HOW TO TRANSLATE ERICKSON'S UTILIZATION PRINCIPLE INTO TERMS OF CHRONO-BIO-GENOMICS IN ORDER TO OBTAIN EPIGENETIC EFFECTS BOTH IN PSYCHOTHERAPY AND WITH BREAST CANCER PATIENTS

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Disclaimer

Materials that are included in this course may include interventions and modalities that are beyond the authorized practice of mental health professionals. As a licensed professional, you are responsible for reviewing the scope of practice, including activities that are defined in law as beyond the boundaries of practice in accordance with and in compliance with your professional standards.

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Today's objectives

This short course is divided into two parts. In the first, we are going to:

- Explain how to translate the Ericksonian Utilization principle into terms of chrono-bio-genomics
- Demonstrate that the change produced by Ericksonian therapies integrated with chrono-bio-genomics is so deep that it has epigenetic effects
- Define how the MBT-T method activates the genes associated with a reduction in inflammatory processes and with the strengthening of the immune system

In the second part, we are going to give a clinical demonstration that will involve the whole audience.

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- Today we are going to explain how the MBT-T method activates a mind-body-gene therapeutic transformation.
- The innovative quality of MBT-T lies in its capacity – in a single session – to reduce stress, induce epigenetic effects and activate the genes associated with a reduction in inflammatory processes and with the strengthening of the immune system (Cozzolino et al. 2017).
- Among the advantages of MBT-T is the possibility to obtain these results even in medium sized and/or large groups.

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Erickson's Utilization principle

"Utilization" is utilizing whatever response a client offers the therapist in a positive way

It is a **mind set** allowing an expert therapist to utilize anything they can to induce change

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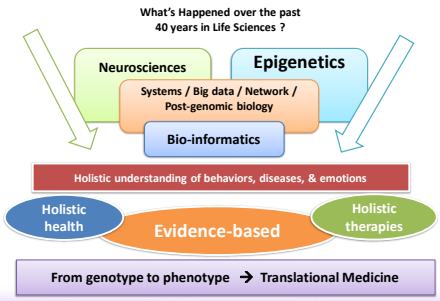

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The Utilization principle

- The Utilization principle lies at the basis of Erickson's amazing ability to facilitate the natural self-healing, growth and evolution processes that every patient possesses inside.
- To date, only few therapists have integrated the chro-bio-genomic dimensions that are inherent in the Utilization principle, in their clinical practice.

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Erickson's Utilization Principle into Terms of Chrono-Bio-Genomics

- For some time now, our research group has been working along this path to develop (Rossi et al., 2006) the possible chrono-bio-genomic implications (Cozzolino, & Celia, 2015) and translate them into therapeutic practice.

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Erickson's Utilization Principle into Terms of Chrono-Bio-Genomics

- Research in this field demonstrates that the experience of novel environmental situations and exercise promotes such benefits as activity and experience-dependent gene expression, brain plasticity and stem cell healing processes (Atkinson et al., 2010; Rossi, 2002; Rossi, Cozzolino, Mortimer, Atkinson, & Rossi, 2011; Rossi & Rossi, 2006) as well as the genome capacity to quickly respond to individuals' psychosocial experiences.

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Erickson's Utilization Principle into Terms of Chrono-Bio-Genomics

- There is a growing need for mind-body methods to allow the mind-body-gene dialogue to be used to its full potential.
- The psychosocial genomics theoretical paradigm of hypnosis encompasses a clinical method called mind-body transformations therapy (MBT-T), which is included among mind-body therapies and applies to both group and individual sessions.

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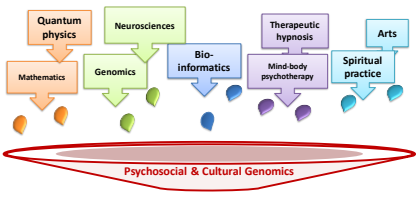
Psychosocial & Cultural Genomics (Rossi, 2002) (3)



A half-century long evidence-based growth

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The Psychosocial Genomics As Theoretical Model

The Psychosocial Genomics (Rossi, 2002) introduces a new foundation of mind-body medicine, based on the study of the processes by which psychological and social experiences may influence gene expression (genomics) and protein synthesis (proteomics) contributing to improve health and quality of life.

It proposes a holistic perspective of the individual considering at the same time physical, psychological and genomic aspects of health and disease in order to promote a mind-body integrated approach where scientific research is translated into effective clinical interventions.

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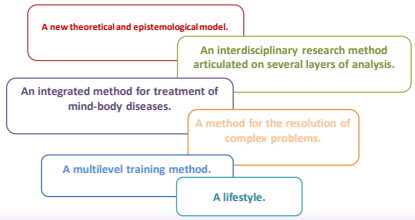
Multiple Implications of Psychosocial & Cultural Genomics



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Erickson's Utilization Principle into Terms of Chrono-Bio-Genomics

- These aspects have been integrated in a specific treatment method called MBT-T (Rossi et al., 2010)
- MBT-T is based on the utilization of the 4-stage creative process (Rossi, 2008), ultradian rhythms, the basic rest-activity cycle (BRAC; Rossi, 1992), the neuronal and biological plasticity, and the relaxation response (RR; Benson, Beary, & Carol, 1974).

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Mind-Body Transformation Therapy (MBT-T)
Previously
Creative Psychosocial Genomic Healing Experience (CPGHE)

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Mind-Body Transformation Therapy (MBT-T)

- MBT-T moves from a naturalistic perspective of hypnosis, and is founded upon the "utilization" of our natural biological rhythms to set the best conditions to activate inner mind-body healing processes to cope with the challenges our organism can be faced with (Cozzolino et al., 2014; Rossi, Iannotti, Cozzolino, Castiglione, Cicatelli, & Rossi, 2008; Rossi et al., 2010; Rossi et al., 2011).

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The Mind-body trasformations therapy (MBT-T)

- Like other types of hypnosis, MBT-T can be used to induce analgesia and anesthesia, stimulate human resilience, promote wellbeing, problem-solving capacity, effective coping and self-empowerment.
- Importantly, MBT-T allows us to make an important contribution to the dialogue between psychosocial genomics-oriented hypnosis and anesthesia (Rossi et al., 2006; Rossi et al., 2011, Cozzolino et al., 2019 in press).

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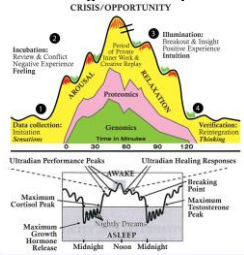
Wave Nature of 4-Stage Creative Cycle



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Human Brain-Hand Communication

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THE INTERNATIONAL PSYCHOSOCIAL GENOMIC TEAM
-THE RESEARCH-

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ABOUT US

THE INTERNATIONAL PSYCHOSOCIAL GENOMIC TEAM

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PSG-Lab

Laboratory of Clinical and Experimental Research on Psycho-Social Genomics, Translational Neuroscience and Hypnosis (PSG-LAB "Ernest Rossi")

Scientific Director
Professor Mauro Cozzolino

University of Salerno (Italy)

https://sites.google.com/a/unisa.it/psg-lab/home

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PSG-LAB

- Founded in 2012 and located within the Department of Humanities, Philosophy and Education at the University of Salerno, the PSG-Lab does research, training and intervention in the fields of Neuroscience, Hypnosis, neuroscientific oriented Psychotherapy and mind-body communication, with special regard to the relationship between psychological experience and gene expression.
- PSG-Lab has achieved worldwide excellence with its clinical and experimental research on the mind-gene relationship.
- The Lab also carries out transdisciplinary, translational and international research and intervention projects on a regular basis in collaboration with universities, research bodies and public and private institutions with a view to promoting psychosocial wellbeing and mind-body health.
- Currently underway is collaboration with the National Cancer Institute of Naples, Italy (Istituto Nazionale Tumori Pascale di Napoli), IGB-CNR (Naples, Italy), Biogem (Ariano Irpino, Italy), Scuola di Specializzazione in Psicoterapia Seraphicum (Rome), The Milton Erickson Foundation (Phoenix, USA), The Psychosocial Genomics Institute (USA), The European Society of Hypnosis, The World Society of Hypnosis, Neuropsychotherapist Network (Australia), Rochester University (USA), Sarvasumana Association, (India), World Association of Psychosocial Genomics (www.psychosocialgenomics.com).

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Therapeutic Hypnosis and Psychotherapy Modulate Gene Expression in Human Leukocytes

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First Pilot Study (2008) [4]

Objective :
Utilize DNA microarrays + bioinformatics software to explore the molecular-genomic basis of therapeutic hypnosis.

Hypothesis:
Therapeutic hypnosis would be related to the expression of immediate-early and experience-dependent genes associated with novel stimuli, growth, brain plasticity, and psycho-neuro-immunology.

A Pilot Study of Positive Expectations and Focused Attention via a New Protocol for Optimizing Therapeutic Hypnosis and Psychotherapy Assessed with DNA Microarrays: The Creative Psychosocial Genomic Healing Experience

Ernest Rossi[1], Salvatore Iannotti[2], Mauro Cozzolino[3], Stefano Castiglione[4], Angela Cicatelli[5], Kathryn Rossi[6]

Results:
Assessed with DNA microarrays, we documented changes in the expression of 15 genes within one hour, and subsequent change in the expression of 77 genes 24 hours after a single intervention of MBT-T.

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Extending our Pilot Study

Objective:
Expanded analyses on our pilot study to further assess the hypothesis that **therapeutic hypnosis is associated with measurable, meaningful changes in gene expression**.

Protocol:
3 human subjects experienced a single session of therapeutic hypnosis conducted via our MBT-T protocol.

Method:
DNA microarrays assessed the expression of **15,508 genes** from each subject's leukocyte RNA immediately prior to, **1 hour after**, and **24 hours after** the session.

A New Bioinformatics Paradigm for the Theory, Research, and Practice of Therapeutic Hypnosis

David Aikawa[1], Salvatore Iannotti[2], Mauro Cozzolino[3], Stefano Castiglione[4], Angela Cicatelli[5], Bhaskar Vyas[6], Jane Mortimer[6], Richard Hill[7], Linka Clovance[8], Aksaia Chamberlain[9], Jorge Cuadros[10], Claude Virot[11], Michel Kennaz[12], Thierry Kalfass[13], Stanley Krippner[14], Claire Frederick[15], Ernest Gregory[16], Michael Shaffran[17], Margaret Bullock[18], Ella Solomany[19], April Cybelle Rossi[20], Kathryn Rossi[21], Ernest Rossi[22]

Using **Gene Set Enrichment Analysis** (GSEA), a publicly available software tool (http://www.broadinstitute.org/gsea/index.jsp), we examined 15,508 genes for functionally meaningful up-regulation or down-regulation of **established cellular pathways and biological processes**.

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General Conclusion from 2008 Pilot Study

A single session of therapeutic hypnosis, utilizing the MBT-T protocol (previously CPGHE), is associated with a positive changes in experience-dependent gene expression.

- Stem Cell Activation
- Reduced inflammation
- Reduced cellular stress

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The Second Study [5]

Hypothesis:
changes in gene expression over relatively brief time periods (1 hour and 24 hours) following a single intervention of MBT-T protocol.

Sample:
18 individuals (9 females and 9 males) aged from 30 to 50 years.

Objective :
- confirm our previous pilot study.
- Give further evidence to the hypothesis that MBT-T could modulate gene expression in human white blood cells .
- Contribute to the development of a new mind-body treatment model which integrate scientific evidence for facilitating therapeutic approaches to stress related dysfunctions in psychiatry, psychology and rehabilitation.

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The Second Study: Materials & Methods

All the subjects underwent the MBT-T (previously CPGHE) protocol

Approximately 10 ml of peripheral blood was collected from the 18 volunteers just before (condition A), one hour (condition B) and 24 hours (condition C) after the MBT-T session.

A DNA microarray data analysis of the white blood cells of the subjects was performed and then a Real-time quantitative RT-PCR analysis was carried out on a subset of 11 genes in order to validate the microarray analysis

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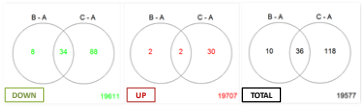
Differential Gene Expression Analyses



The Venn diagrams illustrate the intersection among different expressed genes identified in the comparisons (condition B or C vs. A).

Among the 200 differentially expressed genes identified in this study, 34 genes were down-, and 2 up-regulated at both conditions

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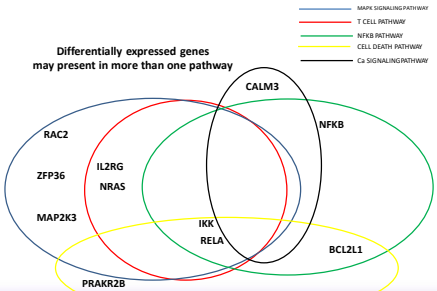

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What do these functional pathways mean ?

MRPK	External signals, cellular responses, incl. **growth, differentiation, inflammation** and **apoptosis.** crucial during neuronal maturation and plasticity, ultimately, to **learning** and **memory**
NF-kB	Rapid regulation of **innate immune response**, **inflammation** and **anti-apoptotic** and **development** processes. Inflammatory cytokines, chemokines and NF-kB in a positive feedback mechanism, if aberrantly active, may lead to **inflammatory diseases, neurological and psychiatric conditions, and neurodeneratvie diseases.**
Ca SIGNALING	Spatial and temporal signals, control processes of **proliferation, development, learning** and **memory**. Responding to antigens through increased proliferation. **Ca2+/CALM3** signaling pathway reported as having an important role the **etiopathogenesis of the AD.**
CELL DEATH	Four genes (**BCL2L1, PRKAR2B, IKBKG=NEMO, RELA**) playing important roles in the **regulation of the life cycle of leukocytes**.
T-CELL SIGNALING	Key role in the **immune system**. **R-Cell receptors**: T-cell activation, formation of immunological synapses in response to antigen exposure.

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The Third Study: the Epigenetic Response to a Mind-Body Treatment

- We conducted another pilot study on epigenetic response to a mind-body treatment using DNA microarray technology to show the involvement of the stress response pathways both in the case of disease and stress and as an effect of mind-body therapies.
- DNA samples were obtained from 20 individuals who experienced a mind-body therapeutic protocol (MBT-T), were analyzed from the bio-molecular point of view by means of an epigenetic marker (MSAP molecular tool), in order to estimate the different status of methylation. The subjects were compared at 3 different times: prior to, 1 hour after, and 24 hours after the treatment.

Cozzolino, M., Guarino, F., Castiglione, S., Cicatelli, A., Celia, G. (2017). Pilot Study on Epigenetic Response to a Mind-Body Treatment. *Translational Medicine @ unisa*, 17(7), 40-44.

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Pilot Study on Epigenetic Response to a Mind-Body Treatment

- The molecular data were processed through different biostatistics approaches: the Bayesian statistics approach, in order to estimate the clustering membership of the subjects (Structure), and the statistical estimation of the DNA methylation level (MSAP statistical tool).
- The structure analysis revealed that the clusters and their membership changed among the three time points moving from higher heterogeneous distribution to higher homogeneous clusters.

Cozzolino, M., Guarino, F., Castiglione, S., Cicatelli, A., Celia, G. (2017). Pilot Study on Epigenetic Response to a Mind-Body Treatment. *Translational Medicine @ unisa*, 17(7), 40-44.

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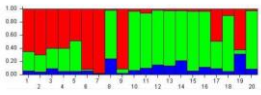
Evaluation of epigenetic state At three different times: MSAP tool

- Before the treatment (time A), the subjects' epigenetic profiles were heterogeneous.



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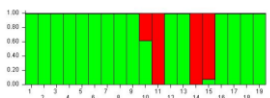
Evaluation of epigenetic state At three different times: MSAP tool

- At time B (an hour after treatment) we found that epigenetic profiles were converging to more homogeneous DNA methylation status.



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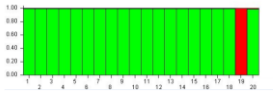
Evaluation of epigenetic state At three different times: MSAP tool

- At time C (24 hours after treatment), epigenetic state of all but subject 19 could be grouped into a single meta-population.



Cozzolino, M., Guarino, F., Castiglione, S., Cicatelli, A., Celia, G. (2017). Pilot Study on Epigenetic Response to a Mind-Body Treatment. *Translational Medicine @ unisa*, *17*(7), 40-44.

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Pilot Study on Epigenetic Response to a Mind-Body Treatment - Results

- Results showed that 1 hour after and 24 hours after the MBT-T treatment the number of meta-populations decreased from three to two.
- Moreover, the membership was more homogeneous at time C than at time B.
- In fact, before the treatment the subjects' epigenetic profiles were heterogeneous whereas after the mind-body treatment we found that the epigenetic profiles converged toward a homogeneous DNA methylation status.
- Regarding the DNA methylation level, we observed that after the treatment the double strand methylation of inner cytosine or hemi-methylation of inner cytosine was the most abundant DNA methylations status.
- These results suggest that the DNA epigenetic status of the subjects was affected by the MBT-T treatment.

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An ongoing study: Psychosocial Genomics Research Program in Oncology (PSGPO)

- PSGPO aims to integrate psychological and biomedical knowledge on the basis of neuroscientific findings, genomic research and mind-body medicine to explore if a new mind-body therapeutic approach can improve quality of life of patients at risk of cancer relapse after the completion of locoregional treatment and adjuvant chemotherapy.
- To achieve this objective we are currently conducting a randomized clinical trial at Istituto Nazionale Tumori Pascale di Napoli (The National Cancer Hospital of Naples, Italy)
- **The study is still on-going, but we have made preliminary analyses of part of the psychological and genomic data, which we are going to present today**

The Psychological part of the study is being conducted by: Mauro Cozzolino, Francesco De Falco, Daniela Barberio, Valentina Abate, Giovanna Celia, Laura Girelli, Deborah Vivo

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Psychosocial Genomics Research Program in Oncology (PSGPO) Objectives

- validate the effectiveness of an innovative therapeutic strategy in improving the quality of life and therapeutic outcome of cancer patients in terms of improvement of physical and psychological well-being
- translate the most recent findings in the field of neuroscience, genomic research and mind-body medicine into cancer clinical practice through the conduct of a randomized clinical trial that aims to demonstrate the greater effectiveness and sustainability of a particular mind-body approach (Mind-Body Trasformations Therapy – MBT-T) compared to traditional approaches
- understand the determinants of the therapeutic outcome through the study of the genome that can clarify the molecular mechanisms underlying the clinical efficacy of our MBT-T approach on cancer patients

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Psychosocial Genomics Research Program in Oncology (PSGPO) Study Design and Participants

- The study is an interventional, non pharmacological, open-label, randomized study on patients with non metastatic breast cancer, involved in a follow-up procedure to experimentally validate the genomic and epigenetic effects of innovative mind-body therapy (MBT-T).
- The study is being carried out on 90 subjects with the same characteristics in terms of age, gender, education level, stage of disease. The sample will be recruited at the end of the standard adjuvant treatments (surgery, chemotherapy, radiotherapy) after an interview with the reference oncologist and psychologist.
- The 90 patients will be randomized into two arms:
  - A: standard follow-up (control arm) - The control arm consists of patients with the same characteristics as the subjects in the experimental group except for undergoing only the standard follow-up procedure (as decided by the reference oncologist).
  - B: standard follow-up + MBT-T (experimental arm)- In this arm there are patients who are undergoing the standard follow up procedure according to the reference oncologist with the addition of a biweekly psychological treatment (MBT-T) for a duration of 4 months (8 sessions in total).
- The therapy is organized in a 90-120 minutes group sessions.

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Psychosocial Genomics Research Program in Oncology (PSGPO) Materials and Procedures

- All the patients are being assessed before and after the first clinical intervention through psychological and genomic indicators.
- Patients are requested to provide 6/8 ml blood sample before (T0) and after the clinical session (T1) in order to evaluate the expression of the relevant genes and their pathways through molecular biology and bioinformatics procedures.
- Afterwards, the same blood sample are being collected after two months from the first clinical session (T2), at the end of the treatment (T3) and after 6 months (T4).

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Psychosocial Genomics Research Program in Oncology (PSGPO)
Psychological Assessment Instruments

- The CORE-10 is a brief outcome measure comprising 10 items drawn from the CORE-OM, which is a 34-item assessment and outcome measure. The CORE-10 has been designed to tap into a pan-theoretical 'core' of users' distress, including commonly experienced symptoms of anxiety and depression and associated aspects of life and social functioning. In addition, there is a key item on risk to self.
- The Hospital Anxiety Depression Scale (HADS) is a self-assessment questionnaire developed to detect states of depression and anxiety in a general medical population of patients. The questionnaire comprises two scales including seven questions for anxiety and seven questions for depression.

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Psychosocial Genomics Research Program in Oncology (PSGPO)
Psychological Data Analysis

- It is important to highlight that the study is still ongoing and the preliminary results are related to a very small number of subjects (<15 for each group)
- A 2X2 mixed factors anova (within/between subjects) was conducted.
- The analyses were performed using IBM SPSS V.
- The preliminary results of the mixed analysis of variance (anova)of CORE-10 and HADS will be shown next.

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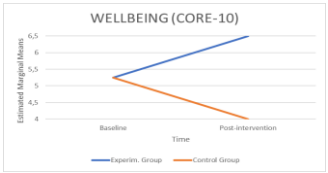
Preliminary results: mean differences in wellbeing

No statistically significant interaction effects were found in well-being ($F = 1.302$; $p = .287$).

However, results indicate that the experimental group, as compared to the control group, showed an increase in wellbeing as measured by CORE-10.

This interaction effect is in line with the research hypothesis.



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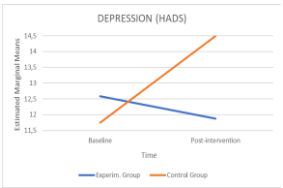
Preliminary results: mean differences in levels of anxiety and depression

No statistically significant interaction effects were found in depression ($F = 1.948$; $p = .188$).

However, results indicate that the experimental group, as compared to the control group, showed a reduction in depression as measured by HADS.

This interaction effect is in line with the research hypothesis.



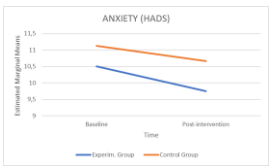
46

Preliminary results: mean differences in levels of anxiety and depression

No statistically significant interaction effects were found in anxiety ($F = 1.470$; $p = .249$).

However, results indicate that the experimental group, as compared to the control group, showed a greater reduction in anxiety as measured by HADS.

This interaction effect is in line with the research hypothesis.



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Preliminary Conclusions of Psychological Assessment

- The preliminary results of the psychological assessment of wellbeing, depression, and anxiety indicate that the experimental group, as compared to the control group, showed an increase in wellbeing as measured by CORE-10 and a reduction in depression and anxiety, as measured by HADS.
- This interaction effect is in line with the research hypothesis.
- The fact that the results are not statistically significant is probably due to the small sample size (<15 subjects per group)
- Data from a greater number of patients are currently being collected and we will be able to present the final results in the next few months.

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Psychosocial Genomics Research Program in Oncology (PSGPO) Genomic Assessment Instruments

- The levels of different cytokines, chemokines, and growth factors were evaluated in sera of patients by the multiplex biometric ELISA-based immunoassay, containing dyed microspheres conjugated with a monoclonal antibody highly specific for a target protein.
- Protein levels were determined using a Bio-Plex array reader (Luminex, Austin, TX, USA) that quantifies multiplex immunoassays in a 96-well format with very small fluid volumes.
- The analysis level was calculated using a standard curve, with software provided by the manufacturer (Bio-Plex Manager Software).

The Genomic part of the study is being conducted by: Mauro Cozzolino, Michele De Laurentiis, Michela Piezzo, Stefania Cocco, Alfredo Baudillon, Susan Costantini, Stefano Castiglione, Francesco Guarino, Angela Cicatelli, Alessandra Calabrese, and Gabriele Madonna.

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The importance of Cytokines and Chemokines

- Cytokines and chemokines are small proteins that play a role in cell-to-cell communication by paracrine or autocrine signaling.
- They were thought to induce immune responses to foreign threats or inflammation and play prominent roles in human biology and diseases (Commins et al. 2010)
- Several studies have showed that the dynamics of cross talk between immune system and cancer cells mediated by cytokines and chemokines changes during cancer initiation, progression, and therapeutic interventions.
- Indeed, tumor-secreted cytokines and chemokines play a key role to shape tumor microenvironment and promote metastasis by facilitating tumor dissemination, motility and invasion (Hanahan et al. 2011).

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Preliminary Genomic Results

- The score plot in figure 1 (below) shows the behavior of cytokines at the three time points and their evolution during the observational period: the levels of pro-inflammatory cytokines tend not to increase over time.
- In contrast, score plot in figure 2 (below) shows the behavior of cytokines in control group, indicating an increase in pro-inflammatory cytokines over time.
- Since the baseline profiles of the two groups are comparable, as shown in fig. 1 and 2, the trend observed in our results leads us to suppose that the MBT intervention is able to modulate the cytokinome profile in favor of a low-inflammatory profile (red dots have the same behavior in the space because the study is randomized -> randomization allows to reduce differences in groups so that the effect of confounders can be neglected)

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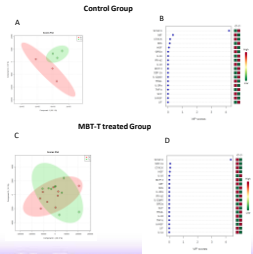
Preliminary Genomic Results - Figure 1

Score plot (A, C) and loading plot (B, D) on cytokines profiling evaluated on sera from Breast Cancer Patients enrolled in the randomized MBT-T study during follow-up after curative treatments, at baseline (T0) and 24 h after the first MBT treatment (T1).



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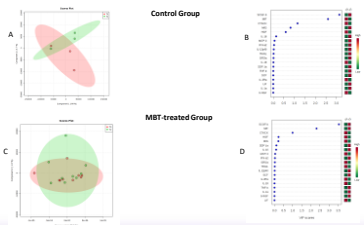
Preliminary Genomic Results - Figure 2

Score plot (A, C) and loading plot (B, D) on cytokines profiling evaluated on sera from Breast Cancer Patients enrolled in the randomized MBT-T study during follow-up after curative treatments, at baseline (T0) ant the end of the MBT treatment (T2).



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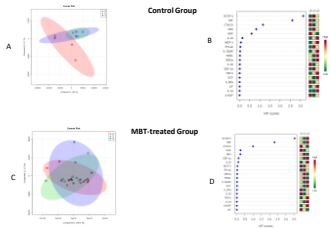
Preliminary Genomic Results - Figure 3

Score plot (A, C) and loading plot (B, D) on cytokines profiling evaluated on sera from Breast Cancer Patients enrolled in the randomized MBT-T study during follow-up after curative treatments, at baseline (T0), 24 h after the first MBT (T1) and the end of the treatment (T2).



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Preliminary Genomic Results

- At time 1, as compared to time 0, the patients who received the MBT-T treatment showed a decrease in SCGF, SDF-1a, MCP3, IL-12p40, and IL-18 cytokines, whereas the control patients (who did not receive the treatment) showed an increase in these cytokines.
- SDF-1a (CXCL12) and MCP3 are two well-known pro-inflammatory chemokines; IL-18 and IL12 are pro-inflammatory as well. SCGF is a growth factor. The decrease shown in these proteins is therefore very interesting.
- At T2, the patients who received the treatement showed a decrease in MIG, MCP3 and GROa cytokines, which increased in control patients. In this case too, MIG(CXCL9), Gro-a(CXCL1), and MCP3 are pro-inflammatory chemokines.

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Preliminary Genomic Results

- IL8 is a proangiogenic cytokine correlate with development of chemoresistance, high stage and mortality while IL-12p40 is able to inhibit the anti-tumor immune response.
- The expression of chemokin SDF-1a is associated with increased invasion, mamosphere formation, metastasis, chemoresistance and angiogenesis.
- MCP3, GROa and MIG are involved in mechanisms of drugs resistance and tumor progression in breast cancer, supporting molecular mechanisms of growing and metastasis of breast cancer cells (King J, et al 2017).
- Stem cell growth factor (SCGF) is a novel cytokine for primitive hematopoietic progenitor cells that could be involved in the survival of cancer stem cells, and, consequently, implicated in the malignant progression in cancer (Ulivi et al. 2004).

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Preliminary Genomic Results

- Our preliminary data show that MBT induce a significant reduction of several pro-inflammatory cytokines and chemokines, involved in mechanisms of drugs resistance and tumor progression in breast cancer (King et al. 2017).
- In particular, the expression of SCGF, SDF-1a, MCP3, IL-12p40 and IL-18 was significantly reduced in sera from patients collected after just 1 MBT (T1) compared to the control group (untreated patients), while the reduction of MIG, MCP3 e GROa was observed at the end of treatment (EOT).
- These results indicate that MBT exert an inflammatory pathway modulation, both in acute and during long period therapy, supporting the prevention of recurrence risk in Breast Cancer Patients.

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Limitations of the Research and Potential Risks

- It is important to highlight that the Psychosocial Genomics Research Program in Oncology (PSGPO) is still ongoing.
- Therefore, all the results shown in this presentation are preliminary and do not allow us to draw any definitive conclusions relating to the subject matter of the study.

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Conclusions

- We explained how to translate the Ericksonian Utilization principle into terms of chrono-bio-genomics
- We demonstrated that the change produced by Ericksonian therapies integrated with chrono-bio-genomics is so deep that it has epigenetic effects
- We defined how the MBT-T method activates the genes associated with a reduction in inflammatory processes and with the strengthening of the immune system

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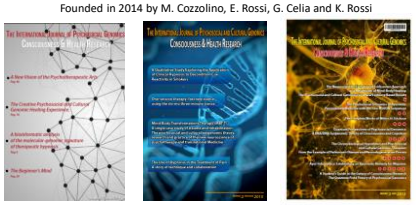
The International Journal of Psychosocial Genomics: Consciousness & Health Research

Founded in 2014 by M. Cozzolino, E. Rossi, G. Celia and K. Rossi



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