TO MAGNIFICO RETTORE OF UNIVERSITA' DEGLI STUDI DI MILANO **ID CODE 5819**

I the undersigned asks to participate in the public selection, for qualifications and examinations, for the awarding of a type B fellowship at **Dipartimento di Scienze Agrarie e Ambientali - Produzione, Territorio, Agroenergia**

Scientist- in – charge: **Prof.ssa Laura Rossini**

[Roberta and Rossi]

CURRICULUM VITAE

PERSONAL INFORMATION

Surname	Rossi
Name	Roberta

PRESENT OCCUPATION

Appointment	Structure
Unemployed	

EDUCATION AND TRAINING

Degree	Course of studies	University	year of achievement of the degree
PhD	Agriculture, Environment and Bioenergy (AAB) XXXV Cycle	University of Milano, Milano (Italy)	Final defence on June 28, 2023
Master	Master of Science in Agricultural and Environmental Biotechnology (BAA) LM-7	University of Perugia, Perugia (Italy)	2017
Degree	Bachelor of Science in Biotechnology L-2	University of Perugia, Perugia (Italy)	2014

REGISTRATION IN PROFESSIONAL ASSOCIATIONS

Date of registration	Association	City
N/A	N/A	N/A

FOREIGN LANGUAGES

Languages	level of knowledge
Italian	Mother tongue
English	B2

AWARDS, ACKNOWLEDGEMENTS, SCHOLARSHIPS

Year	Description of award
2022	Traineeship mobility grant Erasmus+ 2021/22 (II ED.). Internship number: 28 (6 month)
2018	Fellowship at CREA-GB (Research Center for Genomics and Bioinformatics), Fiorenzuola d' Arda (Italy) (1 year)

TRAINING OR RESEARCH ACTIVITY

October 2019 - June 2023 (3 years)

PhD Student in Agriculture, Environment and Bioenergy (AAB) XXXV Cycle

Institution: University of Milano, Milano (Italy) - Department of Agricultural and Environmental Sciences Production, Territory, Agroenergy (DiSAA)

Supervisor: Prof. Laura Rossini; Co-supervisor: Dr. Salar Shaaf

Defense Date: 28/06/2023

PhD thesis title: **Identification and characterization of genetic loci for culm morphology traits in barley (*Hordeum vulgare* L.)**

PhD objectives:

1. to characterize two major Quantitative Trait Loci (**QTL**s) for culm morphology by developing two **segregating populations** which were subsequently genotyped and phenotyped under field conditions. Both phenotypic and genotypic data were integrated to run Genome Wide Association Studies (GWAS) analyses for culm morphology traits and a series of relevant agronomic traits.
2. to identify genes associated to culm features by performing both **reverse and forward genetic screening of two TILLING populations.**

(Please see the attached documents for detailed information)

Funding: This work was supported by the project BARISTA (Advanced tools for breeding BARley for Intensive and SusTainable Agriculture under climate change scenarios) funded by the SusCrop-ERA-NET call 2019-2020 (Grant No. 771134) and FACCE-JPI project ID: 77; Italian Ministry of Research

MUR DM 2521 dated 12/12/2019).

Skills acquired:

- **Phenotyping** of plant morphology and architecture traits: beside the most **relevant agronomic traits** (i.e. plant height, tiller number, leaf size and number, yield). I developed expertise in **image-based phenotyping** to measure **culm morphology** traits (sample collection and processing, acquisition of data)
- **Greenhouse and field management**: experimental design, sowing and collection of phenotypic data.
- Phenotypic and molecular characterization of both **induced** and **natural allelic variation** for culm morphology and other agronomic traits in barley
- **Statistical analyses** of genotypic and phenotypic data (data manipulation and quality check, ANOVA and linear models, data visualization, **single- and multi-locus GWAS**.
- **Genotyping**: **Sanger sequencing results** (primer design and optimization, PCR reaction and analysis of the results), **High Resolution Melting (HRM) Analysis** (primer design and optimization for SNP genotyping, PCR reaction optimization, processing melt curve profiles with HRM software), **High-throughput SNP genotyping (**downstream data quality check using SAS).
- Improved use of **genomic, protein and transcript databases**, **sequence analysis tools**, **comparative genomics tools** and **phylogenetic analyses** for candidate gene identification
- Time and resource management, teamwork coordination
- Communication skills
- Public speaking

March 2022 - September 2022 (7 months)

Visiting PhD Student at Martin Luther University Halle Wittenberg, Halle, Germany

During my stay in Halle, I carried out a field trial of two **segregating populations** developed in my PhD. I took care of the plants in the field and collected phenotypic data for flowering time, plant height, tiller number. In addition, internode samples to **measure culm-related traits** were collected. In parallel, I received basic training on SAS programming to handle big datasets in order to evaluate both genotypic and phenotypic data and to set up preliminary **QTL analyses.**

Host professor: Dr. Klaus Pillen; Supervisor: Dr. Andreas Maurer

Funding: I was awarded the Traineeship mobility grant Erasmus+ 2021/22 (II ED. Internship number 28) for 6 months.

Skills acquired:

- Management and analysis of big genotype and phenotype datasets to perform **QTL mapping** and **GWAS**
- Basic understanding of **SAS programming** language
- Improved skills on using **R** to build genetic maps

- Monitoring and management of large field trial
- Improved organization skills for **phenotypic data collection** from large experiments
- Improved ability in coordinating **teamwork** and communication skills

October 2018 – March 2019 (5 months)

Visiting research fellow at Faculty of Agriculture, Niigata University, Niigata, Japan

Topic: “Cellular localization of SWEET sugar transporters in barley”

During this period, the research activity addressed the cellular localization of two barley SWEET proteins involved in sugar transport through transient gene expression of the selected genes in barley protoplasts and onion cells and Agrobacterium-mediated transient transformation of *Nicotiana benthamiana*’s leaf tissues.

Host professor: Dr. Toshiaki Mitsui, Supervisor: Dr Marouane Baslam

Funding: project H2020- MSCA-RISE ExpoSEED (Exploring the molecular control of seed yield in crops) funded under EXCELLENT SCIENCE - Marie Skłodowska-Curie Actions (Grant agreement ID: 691109)

Skills acquired:

- Gateway construct preparation for **cellular localization**
- **Barley protoplast isolation**
- **Particle bombardment** of barley protoplasts and onion cells
- Improved use of laser-scanning **confocal microscopy**

April 2018 – September 2018 (6 months)

Visiting research fellow at LANGEBIO (Laboratorio Nacional de Genómica para la Biodiversidad), Irapuato, Mexico

Topic: “Immunolocalization assays to study cytokinin distribution during wheat inflorescence development”

During this period, I’ve been involved in experiments focused on understanding Cytokinins distribution during floral formation in *Arabidopsis thaliana* and durum wheat by performing immunolocalization assays on both inflorescence and roots.

Host professor: Dr. Stefan de Folter

Funding: project H2020- MSCA-RISE ExpoSEED (Exploring the molecular control of seed yield in crops) funded under EXCELLENT SCIENCE - Marie Skłodowska-Curie Actions (Grant agreement ID: 691109)

Skills acquired:

- Dissection, tissue embedding and sectioning of wheat shoot apex at different developmental stages.
- **Hormone Immunlocalization** assay
- Basic use of laser-scanning **confocal microscopy**

Apr 2018 - Mar 2019 (1 year)

Research fellow at CREA - Research Centre for Genomics and Bioinformatics

During this period, I implemented two research secondments planned within the H2020-RISE-MSCA-ExpoSEED project (See above sections "April 2018 – September 2018" and "October 2018 – March 2019"

Supervisor: Dr Raffaella Battaglia

November 2017 - March 2018 (5 months)

Research activity at CREA - Research Centre for Genomics and Bioinformatics

I carried out the construction of RNA-Guided Genome-Editing Vectors to knockout the function of two target *SWEET* genes in barley selected during my Master thesis project.

Supervisor: Dr Raffaella Battaglia

October 2016 - October 2017 (1 year)

Trainee student at CREA Research Centre for Genomics and Bioinformatics

Master thesis project aimed to the identification and functional characterization of the *SWEET* family genes in barley (see below section)

Supervisor: Dr Raffaella Battaglia

Funding: project H2020- MSCA-RISE ExpoSEED (Exploring the molecular control of seed yield in crops) funded under EXCELLENT SCIENCE - Marie Skłodowska-Curie Actions (Grant agreement ID: 691109)

Skills acquired:

- Genomic, protein and transcript **online databases searches** for gene family identification
- **Dissection** of barley shoot and inflorescence apex
- Detailed **expression profile studies** of *SWEET* genes at different developmental stages
- Molecular biology techniques: Nucleic acid extraction, agarose gel quantification and visualization, primer design, PCR, **qRT-PCR**, (primer design and optimization, RNA extraction, cDNA synthesis, reaction optimization, quantitation and data analysis), cloning for genome editing construct assembly (Golden Gate assembly), restriction enzyme digestion, **Sanger sequencing** (PCR amplification and cleanup, Cycle sequencing, capillary electrophoresis, data analyses)
- Management and **analysis** of nucleic acid and protein **sequences**: GeneRunner, SnapGene, MEGA, Clustal, DnaSP, PopARTe with your other computer skills
- Exploration of **natural allelic variation**

Bioinformatic skills

- **gRNA design** and off-target searches with Cas-Designer and CasOT online tools
- DNA and protein **sequence alignments** and **phylogenetic analysis**
- **Allele mining** using VCFtools, SAMtools, BCFtools and SnpEff
- **Haplotype** network construction using PopART

October 2014 – October 2017

Master of Science in Agricultural and Environmental Biotechnology (BAA)

University of Perugia, Perugia (Italy)

Dissertation: “Identification and functional characterization of *SWEET* genes in barley”

The Master thesis aimed to identify the *SWEET* (*Sugars Will Eventually be Exported Transporters*) gene family in barley and to characterize those genes that were expressed during inflorescence and caryopsis development from a functional point of view. Among the genes that were expressed in the caryopsis, we selected a candidate for the **genome editing** and part of the construct for the editing through CRISPR/Cas9 system was developed. Finally, **allele mining** was carried out to identify SNPs from the exome capture in a range of cultivars, landraces and wild barleys.

Final degree mark: 110/110 *cum laude*

Thesis supervisors: Prof. Daniele Rosellini (University of Perugia), Dr. Raffella Battaglia PhD (CREA Research Centre for Genomics and Bioinformatics)

Graduation date: 23/10/2017

Funding: project H2020- MSCA-RISE ExpoSEED (Exploring the molecular control of seed yield in crops) funded under EXCELLENT SCIENCE - Marie Skłodowska-Curie Actions (Grant agreement ID: 691109)

October 2010 – October 2014

Bachelor of Science in Biotechnology

University of Perugia, Perugia (Italy)

Dissertation: “Molecular characterization of local and ancient pear accessions”

Final degree mark: 103/110

Thesis supervisors: Prof. Emidio Albertini, Dr. Renzo Torricelli

Graduation date: 15/10/2014

Attendance to courses/workshops:

16th – 24th November 2022 (26 hours - 4 CFU/ECTS)

Phenotypic modelling of crop adaptation (lecture/workshop)

Position: PhD student

Organised by PhD school in Agriculture, Environment and Bioenergy (AAB), University of Milano, Italy

Host: Professor Laura Rossini

Held by Professor Daniela Bustos-Korts, Wageningen University, NL

This course focused on how to deal with Genotype by Environment by Management interactions (GxExM) by provided me with general principles experimental design, statistical analysis of single- and multi environment data to quantify sources of phenotypic variation.

Skills acquired:

- Experimental designs and analysis
- GxE concepts and mixed models for GxE

- Linear-bilinear models for GxE

14th-25th June 2021 (36 hours – 6 CFU)

Insights on the plant biosystem: enemies, friends or just biomes (Summer School 2020- 2021)

Position: PhD student

Organised by PhD school in Agriculture, Environment and Bioenergy (AAB), University of Milano, Italy

Hosts: Professor Laura Rossini, Professor Piero A. Bianco, Dr. Alessandro Passera

Held by Professor Davide Bulgarelli, University of Dundee, UK; Professor Sébastien Massart, Liège University, BE

This course focused on plants-microbiome/virome interactions and how their associated aspects (e.g. plant genetics, nutrition, pathology, and biosecurity) can be employed in agriculture to cope with future challenges (climate changes, input reductions, higher production)

Skills acquired:

- Key notions about main descriptors of microbiota composition and ways of studying the plant microbiota
- Key notions about the impact of High Throughput Sequencing (HTS) for future application in plant virology

28th January – 13th February 2019 (24 hours - 4.8 CFU)

Novel strategies to accelerate crop improvement (lecture/workshop)

Position: PhD student

Organised by PhD school in Agriculture, Environment and Bioenergy (AAB), University of Milano, Italy

Host: Professor Laura Rossini

Held by Professor Jose F. Gutierrez-Marcos, University of Warwick, UK; Host: Professor Laura Rossini

This course allowed me to gain knowledge in novel tools for genome assisted breeding in crop species.

Skills acquired:

- Improved knowledge of crop genomics and its relevance to plant breeding
- Critically assess advantages and disadvantages of novel genome editing tools
- Improved communication skills about the analysis of experimental data and evaluate findings

Teaching activity:

October 2019 - June 2023

Tranining/Supervision of undergraduate and master’s students

During my PhD I worked as co-supervisor of three master's students and one bachelor's student
October 2021 – January 2022 (20 hours) **Teaching assistant at the University of Milano, Milano, Italy** During this period, I helped Professor Laura Rossini with 20 hours of training sessions on solution of genetics problems in the frame of the Plant genetics course. Bachelor's degree course: Plant genetics Production and Protection of Plants and Green Areas A.A. 2021/2022
October 2020 – January 2021 (20 hours) **Teaching assistant at the University of Milano, Milano, Italy** During this period, I helped Professor Laura Rossini with 20 hours of training sessions on solution of genetics problems in the frame of the Plant genetics course. Bachelor's degree course: Plant genetics Production and Protection of Plants and Green Areas A.A. 2020/2021

PROJECT ACTIVITY

Year	Project
2019-2022	BARISTA (Advanced tools for breeding BARley for Intensive and SusTainable Agriculture under climate change scenarios) - FACCE-JPI project ID: 77H2020-MSCA-RISE Objectives: deliver new breeding strategies and toolkits for boosting crop improvement to obtain high-yielding varieties suitable to cope with future climatic conditions WP2 Genetic and physiological dissection of traits My contribution: **Candidate genes identification** for TILLING screening WP3 Development of new genotypes My contribution: **Development of two segregating population** from crosses between barley cultivars carrying contrasting alleles for QTLs for culm morphology. WP4 Validation of predictive breeding tools and selection of new genotypes My contribution: • **Phenotypic characterization** of **TILLING** lined carrying allele variants of a selected candidate gene grown under controlled conditions. • Phenotypic characterization of two **segregating population** developed in WP2 for **culm morphology traits** grown under field conditions. Role: PhD student
2016-2019	H2020-MSCA-RISE ExpoSEED (Exploring the molecular control of seed yield in crops) Objectives: dissect the molecular mechanisms controlling yield in Arabidopsis and rice and to transfer the acquired knowledge to selected crops such as wheat and barley.

	My contribution: to identify barley *SWEET* gene family encoding for sugar transporters and to functionally characterize those genes that were expressed during inflorescence and caryopsis development. Role: Master student (2016-2017), Research fellow (2018-2019)

PATENTS

Patent
N/A

CONGRESSES AND SEMINARS

Date	Title	Place
13th - 14th December 2022	BARISTA End-term meeting: **Oral Presentation**	Martin Luther University Halle Wittenberg, Halle, Germany
3rd - 7th July 2022	13th International Barley Genetics Symposium (IBGS13): **Poster Presentation** “Progress towards QTL mapping and identification of mutants for culm-related traits in barley” **Presenting author**	Riga, Latvia
8th April 2022	Kolloquien der Professur für Pflanzenzüchtung. Sommersemester 2022: **Oral Presentation** “Identification and characterization of major QTLs for culm diameter in barley” **Presenting author**	Martin Luther University Halle Wittenberg, Halle, Germany
14th -16th September 2021	LXIV Congress of the Italian Society of Agricultural Genetics (LXIV SIGA) annual congress: **Poster presentation** “Identification and characterization of major QTLs for culm diameter in barley” **Presenting author**	Online
28th - 01st July 2021	Plant Biology Europe 2021 (PBE2021): **Poster presentation** “Identification and characterization of genetic loci for culm diameter in barley” **Presenting author**	Online

PUBLICATIONS

Books

N/A

Articles in reviews

Bretani G., Shaaf S., Tondelli A., Cattivelli L., Delbono S., Waugh R., Thomas W., Russell J., Bull H., Igartua E., Casas A. M., Gracia P., **Rossi R.**, Schulman A. H., Rossini L. *"Multi-environment Genome Wide Association mapping of culm morphology traits in barley"*, Frontiers in Plant Science, 13, 2022, DOI=10.3389/fpls.2022.926277, ISSN=1664-462X

My contribution: candidate gene searches

Congress proceedings

Rossi R., Shaaf S., Gipli V., Nesi F., Tondelli A., Cattivelli L., Salvi S., Rosignoli S., Tamm Ü., Maurer A., Pillen K., Gajecka M., Chmielewska B, Zbieszczyk J., Daszkowska-Golec A., and Rossini L.: *"Progress towards QTL mapping and identification of mutants for culm-related traits in barley"*. 13th International Barley Genetics Symposium (IBGS13), Riga, Latvia, 3rd-7th July 2022. Abstract e-book: https://ibgs.arei.lv/wp-content/uploads/2022/09/Abstracts_E_Book_15_09_2022.pdf

Poster Presentation - 65 (presenting author)

Michelotti V., **Rossi R.**, Crosatti C., Kitajima-Koga A., Colombo M., Cattivelli L., Battaglia R.: *"Sporophytic control of male fertility, the role of the HvSWEET4 gene"*. 13th International Barley Genetics Symposium (IBGS13), Riga, Latvia, 3rd-7th July 2022. Abstract e-book: https://ibgs.arei.lv/wp-content/uploads/2022/09/Abstracts_E_Book_15_09_2022.pdf

Poster Presentation - 61

Rossi R., Shaaf S., Gipli V., Tondelli A., Cattivelli L., Salvi S., Rosignoli S., Daszkowska-Golec A., Gajecka M., Rossini L.: *"Identification and characterization of major QTLs for culm diameter in barley"*. LXIV SIGA Annual Congress, Online, 14th-16th September 2021. ISBN: 978-88-944843-2-8

Poster Communication Abstract - 4.27 (presenting author)

Crosatti C., Michelotti V., Tafuri A., Gazzetti K., **Rossi R.**, Migliorini C., Guerra D., Cattivelli L., Mica E., Battaglia R.: *"Identification and functional characterization of key genes Influencing yield potential in barley"*. LXIV SIGA Annual Congress, Online, 14th-16th September 2021. ISBN: 978-88-944843-2-8

Oral Communication Abstract – 2.04

Rossini L., Ferrario C., Arrighi M., **Rossi R.**, Cornaro L., Beretta V., Caselli F., Zanzani V., Mendes M., Cavalleri A., Shaaf S., Biswas A., Vajani A., Janiak A., Chmielewska B., Battaglia R., Von Korff M., Horner D. S., Gregis V.: *"CLIMBER - Confronting CLIMate change Impacts in BarlEy and Rice"*. LXIV SIGA Annual Congress, Online, 14th-16th September 2021. ISBN: 978-88-944843-2-8

Poster Communication Abstract – 5.21

Rossi R., Shaaf S., Gipli V., Tondelli A., Cattivelli L., Silvio Salvi S., Rosignoli S., Daszkowska-Golec A., Rossini L.: *"Identification and characterization of genetic loci for culm diameter in barley"*. Plant Biology Europe 2021 (PBE2021), Online, 28th-1st July 2021. Abstract e-book: https://pbe2021.streamcloud.it/download/PBE2021-ABSTRACT%20BOOK_12.07.21.pdf

Poster Communication Abstract - 624 (presenting author)

Shaaf S., Bretani G., **Rossi R.,** Tondelli A., Cattivelli L., Delbono S., Waugh R., Thomas B., Russell J., Bull H., Igartua E., Casas A. M., Monteagudo A., Gracia P., Schulman A. H., Rossini L.: *"Genetic architecture of culm morphology involved in barley lodging resistance: multi-environment genome-wide association"*. PBE2021, Online, 28th-1st July 2021. Abstract e-book: https://pbe2021.streamcloud.it/download/PBE2021-ABSTRACT%20BOOK_12.07.21.pdf

Poster Communication Abstract - 586

Rossini L., Ferrario C., **Rossi R.,** Cornaro L., Beretta V.M., Caselli F., Zanzani V., Mendes M., Shaaf S., Biswas A., Vajani A., Janiak A., Chmielewska B., Battaglia R., von Korff M., Horner D.S., Gregis V.: *"CLIMBER - Confronting CLIMate change impacts in BarlEy and Rice"*. PBE2021, Online, 28th-1st July 2021. Abstract e-book: https://pbe2021.streamcloud.it/download/PBE2021-ABSTRACT%20BOOK_12.07.21.pdf

Poster Communication Abstract - 626

Rossi R., Michelotti M., Mica E., Crosatti C., Masiero S., Cornaro L., Baslam M., Tafuri A., Battaglia R.: "*Sugar transport in barley, the role of the SWEET4 gene*". LXIII SIGA Annual Congress, Napoli, Italy, 10th-13th September 2019. ISBN: 978-88-904570-9-8

Oral Communication Abstract – 8.05

Mica E., Michelotti V., Gregori G., Ventrelli C., **Rossi R.**, Cornaro L., Masiero S., Crosatti C., Brunoud G., Battaglia R.: *"Functional dissection of starch turnover during barley inflorescence and seed development"*. LXII SIGA Annual Congress, Verona, Italy, 25th-28th September 2018. ISBN: 978-88-904570-8-1

Poster Communication Abstract – 7.09

Michelotti V., Ventrelli C., **Rossi R.**, Comaro L., Mica E., Crosatti C., Battaglia R.: *"Functional dissection of starch turnover during barley inflorescence formation"*. Second International Barley Mutants Workshop (iBMW2018), Dundee, Scotland, 25th-27th June 2018. Abstract e-book: https://ics.hutton.ac.uk/ibmw2018/

Poster Communication Abstract

Battaglia R., Guerra D., Tondelli A., Comaro L., **Rossi R.,** Bernardi J., Bagnaresi P., Cattivelli L.: *"Towards the molecular dissection of seed yield determination in crops, a comparative approach"*. KAAB International Symposium 2017: "Frontiers in Plant Science and Biotechnology", Niigata, Japan, 25th September 2017.

Oral Communication Abstract

OTHER INFORMATION

Driving License B

Skills:

- **Phenotyping** of morphology, architecture, and yield traits of small- and large-scale experiments by using both classical and image-based methods
- Excellent use of genomic, transcript and protein databases
- Genotyping (PCR-based methods, High-throughput SNP arrays)
- Management and analysis of big genotype and phenotype datasets
- RNA and DNA extraction, cDNA synthesis, Cell Culture, PCR, Real Time PCR, HRM, Sanger sequencing, sequence analysis, protoplasts isolation and transformation, CRISPR/Cas9 mediated genome editing.
- GWAS data analysis, Principal component (PCA), quantitative genetics
- Excellent ability in organizing work and report preparation
- Excellent teamwork and problem-solving
- Tranining/Supervision of undergraduate and master's Students

Programming Languages:

Basic usage of R and SAS

Declarations given in the present curriculum must be considered released according to art. 46 and 47 of DPR n. 445/2000.

The present curriculum does not contain confidential and legal information according to art. 4, paragraph 1, points d) and e) of D.Lgs. 30.06.2003 n. 196.

Please note that CV WILL BE PUBLISHED on the University website and It is recommended that personal and sensitive data should not be included. This template is realized to satisfy the need of publication without personal and sensitive data.

Please DO NOT SIGN this form.

Place and date: ____Milano______, ____03/07/2023___