TO MAGNIFICO RETTORE OF UNIVERSITA' DEGLI STUDI DI MILANO **ID CODE 6459**

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 Rossi

CURRICULUM VITAE

PERSONAL INFORMATION

Surname	Rossi
Name	Roberta

PRESENT OCCUPATION

Appointment	Structure
Assegnista di ricerca (B)	Dipartimento di Scienze Agrarie e Ambientali - Produzione, Territorio, Agroenergia

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)	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)
2019	Borsa di dottorato ministeriale XXXV Ciclo "Agriculture, Environment and Bioenergy (AAB)"
2018	Fellowship at CREA-GB (Research Center for Genomics and Bioinformatics), Fiorenzuola d' Arda (Italy) (1 year)

TRAINING OR RESEARCH ACTIVITY

August 2023 – current (6 month)

Assegno di tipo B

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

Supervisor: Prof. Laura Rossini

I focused on the collection of phenotypic data in barley populations segregating for culm morphology traits.

In parallel, I carried out an **RNA-Seq experiment** to compare transcriptomes of a **TILLING** mutant for a target strigolactone and its background cultivar.

Funding: project RecoBar (Recovering and Exploiting Old and New Barley Diversity for Future-Ready Agriculture) funded by the SusCrop-ERA-NET and FACCE-JPI (project ID: 81)

Skills acquired:

- Manual dissection of root tissues in barley
- Experimental design, sampling strategies, RNA extraction and quality check to set up RNA-Seq experiments

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. Characterization of two major QTLs for barley **culm morphology** traits in two crossing populations. The development of both segregating populations was monitored by **genotyping** and, during the final field trial, **phenotypic data for morphology traits** were collected. Finally, phenotypic and genotypic data were used for a Genome Wide Association Studies (GWAS) analysis for a series of relevant agronomic traits.
2. Genetic analysis of barley morphology traits by **forward** and **reverse screening** of two **TILLING** populations.

(Please see the attached PhD thesis and publications 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 **morphology** and architecture **traits** in **barley** in both greenhouse and field conditions: I developed expertise in measuring many relevant agronomic traits i.e. plant height, tiller number, yield, leaf morphology, culm morphology. I developed skills in image-based phenotyping to measure culm morphology traits.
- Phenotypic and molecular characterization of both induced (i.e. **TILLING populations**) and **natural allelic variation** for morphology and other agronomic traits in barley
- **Genotyping** methods: **Sanger sequencing** (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** (data quality check using SAS software).
- **Management** and **statistical analyses** of genotypic and phenotypic data: data manipulation, quality check, analysis (ANOVA, linear models, GWAS), data visualization. I improved my ability in using **reference sequence databases** (genomic, protein and transcript), **sequence analysis tools** (BLAST, sequence alignments, primer design) 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 time in Halle, I conducted a field trial of the two barley populations developed in my PhD. I collected phenotypic data for flowering time, plant height, tiller number and culm morphology. In addition, I learned how to run 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:

- **Handling and analysis of big genotype and phenotype datasets** to perform QTL mapping and GWAS
- Basic skills of SAS programming language and improved skills on using R
- Overseeing and managing of large field trial
- Improved ability in coordinating **teamwork** and communication skills

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Apr 2018 - Mar 2019 (1 year)

Research fellow at CREA - Research Centre for Genomics and Bioinformatics

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

Supervisor: Dr Raffaella Battaglia

October 2018 – March 2019 (5 months)

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

Topic: "Cellular localization of sugar transporters in barley"

During my stay in Niigata, I carried out the sub-cellular localization of two barley sugars transporters. This was achieved through **transient gene expression** of the target genes in **barley protoplasts** and onion cells, as well as through Agrobacterium-mediated 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:

- **Molecular cloning:** plasmid construct preparation (isolation of target sequences, Gateway cloning method, transformation of competent cells), screening/selection of transformed cells (Colony PCR, Plasmid purification, Sequencing)
- **Protoplast isolation** from barley leaves
- **Particle bombardment** of barley protoplast and onion epidermal tissues for transient gene expression
- Basic use of **laser-scanning confocal microscopy** and downstream **image analyses** (Fiji software)

April 2018 – September 2018 (6 months)

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

Topic: "Cytokinin and Auxin immunolocalization in wheat"

During this period, I've been involved in experiments focused on understanding Cytokinin and Auxin distribution during floral formation in 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:

- Tissue processing: manual dissection, embedding (Technovit 7100) and sectioning of wheat shoot apex at different developmental stages and root tip from germinated seeds.
- To set up an **Immunolocalization assay** with CK and IAA primary antibodies
- Basic use of laser-scanning confocal microscopy and image analysis

November 2017 - March 2018 (5 months)

Research activity at CREA - Research Centre for Genomics and Bioinformatics

In this time, I had the opportunity of carrying on the work started during my Master thesis. I focused on the assembly of RNA-Guided Genome-Editing Vectors to knockout the function of two candidate genes for sugar transporters in barley.

Supervisor: Dr Raffaella Battaglia

October 2016 - October 2017 (1 year)

Trainee student at CREA Research Centre for Genomics and Bioinformatics

The Master thesis project aimed at identifying and functionally characterize the *SWEET* gene family 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:

- **Databases searches** (genomic, protein and transcript), **sequence analysis** (BLAST, sequence alignments) and **phylogenetic analyses** for gene family identification
- **Manual dissection** of barley shoots and inflorescence apex at different developmental stages
- Detailed **gene expression analyses** of *SWEET* genes
- Molecular biology techniques: Nucleic acid extraction, agarose gel quantification and visualization, PCR and **qRT-PCR** (primer design and optimization, RNA extraction, cDNA synthesis, reaction optimization, quantitation, and data analysis), **genome editing** (target site searches for guide RNA, off-target sites prediction, construct assembly through Golden Gate method), screening and selection of transformed competent cells (restriction enzyme digestion, Sanger sequencing)

- Management and analysis of nucleic acid and protein sequences: GeneRunner, SnapGene, MEGA, Clustal, DnaSP, PopART
- Exploration of **natural allelic variation** (SNP searches using in-house scripts and databases, effect prediction using SIFT sequence, haplotype network construction using PopART software)

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 their **expression profile** at different developmental stages. In addition, we selected a candidate gene to target through **CRISPR/Cas9 system** and part of the construct was developed. Finally, **allele mining** was carried out to identify SNPs 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:

25th – 26th January 2024

Genomica: tecnologie avanzate (workshop)

Organised by Federazione Italiana Scienze della Vita (FISV)

The objective of the course was to provide a detailed overview of genomic technologies and their applications: Sequencing strategies, Whole Genome Sequencing (WGS) and targeted resequencing, Genome and Pangenome assembly, GWAS, **Transcriptome analyses**, Epigenetics.

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) and provided me with general principles of 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 activities:

October 2019 – current

Training/Supervision of undergraduate and master's students

During my PhD and my postdoc, I worked as co-supervisor of four 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
2023-2023	RecoBar - FACCE-JPI project ID: 81 Objectives: Harnessing barley diversity to expand the crop genetic base Role: Assegnista di tipo B
2019-2022	BARISTA - FACCE-JPI project ID: 77 Objectives: deliver new breeding strategies and toolkits for boosting crop improvement to obtain high-yielding varieties suitable to cope with future climatic conditions My contributions: Candidate genes identification for **TILLING screening**, Phenotypic characterization of TILLING line carrying allele variants of a selected candidate gene grown under controlled conditions, **Development and characterization of two segregating populations** from crosses between barley cultivars carrying contrasting alleles for QTLs for culm morphology.

	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
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 My contribution: candidate gene searches

Congress proceedings
Gipli V., **Rossi R.**, Shaaf S., Nesi F., Maurer A., Pillen K., Daszkowska-Golec A., Gruszka D., Chmielewska B., Gajecka M., Zbieszczyk J., Rosignoli S., Salvi S., Cattivelli L., Rossini L.: *"Forward and reverse genetics analyses of culm morphology in barley (Horedum vulgare* L.*)"*. LXVI SIGA Annual Congress, Online, 5th-8th September 2023. ISBN: 978-88-944843-4-2 **Poster Communication Abstract - 2.20**
Michelotti V., **Rossi R.**, Crosatti C., Mica E., Guerra D., Colombo M., Masiero S., Radchuk V., Cattivelli L., Battaglia R.: *"Sporophytic control of male fertility, the role of the sweet4 gene in barley"*. LXVI SIGA Annual Congress, Online, 5th-8th September 2023. ISBN: 978-88-944843-4-2 **Oral Communication Abstract - 3.01**
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, qRT-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
- Use of TILLING populations for reverse and forward genetics

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__________, ___26/02/2024____