فهرست مطالب

برگزار کنندگان

مرکز تحقیقات زیست فناوری کاربردی و مرکز اروپایی پزشکی فردمحور آلمان

حامیان کنگره

- **مرکز مشاوره ژنتیک دکتر مریم اسلامی**
- **شرکت دانش بنیان سینا نوآور ویرا**
- **مرکز پزشکی فرد محور P7 تهران**
- **شرکت سلولهای بنیادی پرنیا**
- **انتشارات تیمورزاده نوین**
- **آزمایشگاه ژنتیک و پاتوبیولوژی پارس ژنوم**
- **شرکت طب بازرگان ایثار**
- **شرکت تحقیقاتی و تولیدی سیناژن**
- **سازمان منطقه آزاد کیش**
- **گروه صنعتی ANG**
- **شرکت سل تک فارمد**
- **پژوهشگاه مرکزی دانشگاه آزاد اسلامی**

رئیس کنگره: پروفسور علیرضا خوشدل، پروفسور کریم نیرنیا

دبیر علمی و اجرایی کنگره: دکتر مریم اسلامی

مراکز همکار

- **مرکز پیشگیری از بیماری های اروپا**
- **آکادمی سلول های بنیادی آلمان**
- **مرکز اروپایی پزشکی فرد محور آلمان**
- **انجمن جراحی پلاستیک و زیبایی ایران**
- **انجمن سلول های بنیادی آلمان**
- **انجمن جراحان مغز و اعصاب ایران**
- **دانشگاه کلن آلمان**
- **انجمن ژنتیک ایران**
- **ستاد سلول های بنیادی دانشگاه علوم پزشکی مشهد**
- **مرکز تحقیقات زیست فناوری و گروه ژنتیک دانشگاه علوم پزشکی آزاد اسلامی تهران**
- **پژوهشگاه مرکزی دانشگاه آزاد اسلامی**
- **انجمن کشت سلول و بافت ایران**
- **بخش بازآموزی وزارت بهداشت و درمان**
- **بخش بازآموزی معاونت علوم پزشکی دانشگاه آزاد اسلامی**

افتخار دریافت امتیاز بازآموزی کنگره برای 29 رشته

تخصصی، فوق تخصصی و علوم پایه با کد شناسه 189368

اعضا کمیته علمی

- دکتر امیر ادهمی اقدم
- دکتر مریم اسلامی
- دکتر ساره اعتماد
- دکتر روزبه باریک بین
- دکتر امیررضا برومند
- دکتر بابک بهنام
- پروفسور جلیل توکل افشاری
- دکتر مسعود خدیوی
- پروفسور علیرضا خوشدل
- دکتر حمیدرضا رحیمی
- پروفسور بیژن رنجبر
- دکتر سجاد سحاب نگاه
- دکترشهرام سواد
- پروفسور داریوش فرهود
- دکترمحمدرضا محمدحسنی
- دکتر امید معمار صادقی
- پروفسور کریم نیرنیا
- پروفسور یوی نیکسدورف
- دکتر بابک نیکو مرام
- پروفسور یورگن هشلر

تهیه و تدوین کتابچه:

- **دکتر مریم اسلامی**
- **زینب فقیه ملک مرزبان**
- **دکتر حانیه فخارباشی زاده**
- **هانیه احمدی**
- **زهرا فقیه ملک مرزبان**

اسامی داوران علمی بخش پوستر

- **دکتر مریم اسلامی**
- **دکتر حانیه باشی زاده فخار**
- **دکتر امیررضا برومند**
- **دکتر نوشین باریک رو**
- **دکتر فاطمه ناجی**
- **دکتر فاطمه روح الله**

سفیران رسانه ای کنگره:

- **کامران نجف زاده**
- **گیتی خامنه**

بخش بازآموزی کنگره: معاونت علوم پزشکی دانشگاه علوم پزشکی آزاد اسلامی تهران

دکتر مهسا هادی پور، مریم سادات کافی

دبیرخانه در محل کنگره: فرشته بخشعلیان، بهزاد اصلانی

اعضا کمیته اجرایی

دکتر کاظم امینی

دکترمجتبی دستوری

دکتر سید علیرضا مکی نژاد

دکتر ابراهیم بلالی

دکتر قاسم بیگ لو

مهندس پروینچی

دکتر حمید جمال الدینی

دکتر محمد مهدی جوکار

مهندس زهرا شیرمحمدی

دکتر فاطمه روح الله

دکتر غلامزاد

دکترمجتبی مالکی

دکترمحمدرضا محمدحسنی

دکتر محمد ناصحی

دکتر مجید نقی پور

دکتر فرشاد هاشمیان

اعضا کمیته اجرایی دانشجویی

دبیر کمیته اجرایی دانشجویی: زینب فقیه ملک مرزبان

دبیرخانه ثبت نام قبل کنگره: غزاله خسروآبادی

واحد روابط عمومی:

- **نسترن دالوند(هماهنگی با سخنرانان)**
- **سیده نادیا محمدی نصرآبادی(مسئول روابط عمومی)**
- **شهرزاد نجفی**
- **پریزاد نجفی**

واحد بین الملل:

- **زینب فقیه ملک مرزبان(مسئول بخش بین الملل)**
- **زهرا فقیه ملک مرزبان(مسئول بخش بین الملل)**
- **دکتر مریم کامی شیرازی(ترجمه داخل سالن)**
- **علی مرادی(ترانسفر بین الملل)**

واحد سمعی و بصری:

- **علی مرادی(مسئول سمعی بصری)**
- **الهه مرادی (عکاسی و فیلمبرداری)**

واحد استقبال و هماهنگی ورود: فاطمه احمدپور

کمیته ثبت نام در محل:

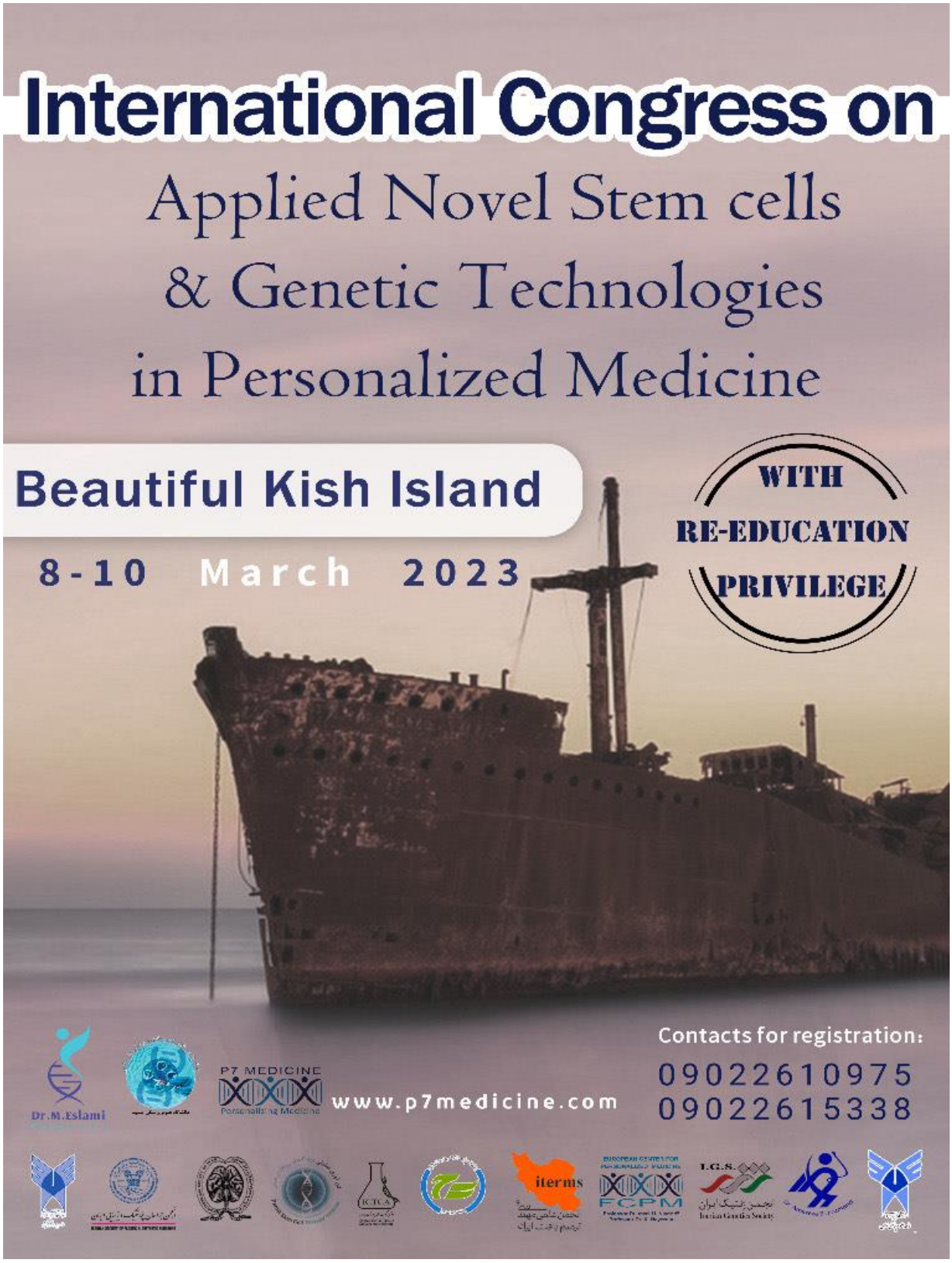
- **پردیس مرادی (ثبت نام در محل امتیاز بازآموزی)**
- **سیده نادیا محمودی نصرآبادی (ثبت نام در محل کنگره و کروز)**
- **مونا معصومی**

واحد نظارت داخل سالن:

- **دلارام حسنی (مسئول بخش نظارت داخل سالن)**
- **سیده نادیا محمودی نصر آبادی(ناظم بخش ابتدایی سالن)**
- **فاطمه حاجی بابایی(ناظم بخش میانی سالن)**
- **نسترن دالوند(ناظم بخش انتهایی سالن)**

واحد تبلیغات کنگره:

- **کیمیا زارع(مسئول بخش تبلیغات)**


International Congress on
Applied Novel Stem cells
& Genetic Technologies
in Personalized Medicine
Beautiful Kish Island
8-10 March 2023
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Dr.M.Eslami
P7 MEDICINE
Personalizing Medicine
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09022615338
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I.G.S.

ساعت	برنامه	نام سخنران
10 – 10:10	افتتاحیه و خوش آمد گویی	ریاست دانشگاه علوم پزشکی (پروفسور علیرضا خوشدل: اپیدمیولوژیست، ریاست کنگره)
10:10 – 10:20	پیشگفتار	دکتر مریم اسلامی(پزشک دکتری تخصصی ژنتیک، فلوشیپ پزشکی بازساختی از دانشگاه هاروارد امریکا: دبیر علمی کنگره)
10:20 – 10:30	مقدمه ای بر پزشکی فردمحور	پرفسور کریم نیرنیا (ریاست مرکز اروپایی پزشکی فردمحور آلمان P7، ریاست آکادمی سلولهای بنیادی آلمان، ریاست کنگره)
10:30 – 11:30	Personalized Cardiovascular Medicine تستهای پزشکی فردمحور در بیماریهای قلبی و عروقی	پرفسور یوی نیکسدورف: پزشک متخصص قلب و عروق ازآلمان (ریاست مرکز پیشگیری از بیماریهای اروپا ریاست مرکز اروپایی پزشکی فردمحور (P7
11:30 – 11:40	پرسش و پاسخ	
11:40 – 12:30	Personalized Cell Medicine کاربردهای سلول درمانی در پزشکی فردمحور	پروفسور یورگن هشلر: پزشک، متخصص نوروفیزیولوژی و سلولهای بنیادی(ریاست انجمن سلولهای بنیادی آلمان، ریاست انستیتو نوروفیزیولوژی دانشگاه کلن آلمان)
12:30 – 12:40	پرسش و پاسخ	
12:40 – 14:00	ناهار و پذیرایی	
14-14:40	Onco Assays & Personalized Medicine شخصی سازی کردن درمان سرطانها (انکواسی)	پروفسور کریم نیرنیا (آلمان) متخصص ژنتیک انسانی:پروفسور سلولهای بنیادی، ناباروری و سرطان
14:50 – 15:20	پزشکی فردمحور و پزشکی بازساختی Personalized Medicine & Regenerative Medicine	دکتر مریم اسلامی (دبیر علمی)

15:20 – 16:00	bFGF Peptide for Vitiligo پپتید bFGFدر بهبود پیسی (ویتیلیگو)	دکتر امید معمار صادقی متخصص ایمونولوژی، متخصص پوست، فوق تخصص جراحی پوست از دانشگاه شیکاگو امریکا
16:00 – 16:20	پذیرایی و ارایه پوسترها	
16:20 – 16:50	کاربرد سلولهای ادیپوز در پزشکی فردمحور Adipose-Derived Stem cells & Personalized medicine	دکتر بابک نیکومرام (ریاست انجمن جراحی پلاستیک ایران)
16:50–17:30	Anti-mitochondrial Therapy: A New Dimention of Personalized Oncology آینده درمانهای فردمحور انکولوژی	دکتر بابک بهنام (پزشک متخصص ژنتیک، فلوشیپ بیوکمیکال ژنتیک بالینی از NIH NSF International امریکا)
17:30 – 18:00	پزشکی فردمحور در تصویربرداری Personalized Imaging	دکتر باریک بین (متخصص رادیولوژی)
18– 19	پانل با حضور سخنرانان روز اول	مدیر پانل: دکتر محمدرضا محمدحسنی؛ فوق تخصص قلب و عروق
19–21	شام و پذیرایی	

نام سخنران	برنامه	ساعت
دکترامیررضا برومند (متخصص مغز و اعصاب، فلوشیپ سلول درمانی از دانشگاه *مونستر* آلمان)	افتتاحیه روز دوم	10 – 10:10
پروفسور کریم نیرنیا (آلمان)	Fertility Assays & Personalized Medicine پزشکی فردمحور و ناباروری و تستهای مرتبط	10:10 – 11:10
	پرسش و پاسخ	11:10 – 11:20
دکترامیررضا برومند	How mesenchymal stem cell therapy effects on neurological diseases اثرات درمانهای فردمحور سلولهای مزانشیمال در بیمارهای مغز و اعصاب	11:20 – 12:20
	پرسش و پاسخ	12:20 – 12:30
	ناهار و پذیرایی	12:30 – 14
پرفسور جلیل توکل افشاری (متخصص ایمونولوژی دانشگاه علوم پزشکی مشهد، فلوشیپ سلول درمانی)	How mesenchymal stem cell therapy would effect on Neuroinflammatory markers in ALS patients اثرات درمانهای فردمحور سلولهای مزانشیمال بر مارکرهای التهابی در بیماران ALS	14:00 –14:30
	پرسش و پاسخ	11:30-14:40
دکتر سجاد سحاب نگاه(دکتری علوم تشریح فلوشیپ سلول درمانی)	The beneficial effects of exosome therapy in the course of traumatic brain injury منافع درمانی اگزوزومها در ضربه مغزی	14:40-15:10
	پرسش و پاسخ	15:10-15:20
پرفسور مسعود خدیوی «دایرکتوری فلوشیپ نورواسپاین» دانشگاه علوم پزشکی تهران، عضو کمیته علمی انجمن جراحان مغز و اعصاب ایران	Personalized medicine in cervical myelopathy پزشکی فردمحور در میلوپاتی سرویکال	15:20-15:40
	پرسش و پاسخ	15:40-15:50

15:50-16:10	Safety & Efficacy of MSC Therapy in ALS امنیت و اثربخشی سلولهای بنیادی مزانشیمال در درمان ALS	دکتر حمیدرضا رحیمی (استادیار دانشکده پزشکی علوم پزشکی مشهد ، متخصص پزشکی مولکولی و سلولهای بنیادی)
16:10 -16:20	پرسش و پاسخ	
16:30 – 16:50	پذیرایی و ارایه پوسترها	
17:10 – 17:30	مراسم رونمایی کتابهای کنگره	
17:30- 18:30	پانل با حضور سخنرانان روز دوم	سخنرانان روز دوم

روز سوم: کروز کورس و برنامه گردشگری خلیج فارس

ساعت	برنامه	نام سخنران
9:30-10	سوار شدن در کروز	
10 – 10:30	Personalized Cell therapy سلول درمانی شخصی سازی شده	پروفسور کریم نیرنیا (آلمان)
10:30-11	CftDNA in Malignant Therapy CftDNAدر درمان بدخیمی	دکتر شهرام سواد پزشک متخصص ژنتیک
11-11:30	Senotherapeutics in cutaneous senescence (skin aging) راهکارهایی در جوانسازی پوست	دکتر امید معمار صادقی
11:30-12	پانل فناوریهای نوین	
12-14	ناهار و پذیرایی	
14-14:30	Mesenchymal Stem Cells for Rejuvenation- A new anti-aging approach نقش سلولهای مزانشیمال در جوان سازی و جلوگیری از پیری	دکترامیررضا برومند

14:45-15:15	ارایه پوسترها	سالن ارایه پوستر
14:30-15	IPS & Stem Cell Therapy for Cardiovascular Diseases رویکردهای پزشکی فردمحور و سلول درمانی در بیماریهای قلبی و عروقی	پرفسور یوی نیکسدورف(آلمان)
15-15:30	Personalized Stem Cell therapy Approach رویکردهای پزشکی فردمحور در سلول درمانی در بیماریهای مختلف	پروفسور یورگن هشلر(آلمان)
15:30-18:00	پذیرایی، برنامه های تفریحی گردشگری خلیج فارس، معرفی و گفتگو با بیماران درمان شده با روشهای پزشکی فردمحور، معرفی پوستر برتر و اعطای جوایز	اختتامیه

کارگاه آموزشی از آزمایشگاه تا بالین: درمانهای پیشرفته سلول درمانی (در سالن برگزاری کارگاهها: ثبت نام در محل) **From Bench to Bedside** **Translational of Advancing Mesenchymal Stem Cell Therapies** **Coordinator:** **-Professor Jalil Tavakkol Afshari,** **PhD, CP(ASCP), CLS(NCA)** **Organizer:** **-PARNIA Stem Cell Tech CO**.		
Module I **14-14:40**	**Fundamentals of Stem Cells,** **Isolation, manufacturing and maintenance** اصول جداسازی، فرآوری و نگهداری سلولهای بنیادی مزانشیمال	دکتر ساره اعتماد: متخصص پاتولوژی دکتر جلیل توکل افشاری
Module II **14:40-15:20**	**Developing Standards (QMS, GMP) and regulations to support the Clinical Translation** استانداردها و آیین نامه ها در فرآیند تولید و کاربرد بالینی	دکتر سجاد سحاب نگاه دکتر حمیدرضا رحیمی
Module III **15:20-16**	**Clinical Trials translation, Experiences and Patient's Concern** کارآزمایی ها، ملاحظات و دغدغه های بالینی	دکترامیررضا برومند امیرادهمی مقدم: فوق تخصص ICU

پیام ریاست عالی دانشگاه آزاد اسلامی

Medical science has shown the heterogeneity of disease expression between individuals. One explanation is that a particular disease can have multiple molecular mechanisms, while another explanation might underscore the genetic heterogeneity in the population. Of course the truth lies somewhere in between and the permutation combination of both elements most likely is at play. The Biotechnology Research Center of Tehran Medical Univesity, Islamic Azad University is proud to present International Congress on Applied Novel Technology of Genetics and Stem cells Congress in Personalized Medicine from March 8-10, 2023, Kish Island, with continuing medical education credits from the Health Ministry of the Islamic Republic of Iran in 29 specialties of medicine and science. The International Congress for the Use of Stem Cells and Genetics for Personalized Medicine is a collaborative effort between The Islamic Azad University of Tehran Medical Sceinces, The University of Cologne, Germany, and The European Center for Personalized Medicine of Germany. This Sceintific event on Personalized Medicine has managed to attract the best and brightest minds from across Iran with the hope of implementing the latest genetic and stem cell research from bench to bedside.

Prof. Mohammad Mehdi Tehranchi

Professor of Physics, Laser and Plasma

President of Islamic Azad Univesity

Prof. Bijan Ranjbar

PhD from Moscow Institute of Physics and Technology (MIPT)

Department of Biophysics, Faculty of Biological Sciences, Tarbiat Modares University

پروفسور بیژن رنجبر

- استاد تمام رشته بیوفیزیک و استاد مدعو گروه نانوبیوتکنولوژی دانشگاه تربیت مدرس
- رئیس اسبق دانشگاه تربیت مدرس
- قائم مقام رئیس دانشگاه آزاد اسلامی در امور هیات ممیزه، شورای گسترش و انتصابات
- معاون سابق دبیر شورای عالی زیست فناوری کشور
- معاون سابق پژوهشی و فناوری دانشگاه آزاد اسلامی
- رئیس پژوهشگاه مرکزی دانشگاه آزاد اسلامی
- عضو کمیته علوم پایه فرهنگستان علوم پزشکی جمهوری اسلامی ایران
- عضو وابسته‌ی فرهنگستان علوم پزشکی جمهوری اسلامی ایران
- مدیرمسئول مجله‌ی زیست فناوری، دانشگاه تربیت مدرس
- استاد نمونه کشوری
- استاد نمونه دانشگاه تربیت مدرس
- برگزیده منتخب گروه علمی علوم پایه جشنواره علمی فرهنگستان علوم پزشکی جمهوری اسلامی ایران
- برگزیده بیست و ششمین جشنواره بین‌المللی خوارزمی جمهوری اسلامی ایران
- پژوهشگر برتر سال های مختلف
- مسئول کمیته فناوری های همگرای NBIC فرهنگستان علوم پزشکی جمهوری اسلامی ایران بمدت ۳ سال
- عضو شورای سیاست گذاری تدوین سند نظام ملی نوآوری- وزارت علوم تحقیقات و فناوری
- عضو شورای سیاست گذاری نظام ایده ها و نیازها-وزارت علوم تحقیقات و فناوری

پیام پروفسور رنجبر

For over a decade, personalized medical care has advanced on multiple fronts, including, diagnostic, preventative and curative modalities. Nowadays this new application is becoming a requisite sector in medicine, medical education, and medical technologies. Early detection and diagnosis opens new avenues for previously hard-to-treat conditions, while reducing some costs of medicine. Personalized medicine has a holistic view on multi-omics in a single person including genomic, transcriptomic, proteomic and metabolic levels. It is able to augment the potential of diagnosis and cure. In this brand new field of medicine, modern genetic technologies such as high throughput sequencing and microarray are used. It can help in diagnosis and prognosis of common and rare diseases. Stem cell studies can provide us with reliable data for corroborating the above mentioned findings and ensuring that personalized medicine advances.

Prof. Alireza Khoshdel

- President of Islamic Azad University, Tehran Medical Sciences
- President of Congress,
- Epidemiologist

پروفسور علیرضا خوشدل (رییس کنگره)

- پزشک متخصص اپیدمیولوژی بالینی
- ریاست دانشگاه علوم پزشکی آزاد اسلامی تهران
- معاون علوم پزشکی استان تهران
- ریاست سابق دانشگاه علوم پزشکی ارتش
- **راه اندازی 11 دوره تحصیلات تکمیلی دانشگاه از جمله دو رشته جدید طب هوافضا و روانپزشکی نظامی**
- **راه اندازی 9 مرکز تحقیقاتی در 3 پژوهشکده دانشگاه**
- **راه اندازی مرکز رشد فناوری دانشگاه و جذب 350 نخبه در پروژه های دانشگاه**
- **تدوین برنامه استراتژیک و نظام جامع علم و فناوری و نقشه راه دانشگاه با رویکرد مدیریت جهادی**
- **ساخت و راه اندازی مرکز جامع دانشورزی و مهارتهای بالینی دانشگاه**
- **راه اندازی پردیس اقدسیه دانشکده دندانپزشکی ارتش**
- **راه اندازی سامانه آموزش مجازی شهاب، حوزه بین الملل و دوره های حرفه ای طب نظامی**
- **طراحی و آغاز عملیات پروژه پردیس یاس فاطمی دانشکده پرستاری**
- **برگزاری اولین کنگره بین المللی طب نظامی در کشور با شرکت 40 کشور خارجی**
- **دبیر بورد تخصصی طب هوافضا به مدت 5 سال و عضو فعلی بورد**

Converging Upon "Personalized Medicine"

The world is witnessing a paradigm shift in medicine that includes several aspects such as smart systems, big-data warehouses, disease networks, and the system biology concept, convergence of sciences, translational medicine, patient-centered care and personalized medicine. This change evolves our understanding of medicine, both in diagnosis and treatment. Furthermore, it makes important reformation in our medical centers.

Our approach to disease management is being transformed to look for interconnected network of disorders as a system and not in isolation. Accordingly, our care plans are changing. A big body of clinical data can now be transferred to data-centers via bionics, cyborg, biosensors and artificial intelligent systems, and smart wearable devices. This data is automatically or purposefully analyzed either for diagnosis, treatment, or monitoring. Furthermore, gathering individual genetic information further empowers modern medicine in specific diagnoses and treatments, including personalized medications. Telemedicine opens windows for around the clock access to care. Robotics further transforms modern medicine in this integrated network by providing exceptional accuracy in the operating room. . Finally, a revolution in regenerative medicine opens new doors for reconstructive and transplantation surgeries.

Consequently, medical universities must be prepared to present a transformed educational curriculum. This includes not only new contents, but also novel approaches to medical training. Moreover, medical universities should evolve their infrastructures, laboratories, faculty structure, and professional academic groups in order to teach the next generation of healthcare providers. In parallel, interdisciplinary research collaborations must be systematically organized to meet these needs

We are now delighted to arrange this international meeting for personalized medicine, in collaboration with a large group of respected scientists and distinguished health care providers as a step towards the era of personalized medicine. Medicine needs close interdisciplinary collaboration for attaining these lofty goals and hence a better future. As the president of Islamic Azad University of Tehran Medical Sciences I welcome all of our respected guests and hope for an all around stimulating experience on the beautiful Kish Island.

Professor Ali Reza Khoshdel, MD-PhD

President, Islamic Azad University of Tehran Medical Sciences

President of Congress

پیام دبیر علمی کنگره

Genetics, cellular and molecular medicines are cutting-edge sciences and technologies that play an important role in improving human health and quality of life. In addition, medical and biological sciences have clearly shown that the onset of diseases differs from person to person due to their different genetic profiles and variations in molecular basis. Therefore, it is feasible that patients respond differently to a single treatment. Personalized medicine is a new field of medicine aims to tailor medical treatments to the individual characteristics of patients. In this review, in addition to genomics and personalized medicine, we touch upon common techniques in this field and the future of personalized medicine. With this development, people can get more information about the possibility of contracting diseases like cancer and early-stage treatments as well as personalized therapies based on their genetic characteristics. Technologies, such as mutation detection in the genome, microarrays or microchips, and next-generation sequencing of the human genome, have not only made molecular detection better and easier but also facilitated the integration of molecular detection with targeted drug delivery for the development of novel personalized treatment.

Dr. Maryam Eslami, MD, PhD

Scientific and Executive Director of Congress

Scientific Representative of European Center for Personalized Medicine

Prof. Karim Nayernia

Head of European Center for Personalized Medicine

President of Congress

پروفسور کریم نیرنیا(رییس کنگره)

- فارغ التحصیل از دانشگاه Göttingen سال ۱۹۹۳
- پروفسور ژنتیک انسانی دانشگاه Göttingen
- پروفسور طب سلول های بنیادی در انستیتو سلول های بنیادی دانشگاه Newcastle
- متخصص بین المللی در زمینه ی سلول های بنیادی
- اولین کاشف اسپرماتوگونیال از سلول های بنیادی
- رییس آکادمی بین المللی سلول های بنیادی
- رییس مرکز اروپایی پزشکی فردمحور
- مدیر گروه شرکت های GENEOCELL
- رییس کنگره

عنوان سخنرانی:

Management of Precision Diagnostics and Personalized Treatment of Cancer

P7CENCER

Management of Precision Diagnostics and Personalized Treatment of Cancer

Prof. Dr. Karim Nayernia
P7MEDICINE
Medical Center Düsseldorf
Germany

P7CANCER is the comprehensive program of International Center for Personalized Medicine (P7MEDICINE) at the Medical Center Düsseldorf for management of precision diagnostics (ONCOASSAY) and personalized treatment (ONCOTHERA) of cancer.

Personalized cancer medicine refers to a novel approach to personalized medicine based on an individual's genome and biological processes. Several investigations have confirmed that specific genes largely control therapeutic outcome in cancer patients and that mutations directly control all stages of cancer development, progression, and response. In personalized cancer medicine, we seek to discover all genetic modifications and variations in each patient's normal and/or cancerous cells after a thorough consultation. Molecular data are used to determine the genetic risk factor in people with hereditary cancers and for disease management in all cancers. Personalized cancer prevention, personalized chemotherapy, radiation therapy, immunotherapy, and gene therapy are some of the leading strategies in personalized cancer medicine today.

ONCOASSAY® is one of our innovated precise personalized medicine approaches, specially designed for the prediction, planning personalized treatment options of cancer in people with or without familial history and personalized monitoring of cancer treatment and recurrence.

Using the most advanced molecular and cellular technologies, ONCOASSAY® investigates the individual tumor as a heterogeneous histologic and genetic tissue, based on patient's tumor biology. To find the most functional types of mutations, complete transcriptional and translational analyses are conducted. There will be a team of oncologists, geneticists, and molecular biologists by the patient's side in order to define the cancer risk and best treatment strategies.

As an important feature of ONCOASSAY®, patient's conventional clinical data is converted to digital format and combined with all the molecular bioinformatic data, leading to a rich and concentrated electronic health file for each patient.

Based on the diagnostic phase, ONCOASSAY® is divided into 3 different services of ONCOASSAY® A, B, and M, that are suggested by the aforementioned team, after first consultation.

ONCOTHERA is a personalized approach of cancer immunotherapy, specifically synthetized from patient's tumor peptides. A new generation of cancer vaccines has been developed for situations where viable tumor tissue is not available for a whole tumor vaccine. This peptide vaccine aims to identify only the immunogenic tumor antigens specific to each tumor. This new vaccine chooses only antigens commonly or expressed by the indication or expressed by the tumor, to create strong targeted and specific tumor vaccines. There are two levels: the first is called The Universal Peptide. It is designed to target general mutations shared across various common indications and to work across a broad range of HLA blood types. It is available right away and works on most patients. The second is The Personalized Peptide. It requires a blood test to determine the HLA typing (Class I – low resolution 2-digit test). It also requires access to your paraffin block or slides to perform a genetic profiling test. Genetic profiling can also be ordered by your oncologist, or coordinated by us. If previously conducted, the same results can be used. The vaccine is personalized to your blood type and to the identified mutations that are unique to your tumor.

Prof. Dariush Farhoud

- **MD, PhD, MG**
- Member of WHO Expert Advisory Panel on Human Genetics, Geneva.
- Member of WHO Committee for Ethics in Medical Genetics, Geneva (1994-2001)
- Funder of Human Genetics in Iran

پروفسور داریوش فرهود

- **دکتری پزشکی از دانشگاه ارلانگن؛ آلمان (۱۹۶۹)**
- **دکتری ژنتیک انسانی و انسان شناسی (PHD) از دانشگاه ماینس آلمان (۱۹۷۲)**
- **پروفسوری در ژنتیک پزشکی (Prof) از دانشگاه مونیخ آلمان(۱۹۹۱)**
- **بنیانگذار،استاد و مدیر اولین گروه ژنتیک انسانی در ایران؛دانشکده بهداشت؛ دانشگاه علوم پزشکی تهران (۱۳۵۲ تا ۱۳۸۲)**
- **کارشناس رسمی رشته ژنتیک انسانی؛ سازمان جهانی بهداشت ؛ ژنو (۱۳۵۵ تا کنون)**
- **عضو کمیته ی ((اخلاق در ژنتیک پزشکی)) سازمان جهانی بهداشت ؛ژنو (۱۳۷۳ تا ۱۳۸۰)**
- **عضو پیوسته و دایمی فرهنگستان علوم جهان سوم ؛تریست (از ۱۳۷۵ تا کنون)**
- **عضو کمیته ی ملی ((اخلاق زیستی)) کمیسیون ملی یونسکو-ایران (۱۳۸۲ تاکنون)**
- **عضو پیوسته و دایمی و دبیر علوم پایه فرهنگستان علوم پزشکی ایران؛ تهران (از ۱۳۸۵ تاکنون)**
- **بنیانگدار ژنتیک انسانی در ایران**

پیام پروفسور فرهود:

Personalized medicine is now, more than ever, a hot topic, especially with greater public awareness of medical issues in wake of a global pandemic. As lifespan and healthspan has grown, we are on a journey to tailor fit medicine to the individual and not the masses. This is the ultimate development of mankind, personalized medicine.

Personalized medicine is focused on a tailor-fit health plan that includes idiosyncratic solutions, including renewal and differentiation of stem cells that are loaded on scaffolds for placement.

Gene therapy will provide an opportunity for innovative treatments of many types of genetic disease including cancer, disease of the skin, heart, e.t.c . The prevention of these diseases with personalized genetic investigations will significantly reduce the cost and subsequently increase both healthspan and lifespan. This Congress strives to create a scientific atmosphere where Iranian and International clinicians, scientists and researchers freely discuss the latest research in personalized medicine. Special attention will be given to the latest on stem cells and their role in medicine. We welcome you and hope that this conference is a primer to future collaborations and advancements on the practice of personalized medicine.

Dr. Maryam Eslami

MD, PhD of Genetics, Regenerative Medicine Fellowship from Harvard Medical School, Scientific & Executive Director of Congress

دکتر مریم اسلامی

- پزشک متخصص ژنتیک، فلوشیپ پزشکی بازساختی از دانشگاه علوم پزشکی هاروارد آمریکا
- نماینده علمی مرکز اروپایی پزشکی فردمحور
- مدیر گروه ژنتیک
- رئیس مرکز تحقیقات زیست فناوری کاربردی واحد علوم پزشکی تهران
- مدیر امور بین الملل دانشگاه
- عنوان برترین زن مخترع سال 2008 از سازمان جهانی مالکیت معنوی ملل متحد (وایپو)
- اولین زن دارنده دو پتنت امریکا در ایران
- دارنده 6 دیپلم افتخار و 6 مدال طلای بین المللی
- مسئول کارگروه زنان نخبه باشگاه پژوهشگران جوان
- مدیر سابق علم سنجی دانشگاه آزاد اسلامی

عنوان سخنرانی:

Scaffold for skin tissue engineering and a method of synthesizing thereof

poly(ε-caprolactone) (PGS-PCL) microfibrous scaffolds are synthesized. The hydrogel is synthesized. The composite scaffold comprising hydrogel and poly (glycerol sebacate)-poly(ε-caprolactone) (PGS-PCL) microfibrous scaffolds is fabricated. A plurality of physico-chemical characteristics of the composite scaffold comprising hydrogel and poly (glycerol sebacate)-poly(ε-caprolactone) (PGS-PCL) microfibrous scaffolds are analysed. The physico-chemical characteristics comprises mechanical properties, swelling ratio and enzymatic degradation and scanning electron microscope imaging. The fibroblast cells are encapsulated within the composite scaffold comprising hydrogel and poly (glycerol sebacate)-poly(ε-caprolactone) (PGS-PCL) microfibrous scaffolds and hydrogels. The fibroblast cells are seeded on composite scaffold and PGS-PCL scaffold. The fibroblast cell viability, fibroblast cell attachment, fibroblast cell spreading, fibroblast cell proliferation and fibroblast cell metabolism are analysed in composite scaffolds, PGS-PCL scaffolds and hydrogels.

Dr.Amir Adhami Aghdam

MD- Fellow of Critical Care Medicine

Anesthesiologist

دکتر امیر ادهمی اقدم

- رئیس بخش ICU
- فلوشیپ مراقبت‌های ویژه (آی سی یو)
- تخصص بیهوشی
- دکترای حرفه‌ای پزشکی

عنوان کارگاه:

Clinical Trials translation, Experiences and Patient's Concern

Clinical Trials translation, Experiences and Patient's Concern

Autologous stem cell therapy is the newest way to control or treat many neurodegenerative diseases, diabetes, osteoarthritis, etc. Sources for cell extraction are bone marrow and adipose tissue. Bone marrow aspiration is an invasive and painful procedure. Many patients do not have a good memory of this procedure due to severe pain. General anesthesia is the best way for the patient to tolerate these conditions. Before anesthetizing, we need to examine the patient. So we are going to explain these topics: patient evaluation, medications for the anesthesia, airway management and the method of bone marrow aspiration.

Dr. Sareh Eatemad

MD, clinical & anatomical Pathologist

دکتر ساره اعتماد

- پزشک
- متخصص آسیب شناسی (پاتولوژی)

عنوان کارگاه:

Fundamentals of Stem Cells, Isolation, manufacturing and maintenance

Fundamentals of Stem Cells, Isolation, manufacturing and maintenance

Stem cells have the ability to build every tissue in the human body, hence have great potential for future therapeutic uses in tissue regeneration and repair. In order for cells to fall under the definition of "stem cells," they must display two essential characteristics. First, stem cells must have the ability of unlimited self-renewal to produce progeny exactly the same as the originating cell. Also they are able to give rise to a specialized cell type that becomes part of the healthy animal. The general designation, "stem cell" encompasses many distinct cell types. Commonly, the modifiers, "embryonic," and "adult" are used to distinguish stem cells by the developmental stage of the animal from which they come, but these terms are becoming insufficient as new research has discovered how to turn fully differentiated adult cells back into embryonic stem cells and, conversely, adult stem cells, more correctly termed "somatic" stem cells meaning "from the body", are found in the fetus, placenta, umbilical cord blood and infants. Therefore, this work shop will sort stem cells into 4 categories based on their biologic properties - Totipotent , pluripotent, oligopotent & unipotent stem cells . Their sources, characteristics, differentiation and breif points of therapeutic applications are discussed.

Dr. Roozbeh Barikbin

Radiologist

دکتر روزبه باریک بین

- متخصص رادیولوژی و سونوگرافی
- عضو آکادمی پزشکی فرد محور آلمان

عنوان سخنرانی

Personalized Imaging in medicine

Personalized Imaging in medicine

This presentation offers a new perspective on personalised medicine (PM) within diagnostic radiography. Personalized medicine refers to the use of a person's genetic information in providing strategies for the detection, treatment, or prevention of disease. Some key issues are raised in light of this new specialty and how it may affect diagnostic imaging. Imaging procedures are adjusted to the clinical problem and patient characteristics. Screening for preclinical disease is done with imaging. Stratification based on imaging biomarkers can help identify individuals suited for preventive intervention. Treatment decisions are based on the in vivo visualization of the location and extent of an abnormality as well as the loco-regional physiological, biochemical and biological processes using structural and molecular imaging. Image-guided biopsy provides relevant tissue specimens for genetic/molecular characterization. In addition, radiogenomics relate imaging biomarkers to these genetic and molecular features. Furthermore, imaging is essential to patient-tailored therapy planning, therapy monitoring and follow-up of disease, as well as targeting non-invasive or minimally invasive treatments, especially with the rise of theranostics. Radiologists need to be prepared for this new paradigm as it will mean changes in training, clinical practice and research. The aim of this article is to begin to acknowledge the importance of personalized medicine, but most importantly, identify aspects where diagnostic imaging plays a pivotal role.

Dr. Amirreza Broumand

Neurologist

Cell therapy fellowship from Münster University

Head of Neurology Department, Parnia Knowledge based Stem Cell institute

دکتر امیررضا برومند

- متخصص مغز و اعصاب و بیماریهای ستون فقرات
- دوره تکمیلی سلولهای بنیادی از دانشگاه مونستر آلمان
- فلوشیپ سایکوسوماتیک از دانشگاه فرایبورگ آلمان

عنوان سخنرانی:

1. How mesenchymal stem cell therapy effects on neurological diseases
2. Mesenchymal Stem Cells for Rejuvenation- A new anti-aging approach

With aging, a portion of cells, including mesenchymal stem cells (MSCs), become senescent, and these senescent cells accumulate and promote various age-related diseases. Therefore, the older age group has become a major population for MSC therapy, which is aimed at improving tissue regeneration and function of the aged body. However, the application of MSC therapy is often unsatisfying in the aged group. One reasonable conjecture for this correlation is that aging microenvironment reduces the number and function of MSCs. Cellular senescence also plays an important role in MSC function impairment. Thus, it is necessary to explore the relationship between senescence and MSCs for improving the application of MSCs in the elderly. Here, we present the influence of aging on MSCs and the characteristics and functional changes of senescent MSCs. Furthermore, current therapeutic strategies for improving MSC therapy in the elderly group are also discussed.

Dr. Amirreza Boroumand, MD

The human body is highly complex and comprises a variety of living cells and extracellular material, which forms tissues and organs. Human cells tend to turn over readily to maintain homeostasis in tissues. However, postmitotic nerve cells exceptionally have an ability to regenerate and be sustained for the entire life of an individual, to safeguard the physiological functioning of the central nervous system. For efficient functioning of the CNS, neuronal death is essential, but extreme loss of neurons diminishes the functioning of the nervous system and leads to the onset of many neurological disorders. Millions of individuals worldwide are suffering from neurodegenerative disorders with little or negligible treatment available, thereby leading to a decline in their quality of life. Neuropathological studies have identified a series of factors that explain the etiology of neuronal degradation and its progression in neurodegenerative disease. The onset of neurological diseases depends on a combination of factors that causes a disruption of neurons, such as environmental, biological, physiological, and genetic factors. There are some of the major pathological factors responsible for neuronal degradation, such as oxidative stress, cell death, aging and neuroinflammation.

Cellular therapy aims to replace damaged resident cells by restoring cellular and molecular environments suitable for tissue repair and regeneration. Among several candidates, mesenchymal stem/stromal cells (MSCs) represent a critical component of stromal niches known to be involved in tissue homeostasis. In vitro, MSCs appear as fibroblast-like plastic adherent cells regardless of the tissue source. The therapeutic value of MSCs is being explored in several conditions, including immunological, inflammatory and degenerative diseases, as well as neurological disorders. An improved understanding of their origin and function would facilitate their clinical use.

Dr.Babak Behnam

MD, PhD of Genetics, Clinical Biochemical Genetics Fellowship, Department of Regulatory Affairs, NSF International

دکتر بابک بهنام

- دکترای پزشکی از دانشگاه علوم پزشکی ایران ۱۳۷۵ (۱۹۹۶)
- دکترای تخصصی ژنتیک انسانی از دانشگاه UCL لندن ۱۳۸۴ (۲۰۰۵)
- فلوشیپ ژنتیک پزشکی با NRSA Award از دانشگاه میشیگان ۱۳۸۵ (۲۰۰۶) و دانشگاه UCF فلوریدا ۱۳۸۶ (۲۰۰۸)
- دانشیار گروه ژنتیک پزشکی دانشگاه علوم پزشکی ایران ۱۳۹۴ (۲۰۱۵)
- راه اندازی کلینیک تخصصی مشاوره ژنتیک پزشکی در بیمارستانهای کودکان و زنان و زایمان دانشگاه و انجام بیش از ۲۰۰۰ مشاوره ژنتیک ۱۳۹۴-۱۳۸۸
- راه اندازی آزمایشگاه تشخیصی بالینی ژنتیک در بیمارستانهای دانشگاهی اطفال (علی اصغر) و زنان و زایمان (مادر) ۱۳۹۳-۱۳۸۹
- فلوشیپ Clinical Biochemical Genetics از انستیتو ملی سلامت امریکا (NIH) و آکردیته بورد ژنتیک بالینی آمریکا
- محقق انستیتو ژنوم انسانی (NHGRI) و برنامه بیماریهای نادر ژنتیکی و شناخته نشده (Rare and Undiagnosed Diseases) از NIH

عنوان سخنرانی:

Anti-mitochondrial Therapy: A New Dimension of Personalized Oncology

Anti-mitochondrial Therapy: A New Dimension of Personalized Oncology

Babak Behnam [1*], MD PhD

Farzad Taghizadeh-Hesary [2,3*], MD

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Farzad Taghizadeh-Hesary: ENT and Head and Neck Research Center and Department, The Five Senses Health Institute, School of Medicine, Iran University of Medical Sciences, 1445613131, Tehran, Iran

Energy is needed by cancer cells to stay alive and communicate with their surroundings. The primary organelles for cellular metabolism and energy synthesis are mitochondria. Researchers recently proved that cancer cells can steal immune cells' mitochondria using nanoscale tubes. This finding demonstrates the dependence of cancer cells on normal cells for their living and function. It also denotes the importance of mitochondria in cancer cells' biology. Emerging evidence has demonstrated how mitochondria are essential for cancer cells to survive in the harsh tumor microenvironment, evade the immune system, obtain more aggressive features, and resist treatments. For instance, functional mitochondria can improve cancer resistance against radiotherapy by scavenging the released reactive oxygen species. Therefore, targeting mitochondria can potentially enhance oncological outcomes, according to this notion. The patients' reactions to radiation are varied, ranging from a complete response to even cancer progression during treatment. This concept illustrates how different levels of mitochondrial metabolism might contribute to this heterogeneity. Considering this notion can help to improve personalized oncological treatments. This article outlines the importance of mitochondrial metabolism in cancer biology and personalized treatments.

Keywords: Mitochondria, Personalized Oncology, Cancer stem cell, T cell

Prof. Seyyed Jalil Tavakkol Afshari

Immunologist

پروفسور سید جلیل توکل افشاری

- استاد دانشگاه علوم پزشکی مشهد
- دکترای متخصصی (Ph.D) ایمنی شناسی (ایمونولوژی)
- دکترای حرفه ای ایمنی شناسی آزمایشگاهی

عنوان سخنرانی:

How mesenchymal stem cell therapy would effect on Neuroinflammatory markers in patients ALS

Evaluation of clinical and specific biomarkers following Mesenchymal Stem Cell transplantation in ALS patients

Prof. Dr. Seyyed Jalil Tavakkol Afshari

Amyotrophic lateral sclerosis (ALS) is a deadly neurodegenerative disorder characterized by progressive degeneration of upper and lower motor neurons. Stem cell-based treatments recently have emerged as potentially effective approaches to delay the progression of ALS. Method: In this single-center, open-label, un-controlled clinical trial, twenty ALS-patients were included considering define inclusion and exclusion criteria. Autologous Bone Marrow-derived MSCs (BM-MSCs) were isolated, expanded and characterized under standard conditions. Concurrent intrathecal (IT) and intravenous (IV) transplantation was applied for patients with equal amount of cells and the patients received cells (1×106 MSCs/kg BW) in two steps with one month interval. The patients followed in three time points (months 0, 1, and 3).At these times, serum and CSF samples were taken from each patient and specific biomarkers were assessed. Results: No serious side effect was observed after cell transplantation in patients. The mean ALS functional rating scale-revised (ALSFRS-R) values remained stable during the follow-up periods. Forced vital capacity (FVC) also showed an increasing trend, and this increase showed significant difference in the third month compared to the before injections (months 0). The changes of oxidative biomarkers including superoxide dismutase (SOD) and nitric oxide (NO) and also inflammatory biomarkers including TNF-α and CCL2 during the follow-up period in none of the serum and CSF samples did not show any significant difference compared to the study' onset. Conclusion: Our obtained results showed that simultaneous IV and IT injection of autologous BM-MSCs is a safe process. Also, the non-significant decrease in ALSFRS-R, and increase in FVC during the study period, as well as the stabilization of inflammatory and oxidative biomarkers' level, indicate the effectiveness of these cells in ALS patients.

Dr.Masoud Khadivi

(Neurological Surgeon; Director of Neurospine fellowship in Tehran Medical University)

دکتر مسعود خدیوی

- **تخصص : جراحی مغز واعصاب دانشگاه علوم پزشکی تهران**
- **رتبه علمی : استادیار**
- **«دایرکتوری فلوشیپ نورواسپاین» دانشگاه علوم پزشکی تهران**
- **عضو کمیته علمی انجمن جراحان مغز و اعصاب ایران**

عنوان سخنرانی:

Personalized Medicine in Cervical Myelopathy

Personalized Medicine in Cervical Myelopathy

Degenerative cervical myelopathy (DCM), a term that has only recently been developed, refers to a number of age- and genetically based pathologies, such as cervical spondylotic myelopathy, degenerative disc disease, and ligamentous aberrations like ossification of the posterior longitudinal ligament. All of these illnesses result in persistent compression of the spinal cord, which results in a clinical condition defined by impaired hand dexterity, unbalanced gait, and possible sensorimotor or genitourinary problems. Heterogeneity in practice patterns has resulted from significant variation in the underlying etiology of DCM and its natural history. Clinical judgment, intervention time, and the best surgical strategy are the three main topics of ongoing discussion in DCM management. We now know more about the pathophysiologic mechanisms of DCM because to important fundamental science investigations conducted over the past two decades. We will be able to develop tailored treatment plans for patients with an increasingly heterogeneous patient population as our understanding of the key pathophysiologic processes grows. This presentation focuses on describing the most innovative methods for tailoring DCM patient therapies, including biomarkers, variables influencing clinical judgment, and selection of the best surgical strategy. Throughout, we give a succinct overview of the ailments that make up DCM and talk about the mechanism behind chronic spinal cord compression. In order to address knowledge gaps and issues in the field of DCM, we also present an overview of clinical-radiologic diagnostic techniques as well as surgical and non-operative therapeutic approaches.

Dr. Hamidreza Rahimi

Assistant Professor of Mashhad Medical University, Specialist in Molecular Medicine and Stem Cells

دکتر حمیدرضا رحیمی

- دکترای حرفه ای پزشکی در رشته پزشکی مولکولی
- استادیار دانشگاه علوم پزشکی مشهد

عنوان سخنرانی

Safety of Efficacy of MSC Therapy in ALS

Safety and efficacy of bone marrow derived-mesenchymal stem cells transplantation in patients with amyotrophic lateral sclerosis

Dr. Hamidreza Rahimi

Stem cell-based treatments have emerged as potentially effective approaches to delay the progression of amyotrophic lateral sclerosis (ALS). This study was designed as a single-center, prospective, and openlabel study without a placebo control group to assess the safety and efficacy of concurrent intrathecal (IT) and intravenous (IV) administration of autologous bone marrow-derived mesenchymal stem cells (BM-MSCs) in patients with ALS. Autologous BM-MSCs were isolated and expanded under standard conditions. Fifteen patients were neurologically examined before BM-MSCs transplantation (1 10 6 cells/kg BW) to evaluate the rate of pre-treatment disease progression. To assess the safety and efficacy, patients were examined at 1, 3, and 6 months following the treatment with BM-MSCs. Adverse reactions were assessed, and the clinical outcome was determined by the evaluation of the ALS functional rating scale-revised (ALSFRS-R) and forced vital capacity (FVC). No serious adverse reaction was observed after combined IT and IV administration of BM-MSCs. The mean ALSFRS-R and FVC values remained stable during the first 3 months of the treatment. However, a significant reduction in ALSFRS-R and FVC levels was observed in these patients 6 months after BM-MSCs administration. Our study revealed that the concurrent IT and IV application of BM-MSCs in patients with ALS is a safe procedure. Furthermore, our data indicate a temporary delay in the progression of ALS after a single combined IT and IV administration of BM-MSCs. Further studies are required to explore if the repeated applications of BM-MSCs could prolong survival and delay the progression of ALS.

دکتر سجاد سحاب نگاه

Dr.Sajjad Sahabnegah

Faculty of Mashhad Medical University

- عضو هیات علمی گروه علوم اعصاب دانشکده پزشکی مشهد
- نماینده معاون تحقیقات و فناوری وزارت بهداشت، درمان و آموزش پزشکی
- استادیار دانشگاه علوم پزشکی مشهد

عنوان کارگاه:

Developing Standards (QMS, GMP) and regulations to support the Clinical Translation

Dr.Shahram Savad

MD, PhD of Genetics

Founder of NGS Panels in Iran

دکترشهرام سواد

- **پزشک متخصص ژنتیک**
- **گواهینامه تاییدیه مهارت پزشکی از کشور آمریکا (ECFMG Certification) سال 2006**
- **اولین WES در ایران**
- **اولین پنل NGS در ایران**
- **اولین NIPT در ایران**
- **اولین سکانس کروناویروس در ایران**
- **اولین غربالگری ازدواج فامیلی در ایران**
- **اولین تشخیص فردمحور سرطان برپایه NGS در ایران**
- **بیشترین گزارش انواع ژنوم انسانی در خاورمیانه**

عنوان سخنرانی:

CftDNA in Malignant Therapy

CftDNA in Malignant Therapy

Most medical treatments are designed for the "average patient" as a one-size-fits-all-approach, which may be successful for some patients but not for others. Precision medicine, sometimes known as "personalized medicine" is an innovative approach to tailoring disease prevention and treatment that takes into account differences in people's genes, environments, and lifestyles. The goal of precision medicine is to target the right treatments to the right patients at the right time.

Advances in precision medicine have already led to powerful new discoveries and FDA-approved treatments that are tailored to specific characteristics of individuals, such as a person's genetic makeup, or the genetic profile of an individual's tumor. Patients with a variety of cancers routinely undergo molecular testing as part of patient care, enabling physicians to select treatments that improve chances of survival and reduce exposure to adverse effects.

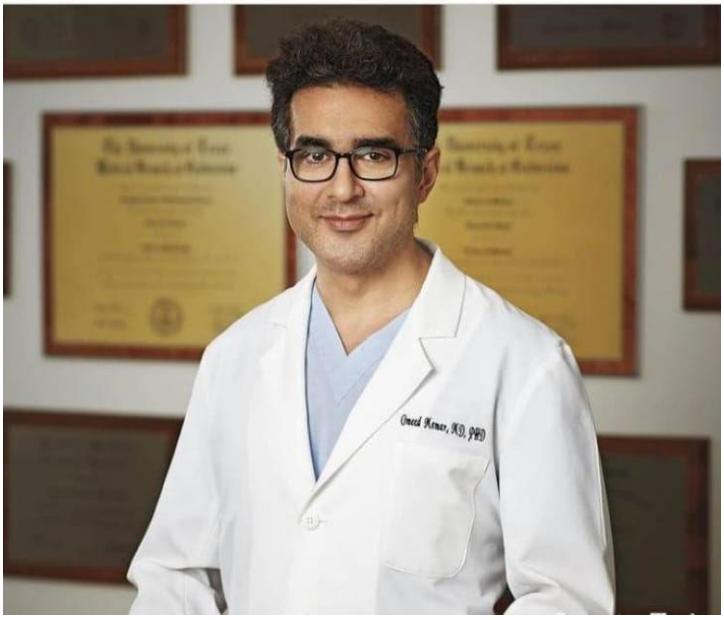
Precision care will only be as good as the tests that guide diagnosis and treatment. Next Generation Sequencing (NGS) tests are capable of rapidly identifying or 'sequencing' large sections of a person's genome and are important advances in the clinical applications of precision medicine. Patients, physicians and researchers can use these tests to find genetic variants that help them diagnose, treat, and understand more about human disease.

دکتر امید معمار صادقی

Dr. Omid Memar Sadeghi

Immunologist, Dermatologist, skin surgery subspecialist
from Chicago University, USA

- پزشک متخصص پوست
- فوق تخصص جراحی پوست از دانشگاه شیکاگو امریکا
- دکتری تخصصی ایمونولوژی
- دانشیار سابق دانشگاه Northwesternامریکا
- استاد افتخاری دانشگاه علوم پزشکی آزاد اسلامی تهران



عنوان سخنرانی:

1. bFGF Peptide for Vitiligo

2. Senotherapeutics in Cutaneous Senescence

bFGF Peptide for Vitiligo

O. Memarsadeghi, MD, PhD

Applied Biotechnology Research Center, Tehran Medical Sciences, Tehran, Iran

Vitiligo is an acquired form of skin depigmentation. It is thought to be an autoimmune disease of the skin, in which melanocytes are targeted and eliminated, leaving depigmentation of the skin. Compared to peri-lesional skin, lesional skin is known to have a skewed cytokine profile, with a notable reduction in basic Fibroblast Growth Factor (bFGF). bFGF has been shown to promote the adhesion and migration of melanocytes, suggesting that bFGF may play a role in the regimentation of vitiligo. This was confirmed by using recombinant bFGF to significantly enhance migration of melanocytes through expression of phosphorylated focal adhesion kinase on melanocytes. Either bFGF or an active peptide of bFGF has been shown to induce melanocyte proliferation and melanogenesis in vitro. Topical application of this peptide has been shown to induce regimentation in vitiligo, and stood the rigor of multiple studies, including a double-blind randomized controlled study with and without phototherapy. This peptide is an approved drug in some countries, including Iran for the treatment of vitiligo. This presentation will review the use of bFGF peptide in vitiligo.

Senotherapeutics in Cutaneous Senescence

O. Memarsadeghi, MD, PhD

Applied Biotechnology Research Center, Tehran Medical Sciences, Tehran, Iran

Senescence is a term used for biologic aging. Leonard Hayflick highlighted senescence in the 1960s, when he showed that fibroblasts in culture can replicate 50 times before entering cellular senescence, a new state of existence of the cell without replication. These senescent cells (SCs) are usually larger than non-senescent cells, and tend to have a distinct secretome termed Senescence Associated Secretory Phenotype (SASP). SCs acquire new markers and can be identified. Cellular senescence is a normal and necessary phenomenon. However, a dysregulation of senescence can cause disease and dysfunction. SASP induced secondary to ultraviolet radiation, oxidative stress, radiation exposure, chronic inflammation, carcinogenesis, to name a few, can induce a pro-inflammatory SASP that causes local and distant disease. In fact, transplanting relatively small numbers of senescent fibroblasts into young mice from syngeneic older mice is sufficient to cause persistent physical dysfunction, as well as to spread cellular senescence to host tissues. Transplanting even fewer senescent cells had the same effect in older recipients and was accompanied by reduced survival, indicating the potency of senescent cells in shortening health- and lifespan. Cellular senescence has been studied in many animal models and cell types. It is especially well studied in skin using keratinocytes, melanocytes, fibroblasts, and adipocytes. Numerous studies have shown that using senotherapeutics, senescence can be reduced and diseases caused by senescence minimized. Senotherapeutics are classified as senolytics which kill SCs selectively; senomorphics which modulate functions and morphology of SCs to those of younger cells, or delays the progression of young cells to SCs in tissues; and immune-system mediators of the clearance of SCs. We will review the potential use of senotherapeutics in dermatology.

Prof. Dr. Med.Uwe Nixdorff

Cardiologist and Sports Specialist, Head of European Center for Personalized Medicine, Head of European Prevention Center

دکتر یوی نیکسدورف

- متخصص بیماری های قلب و عروق تمرکز بر طب پیشگیری
- موسس و رییس مرکز پیشگیری از بیماریهای اروپا
- رییس مرکز اروپایی پزشکی فردمحور

دکتر بابک نیکومرام

- **تخصص: جراحی عمومی**
- **فلوشیپ: جراحی پلاستیک صورت از اروپا**
- **فوق تخصص: جراحی پلاستیک، ترمیمی و سوختگی**
- **بورد فوق تخصصی جراحی پلاستیک**
- **استادیار دانشگاه آزاد اسلامی واحد پزشکی تهران**
- **عضو انجمن جراحان پلاستیک زیبایی آمریکا** (ASAPS)
- **عضو انجمن جراحان پلاستیک آمریکا** (ASPS)
- **عضو انجمن بین المللی جراحان پلاستیک زیبایی** (ISAPS)
- **فلوشیپ جراحی پلاستیک صورت از اروپا**(DAFPRS)
- **ریاست انجمن جراحان پلاستیک و زیبایی ایران**

Dr.Babak Nikoomaram

President of Iranian Society of
Plastic & Aesthetic Surgeons

عنوان سخنرانی:

Adipose-Derived Stem cells & Personalized medicine

Adipose-Derived Stem cells & Personalized medicine

Babak Nikoumaram MD

Plastic Surgeon

Assistant Professor of Islamic Azad University – Tehran Medical Sciences

BooAli teaching Hospital

The aging is constant and the aging in the face is mostly seen and noticeable. With aging Face, we have Skeletal volume and density loss; soft tissue volume loss such as fat, collagen and other connective tissues; skin changes due to sun, smoke and natural degeneration of skin elements causing fine wrinkle; the constant force of the face muscle and tissue loss lead to deep wrinkle; and finally, the gravity pulling everything down cause sagging.

To protect and reverse these effects one may use sunscreen, cream and lotion, peeling, lasers, Botulinum toxin injections, dermal fillers and volume enhancers before choosing an aesthetic plastic surgery procedure .Fat transfer is a key in rejuvenating the face not only to reverse the volume loss but also enhancing the quality of the skin for harboring stem cells. The main obstacle in the fat transfer is the survival of the transferred fat. One-year graft survival is reported as low as 10 to 30% and numerous methods and techniques introduced to gain higher fat survival each with varying degree.

In recent years the Regenerative medicine may add some hope in the wellbeing and reverse the aging and the regenerative medicine is a dynamically developing branch of aesthetic surgery and other disciplines. The first cell therapies were intended to slow the aging process. This began in the 1930s with Paul Niehans, a Swiss doctor who was known to have treated famous historical figures such as Pope Paul XII, Charlie Chaplin, Gen. Charles de Gaulle of France, and many Middle East leaders were said to have been among his patients. Niehans would inject cells of fetus of unborn lambs and other animals into his patients in an attempt to rejuvenate them. Nowadays a wide range of autologous products are used for the purpose of facial rejuvenation. The most commonly applied therapies include agents collected from peripheral blood, such as platelet-rich plasma (PRP) or fibrin but its action is not depending on stem cells. Adipose tissue also is a good source of stem cells in the form of Nanofat, SVF and ADSC. All are efficient for facial rejuvenation. The may improve skin quality, they promote remodeling of the dermis, they have antioxidant effect and protect fibroblast from free radicals; and they stimulate secretion of collagen, elastin and anti-inflammatory cytokines. Finally, if adding to fat transfer (Cell-assisted lipotransfer) it promotes fat survival rate and better volume enhancement.

In Personalized Medicine one can use product of the person’s adipose tissue to enhance rejuvenation but harvesting ADSC requires adequate skills and equipment.

Prof.Dr.med.Jürgen Hescheler

Stem Cell Specialist, Head of the German Stem Cell Association, Director of the Institute for Neurophysiology at University of Cologne

پروفسور یورگن هشلر

- رئیس و مدیر موسسه فیزیولوژی عصبی در دانشگاه کلن
- اولین دانشمند در سراسر جهان که آزمایش‌های الکتروفیزیولوژیکی را بر روی سلول‌های بنیادی انجام داد
- در سال 2002 او اولین دانشمندی در آلمان بود که مجوز کار با سلول های بنیادی همبریون انسانی را گرفت
- تأسیس انجمن آلمانی تحقیقات سلول های بنیادی در سال 2005

عنوان سخنرانی:

Stem cells & its application in Personalized Medicine

Pluripotent Stem Cells and Personalized Cell Medicine

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Due to their ability to reproduce the embryonic, neonatal and adult differentiation of all different organotypic cellular phenotypes, pluripotent stem cells represent an ideal tool to study physiological processes of embryogenesis under *in vitro* conditions. They also provide the basis of personalized cellular therapeutics, to build up precision test assay systems for drug discovery or toxicology and to develop novel disease models for companion diagnostics within personalised medicine. In particular, embryonic (ES) and induced pluripotent stem (iPS) cells can reproduce all organotypic electrophysiology, signalling cascades and genes involved in the development (functional genomics). This is spontaneously occurring within three dimensional cell aggregates - embryoid bodies (EBs) – which we developed 30 years ago. Induction of pluripotency by reprogramming allows obtaining individual iPS cells of patients with his/her specific genetic background. This provides a unique new tool to build up test systems for representing the patient for personalized medicine. Moreover, novel disease models can be generated. To demonstrate the proof of principle, reprogramming of fibroblasts from patients with LQT3 or CPVT syndrome by ectopic expression of the Yamanaka's transcription factors was performed resulting in generation of iPS cells for disease modelling. This novel approach may also enable patient-specific cell replacement therapies, which appears an indispensable prerequisite for a later use in clinics. iPS cells from patients may also represent a new diagnostic tool to precisely analyse the pathophysiology and to develop personalised strategies for an optimized therapy.

Accepted Posters

	Title	Author
1	Phenylacetate as a new inducer for neural differentiation of human adipose-derived mesenchymal stem cells in vitro	Hanieh Ahmadi[1], Mohammad Hajipour[2], Mohsen Ghiasi[3], Raheleh Halabian[4], Ali Salimi*[5]
2	Osteogenic differentiation of hWJ-MSCs in the presence of Rubia tinctorum extract nanoemulsion and Alizarin active ingredient	Nafiseh Abasabadi[1], Hossein Dehghan[2], Raheleh Halabian[3], Arash Padash[4], Hanieh Ahmadi[5], Ali Salimi[6]*
3	Osteogenic differentiation of human adipose-derived mesenchymal stem cells in the presence of schizophyllan polysaccharide and its role in treatment of bone defects	Saideh Hemati[1], Raheleh Halabian[2], Mohsen Ghiasi[3], Ashrafalsadat Hatamian-Zarmi[4], Ali Salimi[5]*
4	The Effects of anti-inflammatory of phycocyanin extracted from Spirulina platensis by evaluating TLR2 pathway in HEK293.TLR2 cells	Arineh Hartoonianpoor[1], Tahereh Naji [1*], Rahim ahmadi[2]
5	ceRNome world as a milestone player in personalized medicine of breast cancer	Mahsa M.Amoli*[1], Forough Taheri[1]
6	Encapsulation of phenolic compounds of Smirnovia iranica as a novel anticancer and antioxidant potential	Negin Shafaei[1], Helia Ghafaripour[1], Ehsan Karimi[1*]
7	Differentiation of Mesenchymal Stem Cells(MSCs) to Osteogenic Cells on Composite Scaffolds Containing vitamin D2 and Chondroitin Sulphate(CS)	Kiana Tabari[1], Raheleh Halabian[2], Maliheh Entezari[3,] Mohsen Ghiasi[4], Ali Salimi[5*]
8	Personalized Skin Care; A review	Negin Noorbakhsh[1, 2†], Ali Akbari[1, 3†], Kambiz Akbari Noghabi[1]
9	DNA Methylation Profile of Stem Cells as Cellular Mediators for Bone differentiation	Seyede Atefe Hosseini[1*], Seyed Javad Hoseini[1]
10	Comparison of the therapeutic effects of amniotic membrane mesenchymal stem cells, directly and indirectly in renal failure induced by acute cardiac ischemic in male wistar rats	Amir Akbari Armand[1], Mahsa Ale-Ebrahim[2*],Nooshin Barikrow[1], Fatemeh roholah[1]
11	Combined application of amniotic membrane mesenchymal stem cells differentiated to cardiomyocyte and modified PGS-co- PCL scaffold in an experimental model of myocardial ischemia-reperfusion	Nastaran Bahrami[1], Mahsa Ale-Ebrahim[2*], Yasin Asadi [3] ,Nooshin Barikrow[1], Ali salami[4] Fatemeh roholah[1]

12	Inhibitory effect of mesenchymal stem cell derived from the amniotic membrance on SK-Br-3 breast cancer cells and CDK2 and Caspase3 genes expression	Parnian Azari [1], Fatemeh Rouhollah [1*], Nooshin Barikrow[1]
13	Diagnostic Chlamydia Trachomatis by PCR in Women with Frequent Abortions in Chalus (North of Iran)	Melika Jalalian[1], Haniyeh Bashizadeh Fakhar[2*],
14	Evaluation of genetic changes in exon 1 of human beta hemoglobin (HBB) gene in patients with thalassemia in Mazandaran province using the technique PCR-sequencing	Parnian Sadat Shahidi[1], Haniyeh Bashizadeh Fakhar[2*],
15	Proteome Profiling of Ductal Carcinoma in Situ	Haniyeh bashi zadeh fakhar*[1], Mohamd Esmaeel Akbari[1],Mostafa Rezaei-Tavirani [2] ,
16	Investigating the role of BRCA2 gene in breast and pancreatic cancers	Sara Kazemirad rad[1], Haniyeh Bashi zadeh Fakhar[2]
17	Stem cells, therapeutic impasses and new clinical perspectives focusing on conditioned media and exosomes: Review	Yousef Terme[1] , Mohsen Marzban*[2], Paniz Sadafi[1]
18	miR-6089 regulates the N-Glycan biosynthesis signaling pathway in the retinoblastoma development by modifying the expression of ST6GAL2: Integrated High-throughput bioinformatics investigation	Mohammad Rezaei[1, 2], Reza Ghelich[1, 2], Mohammad Hossein Donyavi[1, 2], Saina Adiban[1, 2], Mansoureh Azadeh[2, *]
19	lncRNA HELLPAR modulates Ion binding process and Metabolism of Water-Soluble Vitamins signaling pathway through the up-regulation of MTHFD2 in retinoblastoma patients	Reza Ghelich[1, 2], Mohammad Rezaei[1, 2], Mohammad Hossein Donyavi[1, 2], Saina Adiban[1, 2], Mansoureh Azadeh[2, *]
20	Identification of interaction between lncRNA and mRNAs of GABRB2 and GRM3 and neuron signaling pathways associated with the immune system in Lupus (SLE) background	Mahdieh Bakhshayesh[1], Parisa Rabiei Chamgordani[1] , Mohammad Rezaei[1], Mansoureh Azadeh[1]*,
21	Stem Cells and Personalized Medicine; New hopes for cancer therapy	Kimia Sadat Esfahani [1], Maryam Eslami [1,2*]
22	Rs546479213 modulates endocytosis signaling pathway via increasing the binding probability of miR-548bb to SH3GL2 in gastric cancer patients: integrated bioinformatics and high-throughput analyses	Fariba Heidari Esfahani[1], Erfaneh Heidari Esfahani[1], Mohammad Rezaei[1], Mansoureh Azadeh[1, *]

23	SPINT1 regulates cell proliferation through positive co-expression with TMPRSS4 in the pancreatic ductal adenocarcinoma cancer patients	Tahereh Honarmand[1,2], Niloufar Taherikalehmasihi[2], Nima Masaeli[2], Mohammad Rezaei[2], Mansoureh Azadeh[2,*]
24	Whole exome sequencing identifies a novel variant in COL1A2 gene in Iranian child with Osteogenesis imperfecta disease	Syedeh Faezeh sherafat[1]
25	A closer look at changed biomarkers in response to Mesenchymal Stem Cell - therapy in Muscular dystrophies. A scoping review of clinical and experimental studies	Neshat Najaf Najafi1[, 2, 3], Amir Reza [4,2] Boroumand, [5,2,6] Maedeh Amiri-Shahri, [5,2,6] Fatemeh Rasouli [5,2,6] Negin Armide, 7,2 Najmeh Kaffash Farkhad[*, 7,2] Jalil Tavakol-Afshari[*]
26	lncRNA HEPPLAR regulates cell proliferation through positive co-expression with CCNB1 in the liver cancer patients	Parisa Samani[1], Mohammad Rezaei[1], Mansoureh Azadeh1 *
27	A scoping review of diagnostic biomarkers in response to Mesenchymal Stem Cell - therapy in Amyotrophic lateral sclerosis disease	Parizad Najafi[1,2,] Amir Reza Boroumand[3,2,] Shahrzad Najafi [1,2], Jalil Tavakol-Afshari[4,2] Zahraa Al-Khazaali[4,2] Amir Shokr[i5,2] Amir Mehdi Davari, [, 6, 2] Reza Assaran-Darban[1,2,] Sajad Sahab-Negah[3,2]*, Najmeh Kaffash Farkhad [*4,2,]
28	Evaluation of clinical and specific biomarkers following Mesenchymal Stem Cell transplantation in ALS patients	Shahrzad Najafi [1,2],Parizad Najafi[1,2], Reza Assaran Darban [1], Amir Reza Boroumand [2,3] , Sajad Sahab-Negah[2,3],Najmeh Kaffash Farkhad [2,4], Jalil Tavakol-Afshari. [2,4]*
29	Evaluation of genetic variations in exon 6 of the SPATA6 gene in infertile men with acephalic spermatozoa syndrome	Seyedeh-Nadia Mahmoudi Nasrabadi[1] ,Maryam Eslami [1, 2] ,Marjan Sabbaghian [3]
30	Stiff Person Syndrome: A successful Case Report of Mesenchymal Stem Cell and exosome-therapy for a young female patient with coexistence of sero-positive antibody to Glutamic Acid Decarboxylase	Amirreza Boroumand[1], Najmeh Kaffash[2] Farkhad,Mohammad Ali Khodadoust [2],Jalil Tavakol Afshari [2]*
31	A scoping review of biomarker changes in response to Mesenchymal Stem Cell-therapy in Ataxia disease.	Sajjad Mollaei [1,2] , , Amirreza Boroumand [2,3] , Sahel Ghorbani Kalateh [1,2] , Kimia Zare [1,2] ,Sahar Ghorbani Kalateh [1,2] , Reza Assaran-Darban [1,2] , Najmeh Kaffash Farkhad[2,4]*, Jalil Tavakol Afshari
32	The Karyotype of Patients with Aneuploidy and Their Parent's Age , Geographic Region, and Family History	Zeinab Faghih Malek Marzban [1,2]**, Fatemeh Nemati [2,3] ,[*] Maryam Eslami[2,3]** , Dariush Farhoud [4,5,6]**, Mehdi Afshari [7], Alireza Khoshdel [8,]
33	A scoping review of clinical trials using Mesenchymal Stem Cells for Parkinson's disease. Which biomarkers have diagnostic value?	Sahel Ghorbani Kalateh[1,2], Amirreza Boroumand [2,3] ,Sahar Ghorbani Kalateh [1,2] , Sajjad Mollaei[1,2], Kimia Zare[1,2],Najmeh Kaffash Farkhad [2,4] *, Jalil Tavakol Afshari[2,4] *

34	Recognition of biomarkers with diagnostic value in response to Mesenchymal Stem Cell-therapy in Multiple sclerosis patients. A scoping review of clinical studies	Sahar Ghorbani Kalateh [1,2] ,Amirreza Boroumand [2,3] ,Sahel Ghorbani Kalateh [1,2] , Fatemeh Ghorbanisaber [2,4] , Shokofeh rezapour mashhadi[1,2],Fateme Kalhori [1,2],SeyedehKimia Arabi[1,2], Reza Assaran-Darban[1,2],Najmeh Kaffash Farkhad [2,5] *, Jalil Tavakol Afshari[2,5] *
35	Which biomarkers mainly change in response to Mesenchymal Stem Cell (MSC) - therapy in Autism disease? A scoping review of clinical and experimental studies	Mohammad Ali Khodadoust [1,2] , Amirreza Boroumand [2,3] , Sajjad mollaei [2,4] , Maryam Boozari [2,5] , Sana Pournazari[2,5], Navid Pousti Gonabadi [2,6,7] , Reza Assaran-Darban [2,4], Najmeh Kaffash Farkhad [1,2] *, Jalil Tavakol Afshari[1,2] *
36	Personalized therapy in Retinitis pigmentosa: Novel therapeutic horizons appear over current treatments	Mojtaba Ghorbani[1], Reza Salarinia[2]*
37	The role of Epithelial Mesenchymal Transition (EMT) in pathogenesis of cardiotoxicity: Diagnostic & Prognostic approach	Ali Kardooni [1] , Aida Bahrampour [2] , Somaye Golmohammadi [3] , Arsalan Jalili [4,5] , Mohammad Mobin Alishahi [6]*
38	Resveratrol; promising agent for improving the ability of adipose-derived stem cells	Alireza Salimi[1], Zahra Najafpourshehni[2], Reza Salarinia*[1]
39	GK-AS1 LNCRNA axis regulates the PCK1 mRNA in pathways leading to Glycolysis and Gluconeogenesis: Differential Expression of hepatocyte-like cells (HLCs) differentiated from human induced pluripotent stem cells (iPSCs)	Mahdieh Bakhshayesh, Fariba Tahmasebi,Mohammad Rezaei, Mansoureh Azadeh*
40	Examination genes profile changes after treatment of MS disease using stem cells by in silico method	Sayedeh Zahra Shirdeli [1] Mohammad Rezaei [1] Mansoureh Azadeh [1]
41	Integrated systems biology analysis of differentially expressed coding and non-coding RNAs in multiple sclerosis patients: High-throughput expression analysis	Fatemeh Amini[1], Mohammad Rezaei[1], Mansoureh Azadeh1, *
42	The medicinal role of propolis and caffeic acid in controlling the function of pro-inflammatory cytokines interleukin-1β, IFN-γ and interleukin-6 in Alzheimer's disease	Fatameh Rouhollah*
43	Evaluation of the Expression Levels of HRG-AS1 and LOC124905242 in Multiple Sclerosis	Mohammad Hashemiana, +, Melika Khorsandia, +, Mansoureh Azadehb,*

44	Effect of LEF1 gene in gastric cancer	Negar Pedaran [1] , Tayebeh Bahrami [1] , Mansoureh Azadeh [1] , Mohammad Rezaei [1]
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Phenyl acetate as a new inducer for neural differentiation of human adipose-derived mesenchymal stem cells in vitro

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Background: The increase in damages observed in the peripheral and central nervous tissues has led caused scientists to pay special attention to the applications of regenerative medicine in the nervous tissue. Stem cells have raised hope for potential treatments of diseases that currently lack therapeutic methods and they are capable of self-renewal and differentiation into many cell types. Mesenchymal stem cells derived from the human adipose tissue (hADMSCs) could transform into different types of cells such as bone cells and cartilage among others. Specifically, stem cells can be differentiated into different types of cells such as neuronal cells.

Methods: Human ADMSCs were cultured in DMEM (high glucose) culture medium containing 10% fetal bovine serum and 1% Penicillin-Streptomycin. Induction of hADMSCs was done in the differentiation medium containing retinoic acid, IBMX and forskolin with and without phenylacetate during two weeks. The optimal dosage of phenylacetate was calculated by MTT assay. Then, the expression of MAP-2 and NSE genes were evaluated by the real time RT-PCR technique on days 7 and 14 after neural induction of hADMSCs. Also, the expression of neural specific proteins was evaluated by immunocytochemical technique (ICC).

Results: The obtained results showed that the expression of MAP-2 and NSE genes as well as MAP-2 and Gamma-enolase proteins in differentiated cells with phenylacetate was increased compared to the control group.

Conclusion and discussion: Our results showed phenylacetate increased the neural differentiation efficiency of hADMSCs. This outcome can be used in vivo experiments in the future.

Keywords: Mesenchymal stem cell, Differentiation, Neural cells, Phenylacetate, Tissue engineering

Osteogenic differentiation of hWJ-MSCs in the presence of Rubia tinctorum extract nanoemulsion and Alizarin active ingredient

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Background: Bone is a mineralized connective tissue that has the ability to regenerate with high perseverance and is also known as the strongest tissue in the body. Human mesenchymal stem cells (MSCs) are powerful cells which play an essential role in regeneration and reconstruction of demaged tissue by enhancing cell proliferation and differentiation.This study aimed to evaluate the expression of bone specific genes in the differentiation process of human Wharton's jelly stem cells (hWJ-MSCs) in the presence of Rubia tinctorum extract nanoemulsion (R.tENe) with Alizarin active ingredient in vitro.

Methods:hWJ-MSCs were cultured in vitro and differentiation was induced by bone differentiation medium containing R.tENe as well as active ingredient. The optimal doses of R.tENe and active ingredient were determined using the MTT method and Acridine orange-ethidium bromide (AO/EB) staining. Bone differentiation was evaluated by alkaline phosphatase (ALP) activity, Alizarin Red staining and calcium content assay on the 7th and 14th days after induction.

Conclusion and Discussion: The results of MTT and AO/EB assays showed that the optimal doses for the R.tENe and Alizarin were 10 and 25 µg/ml, respectively. The results of ALP activity showed that differentiated hWJ-MSCs in the presence of R.tENe and active ingredients had more ALP activity and calcium content than the control sample, which was obviously confirmed by Alizarin Red staining. It was also found the R.tENe and Alizarin active ingredient can increase the efficiency of osteogenic differentiation of hWJ-MSC ($p\text{-value} \leq 0.05$).

Keywords: Wharton's jelly-Mesenchymal Stem Cells, Osteogenic differentiation, Nanoemulation, Rubia tinctorum, Extract, Alizarin

Osteogenic differentiation of human adipose-derived mesenchymal stem cells in the presence of schizophyllan polysaccharide and its role in treatment of bone defects

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Background: Bone is a dynamic tissue with special properties and has the ability to regenerate and have high strength. Although the remodeling process is mediated by osteoblasts and osteoclasts, some bone defects and injuries from trauma, infections, and surgery are too severe for autorepair. Human mesenchymal stem cells play a very important role in regeneration processes in the body, finding a suitable inducer for the treatment of osteogenesis disorders and diseases is very important.

Materials and methods: Human adipose tissue derived mesenchymal stem cells (hADSCs) were cultured in DMEM culture medium containing 10% fetal bovine serum (FBS) and 1% antibiotic penicillin/streptomycin. Induction of differentiation was done by bone differentiation medium on mesenchymal stem cells. Schizophyllan was also used as an inducer in this study. The optimal dosage of schizophyllan was calculated by MTT technique and Acridine orange-ethidium bromide (AO/EB) staining. Bone differentiation was evaluated using alkaline phosphatase (ALP) activity test and Alizarin Red staining on the days 7 th and 14 th.

Results: The results of MTT assay and Acridine orange-ethidium bromide staining showed that the optimal dosage of schizophyllan is 10 µl/ml. Subsequently, the results of alkaline phosphatase (ALP) activity indicated that the medium containing schizophyllan demonstrated higher alkaline phosphatase expression than the medium containing bone differentiation factors alone, which was also confirmed by Alizarin Red staining.

Conclusion: This study obviously declares that schizophyllan can induce bone differentiation mechanism in hADSCs by increasing the production of ostegenic enzymes (p- value≤0.05).

Keywords: Mesenchymal stem cell, Osteogenic differentiation, Schizophyllan, Tissue engineering

The Effects of anti-inflammatory of phycocyanin extracted from Spirulina platensis by evaluating TLR2 pathway in HEK293.TLR2 cells

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Running title: Anti-inflammatory effects of phycocyanin extracted from Spirulina platensis

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Abstract

Inflammation is the immune system's natural response to injury or disease and is a defense mechanism in the body. The aim of this study was to evaluate the anti-inflammatory effects of phycocyanin extracted from Spirulina platensis by evaluating the TLR2 pathway in HEK293.TLR2 cells. HEK293.TLR2 cell line was prepared and cultured in DMEM medium and phycocyanin was extracted from the S. platensis and MTT test was performed to evaluate the cytotoxic effects. Then the expression of NFKB, Map kinase and MyD88 genes was evaluated by Real Time PCR. The results of our study showed that there was not any significant difference in the viability of HEK293.TLR2 cells in the groups receiving phycocyanin. The expression of Map Kinase, MYD88, NFKB enzymes in the groups receiving lipoticoic acid were significantly higher than phytocyanin and control group. The results displayed that the expression of MYD88, Map Kinase and NFKB was higher in the group receiving lipothic acid and the group receiving lipothic acid / phycocyanin than the group receiving phycocyanin and the control group. The NFKB study also showed that the gene expression in the groups of phycocyanin, lipoic acid and lipoic acid / phycocyanin group was significantly higher than the control group.

Keywords: Inflammation, MYD88, Map Kinase, NFKB

ceRNome world as a milestone player in personalized medicine of breast cancer

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Abstract:

Breast cancer is the most prevalent diagnosed and second leading cause of mortality in women. Despite noteworthy efforts to improve early detection and therapeutic efficacy of BC, the predominant basis for the poor prognosis of cancer patients harboring various malignancies maintains as a drawback, which is greatly due to the intricacy and sever heterogeneity in various levels of its etiology, especially in transcriptomic profiles. Since the introduction of "ceRNome", combined terms competing endogenous RNA (ceRNA) network (ceRNET) and –ome, as a notion referring to the integration of reciprocally tying RNA molecules in a comprehensive cellular environment, there have been tremendous advances in the ceRnome profiling specific to every subtype of breast cancer, which can hold great promise in guiding personalized treatments. ceRNomes are known to affect a variety of components of genome function, including epigenetics, gene transcription, splicing, translation, as well as many central biological processes like cell cycle progression, cell differentiation, development, and pluripotency. Growing computational, mathematical, and experimental tools have been applied for decoding ceRNomes and deciphering various aspects, in which how they impact patients' response to treatment. When combined with other regulatory mechanisms, these ceRNETs in a specific global post-transcriptional context form a complex orchestration of signaling that eventually lead to a better prognosis. We propose that ceRNETs that implicate in diverse view of breast malignancy could be used to develop new targeted and tailored therapeutics providing an avenue perspective to introduce promising personalized treatment modalities and unique opportunities to circumvent ongoing shortcomings in breast cancer patients.

Keywords: Breast cancer, ceRNA, ceRNETs, ceRNome, Personalized medicine

Encapsulation of phenolic compounds of Smirnovia iranica as a novel anticancer and antioxidant potential

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ABSTRACT

Nowadays polyphenols have been applied as a natural anticancer and antioxidant agent. They are important metabolites responsible for therapeutic benefits to treat and prevent numerous degenerative diseases. This is because natural compounds have incomparable structural diversity 1and "drug-like" properties with relatively small molecular weight. The encapsulation technology has great attention and interest in the delivery of phenolic compounds as this technology could help in maintaining all features of bioactive compounds such as potent and strong protection. Smirnovia Iranica (Fabaceae) popularly known as Dome-Gavi in Iran. This herb has a wide range of traditional medicine use as immunomodulator, anti-bacterial, disinfection, antidiabetic, anti-inflammatory agent. This study was conducted to determine the cytotoxicity and antioxidant properties of the phenolic rich extract (PRE) loaded microcapsules obtained from Smirnovia Iranica. For this purpose, The PRE was obtained from Smirnovia Iranica using fractionation by different polarity solvents and the highest PRE was encapsulated by the combination of modified starch, maltodextrin, and whey protein concentrate as wall materials using a spray dryer. After characterization by DLS, SEM and ZETA potential methods, its toxicity effect against normal (HFF) and pancreatic cancer (PANC) cells were evaluated by MTT assay. The occurrence of apoptosis in cancer cells was assessed by flow cytometry and molecular analysis. The obtained results illustrated that synthesized microcapsules had a capsulation efficiency of 91.3% with a particle size of 376 nm and had strong antioxidant activity through inhibiting DPPH free radicals and ferric reducing ability. Through MTT assay, the selective toxicity of synthesized microcapsule against of pancreatic cancer cells (IC_{50}:92.75 µg/ml) is reported while HFF cells indicate no cytotoxic impacts. The gene profiling indicated the significant enhancement of caspase 3 and 9 genes through activation of the intrinsic apoptotic pathway. Our funding recommended that, the developed microcapsules loaded PRE of Smirnovia iranica has the potential to be applied as a selective anticancer and antioxidant agent.

Keyword: Anticancer activity, Encapsulation technology, Pancreatic cancer, Gene profiling.

Differentiation of Mesenchymal Stem Cells(MSCs) to Osteogenic Cells on Composite Scaffolds Containing vitamin D2 and Chondroitin Sulphate(CS)

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Background: Current failures in tissue grafts can be a main reason for developing tissue engineering products. Scaffolds are new biomaterials which able to boost bone repair or regeneration. Collaboration of stem cells and bioscaffolds can be a treatment instead of bon grafting. Mesenchymal stem cells are able to differentiate to many cell linages such as, osteogenic cells.

Methods: Carboxy Methyl Cellulose (CMC) and Glycerol Sebacic Acid (PGS), are natural and synthetic polymers in turn. In this study CMC and PGS scaffolds were made by salt washing method. Inducers (D2 and CS) loaded in scaffolds structure. Then, they characterized whit polymer test. Such as, FTIR and SEM. For next cell tests at first, scaffolds were sterilized with 70% ethanol for 12 hours, after drying they were exposed to UV for a hour. They prepared for following test with punching to little disks. Isolated MSCs from adipose tissue (ADSCs) seeded and cultured on both control and induced scaffolds. Optimal doses of inducers for Cell viability, growth and proliferation checked by MTT assay and Acridine Orange (AO) staining in 2,4 and 6 days of cell culturing. Cell differentiation checked by Alkaline Phosphatase activity and Alizarine Red staining Osteonectin and Runx-2, two bone gene markers, expression studied by Real Time PCR(RT-PCR).

Results: Polymer tests results confirmed suitable properties of scaffolds for cell culturing. The obtained results from MTT and AO showed that not only the scaffolds cause cell viability, but the cells show increased growth on induced scaffolds. Observations of more ALP activity and more Calcium deposits secretion during Alizarin Red test on induced scaffolds confirmed better biological ASCs behavior in differentiation to bone cells on them. Increasing in Osteonectin and decreasing in Runx-2 genes expression results support CMC and PGS scaffolds as a suitable substrate for tissue engineering.

Conclusion and discussion: Our results showed that CMC and PGS scaffolds and vitamin D2 and Chondroitin Sulphate are effective on cell growth and differentiation. This outcome can be used in vivo experiments in the future.

Keywords: Differentiation, proliferation, Scaffolds, Stem cells, Tissue engineering.

Personalized Skin Care; A review

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Abstract:

The skin, which is also the biggest organ in the body, is frequently the first line of defense against environmental toxins, earning it the reputation as the sentinel organ of the human body. Additionally, the microbiome on the surface of our skin, an ecosystem made up of microscopic creatures, is a separate organ. To put it simply, the microbiome is a bacterial ecosystem that lives on the skin's surface. The health of the skin is one benefit of having a balanced microbiome. Everyone has their own unique microbiome. This is partially formed at birth and is impacted by our genetic heritage. Afterward, a variety of factors, like our nutrition, the environment, where we live, the air we breathe, or even the things or people we come into contact with, might change it during the course of our lives. A greater comprehension of how the genes in the cells that make up the skin are regulated and how this regulation results in changes in biological response is needed in order to better grasp the molecular events that take place when the skin adapts to its environment. Numerous genes have been linked to the regulation of the synthesis of functional proteins that are related to skin conditions like inflammation sensitivity, anti-oxidation, anti-glycosylation, aging, collagen regeneration, moisturizing, and others. These genes have been found to have associations with people's skin colour, skin inflammation, skin type, sensitivity, and other traits. Using a variety of anti-aging creams may or may not be able to treat or even prevent skin changes. As a result, not everyone will experience these items' effects or the body's response in the same way. As a result, the book on the human genome may be the best resource for locating the most precise answer. An individual's skin type can be determined, and the proper skin care can then be employed. An approach that can be used to find substances to include in cosmetic formulations that improve the appearance of aged skin is global gene expression profiling, also known as genomics. The advancement of genetic science in the creation of tailored medicine in the area of skin care is examined in this study.

Keyword: Personalized- Skin Care—Review

DNA Methylation Profile of Stem Cells as Cellular Mediators for Bone differentiation

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Abstract:

Stem cells (SCs) nowadays are regarded as promising candidates with excellent properties in cell-based therapy for the regeneration of damaged bone tissues that are either incurable or intractable due to the insufficiency of current therapies. Epigenetic mechanisms play essential roles in stem cell maintenance, differentiation and expression pattern during bone regeneration processes. Recent studies suggest that SCs differentiate into osteoblasts, and this differentiation is regulated by some specific patterns of epigenetic modifications. In osteogenic differentiation of stem cells, DNA methylation, histone modifications, and microRNAs (miRs) regulation are involved in bone repair. For instance, CpG methylation of the osteocalcin promoter considerably decreases during in vitro osteoblast differentiation of SCs. However, many of the mechanisms and the role of epigenetic changes are far from being fully understood. In this review, we studied DNA methylation patterns to determine whether specific differences existed among various stem cell types and summarize the recent advance about the methylations that control SCs commitment to osteoblasts and the potential clinical application of SCs epigenetics in future. In conclusion, this study suggested that the differential DNA methylation profiles could be related to the osteogenic potential of different stem cell populations. Additionally, the increased osteogenic potential of various stem cell might aid researchers or clinicians in making better choices regarding tissue regeneration and clinical therapies.

Keyword: Stem Cell, Epigenetic, Methylation profile, Bone Regeneration

Comparison of the therapeutic effects of amniotic membrane mesenchymal stem cells, directly and indirectly in renal failure induced by acute cardiac ischemic in male wistar rats

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Background: According to the World Health Organization (WHO), ischemic heart disease (IHD) and subsequent kidney failure have a very high prevalence. Scientists hope that by implanting mesenchymal stem cells (MSCs), they can replace the dead tissues and cause the damaged parts of the heart to function again and thus the kidney tissue.

Methods: In this study, MSCs were investigated using flow cytometry technique and then differentiated into osteoblast and adipocyte. Rats were divided into 3 groups including 12 animals including heart failure (HF) as a control group, HF+ hAMSCs injection to heart, HF+ hAMSCs injection to kidney. Then, Ischemia was induced by ligation of the left anterior descending (LAD) artery and the cells were injected into the damaged heart and kidney. After 2 days and 30 days, echocardiography was performed, and TNF-α was investigated in kidney tissue using immunohistochemistry technique and serum levels of urea and creatinine was examined.

Results: Flow cytometry results and differentiation of MSCs to adipocyte and osteocyte, confirmed the MSCs. In the in vivo, ejection fraction fractional shortening (FS), stroke volume (SV) have been increased in treatment groups in comparison with control. The expression of TNF-α protein on day 30, in the kidney cell injection group have significantly decreased compared to the control group ($P<0.05$). Levels of urea and creatinine on day 30 significant difference were observed between the kidney cell injection group and the control group.

Conclusion: As expected, the treatment using MSCs on day 2 after the induction of cardiac ischemia and subsequent kidney damage did not have a significant therapeutic effect compared to the control group, but after 30 days, the treatment groups especially, cell+ kidney treatment group has been able to reduce inflammation, improve the damaged area in the kidney tissue.

Keyword: Mesenchymal stem cells, Amniotic membrane, Cardiac ischemic, Kidney failure.

Combined application of amniotic membrane mesenchymal stem cells differentiated to cardiomyocyte and modified PGS-co- PCL scaffold in an experimental model of myocardial ischemia-reperfusion

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Background: According to the World Health Organization (WHO), about 3.9 million people die from ischemic heart disease (IHD) every year. Several clinical trials have shown that stem cell therapy is a hopeful therapeutic approach for IHD. Human amniotic membrane mesenchymal stem cells (haMSCs) have positive effects on the repair of myocardial ischemia/reperfusion (MI/R) injury via stimulation of endogenous repair mechanisms. Methods: Human amniotic mesenchymal stem cells were differentiated to cardiomyocytes using the CHANG differentiation medium (butyric acid, hyaluronic acid and retinoic acid). Ischemia-reperfusion was induced by ligation of the left anterior descending (LAD) artery in 48 male Wistar rats. The rats were divided into four groups each containing 12 animals, including heart failure (HF) as the control group, HF+ hAMSCs, HF+ hAMSCs+ scaffold, and HF+ scaffold. Echocardiography was performed 2 and 4 weeks after ischemic reperfusion to evaluate cardiac factors (ejection fraction, fractional shortening and stroke volume). The expression of VEGF protein was assessed in the rat heart tissue by immunohistochemistry. Result: In the in vitro our result shows fantastic cell survival when seeded on film. In the in vivo left ventricle ejection fraction (LEVD), fractional shortening (FS), end-diastolic (EDV), and stroke volume (SV) have been increased and systolic volumes decreased in all treatment groups in comparison with control. Although combination therapy has more positive effect in hemodynamic parameters, there is no significant difference between (HF + MSCs + scaffold) with other treatment groups. Also, In the IHC assay expression of the VEGF protein significantly increased in all interventions group. Conclusion: The implantation of MSCs and the modified scaffold significantly enhanced the cardiac functional outcome in this regard enhancement in cell survival and VEGF expression are involved as underlying mechanisms in which cardiac scaffold and MSCs exert a beneficial effect.

Keyword: Ischemia-reperfusion, Modified PGS-co- PCL, Cardiomyocyte, Amniotic membrane, Mesenchymal stem cells.

Inhibitory effect of mesenchymal stem cell derived from the amniotic membrane on SK-Br-3 breast cancer cells and CDK2 and Caspase3 genes expression

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Background: Despite significant advances in molecular basis of cancer and advances in cancer detection and treatment, it is still the main cause of death. Mesenchymal stem cells (MSCs) are a hopeful tool in cell therapies due to their multipotent, self-renewal, and immunomodulatory properties. Mesenchymal stem cell therapy is considered as a proper tool for biological activities and treatment of diseases and cancer. Methods: In this study, the suppressing effect of mesenchymal stem cells derived from human amniotic membrane (haMSCs) on SK-Br-3 breast cancer cells was studied. MSCs were isolated from human amniotic membrane and identity tests were performed. HaMSCs and SK-Br-3 cells were co-cultured. Apoptotic effect of hAMSCs on cells was studied by Acridine orange staining. Expression of CDK2 and caspase3 genes was performed by Real-time PCR and the effect of haMSCs on the cells migration was determined by scratch test. Results: haMSCs induce apoptosis in SK-Br-3 cells. Real-Time PCR analysis revealed a significant ($P<0.05$) decline in expression of CDK2 and an increase in expression of caspase3 genes. Positive result of scratch assay suggested that haMSCs prevented the migration of cancer cells. Conclusion: HaMSCs showed anticancer effects against SK-Br-3 cell line and according to its easy availability compliance with the principles of medical ethics, it can be considered as a confident way to treat this type of cancers. Then, more studies in this area are necessary and may be useful in the treatment of breast cancer.

Keyword: Amniotic membrane, Mesenchymal stem cells, SK-Br-3 breast cancer cells, Caspase 3

Diagnostic Chlamydia Trachomatis by PCR in Women with Frequent Abortions in Chalus (North of Iran)

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Background: Chlamydia trachomatis (C. trachomatis) has been reported to be the most common cause of bacterial sexually transmitted infections.This study aimed at scrutinizing the Chlamydia trachomatis screening tests using vaginal samples and at investigating the correlation between Chlamydia trachomatis infection and the incidence of abortion.

Materials and Methods: This Cross sectional study was conducted at gynecology clinic of Razi Hospital in Chalus, Iran from August 2017 to January 2018. A total of 50 vaginal swabs were collected. Detection of C. trachomatis DNA was performed from vaginal swabs.Independet t-test and chi-square were used yo compare the variables. $P < 0.05$ was significant.

Results: The total prevalence of C. trachomatis infection was 5(10%) in endocervical swabs of women. There were significant differences between chlamydia infection and duration of sexual activity. We did not find any significant difference between detection of chlamydial and abnormal vaginal discharged.

Conclusion: The results of our study suggested that all women experiencing a miscarriage should be screened for Chlamydia trachomatis infection and, if positive, adequately treated to prevent recurrent miscarriages.

Keywords: Diagnostic - Chlamydia Trachomatis -PCR - Frequent abortions

Evaluation of genetic changes in exon 1 of human beta hemoglobin (HBB) gene in patients with thalassemia in Mazandaran province using the technique PCR-sequencing

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Background: Thalassemia is the most common hereditary anemia which has a relatively high prevalence in Iran. In most cases, more than 300 mutations have been identified, which affect genes of alpha and beta globin chains and lead to lack of production or reduction of chains. Iran's population is composed of different ethnic groups, thus, determining the frequency and distribution of these mutations is essential in different parts of the country. We aimed to assess Thalassemia gene mutations in Mazandaran province.

Methods: In this cross-sectional study, 50 β-thalassemia patients with Age range 15-29 years old (23±7 years) were selected and their Genomic DNA was extracted by DNA extraction kit method and tested using multiplex gap-polymerase chain reaction (gap-PCR), amplification refractory mutation system-PCR (ARMS-PCR), and DNA sequencing. Finally 41 samples had the appropriate sequencing for analysis.

Results: 4 mutations were found on HBB genes. we identified mutations in codon 31 (T> C), codon32 (T> C) and codon30 (G> C) in the sequencing sequences. No change in codon 11 (C> T) was reported in normal NCBI mutations.

Conclusion: The frequencies of these mutations were different in various parts of the country. Therefore, defining thalassemia mutations is necessary to establish prenatal diagnosis programs leading to lower medical cost in Mazandaran province.

Keywords: Exon 1 - HBB- Gene - Thalassemia - PCR-Sequencing

Proteome Profiling of Ductal Carcinoma in Situ

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Background and aim: DCIS is the most common type of non-invasive breast cancer, accounting for about 15 to 30 percent. Proteome profile is used to detect biomarkers in the tissues of breast cancer patients by mass spectrometry. This study aimed to obtain the expression profile of DCIS proteome, and the expression profile of invasive biomarkers, and finally to introduce a dedicated biomarker panel to facilitate the prognosis and early measures for in situ breast cancer patients.

Methods and Materials: In this study, 10 patients with breast cancer (DCIS) were studied. Healthy (marginal) and cancerous tissue samples were obtained from patients for proteomics. Initially, all tissue proteins were extracted using standard methods, and the proteins were separated using two-dimensional electrophoresis. Then, the expression amount of the extracted proteins was determined by ITRAQ. The data were analysed by R software, and gene ontology was utilised for describing the protein in detail.

Results: 30 spots on gel electrophoresis were found in the tumor tissue group (sample), and 15 spots in the margin group (control) with $P<0.05$. Healthy and cancerous tissue gels showed that 5 spots had different expression. VWF, MMP9, ITGAM, MPO and PLG protein spots were identified using the site www.ebi.ac.uk/IPI. Finally, protein biomarkers for breast tumor tissue with margin were introduced with the names of P04406, P49915, P05323, P06733, and P02768.

Discussion: There are 5 critical proteins in inducing cancer pathways especially complement and coagulation cascades. The hall markers of a healthy cell to be cancerous are proliferation, invasion, angiogenesis, and changes in the immune system. Hence, regulation of protein plays a key role in developing recurrence to breast cancer in margins.

Keywords: Proteome, Profile, DCIS, Ductal Carcinoma in Situ

Investigating the role of BRCA2 gene in breast and pancreatic cancers

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Abstract :Breast cancer is the most common cancer among women worldwide, with about 2.3 million new diagnoses worldwide in 2020. Pancreatic cancer is one of the deadliest cancers of the digestive system and ranks fourth in cancer-related deaths. It is estimated that it will become the second cause of death by 2030. Various factors play a role in causing all types of cancers, but the importance and role of genetics has been proven in many studies. Genetic predisposition caused by mutations in autosomal dominant genes is the cause of 5 to 10% of all breast malignancies. Among these factors, germline BRCA2 mutations have been clearly associated with the development pancreatic cancer and breast cancer. BRCA2 is the larger than BRAC, located on chromosome 13q12-131 and primarily mediating homologous recombination (10). The role of BRCA2 is mainly as a DNA repair gene, mediating double-stranded DNA repair and thus chromosomal stability. In recent studies, the role of the Brca2 gene in cancers such as breast and pancreas has been discussed, because the identification of prognostic factors plays a very important role in the process of rapid treatment of patients. Therefore, considering the importance of this issue, this study investigates the role of the BRCA2 gene in the identification of cancers. Breast and pancreas have been paid.

Keyword: Investigating- the role - BRCA2 gene -Breast -Pancreatic Cancers

Stem cells, therapeutic impasses and new clinical perspectives focusing on conditioned media and exosomes: Review

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Introduction: In the last decade discussion about stem cells have opened a new hope in the treatment of many acute and chronic diseases, but despite all the advertisements and heavy costs, this treatment method has not been able to show its rightful place in clinical use. In this review article, we try to open up the reasons for this clinical impasse and new solutions to solve the problems facing cell therapy and point to the latest new findings to make the use of these cells more effective. Materials and methods: First, we searched the topic in reliable scientific databases such as PubMed, Scopus, and Science Direct matching the keywords of the article. Then, according to our strategy, we data extracted them. Result: A summary of the problems of direct use of stem cells is as follows 1. principle of Anoikis: Any cell that is separated from its microenvironment and placed in another tissue is prone to cell death. In many systemic injections, only 3% of cells reach the lesion site, and among this 3%, many of them undergo apoptosis.2. Problems of cellular proteomics: Stem cells also produce harmful soluble factors along with beneficial ones. Although these factors will eventually lead to recovery, in practice this recovery will not be very effective.3. Problems of blood-brain barriers 4. fusing stem cells with tissue cells. 5. Problems of the transplant method 6. Problems of the cultivation process, etc. **Conclusion:** Using the supernatant of stem cells and exosomes, which contains useful and anti-inflammatory factors and is discarded for cell transplantation, can be the best option for therapeutic uses. Therefore, the researchers of this project study a pre-conditioned medium with different protocols and try to create an ideal culture medium for treating many diseases.

Keywords: Stem Cell, Transplant, New Strategy, Therapeutic Effect

miR-6089 regulates the N-Glycan biosynthesis signalling pathway in the retinoblastoma development by modifying the expression of ST6GAL2: Integrated High-throughput bioinformatics investigation

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Introduction: The majority of retinoblastomas in one or both of the developing retinal cells of young children are caused by biallelic mutations of the retinoblastoma tumor suppressor gene, RB1. Retinoblastoma is the model genetic malignancy. Even though 95% of patients with bilateral retinoblastoma have not acquired the RB1 mutation, they all have heritable malignancies. In this study, we aimed to find novel biomarkers of retinoblastoma based on integrated systems biology approach and bioinformatics analyses.

Method: Dysregulated protein-coding genes in retinoblastoma patients were demonstrated based on microarray analysis (GSE58780). Pathway enrichment analysis was performed by KEGG online database. miRNA-mRNA interaction analysis was performed by the STRING online database. miRNAs with the following characteristics were selected as the novel regulators of retinoblastoma: binding probability (score): 1; binding site: 3'UTR; located in the seed region.

Results: Based on microarray analysis, ST6GAL2 has a significantly low-expression in the retinoblastoma patients compared to the control (logFC: -3.8314, adj. P. Value < 0.0001). Based on pathway enrichment analysis, ST6GAL2 regulates the N-Glycan biosynthesis signalling pathway. Protein-protein interaction analysis revealed that ST6GAL2 has significant interaction with B4GALT1-3, KMO, WDR64, PCDH9, KDM7A, and SLC5A7 proteins. miRNA interaction analysis revealed the top 25 regulatory miRNAs interacted with ST6GAL2. miR-6089 has stronger and the most significant interaction with ST6GAL2 mRNA (score: 1, position: 3'UTR, binding energy: -39.4).

Conclusion: miR-6089 could regulate the N-Glycan biosynthesis signalling pathway in the retinoblastoma patients, by reducing the expression level of ST6GAL2 as a potential tumour-suppressor and diagnostic biomarker of retinoblastoma. There was no previous study about the possible role of mentioned RNAs in retinoblastoma development.

Keywords: Retinoblastoma, microRNA interaction, systems biology, microarray, pathway enrichment

lncRNA HELLPAR modulates Ion binding process and Metabolism of Water-Soluble Vitamins signalling pathway through the up-regulation of MTHFD2 in retinoblastoma patients

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Background: Retinoblastoma is a form of growing retinal cancer that develops in children and is brought on by the biallelic inactivation of the RB1 gene. Retinoblastoma and other cancers are likely to occur in adulthood in children with RB1 germline mutations. While there are some parallels between genetically modified mouse models of retinoblastoma and human retinoblastoma, there are also variances in their cellular development. In this bioinformatics investigation, we aimed to evaluate the expression level on novel retinoblastoma biomarkers and demonstrate a significant lncRNA-mRNA interaction network in retinoblastoma patients.

Methods: microarray analysis was performed to find novel dysregulated genes in the retinoblastoma samples. GSE58780 was analyzed using R Studio. Pathway enrichment analysis was performed by Reactome online database. Gene ontology analysis was performed by enrichr. lncRNA – mRNA interaction analysis was performed by lncRRIsearch online software.

Results: Microarray analysis revealed that MTHFD2 has a significant up-regulation in the retinoblastoma samples, compared to control (logFC: 4.9455, adj. P. Value < 0.0001). Based on gene ontology analysis, MTHFD2 contributed in the folic acid metabolic process. MTHFD2 is involved in Phosphate and magnesium ions binding function in the mitochondrial matrix and intracellular organelle lumen. Pathway enrichment analysis revealed that MTHFD2 regulates the Metabolism Of Water-Soluble Vitamins And Cofactors signalling pathway. lncRNA-mRNA interaction analysis revealed that lncRNA HELLPAR has significant interaction with MTHFD2 (sum of energy: -2765.56 kcal/mol).

Conclusion: lncRNA HELLPAR might regulate the expression level of MTHFD2 and affect the Metabolism Of Water-Soluble Vitamins signalling pathway in retinoblastoma patients. Dysregulation of HELLPAR could disturb the ion binding process in normal cells. MTHFD2 is a novel oncogene and diagnostic biomarker of retinoblastoma.

Keywords: HELLPAR, High-throughput analysis, Bioinformatics, microarray, lncRNA

Identification of interaction between lncRNA and mRNAs of GABRB2 and GRM3 and neuron signalling pathways associated with the immune system in Lupus (SLE) background

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Background: We want to study the interaction between lncRNA and mRNAs of GABRB2 and GRM3 and also their function as potent receptors that regulate different signaling pathways investigate.

METHOD: The GSE61635 dataset was analysed using the dataset Affymetrix was chosen and Microarray analysis was based on the R studio. This dataset was found in the GEO online database. By using lncRRIsearch, we investigated the interaction between mRNA and lncRNA. All miRNAs were regained from DIANA-Tar Base v.8 and miRNA-mRNA interactions were investigated using miRWalk. The other databases include KEGG, Reactome, and STRING online software.

RESULT: The expression of mRNAs of GABRB2, GRM3, PAK3, and ROBO2 has considerably increased. These RNAs have a single local base-pairing interaction (Energy = -38.61 kcal/mol) and (Energy = -13.36 kcal/mol). The miRNA interaction analysis has revealed that hsa-miR-218-5P could regulate the expression of GABRB2, GRM3, and PAK3 mRNAs and linc00461 lncRNA in the cell line blood in an interaction axis. GRM3 could regulate the following signalling pathway: Glutamatergic Synapse. GRM3 in Glia cells acts on Growth factor production and then, role plays as an Auto receptor in the Presynaptic terminal, Glutamate can act on metabotropic glutamate receptor GRM3 in Postsynapse that is important to many cellular processes, including Differentiation, Proliferation, and Apoptosis.

CONCLUSION: GABRB2 and GRM3 might be prognostic biomarkers. In blood and brain tissue, has-miR-218-5P can form a complex network with GABRB2, GRM3 mRNAs, and linc00461. In Neuroactive ligand-receptor interactions, GABRB2 and GRM3 play an important role.

Keywords: R Studio, Microarray analysis, microRNA interaction, Pathway enrichment

Stem Cells and Personalized Medicine; New hopes for cancer therapy

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Introduction: One of the most important causes of death in the world is cancer. The hallmarks of cancer are proliferative signaling, escape from growth suppressors, persistent replication, resistance to cell death. Functional profiling of tumor cells of a cancer patient has good potential for personalized cancer treatment. The present study examines new methods of cancer treatment through stem cells and personalized medicine.

Methodology & Theoretical Orientation: Many problems that existed in traditional cancer treatments, such as side effects on healthy cells, drug resistance, tumor recurrence; can now be solved by using the unique properties of stem cells (SCs), such as self-renewal, differentiation, tumor tropism. Also, Personalized Medicine, which means giving the right drug to the right person at the right time, based on pairing tumors with genotype-guided drugs that target selected tumor mutations, can help to treat cancer with the homing properties of MSCs towards the tumor site.

Findings: MSCs as carriers for anti-cancer agents, including MSC expressing IL-18, TRAIL, oncolytic adenovirus (CRAd5/F11), and paclitaxel-encapsulated nanoparticles in the treatment of breast cancer cells, B-cell acute lymphocytic leukemia, colorectal cancer, and lung cancer respectively. These interventions resulted in the inhibition of cancer proliferation and metastasis, induced apoptosis, and improved survival of patients. hBMSC-exos overexpressing miR-187 may function as a promising target for the prostate cancer treatment. The combination of IGF-1R mAbs/TKIs and other RTKs as anti-tumor agents is considered to a more effective strategy in cancer therapy.

Conclusion & Significance: Despite many studies aimed at using mesenchymal stem cells in cancer treatment and their tumor suppressive capabilities, these cells may contribute to tumor progression by increasing metastasis, tumor angiogenesis, epithelial-mesenchymal transition, and immune dysregulation. With The high potential of stem cells and the prominent role of personalized medicine, we can see definitive treatment for cancer patients in the future.

Keywords: Cancer therapy, Personalized Medicine, Stem Cells

Rs546479213 modulates endocytosis signalling pathway via increasing the binding probability of miR-548bb to SH3GL2 in gastric cancer patients: integrated bioinformatics and high-throughput analyses

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Background: Gastric cancer (GC) was the fifth most common malignant tumour in the world in 2020 with approximately 1.1 million new cases, and is the fourth leading cause of cancer death, with around 800000 deaths. SH3GL2 Enables identical protein binding activity. Involved in negative regulation of blood-brain barrier permeability; negative regulation of gene expression; and negative regulation of protein phosphorylation. Located in perinuclear region of cytoplasm.

Methods: Using GEO2R, GSE801948 was analysed and genes with significant differential expressions (|logFC| >2 and adjusted p-value <0.05) were selected. GEPIA2 and ENCORI online databases were used to validate the differential expression analysis. survival and co-expression analyses were performed by GEPIA2 and ENCORI. STRING online software was performed to demonstrate the protein-protein interaction analysis. Finding the possible dangerous single nucleotide polymorphisms (SNPs) in the 3'UTR region of selected genes was performed by miRNASNP. Using enrichr, gene ontology and biological pathways were determined. miRNA interaction was performed using miRWalk.

Results: SH3GL2 is significantly down-regulated (logFC = -1.319, adj. P value =3.21e-06) in gastric cancer samples. SH3GL2 has a significant role in the Endocytosis is a mechanism for cells to remove ligands, nutrients, and plasma membrane (PM) proteins. SH3GL2 and CADM2 had several significant interactions. hsa-miR-6756-5p significant interaction with SH3GL2 mRNA in the 3' UTR. rs546479213 SNP cause high desire to connected between hsa-miR-548bb-5p and SH3GL2 so this SNP cause SH3GL2 expression decreases. Low-expression of SH3GL2 has a significant negative correlation whit the survival rate of patients.

Conclusions: miR-6756-5p regulates the Endocytosis signaling pathway through regulation of SH3GL2 gene in gastric cancer samples. Rs546479213 might be one of the main causes of low-expression of SH3GL2 in GC samples.

KEYWORDS: Gastric cancer (GC), miRNA interaction, Pathway enrichment, Diagnostic Biomarkers

SPINT1 regulates cell proliferation through positive co-expression with TMPRSS4 in the pancreatic ductal adenocarcinoma cancer patients

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Background: Pancreatic adenocarcinoma (PAAD) is a highly lethal disease for which mortality closely parallels incidence. There is no standard program for screening patients at high risk of pancreatic cancer. In this study, we performed an integrated bioinformatics and systems biology investigation to evaluate a novel regulatory network in pancreatic ductal adenocarcinoma cancer.

Methods: Microarray analysis was performed on the GSE183795 dataset using GEO2R, ENCORI, KEGG, Ractome, and Enrichr performed pathway enrichment and gene ontology analyses. STRING performed Protein- Protein correlation analysis.

Results: Microarray analysis revealed that TMPRSS4, TSPAN1, and KRT19 have significant up-regulation; CERS4 and SYPL2 have significant down-regulation in pancreatic ductal adenocarcinoma cancer patients. Survival analysis based on GEPIA2 and ENCORI revealed that increased expression of TMPRSS4, TSPAN1, and KRT19, and decreased expression of CERS4 and SYPL2 have significant effects on the survival rate of pancreatic ductal adenocarcinoma cancer patients. Furthermore, Pathway enrichment analysis based on the Reactome database showed that TMPRSS4 regulates cell proliferation in PAAD patients. So, TMPRSS4 involved positive regulation of CLEC7A (also known as Dectin-1) in a pattern-recognition receptor (PRR) expressed by myeloid cells (macrophages, dendritic cells, and neutrophils) that detects pathogens by binding to beta-1,3-glucans in fungal cell walls and triggers direct innate immune responses to fungal and bacterial infections. Protein- Protein correlation analysis based on the STRING online website illustrated that TMPRSS4 has a significant correlation with SPINT1 (r: 0.590, p-value < 4.63e-18).

Conclusion: Protein TMPRSS4 regulates cell proliferation in pancreatic ductal adenocarcinoma cancer patients. TMPRSS4, as a potential oncogene, has a significant up-regulation in PAAD cancer samples. The high amount of TMPRSS4 has a significant effect on the survival rate of pancreatic ductal adenocarcinoma cancer patients and SPINT1 interaction.

Keywords: Systems Biology, Microarray analysis, Pathway enrichment, TMPRSS4

Whole exome sequencing identifies a novel variant in COL1A2 gene in Iranian child with Ontogenesis imperfect disease

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Background: Short stature is a common disorder in pediatrics that can be caused by various metabolic diseases or early growth disorders that affect the function of the growth plate. Skeletal dysplasia is a group of diverse and heterogeneous clinical genetic disorders that include abnormalities. Growth, bone tissue or cartilage. The overall prevalence of these diseases is 2.3 to 7.6 per 10,000 live births in various epidemiological studies. Whole exome sequencing is known as an important method in identifying pathogenic genetic mutations in humans.

Methods: In this study, a 19-month-old boy from a non-consanguineous marriage with short stature, multiple fractures in the femur bone, and a history of femoral bone curvature was investigated in the third trimester fetal ultrasound. Blood samples were collected from the patient and family members. Genomic DNA was extracted using the column method. The genome of the patient was examined using whole exome sequencing and the genetic findings were confirmed through Sanger sequencing in the patient and other family members.

Results A new heterozygous pathogenic change with COL1A2:NM_00089:c.2404G>A:p.G802S was found in the whole exome sequencing data. The change in the patient's parents was checked, which was done in both Normal Homozygous changes.

Conclusions: The present study has shown the importance of proper genetic counseling and genetic diagnostic tests based on NGS for early diagnosis of patients. It also showed the vital impact of accurate molecular diagnosis in optimizing the clinical care provided to patients by providing early and appropriate treatment and the impact this has on improving the quality of life of the patient and his family.

Keyword :Skeletal dysplasia, Short Stature, Whole Exome Sequencing

A closer look at changed biomarkers in response to Mesenchymal Stem Cell - therapy in Muscular dystrophies. A scoping review of clinical and experimental studies

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Introduction: Muscular dystrophies are heterogeneous genetic-based diseases with limited management strategies led to weakness of skeletal muscle and ultimately death. Mesenchymal Stem Cell (MSC)-therapy recently applied for ameliorating progressive harmful symptoms. Finding valid biomarkers in response to this treatment is crucial to assess patient's status which is discuss in this scoping study.

Methods: A comprehensive search was applied through four electronic databases (PubMed, SCOPUS, Cochrane and Web of Science), using PRISMA guideline, up to 16 February 2023. All relevant clinical and pre-clinical studies evaluating biomarkers in response to MSC-therapy in muscular dystrophy disease were included and data were extracted and presented.

Results: From totally 291 searched studies, considering specific inclusion and exclusion criteria, 6 clinical articles including several various biomarkers and 40 experimental articles including nearly 60 biomarkers were finally included. The most repeated laboratory biomarkers in clinical studies were Creatine kinase (CK) and lactate dehydrogenase (LDH). Dystrophin, and dithiothreitol (DTT) were also more repeated than other investigated biomarkers. Muscle strength was also measured in various ways such as a set of CQ Dynamometer computerized force meters and electromyography (EMG). Also, the most important biomarker that was more frequently tested in experimental studies was dystrophin which was tested in twenty studies.

Conclusions: Evaluating muscle strength and other clinical assessments after MSC-transplantation provide valuable information about valid biomarkers in response to cell therapy in muscular dystrophy disease. Confirming that the biomarkers had positive or negative changes in response to this treatment definitely requires more clinical studies with a larger sample size, although in summary the results of this study report relatively favorable changes in response to this treatment.

Keywords: Muscular dystrophy, Mesenchymal Stem Cells, Biomarkers

lncRNA HEPPLAR regulates cell proliferation through positive co-expression with CCNB1 in the liver cancer patients

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Background: liver cancer is the third leading cause of death, especially in developing countries, where it is increasing daily. Because of its essential role in tumor suppression, p53 has attracted much interest in drug development. Any clinically successful therapeutic agent targeting the p53 pathway would save millions of lives. While the role of mutant p53 as a prognostic factor is well established, therapeutic modulation of its wild-type or mutant activities remains elusive. In this study, we performed an integrated bioinformatics and systems biology investigation to evaluate a novel regulatory network in liver cancer patients.

Methods: Microarray analysis was performed on the GSE121714 dataset using GEO2R. KEGG and Enrichr performed pathway enrichment and gene ontology analyses. lncRNA interaction analysis was performed using the lncRRIsearch database. ENCORI performed lncRNA-mRNA correlation analysis.

Results: Microarray analysis revealed that CDK 1, CCNB1, and RRM2 have significant up-regulation in liver cancer patients. Pathway enrichment analysis revealed that CCNB1 regulates cell proliferation in HCC patients. CCNB1 involved positive regulation of spindle microtubules' attachment to the kinetochore process in cyclin-dependent protein kinase holoenzyme complex. lncRNA HELLPAR has significant interaction with CCNB1 (sum of energy: -132.50 kcal/mol). Co-expression analysis revealed that the expression of HELLPAR has a significant correlation (r: 0.421, p-value < 0.0001).

Conclusion: lncRNA HELLPAR regulates the attachment of spindle microtubules to the kinetochore process through positive regulation of CCNB1 in liver cancer patients. CCNB1, as a potential oncogene, has a significant up-regulation in liver cancer samples. The high amount of CCNB1 protein in the cyclin-dependent protein kinase holoenzyme complex might affect the development of liver cancer.

Keywords: Systems Biology, Microarray analysis, Pathway enrichment, CCNB1

A scoping review of diagnostic biomarkers in response to Mesenchymal Stem Cell therapy in Amyotrophic lateral sclerosis disease

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Background: Amyotrophic lateral sclerosis (ALS) is a deadly neurodegenerative disorder, characterized by progressive degeneration of upper and lower motor neurons. Stem cell-based treatments recently have emerged as potentially effective approaches to delay this disease progression. The aim of the current study was to find out a valid biomarker in response to stem cell therapy at the clinical and preclinical investigations.

Method: Electronic databases (PubMed, SCOPUS, Cochrane and Web of Science) were searched in two complementary steps up to 29 January 2023, using PRISMA guideline, for review clinical and experimental articles assessing all biomarkers in response to MSC-therapy in ALS patients (and ALS-animal models). Relevant data were extracted from the included sources, and a comprehensive summary of results presented.

Results: Considering specific inclusion and exclusion criteria, 18 clinical articles including 52 biomarkers and 11 experimental articles including 48 biomarkers were finally included from the 1223 total searched articles. Clinical biomarkers including ALS-FRS and FVC were the most prominent biomarkers correlated with the patient's status. In addition, several other biomarkers like VEGF, MCP-1, IL-6, IL-10, and TGF-β in nearly connection with these parameters, recognized as markers with diagnostic value in response to MSC- therapy. Also, nine biomarkers were more repeated and common between both clinical and experimental studies including: TNF-α, MCP-1, VEGF, SDF-1, IL1-β, TGF-β, MAP2, NSE and CMAP.

Conclusion: Changes in ALS-FRS and FVC are the most repeated investigated clinical biomarkers in response to MSCs-therapy in ALS patients with close correlation with clinical improvement which can help clinicians and researchers for future studies. However, clinical studies with larger sample sizes will definitely provide more useful information in this field.

Keywords: ALS, Mesenchymal Stem Cells, Diagnostic biomarkers

Evaluation of clinical and specific biomarkers following Mesenchymal Stem Cell transplantation in ALS patients

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Background: Amyotrophic lateral sclerosis (ALS) is a deadly neurodegenerative disorder characterized by progressive degeneration of upper and lower motor neurons. Stem cell-based treatments recently have emerged as potentially effective approaches to delay the progression of ALS.

Method: In this single-center, open-label, un-controlled clinical trial, twenty ALS-patients were included considering define inclusion and exclusion criteria. Autologous Bone Marrow-derived MSCs (BM-MSCs) were isolated, expanded and characterized under standard conditions. Concurrent intrathecal (IT) and intravenous (IV) transplantation was applied for patients with equal amount of cells and the patients received cells (1×106 MSCs/kg BW) in two steps with one month interval. The patients followed in three time points (months 0, 1, and 3). At these times, serum and CSF samples were taken from each patient and specific biomarkers were assessed.

Results: No serious side effect was observed after cell transplantation in patients. The mean ALS functional rating scale-revised (ALSFRS-R) values remained stable during the follow-up periods. Forced vital capacity (FVC) also showed an increasing trend, and this increase showed significant difference in the third month compared to the before injections (months 0). The changes of oxidative biomarkers including superoxide dismutase (SOD) and nitric oxide (NO) and also inflammatory biomarkers including TNF-α and CCL2 during the follow-up period in none of the serum and CSF samples did not show any significant difference compared to the study' onset.

Conclusion: Our obtained results showed that simultaneous IV and IT injection of autologous BM-MSCs is a safe process. Also, the non-significant decrease in ALSFRS-R, and increase in FVC during the study period, as well as the stabilization of inflammatory and oxidative biomarkers' level, indicate the effectiveness of these cells in ALS patients.

Keywords: Amyotrophic lateral sclerosis, Mesenchymal stem cells, safety, efficacy

Evaluation of genetic variations in exon 6 of the SPATA6 gene in infertile men with acephalic spermatozoa syndrom

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Introduction: Acephalic spermatozoa syndrome is one of the most severe forms of teratozoospermia which causes male infertility. In this syndrome, the sperm's head is separated from the flagellum because there is a problem in head–tail junction. This syndrome has genetic implications in many cases. SPATA 6 (Spermatogenesis Associated 6) produces a testis-specific protein that is localized in the mature spermatozoa head-to-tail linkage site and plays a role in the attachment of the head-tail of the flagellum during spermatogenesis.

Background: In this study we investigated the variations of exon 6 of SPATA6 gene in infertile men with acephalic spermatozoa syndrome referred to Royan institute.

Method: In the present study, 10 infertile men with acephalic spermatozoa syndrome as a case group and 10 fertile men as a control group were recruited. DNA was extracted from peripheral blood and after designing primers, PCR reaction and sanger-sequencing were performed. The results of sequenced segments were analyzed by Finch TV and Blast.

Results: A heterozygous genetic variation (A>T) was observed in 3 patients with acephalic spermatozoa syndrome and 3 subjects of the control group in exon 6 of the gene.

Conclusion: Since the observed genetic variation was heterozygous, this variation cannot transform the amino acid and consequently, the protein structure and function. Due to the important role of protein SPATA6 in the attachment of thehead to thesperm tail, it is suggested to study the genetic variants of the other exons of this gene in infertile men with acephalic spermatozoa syndrome.

Keyword: SPATA6 Gene, Male infertility, Acephalic Spermatozoa Syndrome

Stiff Person Syndrome: A successful Case Report of Mesenchymal Stem Cell and exosome-therapy for a young female patient with coexistence of sero-positive antibody to Glutamic Acid Decarboxylase

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Background: Stiff Person Syndrome (SPS) is a rare neurological disorder characterized by fluctuating rigidity and painful muscle spasms. High-titer of anti- Glutamic Acid Decarboxylase (GAD) is common in this syndrome. This case report study, is reported a 24-year-old Iranian female patient with SPS presenting with unusual clinical manifestations of severe increase in anti-GAD up to 700 unit and severe muscle spasms, who underwent successful stem cells and exosome transplantation.Stiff Person Syndrome (SPS) is an extremely rare progressive neurological disorder leading to patient's disability (1). Antibodies against glutamic acid decarboxylase (GAD) are key diagnostic markers, but their role in disease pathogenesis is uncertain. Imunomodulatory therapy and symptomatic treatment synergically applied as a therapeutic strategy (2). In this regard, Mesenchymal Stem Cells (MSCs) and their derivatives like exosomes (3) are good candidates to suppress over-activated immune system leading to reduce auto-antibodies. The biggest advantage of this study is the use of combined cell- and exosome therapy protocol for the first time in the management of this syndrome in Iran.

A scoping review of biomarker changes in response to Mesenchymal Stem Cell-therapy in Ataxia disease.

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Background: Ataxia, a neurological disorder mainly characterized by the imbalance in the voluntary movements, is the main exhibition of cerebellar disease. Unfortunately, there is no definitive diagnostic biomarker and effective treatment method except traditional and complementary treatments in this field. In this regard, Mesenchymal Stem Cell (MSC) - therapy is known as a promising approach recently for ataxia patients. Of course, the changes of biomarkers in response to this treatment have not been well studied yet, and perhaps a comprehensive study in this field can open the way to find new diagnostic biomarkers.

Method: Comprehensive searches were carried out in each of 4 databases (PubMed, SCOPUS, Cochrane and Web of Science) without time limitation up to 29 January 2023 with the help of PRISMA guideline. All related clinical and experimental studies were extracted and relevant results reported.

Results: Considering define entry and exit criteria, 5 clinical studies containing 16 biomarkers and 14 animal studies containing 45 biomarkers were obtained from totally 417 searched articles. In human studies, nine of biomarkers were clinical (SARA- ICARS- ADL-FARS- BBS- SOT- MAS -neuroimaging with MRS-FDGPET) and seven of them were laboratory examinations (WBC- PLT -BG -CRP –CR, ALT, and AST). Motor coordination, motor behavior, and muscle strength were the most prominent repeated investigated biomarkers in animal studies.

Conclusion: Cerebellum imaging and clinical biomarkers, are among the most important diagnostic biomarkers in ataxic patients, most of which have shown relative-definite improvement in treated patients (and animal models) after MSC- therapy.

Keywords: Ataxia, Mesenchymal Stem Cells, biomarker

The Karyotype of Patients with Aneuploidy and Their Parent's Age , Geographic Region, and Family History

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Background:The most common chromosomal abnormality in humans is aneuploidy. Several factors have been shown to be responsible for the occurrence of aneuploidy, including parental age, geographic region, and family history.

Methods: Five ml of venous blood was collected from each patient, which was transferred to heparin-containing tubes and used for karyotyping. The blood was cultured in PRMI 1640 for three days, and then the stage of the slides was determined. Samples were then collected, and colchicine was added during division to stop metaphase. After chromosome separation, the slides were in room temperature for three days. Subsequently, 50 metaphases for each patient were examined by the Giemsa binding method to determine the karyotype. Data were described as mean (standard deviation) and percent frequency. Categorical and continuous variables were compared among different karyotypes using one way anova and chi square tests respectively. All analyses were performed using Stata version 14 software.

Results: It was found that from 682 patients, 126 patients had fathers below 35 years and 163 patients had mothers below 35 years. In addition the fathers in 81 patients and the mothers in 40 patients were older than 35 years old. The statistics of chromosomal changes were as follows: 163 cases of translocation, 103 cases of inversion, 216 cases of ps+, 53 cases of qh+, 30 cases of der and 117 cases of other karyotypes (trisomy 13 & 18, xxx syndrome, Marfan syndrome, frx, 45x, del, mar and klein felter syndrome). 347 patients (50.88%) had no complications and 77 patients (11.29%) had abortion complications.

Conclusions Patients with Ps+ karyotype had older fathers and mothers, suggesting that the type of karyotype is related to the age of the parents. These comprehensive fertility data could be useful for genetic counseling in parenatal diagnosis as well as in newly diagnosed postnatal cases. Many of the investigated cases in different geographical regions showed that most of the patients were from the central provinces and the least from the east of the country. In more than half of the patients, there was no disease history in the family. Among the reported complications, the most common was abortion.

Keywords: Personalized Medicine, Aneuploidy , Kayotype

A scoping review of clinical trials using Mesenchymal Stem Cells for Parkinson's disease. Which biomarkers have diagnostic value?

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Background: Parkinson's disease (PD) is a neurodegenerative disorder characterized by the classical motor symptoms of rigidity and tremor. Stem cell transplantation recently is known as a promising approach in this filed. The aim of this study was to identify the main biomarkers that change in response to this treatment in Parkinson's patients.

Method: Two complementary search steps were applied up to February 6, 2023 in four databases (PubMed, SCOPUS, Cochrane and Web of Science), using PRISMA guideline. All relevant clinical trials containing Mesenchymal Stem Cell (MSC) transplantation in PD disease were comprehensively evaluated.

Results: Regarding to define inclusion and exclusion criteria, from totally 990 articles, 9 studies containing 30 biomarkers were included. The most clinical valuation after cell therapy was based on both F-Fluoro-2-deoxyglucose positron emission tomography scanning (FDG PET) and magnetic resonance imaging (MRI) with close association with patient’s status. Unified MSA Rating Scale (UMSAR) was also used for efficacy assessment. BDNF, PDGF-BB, P-tau, Amyloid-β, NF-L, MCP-1, HGF, VEGF, KGF, and TPO were also more repeated investigated biomarkers.

Conclusion: In summary, the functional tests were the most prominent biomarkers that changed in response to cell therapy. Of course, the sample size of the reviewed studies was mostly small (the maximum sample size was 29), which were hopeful and requires more carefulness and caution regarding the investigation of these biomarkers.

Keywords: Parkinson's disease, Mesenchymal Stem Cells, diagnostic biomarkers

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Recognition of biomarkers with diagnostic value in response to Mesenchymal Stem Cell-therapy in Multiple sclerosis patients. A scoping review of clinical studies

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Background: Multiple sclerosis (MS) is known as the commonest non-traumatic autoimmune disorder of central nervous system with different clinical manifestations including physical disability, cognitive deficiency, and other signs with a sharp increased trend in societies, which mostly affects young people. Using Mesenchymal Stem Cells (MSC) in the treatment of MS patients has been increasing in recent years. Therefore, knowing the changed biomarkers in response to this treatment can be effective in diagnosing the disease process

Method: In this scoping review, 4 databases (PubMed, SCOPUS, Cochrane and Web of Science) systematically reviewed using PRISMA guideline without time limitation up to 5 February 2023.All relevant clinical studies included, their data extracted and reported.

Results: Respecting to define inclusion and exclusion criteria, from the total of 1890 searched articles, 33 clinical articles including 69 biomarkers were selected. 31 of them, were clinical biomarkers and 38 other biomarkers were in the category of immunological and paraclinical biomarkers. The most repeated clinical valuation was based on Expanded Disability Status Scale (EDSS) in studies (84%).Also, nearly all the trials (more than 50%) interpreted MRI lesion changes through T1, T2, and Gd enhanced lesions.

Conclusion: Functional tests and MRI images were the most changed biomarkers in response to MSC-therapy in MS patients, indicating the fact that the diagnosis of MS remains clinical, so their examination can provide optimal help to doctors in diagnosing the progress of the disease or treatment. However, most of the studies had a small sample size (The largest article included 48 patients), so conducting and reviewing studies with a larger sample size can definitely increase or decrease the validity of these findings.

Keywords: Multiple sclerosis, Mesenchymal Stem Cells, biomarker

Which biomarkers mainly change in response to Mesenchymal Stem Cell (MSC) - therapy in Autism disease? A scoping review of clinical and experimental studies

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Background: Autism is a neurodevelopmental disorder characterized by variable deficits in social behavior and language, restrictive interests, and repetitive behaviors. Today, Mesenchymal Stem Cell (MSC) - therapy is known as one of the alternative treatment methods for autistic patients without side effects. This scoping review article tries to find out which biomarkers mainly change in response to this treatment in autistic patients.

Method: Six main databases (PubMed, SCOPUS, Cochrane, Embase, ProQuest and Web of Science) were examined based on PRISMA guidelines, without any time limitation up to 30 January 2023, for assessing clinical and experimental studies of MSC-therapy in autism, and all relevant biomarkers were extracted and reported.

Results: From the totally 1718 searched articles and based on the specified inclusion and exclusion criteria, 9 clinical articles containing 24 biomarkers and 6 experimental articles containing 19 biomarkers proved eligible and included in this study. Behavioral and functional tests were among the most important biomarkers investigated in both clinical and experimental studies. Also, some laboratory tests, including CRP, ESR, and Macrophage-derived chemokine were more repeated evaluated biomarkers in clinical studies.

Conclusion: The results obtained from this scoping review suggests that MSC-therapy significantly improves functional scales and clinical biomarkers of autistic patients (and animal models). However, more clinical studies with larger sample sizes are definitely needed to confirm these results.

Keywords: Autism, biomarker, Mesenchymal Stem Cells

Personalized therapy in Retinitis pigmentosa: Novel therapeutic horizons appear over current treatments

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Background: Among inherited retinal dystrophies (IRDs), Retinitis pigmentosa (RP) has the most prevalence in various populations. RP is a hereditary retinopathy that possesses a heterogeneous genetically pattern that, according to mendelian inheritance, can be inherited via X-linked, autosomal dominant and recessive in which photoreceptor cells die. Initially, Photoreceptors degeneration and pigment migration occur during the early stages of disease followed by cone photoreceptors involvement in later stages. Common clinical manifestations include night vision loss, visual field constriction and central vision loss, which eventually lead to blindness. As a genetically heterogeneous disorder in nature, therapeutic approaches to retinitis pigmentosa require to turn the eye on the field of personalized medicine, including individual gene therapy as well as cell therapy. Although novel therapies hold a great promise to overcome irremediable conditions, the road ahead is challenging both ethically and technologically, so the emergence of more creative methods and strategies to tackle the obstacles is in great demand. Personalized medicine is an ever-changing field of science, and new involved genes appear to be taken into account for retinitis pigmentosa occurrence in different people. Hence personalized medicine, such as gene therapy and cell therapy, could be a promising approach to dealing with this disorder.

Keywords: Retinitis Pigmentosa, gene therapy, cell therapy, personalized medicine

The role of Epithelial Mesenchymal Transition (EMT) in pathogenesis of cardiotoxicity: Diagnostic & Prognostic approach

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Background :Cancer is one of the problems, which it is not still completely curable; the existing treatments are associated with many complications, that double its complexity. One of the causes of cancer cell metastasis is Epithelial Mesenchymal Transition (EMT). EMT can also cause cardiotoxicity and heart diseases such as heart failure, hypertrophy and fibrosis. Here we look at three factors: inflammation, oxidative stress and angiogenesis. Each of these processes through signaling pathways initially leads to EMT, and will subsequently lead to heart problems. The most frequent and important of these pathways are PI3K / Akt signaling, NF-kB signaling and TGF-B signaling. These three pathways are jointly involved in these three processes, and link apoptosis to the occurrence of EMT and cardiotoxicity. MicroRNAs (miRNAs) are another factor that are highly expressed in heart cells; they have very different effects, and inhibit or stimulate oxidative stress, angiogenesis and apoptosis via different signaling pathways, such as p38 / MAPK and Nrf2. Finally, it can be concluded that prevention of EMT and cardiotoxicity is very complex, due to its relationship with different pathways and processes; targeting the mentioned common pathways can have a great impact on controlling them.

Keywords: Epithelial Mesenchymal Transition, Cardiotoxicity, Pathogenesis, Molecular, Diagnosis.

Resveratrol; promising agent for improving the ability of adipose-derived stem cells

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Background: Tissue engineering applications can be achieved using adipose stem cells (ADSCs), which were identified in 2001 as a potential source of stem cells. ADSCs have one of the biggest advantages over MSCs in that they are abundant in number and proliferate faster than MSCs in the bone marrow, which allows them to expand rapidly and produce clinically relevant numbers of cells. Resveratrol (RSV) (3, 5, 4'-trihydroxystilbene) is one of the polyphenolic and phytoalexin compounds first discovered in 1940 in the root of white hellebore (Veratrum grandiflorum).

Method: The present study reviewed studies on the effect of resveratrol on improving the ability of adipose-derived stem cells.

Results: As a result of RSV reactivation, MSCs secreted more PDGF-DD, which stimulated ERK signalling in renal tubular cells, induced angiogenesis in endothelial cells, and improved cisplatin-induced renal injury. The paracrine effect of ADMSCs on INS-1 cells can be preserved by resveratrol by preventing the senescence of ADMSCs. Because of resveratrol's dosage-dependent effect on human stem cells, caution should be exercised when applying resveratrol as an anticancer therapeutic agent or nutraceutical supplement.

Conclusion: By increasing paracrine activity and inhibiting cellular senescence, RSV may be a promising agent for enhancing stem cell capacity derived from adipose tissue. While RSV can facilitate cell growth and maintenance in vitro and enhance differentiation before stem cell therapy, other research in this area is needed to increase RSV's bioavailability in vivo, such as using nanotechnology.

Keywords: RSV; Stem cell therapy; Mesenchymal stem cells; ADSCs

GK-AS1 LNCRNA axis regulates the PCK1 mRNA in pathways leading to Glycolysis and Gluconeogenesis: Differential Expression of hepatocyte-like cells (HLCs) differentiated from human induced pluripotent stem cells (iPSCs)

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Background: An SNP analysis has an important role to construct pedigrees, mapping phenotypic traits, and studying population genetics. Hepatocytes robustly express and release large amounts of proteins into the blood. Therefore, it is possible that the hepatocyte's immune function is to secrete specific proteins into blood. Directed differentiation of human induced pluripotent stem cells (iPSCs) into hepatocytes could provide an unlimited source of liver cells.
Method :The GSE187011 gene expression profile data were downloaded from GEO. The present study included 15 samples, including two hepatocyte differentiation methods that compared the resultant cells phenotypically, functionally, and transcriptomic ally at different stages of hepatocyte differentiation. We used miRNASNP-V3 For the analysis of miRNA Targeted with SNP. Finding lncRNAs and their function by Enrichr databases and lncHUB databases. By using lncRRIsearch, we investigated the interaction between mRNA and lncRNA. The pathways which are related to the PCK1gene were selected from the Reactome and KEGG pathway database.
Result: We found that PCK1 mRNA has decreased significantly (logFC: -8.5, p-value <0.0001) in hepatocyte-like cells (HLCs) differentiated from (iPSCs). From all of the extracted SNPs on the Target gain with SNP, rs757361825 can cause a connection with hsa-miR-3159 in the 3'UTR region PCK1. GK-AS1 lncRNA regulates the expression of PCK1 which can have an important effect on the pathways that ultimately lead to Glycolysis and Gluconeogenesis: AMPK, P13K-AKT, Glucagon, and PPAR Signaling Pathway.
Conclusion:rs757361825 have a role in bonding the miRNA in the 3'UTR region PCK1. Moreover, PCK1 by GK-AS1 through different signaling pathways would be able to regulate Glycolysis and Gluconeogenesis.

Keywords: Hepatocyte-Like Cells (HLCs), Induced Pluripotent Stem Cells (iPSCs), Single Nucleotide Variations, Glycolysis, Gluconeogenesis.

Examination genes profile changes after treatment of MS disease using stem cells by in silico method

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Background: Treatment of multiple sclerosis (MS) as an autoimmune disease using stem cells is one of the challenging methods for scientists, especially in the advanced and strong type. Microarray data can be used to effectively investigate changes in gene expression levels after treating this disease with stem cells. This study aims to find effective genes as biomarkers of MS treatment process.

Method: By using the keywords multiple sclerosis, microarray analysis, stem cell, and human in the GEO database, GSE was selected. Then, using the GEO2R site in order to gene expression analysis between three groups of control, pre-treatment, and two years after treated groups were performed using stem cells. The data were evaluated based on log FC, P-value, and adj. P-value and Common effective genes were selected using the Venn diagram site. Then investigations of signaling pathways were carried out on the KEGG databases. Also

Result: In this bioinformatics study of GSE32988 and 19 genes (IRX5, RRAD, TNFAIP6, SNAI1, CXCL3, CCL23, IL6, ATF3, PTGS2, APOBEC3B, CXCL8, AREG, CXCL2, DRAM1, NR4A3, MAFB, NR4A1, NLRP3, PLAUR) were founded. The Kegg database data show that most of these genes are involved in the cytokine-cytokine receptor interaction and IL-17 signaling pathway. In addition, hsa-miR-3651is micRNA common between CXCL2, CXCL3, CXCL8, and IL6 genes.

Conclusion: This bioinformatics study shows that CXCL family genes such as CXCL2, CXCL3, CXCL8, and IL6 gene have increased expression and could be effective biomarkers in investigating the process of MS disease treatment by stem cells. Also, as the only common microRNA between these genes, hsa-miR-365 is probably responsible for the main regulatory role. However, in order to conduct more detailed studies to select clinical biomarkers, it is necessary to use the real-time PCR method for a more detailed review of these results.

Keywords: Genes profile -Changes - Treatment - MS disease - Stem cells - In silico method

Integrated systems biology analysis of differentially expressed coding and non-coding RNAs in multiple sclerosis patients: High-throughput expression analysis

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Background: Based on genecards, the saposin-like protein (SAPLIP) family contains the GNLY product, which is found in the cytotoxic granules of T lymphocytes that are produced in response to antigen stimulation. This protein has antibacterial action against M. tuberculosis and other pathogens and is found in the cytotoxic granules of cytotoxic T lymphocytes and natural killer cells. Different isoforms are encoded by alternatively spliced transcript variants, which have been discovered. In this investigation, we performed a high-throughput microarray analysis to demonstrate novel RNA interaction network in multiple sclerosis (MS) patients.

Methods: Microarray analysis was performed by R Studio on GSE43591 dataset. Pathway enrichment analysis was performed using KEGG and Reactome. Gene ontology analysis was performed by enrichr. miRNA interaction analysis was performed by miRWalk online database. lncRNA interaction analysis was performed by lncRRIsearch. Protein interaction analysis was performed my STRING.

Results: Based on microarray analysis, GNLY has a significant low-expression in MS patients (logFC: -2.221, adj. P. Val < 0.0001). GNLY in immune system-related pathway (antimicrobial peptids). Gene ontology analysis revealed that GNLY is involved in cellular defense response process. hsa-miR-6804-3p has a significant suppressor interaction with GNLY mRNA (score: 1). lncRNA DBET has a significant interaction with GNLY (sum of energy: -352.86). GNLY has protein interaction with KLRD1, PRF1, GZMH, and NKG7).

Conclusion: miR-6804-3p might regulate GNKY expression level in MS patients. GNKY regulates cellular defense response process and antimicrobial signaling pathway. lncRNA DBET has a significant lncRNA – mRNA interaction with GNLY mRNA and could affect its protein interactome and signaling pathway.

Keywords: miRNA interaction, Microarray, Bioinformatics, Biomarker Discovery

The medicinal role of propolis and caffeic acid in controlling the function of pro-inflammatory cytokines interleukin-1β, IFN-γ and interleukin-6 in Alzheimer's disease

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Background: Inflammatory processes caused by disruption of inflammatory cytokines are one of the vital components that play a part in the pathogenesis of Alzheimer. inflammatory cytokines can be inhibited with various pharmaceutical compounds, including Propolis and caffeic acid, which has anti-inflamatory and anti-oxidant properties. In this study, Wistar rats with Alzheimer's were infected with scopolamine, then the effects of two substances on the expression of pro-inflammatory cytokines interleukin-1β, IFN-γ and interleukin-6 were assessed by Real-time PCR method and changes in the hippocampus of the rats' brains and the assessment of brain tissue cells were investigated through the preparation of histopathology slides. The results showed that the cell changes in the group treated with scopolamine are evident compared to the control and sham groups, but it is similar to the group receiving propolis and the morphological difference in the organization of the cells was visible. While in the group receiving caffeic acid with a dose of 8 mg, a significant reduction in the destruction of neurons was evident. The expression results of interleukin-1β, IFN-γ and interleukin-6 genes obtained by Real-Time PCR method showed the expression of these inflammatory cytokine genes in the groups treated with propolis and caffeic acid (in all concentrations) compared to Alzheimer's group (scopolamine) shows a significant decrease ($p<0.05$) therefore, propolis and caffeic acid can be considered as drug candidates in the treatment of Alzheimer's disease.

Keywords: Cytokine; Alzheimer; Propolis; Interleukin-1β; IFN-γ and interleukin-6

Evaluation of the Expression Levels of HRG-AS1 and LOC124905242 in Multiple Sclerosis

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Background: Multiple sclerosis (MS) is a disease that affects the brain and spinal cord and can cause a variety of symptoms, including problems with vision, movement of arms and legs, sensation, and balance. Long noncoding RNAs (lncRNAs) are playing an increasingly important role as biomarkers for various diseases, including autoimmune diseases. Previous studies have shown that HRG-AS1 and LOC124905242 play a role in the pathogenesis of human autoimmune diseases. However, the potential importance of these two lncRNAs as diagnostic biomarkers for MS has not yet been explored. the aim of this study is to quantitatively assess the expression levels of HRG-AS1 and LOC124905242 in peripheral blood samples of MS patients compared with healthy controls.

Materials and Methods :In this case-control study, blood samples were collected from 10 MS patients and 10 healthy controls. Total RNA was extracted and the expression levels of selected lncRNAs were quantitatively measured using the quantitative real-time-polymerase chain reaction (qRT-PCR) method.

Results :We detected a significant up-regulation in the expression of HRG-AS1 and LOC124905242 in MS patients compared with the control. Based on receiver operating characteristic (ROC) curve analysis, HRG-AS1 was able to effectively discriminate MS patients from healthy subjects. The result of this study indicates that HRG-AS1 is significantly and inversely correlated with the Diastolic Disability Status Scale (EDSS) for prognosis in MS patients.

Conclusion: According to the result of our study, a potential role of HRG-AS1 lncRNA as a diagnostic biomarker to distinguish MS patients has been suggested.

Keywords: Autoimmune Disease, Long Non-coding RNA, Multiple Sclerosis, QRT-PCR

Effect of LEF1 gene in gastric cancer

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Background: Gastric cancer is a serious malignant disorder with a10% mortality rate of approximately. Therefore, it is necessary to identify diagnostic biomarkers and drug targets to improve the of patients. The aim of the current research is to identify key genes and the relevant signaling pathways. LEF1 gene was identified in important signaling pathways such as Transcriptional Regulation of Granulopoiesis , Binding of TCF/LEF , RUNX3 Regulates WNT Signaling, Gastrulation and Extracellular Matrix Organization related to gastric cancer.

Methods: At first we found GSE194261 on the GEO site and analyzed it by GEO2R and selected 9 cancer samples and 9 normal samples and selected the LEF1 gene for testing with the help of the obtained charts and tables. Then LEF1 gene was checked in GEPIA2 by Expression DIY analysis and significant increase in expression of this gene was observed in Box Plot diagram and also Log FC of this gene was positive which confirms this result.

Next, in the Survival Analysis section, we examined the relationship between LEF1 gene expression and the survival of patients, and according to the overall survival chart, we concluded that the increase in gene expression has led to an increase in the death rate of patients but this chart statistically is not meaningful due to Log ranc P = 0.33 .

Based on the P-value number, we entered the first 13 genes in the table obtained from GEO2R into Enrichr and the LEF1 gene was confirmed according to the resulting signaling pathway. We also checked the signaling pathway in which this gene is involved with the help of the Reactome site.

Finally, by examining the gene by miRNASNP and according to the decrease in gene expression with the help of Loss number, we identified the effective microRNAs, which by not binding to LEF1, its expression have increased .

Results and Conclusion : According to the analyzes carried out by various sites, to investigate this disease and one of the most important genes involved in it and the signaling pathways that play a role in it, such as the gastrulation pathway, which is one of the stages of fetal growth and development, followed by Each embryonic layer turns into an organ or tissue. Also, according to the diagrams obtained, the LEF1 gene causes gastric cancer by increasing its significant expression.

Keywords : Gastric cancer , LEF1 gene , Signaling pathway , microRNA

miR-3620-5p and Linc00940 regulates DDC expression level in Retinoblastoma via modulation of metabolism of amino acids and derivatives signaling pathway

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Background: Retinoblastoma (RB) represents one of the most common forms of primary intraocular malnutrition in children which accounts for 3% of all childhood cancers caused by mutations within the gene that codes for retinoblastoma (RB1) in chromosome 13q14.2. Although long non-coding RNAs have been shown to regulate the development and occurrence of cancer, specific lncRNAs can undergo alterations. The purpose of this study is to identify new miRNAs and long noncoding RNAs in retinoblastoma samples which regulate specific gene expression.

Methods: The GEO database, the gene expression profile of GSE208143 by array, including tumor and control samples, was analyzed via the GEO2R. Similar P-Value adjustment and Fold Change (FC) and Adjusted P-Value were made with the lowest quantity to identify lncRNAs fellow associate genes and then identify miRNAs associated with the desired gene using the miRWalk database. Finally, using the LncRRI search web server and the Gene Cards database, the desired lncRNA was most likely to be selected.

Results: Considering the defined criteria, a new abnormal lncRNA was identified. First, by analyzing and comparing signaling pathways and the gene ontology between the selected candidate genes in the Enrichr web-based tool, we selected the DDC gene. The miRNA was selected by the miRWalk database with the most negative ΔG called miR-3620-5p (energy: -33.8, position: 3´UTR, score:1). In the next step, we reached Linc00940 using the LncRRI search web server and determined that we had found an important lncRNA using the Gene Cards database.

Conclusion: The current study may identify novel hsa-miR-3620-5p and Linc00940 lncRNA regulates DDC gene mRNA expression and modulates metabolism of amino acids and derivatives signaling pathway in retinoblastoma samples; however, further research is required to determine the potential functions of these miRNAs and lncRNA in Retinoblastoma occurrence.

Keywords: Retinoblastoma, lncRNA, bioinformatics, miRNA, Biomarker discovery

miR-1233-5p modulates protein digestion and absorption signaling pathway suppressing the expression level of COL10A1 in gastric cancer patients: systems biology investigation

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Background: Gastric cancer is a global health problem, with more than 1 million people newly diagnosed with gastric cancer worldwide each year. Despite its worldwide decline in incidence and mortality over the past 5 decades, gastric cancer remains the third leading cause of cancer-related death. COL10A1 (Collagen Type X Alpha 1 Chain) is a Protein Coding gene.COL10A1is overexpressed in diverse tumours and displays vital roles in tumorigenesis. However, the prognostic value of COL10A1 in gastric cancer remains unclear.

Methods: Gene expression data of (GSE 103236) was analyzed by GEO2R. stomach cancer and healthy control group were compered and then analyzed by GO2R to find differently expressed genes. GEPIA2 and ENCORI databases were then use to correlation and survival Moreover . through the KEGG database ,the signaling pathway was checked. By enrichr was found gene ontology and biological pathways. STRING database was realized to the protein-protein interaction analysis and miRWalk was untilized to find significant miRNA in the 3UTR region.

Results: COL10A1 were selected that has significant increase in expression regulation.we realized that two genes COL10A1 and P4HA2 were correlated and had an effect on survival and in the tumor group. COL10A1 is involved in the protein digestion and absorption process. This signaling pathway is disrupted COL10A1 in positive regulation of multicellular organismal process and positive regulation of cell motility in the intracellular organelle lumen. COL10A1 gene has a strong interaction with the P4HA2 and ACAN genes. hsa-miR-1233-5p has an effect on the expression of COL10A1 gene and this miRNA by regulating the expression of COL10A1 gene can affect the protein digestion and absorption signaling pathway.

Conclusions: miR-1233-5p regulates the protein digestion and absorption signaling pathway through regulation of COL10A1 gene in gastric cancer samples. miR-1233-5p might be one of the main causes of high-expression of COL10A1 in GC samples.

KEYWORDS: Gastric cancer (GC), miRNA interaction, biological pathways, protein-protein interaction

FN1 gene expression changes in PDAC disease, finding new biomarkers for better treatment by investigating through miRNAs and lncRNAs: Integrated bioinformatics investigation

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Introduction: Pancreatic ductal adenocarcinoma (PDAC) is the most common form of pancreatic cancer in recent decades. Also, PDAC is resistant to treatment due to genetic and epigenetic changes. In this bioinformatics research, the goal was to identify and determine a biological network of genes, miRNAs and lncRNAs, which was used for a better study on PDAC.

Methods: The GSE15471 gene expression profile data were downloaded from the NCBI Gene Expression Omnibus (GEO) (https://www.ncbi.nlm.nih.gov/geo). FN1 was selected and by using miRWalk database, plenty miRNAs were found for this gene. In addition, with the purpose of finding lncRNAs related to this network, the miRNA (has-miR-214-3p) was searched in LncBase v.3 and DLGAP1-AS1 and EPB41L4A-AS1 were selected as suitable lncRNAs. Ultimately, the pathway (https://www.genome.jp/kegg/pathway.html) that this gene was involved in were analyzed to find its role in Cancer. Protein network of FN1 was constructed through STRING.

Results: Based on GEO analysis a desired GSE named GSE15471, by using $|\log FC| \geq 1$ and $P < 0.05$ as cut-off criterion, we choose FN1 gene that has an important role in PI3K-Akt signaling pathway. The PI3K regulated signaling pathway network could recognize the dynamic signaling of the tumor microenvironment (TME), and could directly promote a variety of oncogenic processes or activate parallel interconnected signaling nodes. Has-miR-214-3p is a miRNA related to the FN1 gene. Based on the STRING database, we visualized the PPI network of FN1 with proteins such as Integrin alpha-5 and Integrin beta-3. As a result, this miRNA and lncRNAs can act as a ceRNA network which has an effect on FN1 gene regulation.

Conclusions: According to the all mentioned events it is concluded that FN1 with has-miR-214-3p and its CeRNAs affect the progression of PDAC. These results will provide a promising therapy method for the diagnosis and treatment of PDAC patients.

Keywords: Pancreatic ductal adenocarcinoma (PDAC), Has-miR-214-3p, DLGAP1-AS1, EPB41L4A-AS1, microRNA, lncRNA

Up-regulation of TMEM45B and TRIM2 in Multiple sclerosis disease is regulated by a novel ceRNA network: integrated bioinformatics analysis.

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Introduction: Multiple sclerosis (MS) is a chronic autoimmune disease of the central nervous system characterized by inflammation, gliosis, and neuronal loss. In the world, less than one percent have been diagnosed with MS. Although the cause of MS is unclear, the evidence suggests that it is a multifactorial disease, and it can be mentioned immune factors, genetic predisposition along with environmental factors such as exposure to infectious agents. Its symptoms are different and can include visual impairment, bladder, and cognitive dysfunction.

Methods: First of all, raw data(GSE13732) was extracted from GEO and analyzed by GEO2R to obtain differentially expressed genes(DEGs), also, miRWalk, KEGG PATHWAY, lncBasev.3, STRING, GeneCards databases were used.

Results: TMEM45B(with logFC=1.438) and TRIM2(with logFC=1.4) including genes that have the most expression changes among the genes related to this disease. Using the KEGG PATHWAY database, it was determined that the NF-kappa B signaling pathway is effective in this disease, NF-κB(transcription factor) plays a major role in inflammatory diseases such as multiple sclerosis MS by regulating inflammation and cell survival. Then miRWALK was used to find miRNAs in the 3UTR region of these mRNAs and miRNAs hsa-miR-26b-3p (for TMEM45B) and hsa-miR-192-3p (for TRIM2) were chosen.miRNAs were used to find lncRNAs in the lncbasev.3 database and GNG12-AS1)for hsa-miR-26b-3p(; LINC00472)for hsa-miR-192-3p) were selected. GeneCards was also used to validate the selected lncRNAs. Through STRING, it was found that the TRIM2 gene protein interacts with other proteins such as TRIM3 and PUM1.

Conclusion: In conclusion, the higher expression of TMEM45B and TRIM2 genes and the effect on the NF-κB signaling pathway, as well as the creation of a possible ceRNA regulatory network between miRNAs and lncRNAs and their regulatory effect on the mRNA of these genes can cause the development and progression of MS.

Keywords: Multiple sclerosis (MS), TMEM45B, TRIM2, microRNA, lncRNA

Differential Expression of glioblastoma cells and normal in brain tissue and the important role of ERG mRNA in sarcomas: integrated systems biology investigation (in silico)

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Background: There are several types of primary brain cancer, but glioblastoma is the most common and aggressive type among adults that may be related to treatment by stem cells. To explore how LMO2 and ERGmRNAs regulate self-renewal and tumor growth in brain endothelial cells by signaling with a glioblastoma background we used bioinformatics tools. We found the interaction between lncRNA and miRNAs with LMO2 mRNA.

METHODS: The GEO online database was used to find this dataset. GSE137902 dataset Affymetrix was analyzed to find differentially expressed genes (DEGs). The Pathway enrichment analysis was carried out using KEGG online databases. All miRNAs were regained from DIANA-TarBase v7.0 and Enrichr. The expression of lncRNAs in different Pathways has been examined by the lncHUB databases. Was comparing the expression of genes in Glioblastoma by Gepia2 databases—the protein-protein interaction analysis by STRING online software.

RESULTS: We found that ERG and LMO2 mRNAs had low expression changes (adj. P. Val<0.05) in comparison to endothelial cells from glioblastoma and normal brain cultured. miRNAs interaction analysis showed that hsa-miR-103-3p and hsa-miR-107 could regulate the expression of LMO2 and Linc00665 lncRNA in cell line H4 from Brain tissue in an interaction axis. This RNA has a single local base-pairing interaction. We investigated that, there is a common pathway between LMO2 and ERG including in Transcriptional Misregulation in Cancer. ERG plays an important role in Sarcomas by affecting IGF1 causing Tumor growth, and survival also LMO2 is involved by Transcription factor LYL1 which leads to Self-Renewal and Differentiation resistance.

CONCLUSION: LMO2 mRNA and Co-Expression Linc00665 lncRNA and hsa-miR-103-3p and hsa-miR-107 miRNAs could be prognostic biomarkers in cell line H4 from Brain tissue. Moreover, ERG using IGF-1 can playan important role in Sarcomas, affecting Tumor growth and survival.

Keywords: Glioblastoma, H4 cell line, Self-Renewal, Glioma-sarcoma, IGF1

Production of optimized AAVs carrying the RPGR gene for X-linked retinitis pigmentosa type-3 gene therapy

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Background: The most common form of X-linked retinitis pigmentosa is caused by mutations in the RPGR gene, leading to photoreceptor degeneration and loss of vision. Gene therapy using adeno-associated viral (AAV) vectors has proved its safety in clinics and AAV serotype-2 (AAV2) has been widely used for gene delivery into the retina. The aim of this study is to evaluate photoreceptor transduction efficiency of two rAAV2-RPGR vectors with mutant capsids following intravitreal and subretinal delivery in mice.
Methods: We synthesized codon-optimized human RPGR^{ORF15} gene cloned into an AAV vector with CMV promoter. RPGR^{ORF15} transgene expression was analyzed by transfection into cells followed by western blotting using an anti-RPGR antibody. The transgene was cloned into an AAV vector under the control of photoreceptor-specific GRK1 promoter. AAV2-(7m8) and AAV8 capsid vectors were used to introduce tyrosine to phenylalanine mutations by site-directed mutagenesis. To evaluate the function of mutant AAVs, we produced an AAV2 shuttle plasmid encoding an EGFP reporter.
Results: The recombinant AAV(7m8-YF)-EGFP particles were produced in HEK293T cells, purified from cell lysates by Heparin affinity chromatography, concentrated and stored. The activity and titer of the AAV(7m8-YF)-EGFP variant has been assessed by transduction of cultured cells showing a high transduction activity in vitro. We are now analyzing AAV-RPGR^{ORF15} mutant variants and will test the transduction efficiency of these mutant viruses in the mouse retina.
Conclusion: AAVs harbouring capsid surface tyrosine mutations display increased stability and penetration compared with the wild type counterparts.

Keywords: Retinitis Pigmentosa, RPGR, gene therapy, adeno-associated virus

Application of nanoparticles for gene delivery to stem cells

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Background: Gene therapy is an intriguing therapeutic modality which is expected to assume a pivotal role in the treatment of crippling inherited, painful and degenerative disorders by transfer of genetic material into cells. The combination of the stem-cell technology with gene therapy has the potential to provide regenerative tissue and therapeutic agents simultaneously; thus, having the advantages of both technologies. The most common methods for delivering exogenous genetic material to cells are electroporation, microinjection, and utilize natural or synthetic vectors. Although physical techniques like electroporation is considered as a highly effective method for gene delivery, but they are significantly harmful for stem cells. Gene delivery vectors included viral and non-viral vectors. The efficiency of host-cells transfection with viral vectors is relatively high compared to non-viral methods, but the main drawbacks of using virus vectors are its immunogenicity and cytotoxicity. On the other side non-viral vectors have poor effectiveness in transfection and reproducible handling of embryonic stem cells differentiation. Lipofectamine 2000 is the most popular commercial non-viral based method with the gene transfection efficiency of 40%. In recent years, a series of advanced non-viral gene delivery nanomaterials and related methods have been reported, such as nanoparticles, nanocapsules, nanotubes, nanogels, dendrimers, liposomes, cell penetrating peptides and etc. Our review showed that nano-based gene delivery systems such as Angelica sinensis polysaccharide nanoparticles-pDNA, calcium phosphate-pDNA and lipid nucleic acid nanoparticles could be good potential candidates for gene delivery, exhibiting a high transfection efficiency combined with a lower cytotoxicity than Lipofectamine2000. Therefore, nanotechnology has all the potential to revolutionize the gene delivery system in degenerative diseases, so that more diseases can be treated through this simple, safe, convenient, economical and efficient technology platform for gene therapy.

Keyword: Application , Nanoparticles , Gene delivery , Stem cells

Precision medicine in breast cancer and PI3K/AKT/mTOR pathway regulation

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Background: Breast cancer is very common in women, and with the advancement of science in the field of cancer and biological therapy, it remains the fifth leading cause of death worldwide. Breast cancer treatment is multidisciplinary and early detection is very important. Diagnostic methods are often possible by mammography, MRI, and breast tissue biopsy, and today, common treatments are often surgery, chemotherapy, and radiation therapy. Choosing the right method is very important because it affects the patient's quality of life. On the other hand, considering that breast cancer is a disorder with different biological characteristics, it is better to have personalized treatment approaches depending on the patient's genetic structure and use targeted treatment for each person according to targeted cellular pathways and microenvironment.The PI3K/AKT/mTOR pathway consists of complex events that regulate various cellular processes such as growth and proliferation, angiogenesis, differentiation, apoptosis, and energy metabolism of cells. PIK3 with its kinase activity converts PIP2 (phosphatidylinositol 4، 5-bisphosphate) to PIP3 (phosphatidylinositol 3، 4، 5-triphosphate) and then activates the AKT and mTOR pathways. Too many genetic aberrations from this pathway can lead to cancer and resistance to treatment. In contrast, PTEN and INPP4B (inositol polyphosphate-4 phosphatase) are tumor suppressor systems and as negative regulators and inhibit PIK3 with phosphatase activity. Mutations in these suppressor systems also lead to cancer It is hoped that with further progress and better understanding of cellular pathways and tumor microenvironment, more targeted breast cancer treatments will be carried out with precision medicine and we will achieve definitive treatment.

Keywords: Breast Cancer , Precision Medicine, PI3K

Integrated system biology investigation (in-silico) of the effect of the TGFβ signalling pathway on Self-Renewal in Mammary Stem cells with cardiovascular disease after chemotherapy

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Background: Our study demonstrates that INHBB with mRNA and lncRNA are in an interaction axis, indicating the presence of a complex network. TGF-beta coded by INHBB controls breast cancer stem cell self-renewal in the TGF-β Signalling Pathway and also is involved in the development of many tissues, including the heart and blood vessels.

METHODS: The GSE163883 dataset was found in the GEO online database. We examined the interaction between mRNA and lncRNA using lncRRIsearch. With miRWalk, we investigated miRNA mRNA interactions using all miRNAs recovered from DIANA-Tar Base v.8. Additional databases include KEGG, Reactome, and STRING.

RESULTS: We found that INHBB mRNA has considerably increased (adj. P. Val<0.05). miRNA interaction analysis revealed that miR-34a-5p could regulate the expression of INHBB and LINC01747 lncRNA in cell line MCF7 from Memory Gland tissue in an interaction axis which indicates the existence of a complex network. Interaction analysis of INHBB and LINC01747 lncRNA illustrated have a single local base-pairing interaction (Energy = -20.70 kcal/mol) and (Energy = -13.70 kcal/mol). INHBB encodes a member of the TGF-beta in the TGFβ signalling pathway and the different Pathways that are involved in cell growth, cell differentiation, cell migration, apoptosis, cellular homeostasis, and other cellular functions and the development of many tissues, including the heart and blood vessels. Also, INHBB can play a role in Signalling Pathway Regulation Pluripotency of Stem Cells and interact with BMP and SMAD. By increasing the expression of gene INHBB, it can be assumed that TGFβ/Cyclin D1/Smad-mediated inhibition of BMP4 promotes breast cancer stem cell self-renewal activity.

CONCLUSION: We identified the hub lncRNA-mRNA network involved in regulating various biological processes in cell line MCF7 from Mammary Gland tissue. breast cancer stem cells play a role in cell self-renewal pathways. TGF-β inhibitors may be a prognostic factor for cardiovascular disease after chemotherapy.

Keywords: microRNA interaction, STEM CELL, TGFβ signalling, Breast cancer

Methylated septin 9 in various stages of CRC-A meta analysis Study

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Introduction : The prevalence of colorectal cancer (CRC) is increasing, and early detection in low stages is very important. One of these markers is 9-methylated septin, whose expression level is related to different degrees of colorectal cancer. As a result, in this review study, we tried to Investigating the expression level of methylated septin 9 gene in different grades of colorectal cancer.

Method :he present study was a systematic review and synthesis of quantitative evidence. The primary keywords were published in reliable databases such as Pubmed, Google schoolar, Elsevier, Wiley in English were searched until the end of 2022. Two authors independently examined the articles in terms of data extraction, inclusion criteria, and quality assessment of the articles, and the meta-aggregation method synthesized the findings.

Result :Our result on 13 studies shows that total number of participants with colon cancer was 1,943 (57.8 % male and 42.2 % Female) , and the average age of the patients was 62.75 years. The average Septin 9 was positive 65.4 %. In Our study positive detection rate overall, respectively for 0 stage 55.14% , I stage 51.21% ., II stage 70.37% , III stage 64.54% , IV stage 99.99% and for unknown 67.83% . The highest percentage based on different stages of cancer was related to stage IV (99.99%) and the lowest was related to stage I cancer (51.21%) .

Conclusion :The studies considered in this article show that methylated septin-9 is a suitable biomarker for detecting colorectal cancer. Another important point is the relationship between the expression level of septin-9 and different degrees of colorectal cancer, so that in stage 0 and 1, the lowest level of expression and in the stage 4 The highest level of expression was seen.

Keywords: Methylated -septin 9- various stages- CRC

The application of stem cells in the treatment of diabetic wounds

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Background: Classically, wound healing proceeds through sequential but overlapping phases of inflammation, proliferation and remodelling. However, in individuals affected by diseases such as diabetes, the body's natural wound healing process is impaired. Delayed wound healing results in pathological inflammatory state and consequently to chronic wounds which lead to further complications. The application of stem cells has been disclosed to be a promising treatment for non-healing wounds. Stem cells are unspecialized cells of the human body distinguished by their capacity for self-renewal and differentiation towards multiple lineages. They have reduced immunogenicity and contribute to wound healing through stimulating re-epithelialization, wound closure, ECM production and angiogenesis. Furthermore, stem cells have been demonstrated to participate in mediating various growth factors and cytokines which promote wound healing.

Method: Herein, we review the potentials and limitations of the application of different kinds of stem cells, including embryonic stem cells (ESCs), induced pluripotent stem cells (iPSCs), mesenchymal stem cells (MSCs), and adipose-derived stem cells (ASCs) in diabetic wound healing by searching on "Google Scholar" database for publications.

Results: Specifically, MSCs are the most researched due to their safety and ease of harvest from dermal and adipose tissue; however, compared to pluripotent ESCs and iPSCs, multipotent MSCs can only differentiate into tissue-forming cell lineages. Both ECSs and iPSCs have remarkable regenerative potential but their application is limited due to ethical issues and increased risk of cancer development, respectively. ASCs are more favorable candidates for stem cell therapeutics owing to their capacity to differentiate into diverse cell lineages and cell growth promotion.

Conclusion: Overall, stem cell transplantation for the treatment of chronic wounds, which remain a major clinical problem, especially in diabetic patients presents both challenges and new opportunities. Since chronic wounds have a different etiology, personalized stem cell therapy would allow for tailored treatment with maximal efficacy and limited adverse effects.

Keywords: Application ,Stem cells , Treatment , Diabetic wounds

Smart Arginine-Equipped Polycationic Nanoparticles for p/CRISPR Delivery into Cells

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Abstract

An efficient and safe delivery system for the transfection of CRISPR plasmid (p/CRISPR) into target cells can open new avenues for the treatment of various diseases. Herein, we design a novel nonvehicle by integrating an arginine-disulfide linker with LMW PEI (PEI1.8k) for the delivery of p/CRISPR. These PEI1.8k-Arg nanoparticles facilitate the plasmid release and improve both membrane permeability and nuclear localization, thereby exhibiting higher transfection efficiency compared to native PEI1.8k in the delivery of nanocomplexes composed of PEI1.8k-Arg and p/CRISPR into conventional cells (HEK 293T). This nanovehicle is also able to transfect p/CRISPR in a wide variety of cells, including hard-to-transfect primary cells (HUVECs), cancer cells (HeLa), and neuronal cells (PC-12) with nearly 5 to 10 times higher efficiency compared to the polymeric gold standard transfection agent. Furthermore, the PEI1.8k-Arg nanoparticles can edit the GFP gene in the HEK 293T-GFP reporter cell line by delivering all possible forms of CRISPR/Cas9 system (e.g., plasmid encoding Cas9 and sgRNA targeting GFP, and Cas9/sgRNA ribonucleoproteins (RNPs) as well as Cas9 expression plasmid and in vitro-prepared sgRNA) into HEK 293T-GFP cells. The successful delivery of p/CRISPR into local brain tissue is also another remarkable capability of these nanoparticles. In view of all the exceptional benefits of this safe nanocarrier, it is expected to break new ground in the field of gene editing, particularly for therapeutic purposes.

Keywords: nanocarrier, p/CRISPR transfection, gene editing, brain

Precision Medicine and Genetics of Behavioural Disorders

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Background: Any chronic and recurrent pattern of behaviour that flouts social mores or laws, gravely compromises a person's functioning, or causes anxiety in others is considered to be a behavioural disorder. The phrase is used in a very broad sense to refer to a number of different diseases or syndromes. New advances in biomedical sciences and genomic medicine have highlighted the heterogeneity of behavioural disorders and their underlined diverse pathogeneses and molecular mechanisms. The diverse causes and unique progression patterns of behavioural disorders amongst individuals are most likely due to genetic heterogeneity of the general population. Moreover, a difference is further seen in response to treatment of behavioural diseases, and in adverse outcomes of therapy amongst the population involved in them. Therefore, the genetic approach in behavioural disorders is becoming individualized making it as one of the important topics in precision medicine while specialized techniques are becoming more popular…ll Overall, the precision medicine which includes an individually tailored approach encompassing prevention, diagnosis and therapy based on genetic and molecular characteristics of an individual is applicable to behavioural disorders. In this article, we make an effort to pinpoint the influences of genes at various levels of RNA, DNA, and proteins on a person's behaviour. This study aims to show the relationship between precision medicine and behavioural genetics.

Keywords: Precision Medicine - Genetics -Behavioural Disorders

Long non-coding RNA panel as a molecular biomarker in glioma

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Background: Glioma is one of the most malignant brain tumours, accounting for about half of the gliomas that occur in central nervous system (CNS), originates from the glial tissue of the brain. The aim of the present study was to determine the expression levels of 5 lncRNAs (MDC1-AS1, HOXA11-AS, MALAT1, CASC2, ADAMTS9-AS2) in patients with high-grade glioma in comparison with low grade glioma.

Methods: This was a retrospective study which determined molecular biomarker on pathologic glioma samples. We examined 100 patients' pathologic block which consisted of 50 pathology samples of high-grade glioma (case group) and control group consisted of 50 pathology samples of low-grade glioma. This research was performed using real time polymerase chain reaction (PCR) technique.

Results: The results showed that the expression of ADAMTS9-AS2 and HOXA11-AS genes significantly increased with increasing tumour grade. Also the expression of CASC2 gene significantly decreased with increasing tumour grade.

Conclusions: It was concluded that ADAMTS9-AS2 and HOXA11-AS and CASC2 are promising lncRNA markers in prognosis of glioma.

Keywords: Long non-coding -RNA panel -a molecular biomarker -glioma

The correlation of miR-31 and miR-373 expression changes with K-Ras common mutations in Iranian colorectal cancer patients.

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Background: In the present study, two molecular markers (miR-31 and miR-373) involved in the pathogenesis of CRC and their association with histopathological features investigated. As well, the prognostic value of these molecular markers was investigated in CRC patients with or without common K-Ras mutations. Paraffin blocks of tissue samples from 150 patients who underwent colon surgery between 2018 and 2020 were prepared from the Pathology Department of Imam Hossein Hospital (Tehran, Iran). After DNA and RNA isolation, Gene expression of miR-31 and miR-373 was determined using probe-based qRT-PCR. K-Ras mutations were surveyed using conventional PCR and agarose gel electrophoresis. The mean age of the patients was 57.2 ±13.4 years. K-Ras codon 12 and 13 mutations were positive in 31 (20.6%) and 22 (14.6%) respectively. Collectively, our results showed that K-Ras common mutations occurred in 32.6% of Iranian CRC patients. The expression levels of miR-31 and miR-373 increased in CRC patients with K-Ras mutations in comparison with patients without these mutations. Considering the role of miR-31 and miR-373 in CRC tumor progression, it seems that the CRC patients bearing K-Ras mutations have poorer prognosis respective to patients without K-Ras mutations.

Keywords: Colorectal cancer, miR-31, miR-373, K-Ras.

Investigation and bioinformatic analysis of the effect of RRAS gene in MCF7 cell line from Mammary Gland tissue In Silico analysis

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Background: One of the most common cancers among women, breast cancer (BC) is closely related to hormonal imbalances. HSPB8 is involved in the mechanisms that regulate the cell cycle and cell migration. The protein encoded by RRAS is a small GTPase involved in diverse processes including angiogenesis, vascular homeostasis, and regeneration, cell adhesion.

Methods: The GSE179674 dataset was found in the GEO online database. Finding the interaction between lncRNAs and genes by Enrichr databases and lncHUB databases. Comparing the expression of genes in breast cancer by Gepia2 databases. we investigated miRNA-mRNA interactions using all miRNAs recovered from DIANA-Tar Base v.8. Additional databases include KEGG, Reactome, and STRING.

RESULTS: We found that RRAS and HSPBB mRNAs had down and upregulation (adj. P. Val<0.05) in breast cancer. miRNA interaction analysis revealed that hsa-miR-23b-3p could regulate the expression of RRAS with TYMSOS and ILF3-DT lncRNAs in cell line MCF7 from Mammary Gland tissue in an interaction axis which indicates the existence of a complex network. Our Research has mentioned up and down-regulation of RRAS and HSPBB the possibility that function as cell proliferation and transformation in the breast. The Ras proteins are small GTPases that play a crucial role in transmitting signals within cells. RRAS is involved in the MAPK Signaling Pathway and plays an important role in the RAS Signaling Pathway that the MAPK and RAS signaling pathways lead to cell proliferation, differentiation, migration, growth, and apoptosis.

CONCLUSION: We identified the lncRNA-mRNA network complex in regulating various biological functions in cell line MCF7 from Mammary Gland tissue. RRAS mRNA and also, Co-Expression TYMSOS and ILF3-DT lncRNAs and has-miR-23b-3p miRNA could be prognostic biomarkers in breast cancer. Moreover, RRAS can affect MAPK Signaling Pathway/ RAS Signaling Pathway proliferation, differentiation, migration, growth, and apoptosis in Breast Cancer.

Keywords: Breast cancer, HSPBB, RAS Signaling Pathway, MCF7, Pathway enrichment

miR-6778-3p and LINC00940 regulates MGAM expression level in cholangiocarcinoma via modulation of neutrophil degranulation signaling pathway

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Background: Although long non-coding RNAs have been shown to regulate the development and occurrence of cancer, specific lncRNAs can undergo alterations. Our aim in this project is to identify new miRNAs and lncRNAs in cholangiocarcinoma samples which regulate specific gene expression.

Methods: The GEO database, the gene expression profile of GSE89749 by array, including tumor and control samples, was analyzed via the GEO2R. Fold Change (FC) and Adjusted P-value were made with the lowest quantity to identify lncRNAs fellow associate genes and then identify miRNAs associated with the desired genes using the miRWalk database. Finally, using the LncRRI search web server and the Gene Cards database, the desired lncRNAs was most likely to be selected.

Results : The miRNAs were selected by the miRWalk database with the most negative ΔG called hsa-miR-6778-3p (energy: -30.9, position: 3´UTR, score:1) and hsa-miR-4793-5p (energy: -30.6, position: 3´UTR, score:1) for MGAM gene and hsa-miR-6090 (energy: -31.1, position: 3´UTR, score:1) for LCT gene. In the next step, we reached Linc00940 for MGAM gene and Linc0125 for LCT gene using the LncRRIsearch web server and determined that we had found important lncRNAs using the Gene Cards database.

Conclusion: This study may identify novel miRNAs (hsa-miR-6778-3p, hsa-miR-4793-5p) and Linc00940 lncRNA that regulate the expression of the MGAM gene and modulate neutrophil degranulation signaling pathways. It has also been found that hsa-miR-6090 and Linc0125 regulate the expression of LCT mRNA and modulate digestion absorption signaling pathways in Cholangiocarcinoma samples.

Keywords: Cholangiocarcinoma, lncRNA, bioinformatics, miRNA, Biomarker discovery

miR-3170 modulates Bile secretion pathway via suppressing the expression level of SLC22A1 in liver hepatocellular carcinoma patients

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Background: Liver hepatocellular carcinoma (LIHC) is one of the common primary liver cancers worldwide and the major cancer worldwide, responsible for millions of premature deaths every year. The most significant risk factors include lifestyle habits (tobacco, alcohol drinking and diet). Therefore, utilizing reliable biomarkers would highly improve the prognosis and treatment of this illness.

Methods: Microarray analysis was performed on the GSE131329 dataset using GEO2R, GEPIA2, ENCORI, KEGG, Reactome, and Enrichr performed pathway enrichment and gene ontology analyses. STRING performed Protein- Protein correlation analysis.

Results: Microarray analysis revealed that SLC22A1 have significant down-regulation in Liver Hepatocellular Carcinoma (logFC= -4.554, adj.P value= 1.01e-23). A reciprocal miRNA gene was identified, which was hsa-miR-3170 which has the characteristics of score=1 and is effective in the discussed cancer. In addition, the KEGG database and ENRICHR database confirmed that SLC22A1 is a component of the Bile secretion signaling pathway which is involved in tumor progression. SLC22A1 has a role in pathway of Abacavir Transmembrane Transport R-HSA-2161517. SLC22A1 is used in biological process of serotonin transport, also in molecular fonction of pyrimidine nucleoside transmembrane transporter activity, and cellular component of integral component of plasma membrane. Among the proteins that have interacted with the desired gene (based on the STRING online website), we can mention: SPNS3 and SLC47A1.

Conclusion: hsa-miR-3170 might regulate Bile secretion signaling pathway through the regulation of SLC22A1 expression level in LIHC patients. SLC22A1 could be considered as a potential tumor suppressor and biomarker of LIHC.

Keywords: miRNA interaction, Microarray, Bioinformatics, Pathway enrichment.

The effect of Helicobacter pylori infection on CTNNB1 gene expression in gastric cancer and bioinformatic analysis of the relationship between this gene and miR-204-3p

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Background: CTNNB1 gene encodes beta-catenin. Helicobacter pylori infection affects gastric cancer(GC) growth by increasing beta-catenin expression. abnormal expression of beta-catenin by affecting its target genes such as c-myc and cyclin-D, which are involved in apoptosis and cell proliferation, leads to various diseases, including GC. our aim is to investigate the expression of beta-catenin gene in gastric cancer patients infected with H. Pylori.

Method: in this study, 50 tumor tissue samples and 50 adjacent non-tumor tissues samples were studied as controls from GC patients. in the first step, the expression changes of CTNNB1 gene were evaluated in people with GC and in the second step, the expression changes of this gene were evaluated in people with GC infected with H. pylori in Iran. To isolate people infected with H.pylori after bacterial DNA extraction, the final diagnosis was done using specific primers for 16srRNA gene and Real-Time PCR. next, in order to evaluate CTNNB1 gene expression, first, the Total RNA of the tissue samples was extracted using Trizol and then cDNA synthesis was done, changes in CTNNB1 gene expression in the tissue samples of these people were examined using specific primers and Real-Time PCR.

Results: the results showed that the expression of CTNNB1 in the tumor tissue samples compared to the control samples (tumor margin) in the studied population and also the tumor tissue samples infected with H. pylori had a significant increase in expression compared to the non-infected samples. ($P < 0.01$).

Conclusion: based on bioinformatics analysis, miR-204-3p expression has an inverse relationship with CTNNB1 gene And there is no significant relationship between CTNNB1 gene expression changes and the survival rate of GC patients. These studies show that CTNNB1 can be a good biomarker to distinguish GC patients from control samples.

Keywords: Beta-catenin protein, Gastric cancer, H.pylori , miR-204-3p

Application of personalized medicine in tissue engineering and regenerative medicine

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Background: Personalized medicine or precision medicine is a new method of therapy in which we discover everybody's specific characteristics and design a special way of treatment. It seems that mixing up with other fields of paramedicine can be more effective and help scientists have more choices in community health promotion. One of the strongest and most approved branches of new sciences is regenerative medicine, tissue engineering and cell therapy. The application of scaffolds and stem cells led us to present bigger and bigger paths.

Methods: An electronic search was conducted in PubMed and Google scholar search engines with English keywords, including tissue engineering, regenerative medicine, personalized medicine, and cell therapy. A combined search of keywords was done using Boolean operators AND and OR. Data analysis was done qualitatively.

Results: We find that various sources of stem cells, including mesenchymal stem cells, embryonic stem cells and induced pluripotent stem cells (iPSCs), are the options that can be used as a cell therapies bank and could give many advantages. On the other hand, discovering personal genetics features in laboratories is a powerful arm of personalized cell therapy.

Discussion and conclusion: By reviewing past studies, we realized that the approaches of personalized medicine based on tissue engineering exposed two main challenges: the high cost of producing personalized tissue engineering grafts and old protocols of foreign cells usage. From this point of view, with an overview of our country's capacities, we must increase our knowledge withof our country's capacities and increase our knowledge by expanding specific information in the field of personalized medicine. Progressive genetic changes in patients led us to use related cells (amniotic membrane and birth products) to cure with reserved cell banks. New tissue engineering equipment such as bioprinters or bioreactors will take a stronger step toward treatment with more efficient, low-cost & less complicated methods.

Keywords: Tissue engineering, Regenerative medicine, Personalized medicine, Cell therapy

Investigating the effect of chitosan nanogel containing eugenol essential oil in wound healing in rats

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Background: : Skin wounds and reducing their healing time are considered one of the most important aspects of medicine. Eugenol, which is the main ingredient of cloves, has been investigated for its unique properties such as antimicrobial, antifungal, antioxidant, anticancer and anti-inflammatory in wound healing. The main aim of the present study is to investigate the effectiveness of chitosan nanogel loaded with eugenol essence on full-thickness skin wound healing in rat animal model.

Method: For this purpose, chitosan nanogel containing eugenol essence was prepared using ionic gelation technique a. The size of microcapsules was checked by DLS method. In order to investigate the effect of nanogel on wound healing, a number of 12 rats in two control groups and nanogel on days 7, 14 and 21 were examined macroscopically (wound closure rate) and histological (inflammation, tissue granulation and fibrotic tissue) were investigated. The mean ± standard error of comparing two groups was analyzed by one-way ANOVA test and Tukey's post hoc test was used to determine significance between groups. The significance level in all analyzes $p<0.05$ was considered.

Results: DLS results showed that the nanogel particle size is about 126 nm with a particle size distribution of 127 nm. The macroscopic result of the nanogel group show a significant decrease compared to the control group ($p<0.05$). The results of histology showed that in the nanogel group there was a decrease in blood vessels, inflammation and edema in the granulation tissue and the appearance of moderate to high fibrotic tissue .

Discussion and conclusion: The results of the studies show that the use of nanogel containing eugenol can improve wound healing compared to the control group.

Keywords: Wound healing, Chitosan, Nanogel, Eugenol.

DNA-based Nano-biosensors as an emerging platform for the detection of Heart attacks and strokes

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Background: Heart attack and stroke are the main causes of death in various societies annually. To save patients from death and permanent injuries, it is necessary to start diagnosis and treatment in the first few minutes or golden time. In these cases, not only can the patient's life be saved with a quick and timely diagnosis, but unnecessary costs can be avoided by screening real patients from others. Biosensors are brand-new and effective tools in diagnosing diseases, which have not only increased the speed but also the accuracy of diagnosis. Using the unique properties of different compounds together, such as nucleic acids and nanomaterials, can create a revolution in the design of biosensors.

Since genetic compounds like DNA or RNA have a high ability in hybridization, they can increase the sensitivity and specificity of the sensor. for this purpose, they are suitable materials for use in biorecognition systems in sensors. DNAzymes are structures of DNA that have enzymatic properties. These synthetic compounds are like aptamers and are produced by the SELEX (SYSTEMATIC EVOLUTION OF EXPONENTIAL ENRICHMENT) process. Compared to protein enzymes, they are relatively cheaper to produce and easier to reproduce. Also, DNAzymes are resistant at ambient temperature and above and can be stored at room temperature. They can detect target analytes or catalyze chemical and biological reactions. DNAzymes are divided into two groups: peroxidase mimics and RNA cleavage. peroxidase mimics are rich in guanine and have a quadruplex structure, after binding to hemin, they exhibit peroxidase-like activity, which can participate in creating quantitative luminescence and color signals by oxidizing substrates such as ABTS, TMB, and LUMINOL. According to the characteristic of peroxidase mimic DNAzymes, by using suitable compounds as transducers, suitable optical or color sensors can be designed. Therefore, it is possible to use the combination of DNAzyme with ELISA, ALISA, FLISA, QUANTUM DOTS, gold nanorods, silver nanorods, etc.

Fortunately, heart attack and stroke have well-known biomarkers like Troponin T, troponin I, BNP, NT-proBNP, D-dimer, von Willebrand factor, etc. whose aptamers have already been introduced, so making POINT-OF-CARE tools in the mentioned way can be a suitable biosensor.

In conclusion, biosensors are one of the new and effective tools for the rapid diagnosis of diseases, which are receiving attention today. The design of DNA-based nano-biosensors by improving the limit of detection, speed, and accuracy has raised many hopes for making POC tools.

Keywords:-based-DNA Nano-biosensors - platform -detection -Heart attacks -strokes

Integrated system biology investigation (in-silico) of the effect of SLIT2/ROBO2 signaling pathway on Self-Renewal in Mammary Stem cells with Lupus (SLE) background

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Background: Several different types of cells are formed from stem cells in the body. The body may use them to repair itself. target mRNAs that can be highly expressed in SLE disease have functions in different signaling pathways in mammary stem cells. besides, we showed ROBO2, PAK3, and their interactions with mRNAs and lncRNAs in an interaction axis, indicating the presence of a complex network.

METHODS: The GSE61635 dataset was found in the GEO online database and Microarray analysis was based on the R studio. We examined the interaction between mRNAs and lncRNAs using lncRRIsearch.With miRWalk, we investigated miRNA-mRNA interactions using all miRNAs recovered from DIANA-Tar Base v.8. Additional databases include KEGG, Reactome, and STRING.

RESULT: The expression of mRNAs of PAK3 and ROBO2 has increased. SLIT/ROBO2 and PAK3 which were highly expressed in SLE disease can function in different signaling pathways. These RNAs have a single local base-pairing interaction (Energy = -38.61 kcal/mol) and (Energy = -13.36 kcal/mol). The miRNA interaction analysis revealed that miR-101-3p could regulate the expression of ROBO2, PAK3,NEAT1, MALAT1, and GAS5 lncRNAs in an interaction axis which indicates the existence of a complex network. Also, the loss of ROBO2 increases Self-Renewal in Mammary Stem cells whiles increasing SLIT2 can enhance Self-Renewal. In addition, the loss of SLIT/ROBO2 signaling inhibits the expression of p16INK4a, itself a potent suppressor of tumors by regulation of the cell cycle. Moreover, ROBO2 and PAK3 have important roles in the regulation of actin cytoskeleton and Axon guidance.

CONCLUSION: ROBO2, PAK3 mRNAs, and also, Co-Expression of NEAT1, MALAT1, GAS5lncRNAs, and miR-101-3p could be prognostic biomarkers. Our current study in-silico has demonstrated that SLIT2/ROBO2 signaling pathway affects Self-Renewal in Mammary Stem cells ROBO2 and PAK3 have an important function in the regulation of actin cytoskeleton and Axon guidance.

Keywords: R Studio, Microarray analysis, microRNA interaction, Self-Renewal,

ST6GALNAC1 gene expression changes in Pancreatic cancer, and regulation of its expression by miRNAs and lncRNAs: an integrated bioinformatics review

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Background: Pancreatic cancer refers to the carcinoma arising from the pancreatic duct cells,pancreatic ductal carcinoma. Smoking, diabetes, inflammation of the pancreas, family history of pancreatic cancer and some genetic syndromes (About 10% of pancreatic cancers are hereditary) are all causes of this disease. A common symptom of pancreatic cancer is a dull pain in the upper abdomen (belly) and middle or upper back that comes and goes. Pancreatic cancer is the 12th most common cancer worldwide.

Methods: In the first step, GSE46234 was downloaded from GEO and analyzes were performed on it to obtain differentially expressed genes, and databases such as: miRWalk, KEGG PATHWAY, lncBasev.3, GeneCards were used.

Results: The ST6GALNAC1 gene which is among the genes that have the most expression changes in this disease, was selected for further studies. Using this gene in MIRWALK database, various miRNAs were found and among them hsa-miR-365a-5p miRNA was used to find lncRNA in lncBasev.3 database. Two lncRNAs GORAB-AS1 and KCNIP4-IT1 were found and GENECARDS was used for their validation. Also, by using this gene and the kegg pathway database, we found that the Metabolic pathways is effective in pancreatic cancer.

Conclusion: According to these findings, it can be concluded that ST6GALNAC gene expression changes as well as the regulatory effects of hsa-miR-365a-5p (miRNA) and GORAB-AS1 and KCNIP4-IT1 (lncRNAs) in its expression can be effective in this disease.

Keywords: Pancreatic cancer, hsa-miR-365a-5p, GORAB-AS1

Hypermethylated ELMOD1 regulates GTPase activity in retinoblastoma as a potential tumor suppressor and diagnostic biomarker: integrated systems biology investigation

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Background: Children can develop retinal cancer called retinoblastoma, caused by the biallelic inactivation of the RB1 gene. Children with RB1 germline mutations are prone to develop retinoblastoma and other malignancies as adults. While there are some similarities between retinoblastoma in genetically engineered mice and retinoblastoma in humans, there are significant differences in their biological development. Using bioinformatics, we were able to identify a considerable network of lncRNA-mRNA interactions in retinoblastoma patients and assess the degree of expression of new retinoblastoma biomarkers.

Method: gene expression analysis was performed by microarray analysis (GSE58780) and RNAseq datasets. Methylation analysis was performed using R Studio (GSE58783). miRNA interaction analysis was performed by miRWalk. lncRRIsearch was performed to evaluate lncRNA-mRNA interaction analysis. Pathway enrichment and gene ontology was performed by enrichr.

Results: ELMOD1 has a significant low expression in retinoblastoma samples (logFC: -2.555068, adj. P. Value < 0.0001). Methylation analysis revealed that ELMOD1 is hypermethylated in the retinoblastoma samples (logFC: 0.7913, adj. P. Val < 0.0001). hsa-miR-619-5p regulates the expression level of ELMOD1 in the 3'UTR region of its mRNA (score: 1, energy: -38.00). lncRNA SLC25A25-AS1 have a significant interaction with ELMOD1 mRNA (sum of energy: -645.82). ELMOD1 is involved in GTPase regulator activity (GO:0030695).

Conclusion: miR-619-5p and lncRNA SLC25A25-AS1 are the possible regulators of GTPase activity by regulating ELMOD1 expression level. ELMOD1 is a potential tumor suppressor and diagnostic biomarker of retinoblastoma.

Keywords: Methylation Analysis, Microarray Analysis, Biomarker Discovery, RNA interaction

miR-96-5p affects the expression level of ATP6V1G3 in KIRK samples and modulates Collecting duct acid secretion signaling pathway

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Background: Kidney renal clear cell carcinoma (KIRC) is the most common renal cell carcinoma (RCC). However, patients with KIRC usually have poor prognosis due to limited biomarkers for early detection and prognosis prediction. The purpose of this study is to identify proteins by identifying differentially expressed genes in KIRC using microarray analysis.

Methods: Microarray analysis was performed on the GSE168845 dataset using GEO2R, GEPIA2, ENCORI, and Enrichr performed pathway enrichment and gene ontology analyses. STRING performed Protein- Protein correlation analysis. miRNA interaction analysis was performed by miRWalk.

Results: Microarray analysis revealed that ATP6V1G3 have significant down-regulation (logFC= -9.21 , adj.P value = 0.0002674) in Kidney Renal Clear Cell Carcinoma patients. GEPIA2 expression analysis validates mentioned result. This gene has taken to miRWalk to find target mRNAs. Finally, a reciprocal miRNA gene was identified (hsa-miR-96-5p) which has the characteristics of score=1 and is effective in the discussed cancer Furthermore, the result of REACTOM confirmed that ATP6V1G3 is used in pathway of Insulin Receptor Recycling R-HSA-77387. Gene ontology revealed that ATP6V1G3 is used in biological process of phagosome acidification, also in molecular function of ATPase binding, and cellular component of proton-transporting V-type ATPase complex. ATP6V1G3 has a significant interaction with ATP6V1F protein.

Conclusion: hsa-miR-96-5p might regulate Collecting duct acid secretion signaling pathway through the regulation of ATP6V1G3 expression level in KIRC patients. ATP6V1G3 could be considered as a potential tumor suppressor and biomarker of KIRC, based on mentioned results in this study.

Keywords: miRNA interaction, microarray, bioinformatics, pathway enrichment.

Nanostructured Lipid Carriers: A promising tool for transdermal drug delivery

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Background: Human skin has unique properties, and its function as a physical and biological barrier is one of the most obvious. skin is primarily able to prevent the penetration of many molecules from the outside due to the corneal layer of the epidermis. However, some compounds, especially smaller molecules, can across through the skin and reach the lower layers of it. Due to the hydrophobic nature of the stratum corneum layer, this barrier allows fat-soluble molecules to penetrate more easily than water-soluble molecules.Drug delivery through the skin mainly includes topical and transdermal delivery methods. Transdermal delivery has found wider applications as an alternative way for systemic delivery of drugs. Transdermal methods have advantages such as ease of delivery, greater patient cooperation, increased compliance, pain-free, avoidance of first-pass metabolism, and control of drug release.The goal of each skin drug delivery systems is to deliver a sufficient amount of drug into the skin with maximum stability and minimum toxicity. Therefore, a drug delivery system in order to ensure successful skin drug delivery should show favorable characteristics such as drug protection, targeting, biocompatibility and biodegradability. Nanostructured lipid carriers (NLCs) was developed in 2000 and within 12 years after their invention, more than 30 commercially available products have been introduced to the market. NLCs are second generation lipid nanocarrier system which contains both solid and liquid lipids which in turn produced less ordered lipidic core. The NLCs having unstructured matrix, have high drug loading characteristics and provide long-term drug stability during the storage period in comparison to other colloidal systems. Due to the lipophilic matrix, NLCs are useful for the formulation of lipophilic drugs. Since the NLCs exhibits biocompatibility, biodegradability and consider as safe carriers, they can be used in different applications and by different routes such as oral, cutaneous, ocular and pulmonary.

Keywords: Nanostructured Lipid- Carriers- transdermal- drug delivery

Epidemiology, Etiology, Genetic Variants in Non- Syndromic Hearing Loss in Iran: A Systematic Review and Meta-analysis

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** Mohsen Naraghi and Dariush Farhud are joint second authors

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Background: Hearing loss is one of the most common heterogeneous complicated disorders worldwide. We previously analyzed the results of published data on non-syndromic hearing loss in the Iranian population systematically.A broad range of genes is a challenge for molecular screening and clinical diagnosis in our populations on the ground of distinct genetics. The aim of this study was to analyze the role and frequency of the variants accountable for non-syndromic hearing loss (NSHL) in the Iranian population.These were identified with different methods including whole exome sequencing (WES), next-generation sequencing (NGS), targeted genomic enrichment and massively parallel sequencing (TGE + MPS), autozygosity mapping, STR markers, linkage analysis, and direct sequencing. This is the comprehensively study focusing on classifying 13 common NSHL genes according to their frequencies. Previous studies have not studied different regions and the Iranian population, and this is the definitive study on the topic.

Methods: We searched Scopus, PubMed, Science Direct databases, and Google Scholar. After a systematic review of the evidence 95 studies were considered then 31 studies were eligible for meta-analysis. In total, 6995 families, 358 variants, and 117 novel variants were included. Statistical analyses were conducted using Stata SE version 11software.The inverse variance method enjoyed combining data. Heterogeneity of the preliminary results was assessed using Q(Cochrane test),and I square index. Random effects or fixed models were applied to combine the results, relying on the degree of heterogeneity.Point and pooled prevalence of variants acting on different regions were illustrated by forest plots.

Results: The total prevalence of at least one variant of GJB2 and SLC26A genes was estimated at 26% and 5 %, respectively. Variant c.35delG accounted for 18% of the GJB2 variants while 1% of these variants were novel ones. The next most common variants in the GJB2 gene were c.109G>A at 3.5% and c.-23+1G>A at 2.3%. Moreover, the prevalence of GJB2 gene variants varied on average 0.002% from one region to another in Iran (p=0.849). Our meta-analysis also showed that the frequency of at least one variant of MYO15A varied between 1.2% and 12.5%. Corresponding prevalences for the other variants were as follows: ILDR1 (3.5% – 3.7%), CDH23 (2% -10%), PJVK (1.4% - 33%), TECTA (1.3% - 6.7%), MYO6 (2% - 4.8%), TMC1 (1.8% - 2%), MYO7A (0.7% -5%), MARVELD2 (0.7- 5%), OTOF (0.7% – 4%), LRTOMT (0.7% – 2.5%). Finally, we did not find any relationship between geographic area and the presence of these variants.

Conclusion: GJB2 gene variants were the most common cause of NSHL in Iran. Understanding the prevalence of NSHL gene frequency in Iran may be the foundation for future studies in an Iranian population which may lead to future NSHL therapy.

Keywords: hearing loss, non-syndromic, Iranian, population, variant, gene, prevalence

Gjb3 Gene Mutations in Non-Syndromic Hearing Loss of Bloch, Kurd, and Turkmen Ethnicities in Iran

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Background: Hearing loss (HL) is one of the most common heterogeneous congenital disabilities worldwide. Gap junction protein β-3 (GJB3) gene encodes Connexin31 protein (Cx31). The hereditary type of hearing im-pairment in this gene are known to cause both autosomal recessive and autosomal dominant form. In addition, GJB3 mutations have been involved in sensorineural deafness, erythrokeratodermia variabilis (EKV), and neu-ropathy diseases. We aimed to investigate GJB3 mutations in people suffering from HL among three different ethnicities of Iranian population (Baloch, Kurd, and Turkmen).

Methods: In this descriptive study, 50 GJB2-negative non-syndromic hearing loss (NSHL) Iranian individuals from 3 ethnic groups of Baloch (n=17), Kurd (n =15) and Turkmen (n=18) were enrolled. DNA extractions, PCR, and mutation detection was carried out for the two large deletions of the GJB6, del (GJB6 -D13S1830,) and del (GJB6 -D13S1854) followed by direct DNA sequencing method for the GJB3.

Results: DNA sequencing of GJB3 was shown a missense heterozygous mutation rs199689484 (NM_024009.3) GJB3: c.340G>A (p.Ala114Thr) in a Baloch patient, and a polymorphism rs35983826 (NM_024009.3) GJB3: c.798C>T (p.Asn266=) in a Turkman patient, in coding region of the GJB3. We did not detect del (GJB6 -D13S1830) and del (GJB6 -D13S1854) among these three ethnicities in Iran.

Conclusion: Deafness is a heterogeneous disorder. Specific genes and mutations contribute to hearing loss that varies from locus to locus as well as from population to population.

Keywords: Non-syndromic hearing loss (NSHL); Ethnicity; Iran; Connexin31 (Cx31)

LINC00940 and miR-4667-3p modulates 1-phosphatidylinositol-3-kinase regulator activity in MS patients through regulation of CISH expression level

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Background: An SH2 domain and a SOCS box domain are found in the CISH expressed by this gene. The suppressor of cytokine signaling (SOCS), STAT-induced STAT inhibitor (SSI), and cytokine-induced STAT inhibitor (CIS) protein families are all members of which the protein is a member. Known to be cytokine-inducible negative regulators of cytokine signaling are members of the CIS family. In hematopoietic cells, IL2, IL3, GM-CSF, and EPO can all increase the expression of this gene. In this investigation, we demonstrate a RNA interaction network in MS patients, based on a high-throughput data analysis.

Methods: High-thorughput microarray on MS samples data analysis was performed by R Studio on GSE43591. miRNA-mRNA interaction analysis was performed by miRWalk online software. lncRNA-mRNA interaction analysis was performed by lncRRIsearch database. Pathway enrichment analysis was performed by KEGG, Reactome, and enrichr. Also, Gene ontology (GO) analysis was performed by enrichr. Protein-protein interaction analysis was performed by STRING online software.

Results: CISH has a significant low-expression in the MS patients, compared to control samples (logFC: -1.432, adj. P. Val: 0.00012). hsa-miR-4667-3p regulates the expression level of CISH (score: 1, position: 3UTR). LINC00940 also modulates the expression level of CISH via direct lncRNA-mRNA interaction. CISH regulates Growth Hormone Receptor Signaling pathway. GO analysis revealed that CISH involved in cellular response to interleukin-7 and 1-phosphatidylinositol-3-kinase regulator activity. CISH protein interacts with STAT5A, JAK3, GHR, and JAK1.

Conclusion: LINC00940 and miR-4667-3p regulates cellular response to interleukin-7 process via interaction with CISH. CISH as a potential tumor suppressor could be considered as a diagnostic biomarker of MS.

Keywords: miRNA, lncRNA, Microarray, Bioinformatics, Multiple Sclerosis

Day 1 - Wednesday 8th March 2023		
09.30 – 09.50	**Registration**	
09.50 – 10.00	**Welcome & Chair Introduction**	
Part 1: **Opening**		
10.00 – 10.10	**Inaugural**	***Prof. Alireza Khoshdel*** *(President of Islamic Azad University, Tehran Medical Sciences;* *President of Congress, Epidemiologist)*
10.10 – 10.20	***Greeting***	***Dr. Maryam Eslami (****MD, PhD of Genetics, Regenerative Medicine Fellowship from Harvard Medical School, Scientific & Executive Director of Congress)*
10.20 - 10.30	***Prologue***	***Prof. Dr.Karim Nayernia*** *(Head of European Center for Personalized Medicine, Head of International Center for Personalized Medicine (P7MEDICINE), President of Congress)*
Part 2: **Personalized Medicine in Cardiovascular disease and Stem Cells**		
10.30 – 11.30	**Personalized Cardiovascular Medicine**	***Prof. Dr. Med.Uwe Nixdorff*** *(Cardiologist and Sports Specialist , Head of European Center for Personalized Medicine, Head of European Prevention Center)*
11.30 – 11.40	**Discussion**	
11.40 – 12.30	**Personalized Cell Medicine**	***Prof. Dr. Med.Jurgen Hescheler*** *(Stem Cell Specialist, Head of the German Stem Cell Association, Director of the Institute for Neurophysiology at University of Cologne)*
12.30 – 12.40	**Discussion**	
12.40 – 14.00	**Lunch & Networking**	
Part 3 - **Personalized Medicine in Onco Assays, Regenerative Medicine & Skin Aging**		

14.00-14:40	**Onco Assays & Personalized Medicine**	***Prof. Dr.Karim Nayernia***
14.40 – 14.50	**Discussion**	
14.50 – 15.20	**Personalized Medicine & Regenerative Medicine**	***Dr. Maryam Eslami***
15.20 – 16.00	**bFGF Peptide for Vitiligo**	***Dr. Omid Memarsadeghi*** *(Immunologist, Dermatologist, skin surgery subspecialist from Chicago University)*
16.00 – 16.20	**Coffee Break & Poster Presentations**	
Part 4: Personalized Medicine & Adipose-Derived Stem Cells, Oncology and Radiology		
16.20 – 16.50	**Adipose-Derived Stem Cells & Personalized Medicine**	***Dr. Babak Nikoumaram*** *(President of Iranian Society of Plastic & Aesthetic Surgeons)*
16.50 – 17.30	**Anti-mitochondrial Therapy: A New Dimension of Personalized Oncology**	***Dr. Babak Behnam*** *(MD, PhD of Genetics, Clinical Biochemical Genetics Fellowship, NSF international U.S.A)*
17.30 – 18.00	**Personalized Imaging**	***Dr. Roozbeh Barikbin*** *(Radiologist)*
18.00 – 19.00	**Panel with the speakers of first day**	***Panel Director: Dr. Mohammadreza Mohamadhasani (Cardiologist)***
19.00 - 21.00	**Farewell Dinner**	

Day 2 - Thursday 9 th March 2023		
Part 1: **Welcome, Personalized Medicine Role in fertility & Neurological Diseases**		
10.00 – 10.10	**Second day Inaugural**	***Dr. Amirreza Broumand (****Neurologist, Cell therapy fellowship from Münster University)*
10.10 – 11.10	**Fertility Assays & Personalized Medicine**	***Prof. Dr. Karim Nayernia***
11.10 – 11.20	**Discussion**	
11.20 – 12.20	**How mesenchymal stem cell therapy effects on neurological diseases**	***Dr. Amirreza Broumand***
12.20 – 12.30	**Discussion**	
12.30 – 14.00	**Lunch & Networking**	
Part 2: **The New methods of treatment in personal medicine**		
14.00 – 14.30	**How mesenchymal stem cell therapy would effect on Neuroinflammatory markers in ALS patients**	***Prof. Jalil Tavakol Afshari*** *(Immunologist, Cell Therapy Fellowship)*
14.30 – 14.40	**Discussion**	
14.40 – 15.10	**The beneficial effects of exosome therapy in the course of traumatic brain injury**	***Dr.Sajjad Sahab Negah*** *(PhD of Anatomical Sciences, Cell therapy Fellowship)*
15.10 – 15.20	**Discussion**	
15.20 – 15.40	**Personalized medicine in cervical myelopathy**	***Dr. Masoud Khadevi*** *(Neurological Surgeon; Director of Neurospine fellowship in Tehran Medical University)*

15.40 – 15.50	**Discussion**	
15.50 – 16.10	**Safety & efficacy of MSC therapy in ALS**	***Dr. Hamidreza Rahimi*** *(Assistant Professor of Mashhad Medical University, Specialist in Molecular Medicine and Stem Cells)*
16.10 – 16.20	***Discussion***	
16.30 – 16.50	**Coffee Break & Poster Presentations**	
Part 3: **Sponsor & Awards**		
17.10 – 17.30	**Congress Books Introducing**	
17.30 – 18.30	**Panel with the Speakers**	

Third day – Friday 10 th March 2023 Cruise course and Persian Gulf tourism program		
concluding section : Personalized cell theraoy and it's effect and the end of Congress		
09.30 – 10.00	**Landing Cruise Ship**	
10.00 – 10.30	**Personalized Cell Therapy**	***Prof. Dr. Karim Nayernia***
10.30 – 11.00	**CftDNA in Malignant Therapy** ***Dr. Shahram Savad; MD, PhD of Genetics***	
11.00 – 11.30	**Senotherapeutics in cutaneous senescence (skin aging)**	***Dr. Omid Memarsadeghi***
11.30 – 12.00	**New Technologies panel**	
12.00 - 14.00	**Lunch & Networking**	
14.00 – 14.30	**Mesenchymal Stem Cells for Rejuvenation- A new anti-aging approach**	***Dr. Amirreza Broumand***
14.30 – 15.00	**Poster Presentation**	

15.00 – 15.30	**IPS & Stem Cell Therapy for Cardiovascular Diseases**	***Prof. Dr. med.Uwe Nixdorff***
15.30 – 16.00	**Personalized Stem Cell Therapy Approach**	***Prof. Dr. med. Jurgen Hescheler***
16.00 – 18.00	**Persian Gulf tourism entertainment programs & Farewell**	

From Bench to Bed **Translational of Advancing Mesenchymal Stem Cell Therapies Coordinator:** **Professor Jalil Tavakkol Afshari, PhD, CP(ASCP), CLS(NCA)** **Organizer:-PARNIA Stem Cell Tech CO**		
Module I **14-14:40**	**Fundamentals of Stem Cells,** **Isolation, manufacturing and maintenance**	**Prof. J. Tavakkol Afshari** **&** **Dr. S. Etemad (Pathologist)**
Module II **14:40-15:20**	**Developing Standards (QMS, GMP) and** **regulations to support the Clinical Translation**	***Dr. S. Sahabnegah*** ***&*** ***Dr.H. Rahimi***
Module III **15:20-16**	**Clinical Trials translation, Experiences and Patient's Concern**	***Dr. A. Boroumand*** ***&*** ***Dr. A. Adhami (ICU Specialist)***