stimuli (Figure 2). For example, the first transcript in Figure 2 has a relatively high expression across all treatments, with the highest expression in biotic stress treated leaves. This transcript corresponds to a WRKY protein from Group 1 that is highly similar (99%) to a double WRKY protein PPS8 of S. tuberosum, which is a candidate substrate for MAPKs that play pivotal roles in induced defence responses [6].

WRKY transcription factors are part of complex co-regulatory mechanisms and more detailed expression studies are required to identify their role dfence response regulation.

For 77 of the WRKY peptides transcripts were detected among the RNA sequence libraries. Most of the transcripts had a low abundancy suggesting low level of expression, but there are also transcripts that accumulate in large amounts in certain tissues or after biotic or abiotic stimuli (Figure 2 expression across all treatments, with the highest expression in biotic stress treated leaves.

Respuesta de tres variedades de papa en un sistema Aeropónico novedoso para la producción

Julián Mateus[1] • Stef de Haan[2]
Carlos Chuquillanqui[2]
Ian Barker[2] • Alfredo Rodríguez [3]

[1] Corporación Colombiana de Investigación Agropecuaria (CORPOICA). Centro de Investigación Tibaitatá. • Km 14 vía Bogotá – Mosquera. Colombia

[2] International Potato Center (CIP). Germplasm Enhancement and Crop Improvement-Crop Management Division • Av. La Molina 1895. La Molina. Lima 12. Perú

[3] Universidad Nacional Agraria La Molina. Centro de Investigación de Hidroponía y Nutrición Mineral Departamento de Biología. • Av. La Molina s/n. La Molina. Lima 12. Perú

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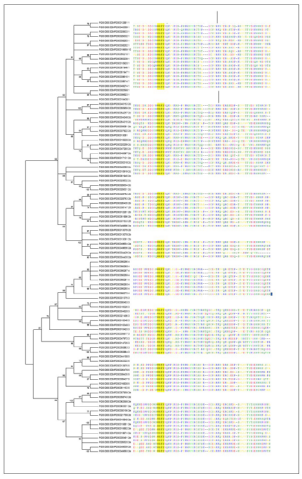

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The evolutionary history was inferred using the Neighbor-Joining method [2]. The bootstrap consensus tree inferred from 1000 replicates [3] is taken to represent the evolutionary history of the taxa analyzed [3]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [3]. The evolutionary distances were computed using the Poisson correction method [4] and are in the units of the number of amino acid substitutions per site. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 61 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 [5]. Sequence alignment of each group with each groups characteristic motifs are shown on the right.

Methods

WRKY Pfam profile PF03106 consisting of the alignment of 34 WRKY type sequences was used to mine the PGSC DM peptides with HMMER algorithm and 135 sequences were obtained. After alignment the proteins lacking either the WRKY motif or part of the zinc finger motif were removed. WRKY domains (75 amino acids) of 96 proteins were subjected to phylogenetic analysis by MEGA4 and NJ consensus tree was computed (Figure 1). Potential leucine zippers, leucine repeats and coiled coil domains were predicted in full length WRKY proteins using 2ZIP server at http://2zip.molgen.mpg.de/.

Potato WRKY protein Phylogeny

The groups previously classified in Arabidopsis [1] were identified: Group 1 proteins contain 2 WRKY domains and based on the C-terminal WRKY domain alone do not form a clearly supported group in phylogenetic tree. Part of the group 2b proteins cluster together with group 2a proteins. However, these groups can be differentiated on the N-terminal region of the protein before the WRKY domain. Only group 2a proteins were found to contain a predicted leucine zipper (LZ) whereas some of the group 2b proteins contain a coiled coil (CC) domain.

Groups 2d and 2e each form well supported phylogenetic groups. Group 4 is new as compared to Arabidopsis and is clearly distinguished by a a different type of zinc finger motif with the C-X4-C motif typical to Group 2 but with a H-X-C motif typical for group 3. Groups 2d and 2e each form well supported

Groups 2d and 2e each form well supported phylogenetic groups. Group 4 is new as compared to Arabidopsis and is clearly distinguished by a a different type of zinc finger motif with the C-X4-C motif typical to Group 2 but with a H-X-C motif typical for group 3.

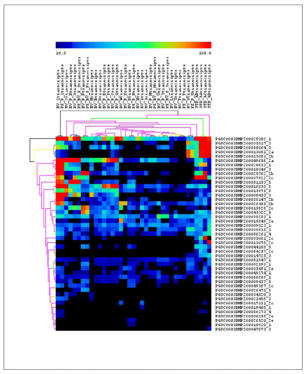


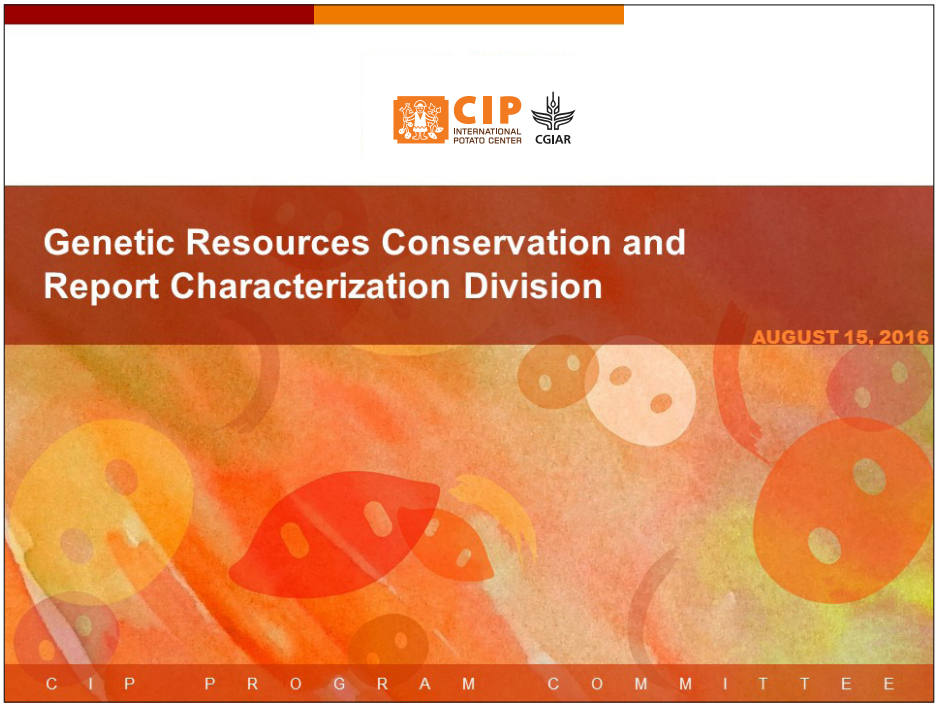
Figure 2. Comparison of transcript accumulation in different tissues and in response to abiotic and biotic stimuli. Expression in DM is determined by FPKM (Fragments Per Kilobase of exon per Million fragments mapped) values (PGSC).

Transcript profiles

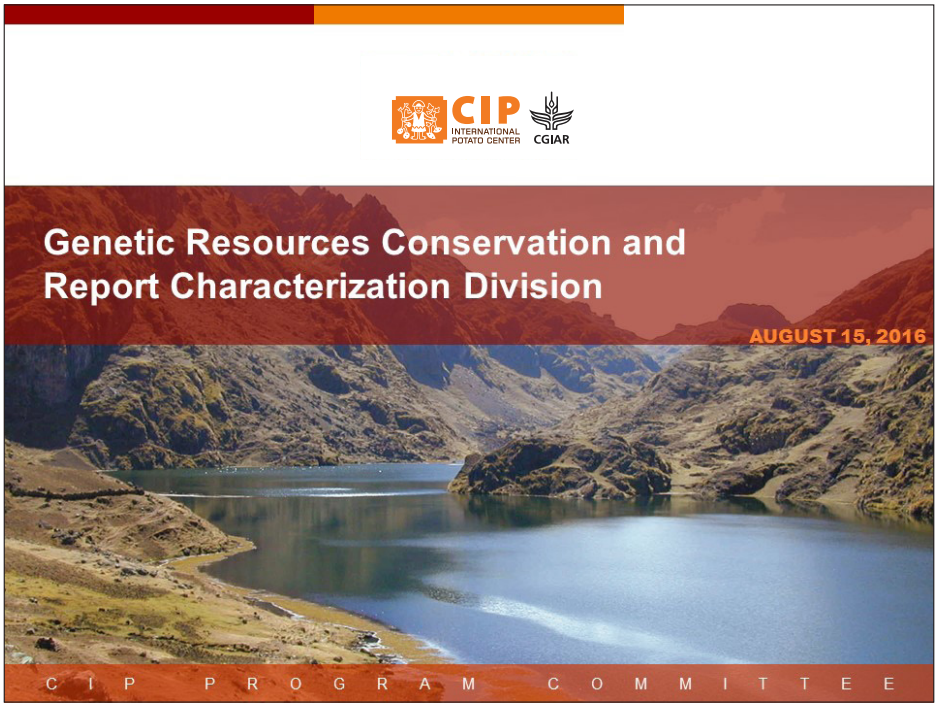
For 77 of the WRKY peptides transcripts were detected among the RNA sequence libraries. Most of the transcripts had a low abundancy suggesting low level of expression, but there are also transcripts that accumulate in large amounts in certain tissues or after biotic or abiotic stimuli (Figure 2). For example, the first transcript in Figure 2 has a relatively high expression across all treatments, with the highest expression in biotic stress treated leaves. This transcript corresponds to a WRKY protein from Group 1 that is highly similar (99%) to a double WRKY protein PPS8 of S. tuberosum, which is a candidate substrate for MAPKs that play pivotal roles in induced WRKY transcription factors are part of complex co-regulatory mechanisms and more detailed expression studies are required to identify their role dfence response regulation.

RESEARCH PROGRAM ON Roots, Tubers and Bananas

Power point presentations (on screen-show)



Power point presentations



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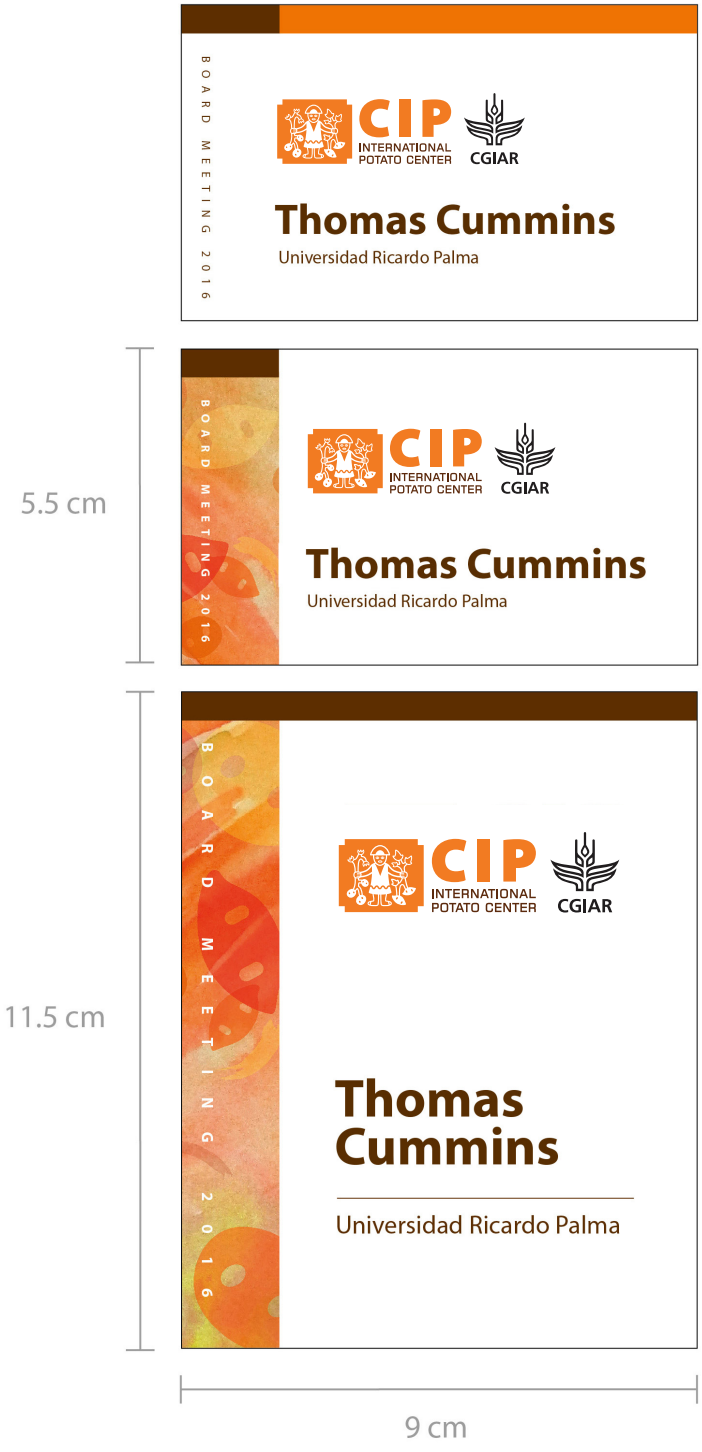
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James Stapleton (CIP)

To: Viviana Infantas
Subject: Board meeting 2022

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James Stapleton | Head of Communications Department
Apartado 1558, Lima 12, Perú
Tel: +51 1 349 6017 ext 3011 / +51 1 317 5303
j.ranck@cgiar.org • www.cipotato.org

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Publications

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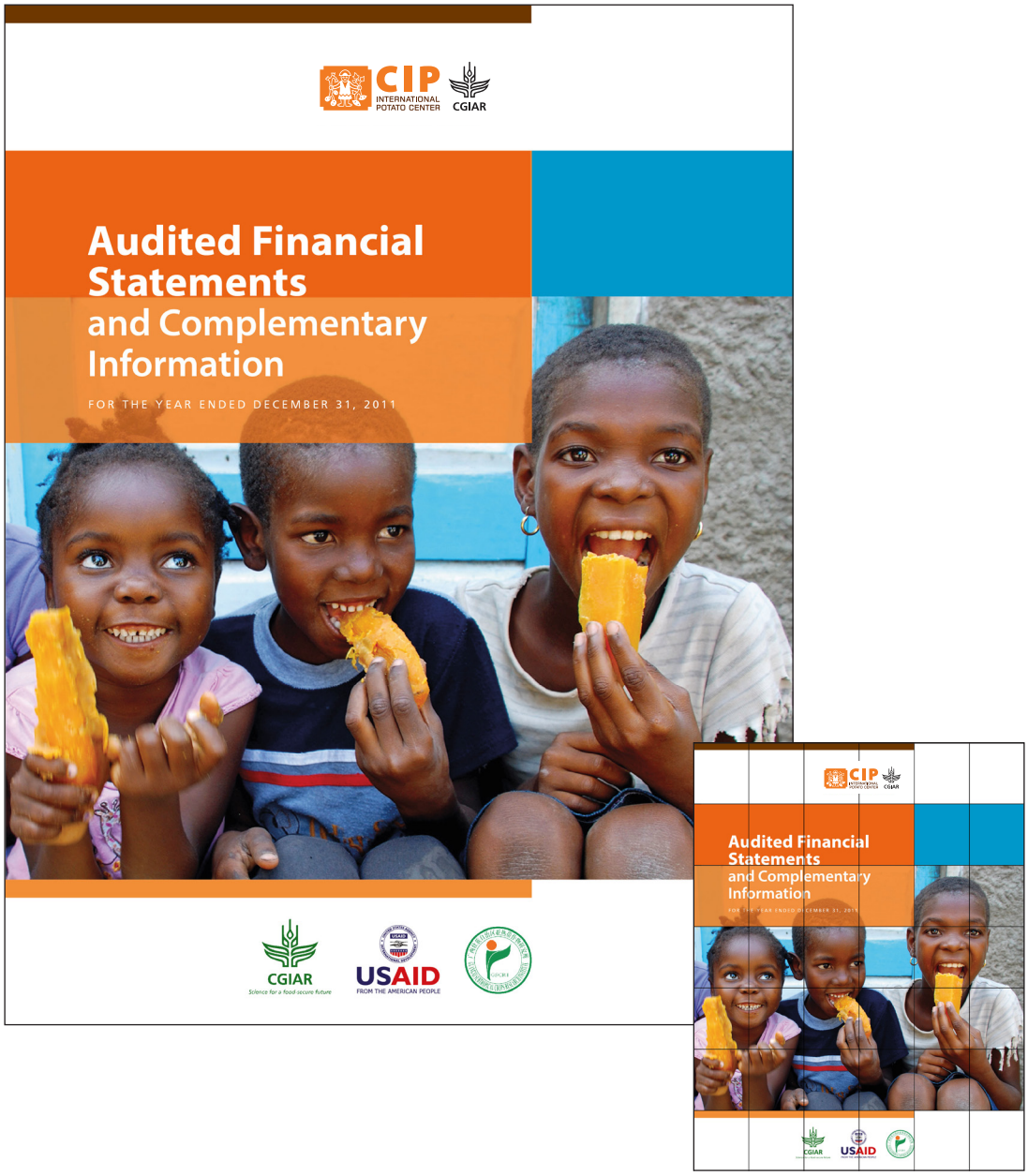

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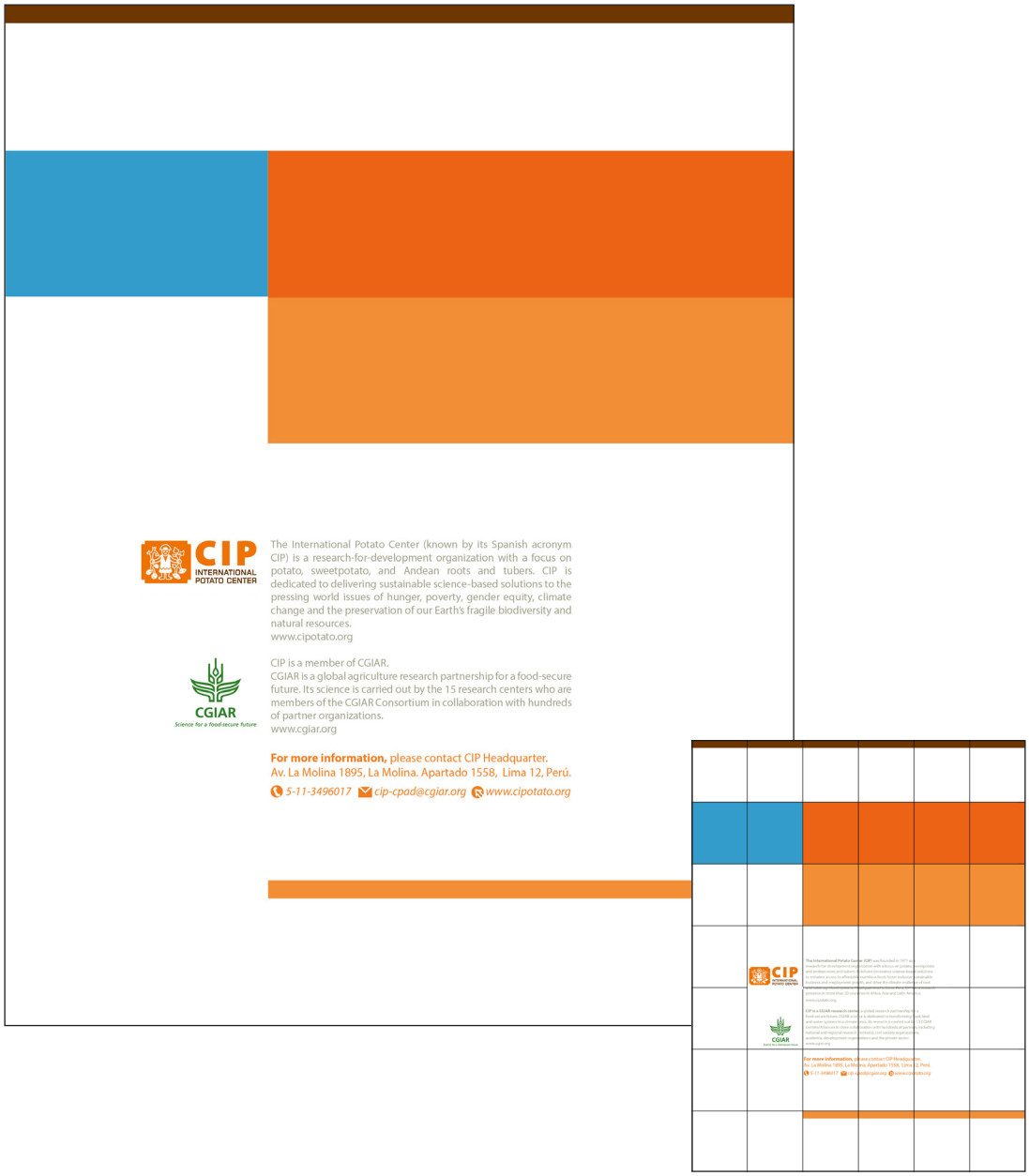

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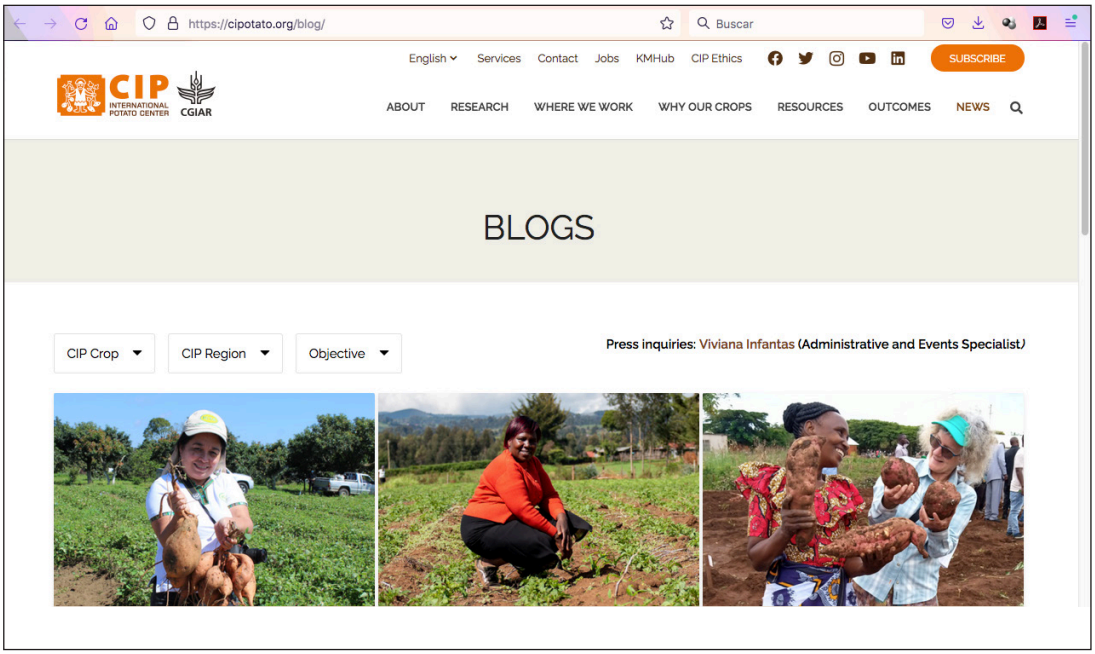

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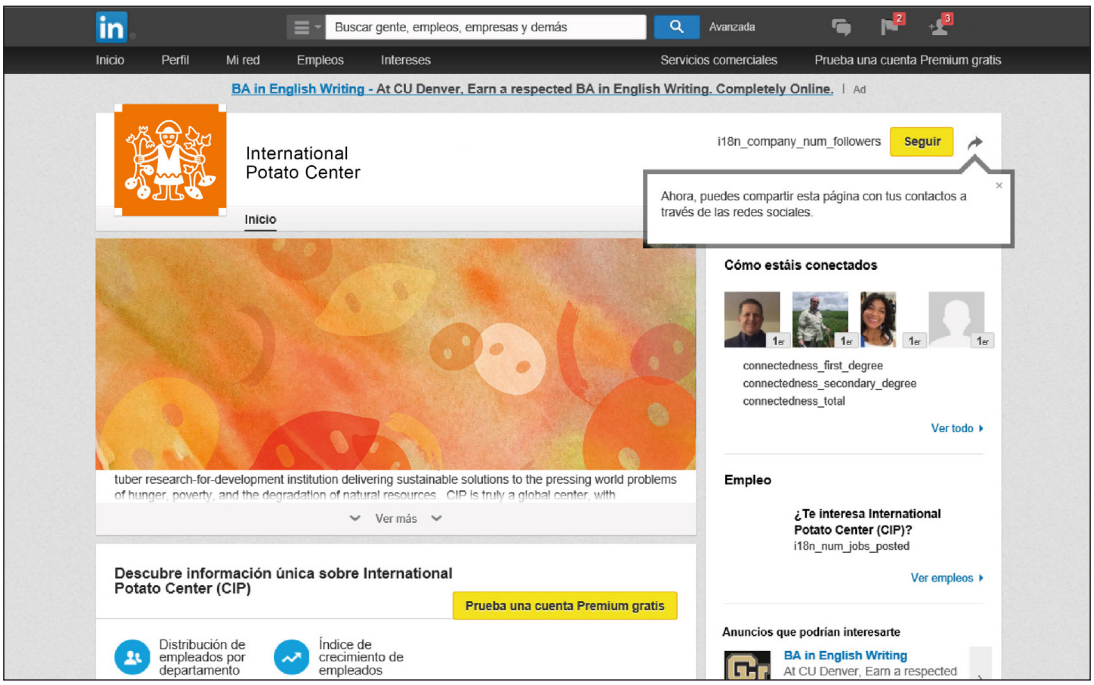

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