Pepper wine and wool as the dynamic factors of the social and economic develo

What influences the social and economic development of a country? 'Economic and social development' refers to the improvement in the standard of living of a population through factors such as wealth distribution, social differentiation, and industrial transformations, as discussed in the sociological literature.

What are the factors affecting economic growth and social development? Social and economic factors include factors such as income, education, employment, community safety and social support. The choices that are available in a community are impacted by social and economic factors. These choices include our abilities to afford medical care and housing and to manage stress.

How does social development lead to economic development? This paper argues that social factors can contribute to sustainable economic growth because social development leads to healthy, educated and productive citizens who can bring economic contributions.

What is an example of social and economic development? Unemployment and low income are one of the best examples to understand socio-economic development. If the unemployment rate is high, people have to work for industries that are lower than their ability on a way lesser pay scale. This suppresses the overall socio-economic development.

How do social factors affect development? Socio-cultural factors influence development by providing it with a social context. The various socio-cultural consequences that a child meets with are learnt by him/her and thus, a child develops a personality which is influenced by his/her experiences.

What are the three factors influencing economic growth?

How do social factors affect the economy? Social economics can relate to how gender norms and stereotypes influence labor markets. For example, social economics relates to hiring practices, promotion opportunities, and wage setting. Women may be pegged for specific roles as opposed to different roles historically occupied by men.

How to promote social and economic development?

How does social development affect social development? Children who have strong social skills are better able to understand others' perspectives, communicate effectively, and find solutions to conflicts. This helps them build better relationships and develop conflict resolution skills that will benefit them throughout their lives.

What factors influence the economic development of a country?

What is economic development influenced by? While year-to-year changes in per capita income are heavily influenced by such factors as weather (which affects agricultural output, a large component of income in most developing countries), a country's terms of trade, and other factors, growth rates of per capita income over periods of a decade or more are strongly ...

What are the social economic influences? Socioeconomic factors affect one's ability to engage in health activities, afford medical care and housing, and manage stress. For example, employment provides income, which enables access to housing, education, childcare, food, medical care, and other needs.

What are the three main influences on a country's level of economic development? Increases in capital goods, labor force, technology, and human capital can all contribute to economic growth.

Leong's Manual of Diagnostic Antibodies for Immunohistology. pS2. Cancer Research. Abstract PS2-29: Artificial intelligence-assisted interpretation of Ki-67 expression and repeatability in breast cancer.

Objective: Ki-67 Label Index (Ki-67LI) is a breast cancer(BC) predictive and prognostic factor. The lack of standardization and reproducibility of evaluation methods limits its use in routine work. In this study, Ki-67 standard comparison card (SRC) and artificial intelligence(AI) software were used to evaluate breast cancer Ki-

67LI. We established training and validation sets and studied the repeatability between observers. Methods: A total of 300 invasive breast cancer specimens were randomly divided into training and verification sets, with each set including 150 cases. Breast cancer Ki-67 standard comparison cards ranging from 5% to 90% were created. The training set was interpreted by nine pathologists of different ages through microscopic visual assessment (VA), SRC, microscopic manual counting (MC), and AI. The validation set was interpreted by three randomly selected pathologists using SRC and AI. Friedman M was used to analyze the difference. The intra-group correlation coefficient (ICC) and Bland-Altman scatter plot were used for consistency analysis. Results: 1.Ki-67LI interpreted by the four methods in the training set did not obey a normal distribution (P<0.05). Friedman M test showed that the difference between pathologists using the same method was statistically significant (P<0.05). After Bonferroni correction, Ki-67LI interpreted using SRC and AI showed that the difference between each pathologist and the gold standard was statistically significant (P<0.05), and the difference between pathologists was not statistically significant (P>0.05); Ki-67LI interpreted using VA and MC showed that the difference between each pathologist and the gold standard and the difference between pathologists were statistically significant (P<0.05). 2. The intra-group correlation coefficient(ICC) obtained by nine pathologists in the training set that used SRC (ICC=0.918) and AI (ICC=0.972) to interpret Ki-67LI, was significantly higher than when VA (ICC=0.757) and MC (ICC=0.803) were used. 3. Through SRC, the initial and intermediate pathologists in the training set had an increased ICC. 4. In the homogeneous group of the training set, the agreement on observers of VA, MC, SRC, and AI among observes was very good, with all ICC values above 0.80. In the heterogeneous group, SRC and AI showed a good agreement among observers (ICC= 0.877 and 0.959, respectively). In the homogeneous and heterogeneous groups of validation sets, the consistency among the pathologists that used SRC and AI was very good, with an ICC of>0.90. 5. In the verification set, using SRC and AI, three pathologists obtained results that were very consistent with the gold standard, having an ICC above 0.95, and the inter-observer agreement was also very good, with an ICC of>0.9. Conclusion: AI has satisfactory inter-observer repeatability, and the true value was closer to the gold standard, which is the preferred method for Ki-67LI reproducibility; While AI software has not been popularized, SRC may be interpreted as breast cancer Ki-67LI's standard candidate

method.Keywords: Breast cancer, Ki-67, Artificial intelligence, Ki-67 standard comparison card, Repeatability

Citation Format: Lina Li, Yueping Liu. Artificial intelligence-assisted interpretation of Ki-67 expression and repeatability in breast cancer [abstract]. In: Proceedings of the 2020 San Antonio Breast Cancer Virtual Symposium; 2020 Dec 8-11; San Antonio, TX. Philadelphia (PA): AACR; Cancer Res 2021;81(4 Suppl):Abstract nr PS2-29.

. SpringerReference. PS1/PS2. Cancer Research. Abstract PS2-28: The gut microbial signatures of premenopausal breast cancer in Taiwan.
Background Unlike western countries, breast cancer tends to occur in older and postmenopausal female; in Taiwan, 40% of patients are younger than 50 years old and are mainly diagnosed in premenopausal women. Increasing evidence has demonstrated that microbiome-host interactions may contribute to breast cancer development and treatment in addition to genetic variations. Interestingly, current studies suggest the gut microbial community likely affects the risk for estrogen-related diseases in older adults. We aimed to explore the gut microbial profiles in regarding with menopausal status and elucidate whether the gut microbiomes and related function pathways were different in premenopausal and postmenopausal breast cancer patients in Taiwan. Methods A total of 70 healthy female controls (premenopausal/Pre-C, n=20; postmenopausal/Post-C, n=50) and 146 stage I/II breast cancer patients (premenopausal/Pre-BC, n=70; postmenopausal/Post-BC, n=76) were enrolled in our study. The microbial composition in fecal samples was analyzed using 16S rRNA amplicon sequencing (V3-V4 region) on the Illumina Miseq platform. The obtained data was analyzed using CLC Microbial Genomics Module (Qiagen, Germantown, MD, USA). Linear discriminant analysis effect size (LEfSe) and Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt) were analyzed with Galaxy/HutLab and Metagenomic Profiles (STAMP) software. Results Alpha diversity of the Shannon index was unexpectedly higher in Pre-BC when compared with that of Pre-C. Weighted beta-diversity with the principal coordinate analysis (PCoA) demonstrated that total microbial compositions were significantly different between Pre-C versus Pre-BC (p=0.001) and Post-C versus Post-BC (p=0.054). The Operational Taxonomic Units (OTUs) and Krona analysis showed that the abundance of Proteobacteria was significantly increased in both Pre-BC and Post-BC (p=0.011 and 0.017), whereas

Bifidobacterium was significantly reduced in both Pre-BC and Post-BC1 (p<0.001 and 0.009) when compared with the matched controls, Pre-C and Post-BC. We further clarified the microbial markers based on the linear discriminant analysis effect size (LEfSe). As compared with Pre-C, Pre-BC had a much higher abundance of pathogens including Shigella, Clostridium, Haemophilus and others. The total microbial composition was also significantly different between Pre-BC and Post-BC (p=0.001). Intriguingly, the abundance of the microbiomes in alpha-Linolenic acid metabolism was reduced in Pre-BC when compared with Post-BC, whereas alpha-Linolenic acid metabolism were increased in both Pre-BC and Post-BC as compared with their matched controls. Conclusion Our results provide hints that, dysbiosis might be one of triggers or niches in contributing to Taiwan Pre-BC and might modulate multiple signaling pathways in relation to lipid metabolism and pathogen infections. The mechanisms underlying the link of specific gut microbiomes to Taiwan breast cancer require further investigations.

Citation Format: Ming-Feng Hou, Chih-Po Chiang, Yao-Tsung Yeh. The gut microbial signatures of premenopausal breast cancer in Taiwan [abstract]. In: Proceedings of the 2020 San Antonio Breast Cancer Virtual Symposium; 2020 Dec 8-11; San Antonio, TX. Philadelphia (PA): AACR; Cancer Res 2021;81(4 Suppl):Abstract nr PS2-28.

. Cancer Research. Abstract PS2-30: The expression of PD-L1 (Ventana SP142) in HER2-positive breast cancer and its relationship with clinicopathological characteristics.

Objective: This article aims to investigate the correlation between the expression of PD-L1 and tumor-infiltrating lymphocytes, clinicopathological features and prognosis in HER2-positive breast cancer.Methods: This study included 156 cases of HER2-positive breast cancer. Three 2mm tumor cores were selected for each case, and the expression of PD-L1 on ICs was detected by Immunohistochemistry. Statistical software SPSS 24.00 was used for analysis, ?2 test and Fisher exact test were used for correlation and consistency analysis; Logistic regression analysis was used for multivariate analysis; Kaplan-Meier analysis was used for univariate survival; Cox regression analysis was used for multivariate survival; TILs and PD-L1 correlation was analyzed by Spearman rank; P<0.05 was considered statistically significant.Results: In HER2-positive breast cancer the expression rate of PD-L1 on

ICs was 31.4%. In HER2-positive breast cancer the expression of PD-L1 on ICs was significantly correlated with the tumor size, the presence or absence of lymphovascular invasion, the expression of TILs, CD4 and CD8 (P<0.05); obtained using Logistic multivariate regression analysis The tumor size, the presence or absence of vascular tumor plugs, the expression of TILs and CD8 were independent factors affecting PD-L1 expression (P <0.05). Spearman rank correlation analysis showed that TILs infiltration level was positively correlated with interstitial immune cell PD-L1 expression in HER2-positive breast cancer patients (r = 0.486,P <0.05). Univariate survival analysis of disease-free survival (DFS) for HER2-positive breast cancer the patient's tumor size, lymphovascular invasion, lymph node metastasis, TILs, tumor immune microenvironment classification-CD4 (TIME-CD4) and tumor immune microenvironment classification-CD8 (TIME-CD8) has a significant effect on patients' DFS (P<0.05); multivariate survival analysis revealed that patients had lymphovascular invasion, TILs, TIME-CD4 and TIME-CD8 as HER2-positive breast cancer independent factors of DFS (P<0.05).Conclusions: The expression of PD-L1 on ICs in HER2-positive breast cancer is related to tumor size, presence or absence of lymphovascular invasion, TILs,CD4 expression and CD8 expression.The independent influencing factors of disease-free survival in patients with HER2-positive breast cancer are the presence or absence of lymphovascular invasion, TILs, TIME-CD4 and TIME-CD8. Among them, patients with no lymphovascular invasion and higher levels of tumor infiltrating lymphocytes had better prognosis; CD4-/PD-L1- group had better prognosis in the TIME-CD4 and CD8+/PD-L1- group had better prognosis in the TIME-CD8. There is a positive correlation between TILs infiltration level and PD-L1 expression, suggesting that HER2-positive breast cancer patients can be accurately treated according to different TILs infiltration levels and PD-L1 expression.Key words: breast cancer; HER2-positive;PD-L1;TILs

Citation Format: Ningning Zhang, Yueping Liu. The expression of PD-L1 (Ventana SP142) in HER2-positive breast cancer and its relationship with clinicopathological characteristics [abstract]. In: Proceedings of the 2020 San Antonio Breast Cancer Virtual Symposium; 2020 Dec 8-11; San Antonio, TX. Philadelphia (PA): AACR; Cancer Res 2021;81(4 Suppl):Abstract nr PS2-30.

. Cancer Research. Abstract PS2-12: Can oncotype Dx risk categories be predicted in invasive lobular carcinoma?.

Background Oncotype Dx Recurrence Score (ODX-RS) is a 21-gene assay used to predict recurrence in early stage breast cancer and guide chemotherapy decisions. Invasive lobular carcinomas (ILC) represent approximately 10-15% of all breast cancers. Many prior studies have shown that they have unique clinicopathologic features when compared to other histological subtypes. Therefore, the aim of this study was to first assess whether ODX-RS can be predicted using clinicopathologic factors in ILC and secondly, to compare these factors in invasive ductal carcinoma (IDC) and invasive carcinoma with mixed ductal and lobular features (IMC). Materials and Methods With IRB approval, the CoPath pathology database was queried for patients who were newly diagnosed with either IDC, ILC or IMC from 2010-2018 and had available Oncotype scores. For ILC cases, the subtype and presence or absence of LCIS was documented. The original pathology report was reviewed, and a chart review was performed to assess treatment decisions, locoregional and or distant recurrences and duration of follow-up. Patients with hormone receptor negative, HER2 positive or lymph node macrometastatic disease were excluded. Results A total of 582 patients were identified. The mean age was 60.1 years (range, 25-80 years). The median follow-up was 49 months (range, 0-145 months). There were 414 (71%), 102 (18%) and 66 (11%) cases of IDC, ILC and IMC, respectively. For ILC, there was a statistically significant relationship between ODX-RS and tumor grade, tubule formation, nuclear pleomorphism, mitotic count, modified Magee score (MME) and associated LCIS (Table 1). When compared to IDC and IMC, ILC had the lowest percentage of Grade 3 tumors, PR expression and high-risk patients by ODX. Factors predictive of high-risk ODX-RS in ILC were nuclear pleomorphism, mitotic count, ER H-score, PR H-score and MME, while for IDC, predictive factors included tumor grade, PR H-score, and MME using TAILORx cutoffs (Table 2). The rate of locoregional recurrences was similar between ILC and IDC (Table 1). No statistically significant correlation was found between ILC variants and RS. Disease free survival (DFS) was best in patients with IMC compared to IDC and ILC. DFS was also significantly better in patients with classic variant of ILC compared to pleomorphic variant.Conclusion We found that although ILC was similar to IDC and IMC based on tumor stage, tumor grade, risk category distribution, they demonstrated different predictors of high-risk ODX. Overall DFS was best in patients with IMC and patients with ILC, classic variant, however, when stratified based on RS scores the results were variable. Table 1. Clinicopathologic features of patients with ILC based on risk

categories.

ODX based on TAILORx<1111-25>25Totalp-valueAge0.534<502 (14)12 (86)014>5018 (20)65 (74)5 (6)88Race, n (%)0.551Caucasian20 (23)62 (72)4 (5)86African American012 (92)1 (8)13Asian02 (100)02Not reported01 (100)01T stage, n (%)0.187111 (21)35 (69)5 (10)51

27 (16)36 (84)04332 (25)6 (75)08Tumor Grade, n (%)<0.000113 (22)11 (78)014216 (19)66 (78)3 (3)8531 (33)02 (67)3Tubule formation, n (%)<0.0001Not reported3 (50)2 (33)1 (17)61000020011317 (18)75 (79)3 (3)95Nuclear pleomorphism, n (%)<0.0001Not reported3 (50)2 (33)1 (17)612 (14)12 (86)014214 (19)58 (80)1 (1)7331 (11)5 (56)3 (33)9Mitotic count, n (%)<0.0001Not Reported321611670187215 39ER %, mean (SD)95 (4)92.6 (10)95.6 (1.3)93.2 (8.5)0.426PR %, mean (SD)74.3 (31.6)54.6 (37)62.2 (19)58.8 (36)0.09Modified Magee Score, mean (SD)13 (6.5)17.3 (5)16.7 (9.8)16.4 (5.8)0.010ILC Variants, n (%)0.169Classic18 (20)68 (77)3 (3)89Pleomorphic2 (15)9 (70)2 (15)13Associated LCIS Variants, n (%)<0.0001Classic15 (19)62 (79)2 (2)79Solid001 (100)1Pleomorphic08 (80)2 (20)10Mixed Pleomorphic and Classic5 (42)7 (58)012Locoregional RecurrenceYes0 (0)3 (75)1 (25)40.12No20 (20)74 (76)4 (4)98Distant recurrenceYes03 (100)030.605No20 (20)74 (75)5 (5)99

Table 2. Demographic data.AgeILCIDCIMCTotalp-value<3003 (0.7)030.00631-402 (2)14 (3.4)1 (1.5)1741-5012 (11.8)67 (16.2)10 (15.2)8951-6021 (20.6)140 (33.8)12 (18.2)17361-7039 (38.2)132 (31.9)31 (47)20271-8028 (27.5)58 (14)12 (18.2)98Total10241466582T stage, n (%)<0.0001T151 (50)303 (73)48 (73)402T243 (42)109 (26)18 (27)170T38 (8)2 (1)0 (0)10Tumor Grade, n (%)<0.0001114 (14)84 (20)9 (14)107285 (83)236 (57)50 (76)37133 (3)94 (23)7 (10)104ER, mean (SD)93 (8)91 (15)93 (7)0.883PR, mean (SD)59 (36)67 (37)62 (38)0.451Oncotype risk categories, n (%)Low risk (<11)20 (20)95 (23)13 (20)128<0.0001Intermediate risk (11-25)77 (75)230 (56)46 (70)353High risk (>25)5 (5)89 (21)7 (11)101Locoregional recurrence0.266Yes4 (4)16 (4)0 (0)20No98 (96)398 (96)66 (100)562Distant Recurrence0.927Yes3 (3)10 (2)2 (3)15No99 (97)404 (98)64 (97)567Predictors of High-risk ODX-RS, p-valueTumor gradeNS<0.00010.045Nuclear pleomorphism0.0060.004NSMitotic count0.003NSNSER H score0.047NSNSPR H score<0.00010.014NSModified

Magee score (MME)0.019NSNSMME based on TAILORx cutoffsNS0.024NS

Citation Format: Akisha Glasgow, Haley Sechrist, Phillip Bomeisl, Hannah Gilmore, Aparna Harbhajanka. Can oncotype Dx risk categories be predicted in invasive lobular carcinoma? [abstract]. In: Proceedings of the 2020 San Antonio Breast Cancer Virtual Symposium; 2020 Dec 8-11; San Antonio, TX. Philadelphia (PA): AACR; Cancer Res 2021;81(4 Suppl):Abstract nr PS2-12.

. Cancer Research. Abstract PS2-21: Analysis of the clinical applicability of modified residual cancer burden system in evaluating the pathological response of breast cancer after neoadjuvant treatment.

Objective: To study the related factors affecting the residual cancer burden (RCB) after neoadjuvant therapy for breast cancer, and to modify the residual cancer burden system for patients after neoadjuvant therapy. To analyze the modified residual cancer burden system in predicting prognosis in patients with different molecular types. Methods: A retrospective analysis was conducted on 1274 patients who were diagnosed with invasive carcinoma of the breast by preoperative coarse needle aspiration pathology from January 2009 to December 2017, and who underwent surgical resection after neoadjuvant therapy. Follow-up was 1186. From 2009 to 2016, 837 patients were randomly assigned to the training set, and combined with HER2 expression before neoadjuvant therapy for revised residual cancer burden system (HER2-RCB). In 2017, 349 patients formed a verification set, which was used to verify the effectiveness of the analytical model. In this study, SPSS21.00 was used for statistical analysis, Spearman was used for correlation analysis, Hosmer-lemeshow test constructed model calibration degree, ROC curve was used to evaluate the efficiency comparison, Kaplan-Meier and Cox were used for survival analysis, P<0.05 was statistically significant. Results: All patients in this study were female, with an average age of 50+8.7 years (24-86 years). Spearman correlation analysis showed that RCB classification was positively correlated with ER, PR expression, clinical stage, and age before neoadjuvant therapy (P<0.05), and negatively correlated with KI67, HER2 expression before neoadjuvant therapy, postoperative vascular tumor thrombus and lymph node metastasis (P<0.05). In the training set and validation set groups, the HER2-RCB classification has a good and consistent calibration between the predicted value of the patient's overall survival (OS) and disease-free survival (DFS) risk and the actual observed value.

Sexuality is high (P>0.05), and the prognostic risk stratification of patients is higher than RCB classification (AUC=0.782, 0.699; 0.819, 0.719). According to the molecular types of breast cancer, and compared with other molecular typing, the differences that the RCB classification predicts the OS of patients with HER2 over-expression and Luminal B HER2 positive breast cancer were statistically significant (P<0.05), but there was no statistically significant difference in DFS (P>0.05), while the differences that the HER2-RCB classification predicts OS and DFS in patients with HER2 over-expression, and Luminal B HER2-positive breast cancer were statistically significant (P<0.05). Conclusions: HER2-RCB classification is more accurate than RCB classification in predicting prognosis, and the prediction of recurrence and metastasis risk in patients with HER2 over-expression and Luminal B HER2 positive breast cancer is better than RCB classification. It is suggested that HER2-RCB classification has better clinical applicability.Key words: Neoadjuvant therapy, Residual cancer burden, Pathologic complete response, Human epidermal growth factor receptor 2, Molecular type

Citation Format: Yanqi Ma, Yueping Liu. Analysis of the clinical applicability of modified residual cancer burden system in evaluating the pathological response of breast cancer after neoadjuvant treatment [abstract]. In: Proceedings of the 2020 San Antonio Breast Cancer Virtual Symposium; 2020 Dec 8-11; San Antonio, TX. Philadelphia (PA): AACR; Cancer Res 2021;81(4 Suppl):Abstract nr PS2-21.

. Cancer Research. Abstract PS2-34: Concordance of breast cancer biomarker testing in core-needle biopsy and surgical specimens: A single institution experience. Accurate diagnostic biomarker testing, including estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (Her2) expression profile, is crucial to appropriate management decisions in breast cancer. Receptor status testing is typically performed on the initial core needle biopsy (CNB) and surgical specimen (SS). The rate of concordance between CNB and SS is unclear as is the impact this has on clinical decision making. The current guidelines on retesting are vague, which results in individual institutions and providers determining retesting policies. Several studies worldwide have assessed the concordance of receptor testing with mixed conclusions. We aim to determine concordance between CNB and SS, and whether this leads to clinically relevant management changes. A retrospective analysis was performed on patients with

invasive breast cancer with available CNB and SS pathology at our institution between January 2010- May 2020. Patients who were treated with primary surgical resection and neoadjuvant chemotherapy with residual disease were included. Concordance rates between CNB and SS were assessed for ER, PR, and Her2 IHC/FISH amplification. ER and PR status were defined per NCCN guidelines as “positive,” “low-positive (ER)” or “negative.” Major discrepancy was defined as a change in label of “positive” or “negative”. Minor discrepancy was defined as change >10% without a “positive” or “negative” label change. Major discordance in Her2 was defined as change in label of “positive” or “negative” based on IHC or FISH amplification results. A minor discrepancy was a change in Her2 IHC (0-3) or FISH amplification without change in label of “positive” or “negative.” The clinical impact of discordant results was determined by investigator review. 748 patients met the eligibility criteria, and 64 of these patients received neoadjuvant therapy. For ER, there was 90.6% concordance, 2.2% major discordance, and 7.8% minor discordance between CNB and SS. For PR, there was 59.64% concordance, 11.9% major discordance, and 28.46% minor discordance. For Her2, there was 54.7% concordance, 1.6% major discordance, and 43.8% minor discordance. Of major discordance, ER (43.8%) led to the most change in management compared to Her2 and PR (12.5% and 2.2%, respectively). Retesting Her2 on SS did not change management when initial CNB was Her2 positive. For major discrepancies, patient demographics, tumor characteristics, treatment course, recurrence, and survival were reviewed. Although discordance was more common in PR and Her2 than ER biomarker profiles, major discordance leading to treatment changes were more common in ER and Her2. Retesting ER and Her2 on CNB and SS may be more clinically beneficial than retesting PR. Guidelines for retesting receptor profiles on CNB and SS are needed to best guide patient care management decisions that maximize clinical benefits while minimizing healthcare costs.

Table: Concordance of ER, PR, and HER2 Expression ProfileConcordanceMajor DiscrepancyMinor Discrepancy# Patients with Change in Treatment with Major DiscrepanciesER90.6%2.2%7.8%7/16 (43.8%)PR59.6%11.9%28.5%2/90 (2.2%)Her254.7%1.6%43.8%5/12 (12.5%)

Citation Format: Jessica Anne Slostad, Nicole Yun, Aimee Schad, Surbhi Warrior, Ruta Rao. Concordance of breast cancer biomarker testing in core-needle biopsy

and surgical specimens: A single institution experience [abstract]. In: Proceedings of the 2020 San Antonio Breast Cancer Virtual Symposium; 2020 Dec 8-11; San Antonio, TX. Philadelphia (PA): AACR; Cancer Res 2021;81(4 Suppl):Abstract nr PS2-34.

. Cancer Research. Abstract PS2-25: Cell-free DNA based detection of mono-allelic versus bi-allelic loss of function for essential genes in breast cancer.
Background: Breast cancer is the top cancer in women, accounting for over 30% of new cancer cases in women worldwide. Breast cancer is a highly heterogenous disease. Treatment of breast cancer is a very active area in cancer research with significant progresses in recent years. Despite of recent progress in liquid biopsy molecular profiling, blood-based detection of mono-allelic versus bi-allelic loss of function for essential genes such as BRCA, PTEN etc. remains an unmet clinical need for targeted therapy in breast cancer.

Methods: We tested over 1000 plasma samples of breast cancer patients using PredicneCARE, a proprietary cell-free DNA (cfDNA) assay, which covered the DNA Damage Repair (DDR) genes in addition to most genes under research in cancer pathways. This blood-based cfDNA assay has a well-tuned capability to reliably detect copy number gain and loss, discriminating bi-allelic versus mono-allelic gene deletions. The assay also has an HRD (Homologous Recombination Deficiency) add-on for the generation of HRD score.

Results: PredicineCARE was used to test over 1000 breast cancer patients. The most frequently mutated genes include TP53(59.7%), PIK3CA(47.6%), BRCA2(16.1%), ATM(12.9%), ESR1(12.1%), and ARID1A(10.1%), with cancer variant detection capability down to 0.1% for hotspots; for copy number gain at ?2.23 and for copy number loss at ?1.75; and for rearrangements at 0.375%. Interestingly, cfDNA-based gene amplifications were founded in ERBB2, PIK3CA, FGFR1, MYC, etc. and gene deletions were found in important genes such as PTEN, RB, BRCA1/2 etc. Interestingly, we observed significant difference in mutations of key driver genes such as PIK3CA in Chinese versus Caucasian mBC cohorts.

Conclusion: The PredicineCARE assay detects blood-based cancer alterations including copy number loss, fusion detection and somatic status evaluation, providing a non-invasive approach to profile important targets including HER2,

EGFR, VEGFR, DNA damage repair (BRCA1/2), cell cycle and growth regulations (CDK4/6-RB and PTEN/PI3K/AKT/mTOR), and TRK/ROS1/RET fusions for the treatment of breast cancer.

Citation Format: Feng Xie, Haoran Tang, Yue Zhang, Yong Huang. Cell-free DNA based detection of mono-allelic versus bi-allelic loss of function for essential genes in breast cancer [abstract]. In: Proceedings of the 2020 San Antonio Breast Cancer Virtual Symposium; 2020 Dec 8-11; San Antonio, TX. Philadelphia (PA): AACR; Cancer Res 2021;81(4 Suppl):Abstract nr PS2-25.

. Cancer Research. Abstract PS2-44: Correlation of thermalytix - an artificial intelligence based thermal breast screening tool in detecting a breast lesion as benign, malignant or normal.
Aim: To correlate results of Thermalytix - an artificial intelligence (AI) based breast screening tool with mammography and the final diagnosis as established by histopathology

Introduction: Screening and early diagnosis has proved to be useful in improving clinical outcome and survival of breast cancer patients. Mammography, the only breast cancer screening modality approved is not accessible or economically sustainable in low and middle-income countries (LMICs). Thermalytix, an artificial intelligence (AI) based breast cancer screening tool is low cost, portable and radiation free and uses AI-based techniques to analyze and interpret breast thermal images captured using a high-resolution infrared camera. Areas of high thermal activity are identified using relative temperature thresholding while vascular structures are analyzed using a novel image processing technique. These hotspots and vascular patterns are further analyzed to extract a set of features that are input to 3 pre-trained machine learning models to generate quantitative scores. The final scores generated based on these parameters are used to label a breast lesion as malignant, benign or normal at first screening. In this study, we present a comparative analysis of the results of thermalytix and mammography with final diagnosis as established by histopathological diagnosis.

Methods:In this retrospective study, 65 patients who had undergone biopsy and histopathological examination of breast for symptoms such as breast lump, pain or discharge were recruited. Each patient had mammography and the non-invasive

Thermalytix test done as a preliminary screening modality prior to biopsy. Automated results generated by Thermaytix were then independently compared with the histopathological diagnosis retrospectively. Similarly, the mammography results were also compared with the biopsy findings to compare the coherence of each modalities in detecting breast lesion independently.

Results:Out of the 65 symptomatic patients who were followed up by biopsy for any suspicious lesion 48/65 were neoplastic with 37/65 malignant lesions 11/65 benign lesions. Rest 17/65 patients were non-neoplastic comprising of 13/65 inflammatory cases and 4/65 normal cases.

1.Thermalytix detected 31/37 malignant cases while mammography detected 35/37 as malignant. 2.Among benign lesions thermalytix came out positive for 6/11 cases while mammography did so in 10/11 cases. 3.For inflammatory cases thermalytix and mammography raised a suspicion for malignancy in 10/13 and 11/13 cases respectively. 4.All 4 cases which were normal on biopsy were all labelled as suspicious by mammography while 3 were labelled as suspicious by thermalytix.

Conclusion:This preliminary study shows that thermalytix fared well with radiological findings in detecting breast lesions as benign, malignant or normal. The findings were somewhat skewed in favour of radiological findings as mammography was done as the primary screening test before the patients underwent biopsy and histopathological examination for any suspicious lesion.

Thermalytix can act as a low cost, portable and radiation-free test that can be of great help in detecting neoplastic lesions of breast at first screening in in low- and middle-income countries (LMICs) where mammography is not accessible or economically scalable. With its automated scoring and annotations of potential neoplastic lesion Thermalytix is poised to be a promising modality for breast cancer screening in future.

Citation Format: Chandan Kumar, Lakshmi Krishnan, Himanshu Madhu, Geetha Manjunath. Correlation of thermalytix - an artificial intelligence based thermal breast screening tool in detecting a breast lesion as benign, malignant or normal [abstract]. In: Proceedings of the 2020 San Antonio Breast Cancer Virtual Symposium; 2020 Dec 8-11; San Antonio, TX. Philadelphia (PA): AACR; Cancer Res 2021;81(4

Suppl):Abstract nr PS2-44.

. The Proceedings of the Asian Pacific Conference on Biomechanics : emerging science and technology in biomechanics. PS2-19 Control of fibrosis by atmospheric pressure plasma(PS2: Poster Short Presentation II,Poster Session). PS2-19 Control of fibrosis by atmospheric pressure plasma(PS2: Poster Short Presentation II,Poster Session). The Pelvic Girdle. . Cancer Research. Abstract PS2-27: Benefits of a rapid diagnostic centre for breast cancer care during the COVID-19 pandemic.
BACKGROUND: Changes in access to breast imaging and suspension of mammographic screening during the COVID-19 pandemic had the potential to significantly delay breast cancer diagnostic pathways. The Gattuso Rapid Diagnostic Centre (GRDC) is an innovative clinic that provides a patient-centered approach for investigation of suspicious breast abnormalities and sees approximately 1200 patients per year. The aim of this study was to assess the impact of the pandemic on patient volumes and imaging at this high-volume breast rapid diagnostic centre.

METHODS: A retrospective review of consecutive patients who presented to the GRDC from the start of the pandemic (March 12, 2020) until May 31, 2020 was performed. The number of patients, reason for referral, cancer detection rate (CDR), and waiting time from appointment to diagnosis were evaluated and compared to a corresponding time period in 2019.

RESULTS: A total of 168 new patients presented to the GRDC during the study period, corresponding to a 32.3% decrease in the number of patients compared to 2019 (n=248). Seventy-eight patients (46.4%) were referred due to the presence of a clinical palpable abnormality, which represented an increase of 13.8% (n=81 [32.7%] in 2019; p=0.005). Out of 168 patients, 69 were diagnosed with a breast malignancy, yielding a CDR of 41.1% during the pandemic versus 111 patients in 2019 (CDR of 44.8%; p= 0.456). The average time from appointment at GRDC to diagnosis was lower at 0.76 days vs 1.21 days in 2019. The rate of same day diagnosis was significantly higher at 39.5% vs 27.0% in 2019 (p=0.008). Twenty-five patients (14.9%) received neoadjuvant systemic therapy compared to 16 patients (6.5%) in 2019 (p=0.005). CONCLUSION: There were fewer patients presenting for breast investigations during the pandemic period and a significant increase in the percentage of patients with palpable masses as the cause for referral with no

appreciable change in the CDR. The presence of a rapid diagnostic breast center enabled patients with concerning breast symptoms to access and receive expedited assessment. This ensured patients did not undergo diagnostic delays despite the health care restrictions that emerged during the COVID-19 pandemic.

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. Cancer Research. Abstract PS2-22: The sensitivity and specificity of routine breast cancer pathology based on breast core biopsies compared with pathology based on surgical resections.
Background: Several studies have reported good or reasonable concordance of biomarker panel based on core needle biopsies (CNB) and the pathology based on the surgical specimen (SS). However, as neoadjuvant therapy (NAC) is becoming more common, the result from the preoperative CNB is crucial as it is the only source for the subtyping of the breast tumor. Incorrect results of subtype could result in suboptimal choice of NAC. The aim of this study was to estimate the sensitivity and specificity of biomarkers and surrogate subtypes based on CNB compared with the surgical specimen (SS) in a three-year cohort of primary breast cancer patients diagnosed at Uppsala University Hospital.

Patients and Methods: We collected data from all patients diagnosed with breast cancer at the University Hospital Uppsala, between 1st of September 2015 and 31st of August 2018 (n=837). Of these, 319 primary operated tumors were available with full biomarker information on CNB and SS. An additional 71 tumors from patients treated with NAC could be identified (not reported). Histopathological results from CNB and SS (n= 319) were used to divide the tumors in five subtypes; luminal A, luminal B, triple negative (TNBC), HER2-luminal and HER2 non-luminal.

Results: The sensitivity/specificity of CNB for the expression of estrogen receptor was 100%/100%, progesterone receptor 96%/77%, HER2 by IHC3+ 77%/99%, Grade 3 49%/89% and high Ki67 72%/78%. The sensitivity and specificity of CNB

and SS in subtype TNBC and HER2 non-luminal subtypes was 100%. Out of 37 cases with HER2-luminal subtype, 27 were correctly diagnosed by CNB (sensitivity 73%, specificity 100%). The sensitivity for correct diagnosis of luminal A was 76% with a specificity of 83% and luminal B subtype had a sensitivity of 74% and 99% specificity.

Conclusions CNB was very reliable in defining TNBC and HER2 non-luminal subtypes, but less accurate in diagnosing luminal subtypes. There is a clear risk for underdiagnosis of HER2-luminal tumors. These patients might therefore receive suboptimal treatment when treated with NAC.

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. Breast Cancer Research and Treatment. Breast Cancer Res Tr. Expression of the pS2 gene in breast tissues assessed by pS2-mRNA analysis and pS2-protein radioimmunoassay. The Proceedings of the Asian Pacific Conference on Biomechanics : emerging science and technology in biomechanics. PS2-14 OBSERVATION OF CELLULLAR RESPONSE TO OXYGEN TENSION USING MICROFLUIDIC DEVICES(PS2: Poster Short Presentation II,Poster Session). PS2-14 OBSERVATION OF CELLULLAR RESPONSE TO OXYGEN TENSION USING MICROFLUIDIC DEVICES(PS2: Poster Short Presentation II,Poster Session). The Proceedings of the Asian Pacific Conference on Biomechanics : emerging science and technology in biomechanics. PS2-17 Development of Sensing System for Three-dimensional Shape and Local Mechanical Properties on Living Tissues(PS2: Poster Short Presentation II,Poster Session). PS2-17 Development of Sensing System for Three-dimensional Shape and Local Mechanical Properties on Living Tissues(PS2: Poster Short Presentation II,Poster Session). The Proceedings of the Asian Pacific Conference on Biomechanics : emerging science and technology in biomechanics. PS2-5 The effect of interstitial flow on the invasion ability and morphology of glioma stem cells(PS2: Poster Short Presentation II,Poster Session). PS2-5 The effect of interstitial flow on the invasion ability and morphology of glioma stem cells(PS2:

Poster Short Presentation II,Poster Session). The Proceedings of the Asian Pacific Conference on Biomechanics : emerging science and technology in biomechanics. PS2-13 DYNAMICS OF ACTIN FILAMENTS DURING ADHESION PROCESS OF MC3T3-E1 CELLS TO SUBSTRATE(PS2: Poster Short Presentation II,Poster Session). PS2-13 DYNAMICS OF ACTIN FILAMENTS DURING ADHESION PROCESS OF MC3T3-E1 CELLS TO SUBSTRATE(PS2: Poster Short Presentation II,Poster Session). The Proceedings of the Asian Pacific Conference on Biomechanics : emerging science and technology in biomechanics. PS2-8 Investigating of skin behavior under compression using a pendulum test(PS2: Poster Short Presentation II,Poster Session). PS2-8 Investigating of skin behavior under compression using a pendulum test(PS2: Poster Short Presentation II,Poster Session)

Who is best suited for narrative therapy? Individuals, couples, or families may use narrative therapy. In a couple or family setting, the technique of externalizing problems facilitates positive interaction. It can also make negative communication more accepting and meaningful.

How can narrative therapy be used in child counseling? The benefits of Narrative therapy are it encourages the child to look at life moments in which the problem was not around, exploring celebrations, achievements, and awards; an opportunity for the child to begin rewriting their story without the problem.

Is the problem the problem in narrative therapy? “The problem is the problem, the person is not the problem” is an oft quoted maxim of narrative therapy. The linguistic practice of externalization, (White, 1988/9; White & Epston, 1990a) which separates persons from problems, is a playful way to motivate children to face and diminish difficulties.

Who are the theorists most often associated with narrative therapy? Narrative therapy was developed during the 1970s and 1980s, largely by Australian social worker Michael White and David Epston of New Zealand, and it was influenced by different philosophers, psychologists, and sociologists such as Michel Foucault, Jerome Bruner, Lev Semyonovich Vygotsky etc.

Who should not use narrative therapy? Narrative therapy may not be suitable when a patient is unwilling to engage in storytelling or lacks the capacity to participate actively in reconstructing their narrative post-trauma.

What are the 5 steps of narrative therapy? This book from one of the developers of narrative therapy takes the reader through the five main areas of narrative therapy, according to White: re-authoring conversations, remembering conversations, scaffolding conversations, definitional ceremony, and externalizing conversations.

What are the techniques used in narrative play therapy? Key techniques used in narrative therapy include externalization (viewing issues as separate from oneself), deconstruction (breaking problems into manageable parts), and unique outcomes (exploring and expanding alternative life narratives).

What is an example of narrative therapy? Techniques of Narrative Therapy Problems are seen as separate from the person. For example, “You did a bad thing” rather than “You are a bad person”. This technique helps the client be less critical of themselves and allows them to examine their narrative more objectively.

What is narrative therapy for families? Narrative therapy is a form of counseling that views people as separate from their problems and destructive behaviors. This allows clients to get some distance from the difficulty they face; this helps them to see how it might actually be helping or protecting them, more than it is hurting them.

What are the disadvantages of narrative family therapy? While narrative therapy has many benefits, there are a few cons to this approach that are important to be aware of. They include: Not appropriate for those with intellectual disabilities or language issues. Non-directive approach may be overwhelming for some clients.

What are the criticism of narrative therapy? Criticisms of Narrative Therapy Much of the criticisms that apply to narrative therapy lie in the opportunity for therapist bias. Because the therapist is a co-discoverer and aids in shaping an individual's perspective, the objectivity of the therapist must be constantly confirmed.

What is the main focus of narrative therapy? An initial goal of narrative therapy is to better understand how a key problem, viewed by the client within an existing life

story, influences or impacts their life. To do so, the therapist begins by asking them a great deal of open-ended questions, leaving room for the client to choose how to tell their story.

Who benefits most from narrative therapy? Narrative therapy can be used to treat almost any concern, but it tends to be most effective with those who are likely to benefit from techniques that help them reframe their circumstances or identity.

What are unique outcomes in narrative therapy? In narrative therapy unique outcomes are the overlooked instances that contradict the unwanted, problem saturated dominant narrative.

Is narrative therapy evidence-based? Some evidence supporting the effectiveness of this approach: One study found that adults with depression and anxiety who were treated with narrative therapy experienced improvements in self-reported quality of life and decreased symptoms of anxiety and depression.

What are the disadvantages of narrative approach? The first drawback of narrative analysis is the problem of subjectivity and interpretation. In other words, a drawback of the focus on stories and their details is that they're open to being understood differently depending on who's reading them.

Is narrative therapy like CBT? In a similar fashion to how the CBT therapist helps the client construct alternative beliefs about themselves, the narrative therapists helps the client construct more useful stories about themselves, helping them to make sense of their experiences, thoughts, and feelings.

What are exceptions in narrative therapy? The process of clients re-authoring their lives involves noticing the “quiet,” unnoticed stories that are able to support clients' budding identities as they separate themselves from their problems. These “quiet” stories are often referred to in narrative practice as “unique outcomes,” or “exceptions.”

What pairs well with narrative therapy? Existentialism - This idea may seem strange at first, as existentialism is the belief that the world has no inherent meaning. But because narrative therapy is all about developing your own story with meaning and purpose, rather than seeking absolute truth, existentialist concepts are well-

aligned with the approach.

How do I start narrative therapy? According to Payne (1), the author of Narrative Therapy: An Introduction for Counselors, the first step of narrative therapy is to allow space for the client to share the “problem-saturated” story. This story could have a negative outlook and be more focused on what's going wrong instead of any hope for the future (1).

What are the boundaries of narrative therapy? Narrative therapy helps individuals examine the stories and beliefs they hold about themselves and their relationships. By reauthoring their narratives, individuals can develop a stronger sense of agency and explore alternative ways of establishing and maintaining healthy boundaries.

What was the journey to the promised land? FORTY YEARS IN THE WILDERNESS Because of their unbelief, God determined that the Israelites would be punished. They were told that they must wander in the wilderness for forty years until all of the men who did not believe Him died; then their children would go into the land.

What is the 11 day journey to the promised land? Deuteronomy 1:2 Amplified Bible (AMP) It is [only] eleven days' journey from Horeb (Mount Sinai) by way of Mount Seir to Kadesh-barnea [on Canaan's border; yet Israel wandered in the wilderness for forty years before crossing the border and entering Canaan, the promised land].

Where in the Bible does it say journey to the promised land? Exodus 13:20-22 So they took their journey from Succoth and camped in Etham at the edge of the wilderness. And the LORD went before them by day in a pillar of cloud to lead the way, and by night in a pillar of fire to give them light, so as to go by day and night.

How long should the journey to the promised land have taken? The journey to the promised land should have taken eleven days, but Israel has wandered for forty years by this point. . The people of Israel complain against Moses and Aaron and accuse them of leading them into the wilderness just to die, so Moses and Aaron ask the Lord what they should do.

Who actually entered the promised land? Joshua and Caleb were the two spies who brought back a good report and believed that God would help them succeed. They were the only men from their generation permitted to go into the Promised Land after the time of wandering.

Why did the Israelites take 40 years to reach the promised land? The reason the Israelites spent so long in the wilderness is because their faith was not very strong. They struggled again and again, worshipping a golden calf instead of God, complaining about the food God provided, rebelling against Moses and Aaron, worshipping pagan gods and more.

How long did Moses wander in the promised land? After 40 years of wandering in the desert, Moses died on Mount Nebo at the age of 120, within sight of the Promised Land. The majority of scholars see the biblical Moses as a legendary figure, while retaining the possibility that Moses or a Moses-like figure existed in the 13th century BCE.

How long did Moses wait to see the promised land? Moses spent 40 years in the desert before God raised him up to lead Israel out of Egypt. As soon as God delivered Israel from bondage, He took them into the desert for another 40 before entering the Promised Land.

How long did Joshua wait to enter the promised land? Are you frightened of the tests and trials that still lie ahead, or do you view your future with courage and faith in God? Forty years of wandering in the wilderness had brought Israel to stand upon a mountaintop overlooking the land of promise.

What did Jesus say about Promised Land? In Luke 21:24, Jesus prophesied that one day Jews would have sovereignty over the land of Israel. They will fall by the edge of the sword and be led captive among all nations, and Jerusalem will be trampled underfoot by the Gentiles, until the times of the Gentiles are fulfilled.

What is the promised land called today? God instructed Abraham to leave his home and travel to Canaan, the Promised Land, which is today known as Israel. God asked Abraham to follow his rules and be a good example to others.

Who did God tell to go to the promised land? The LORD had said to Abram, "Leave your country, your people and your father's household and go to the land I will show you." – Genesis 12:1. The LORD appeared to Abram and said, "To your offspring [or seed] I will give this land." – Genesis 12:7.

Where in the Bible does it say 11 days journey to the Promised Land? The Israelites' 40 years of wandering are a symbol of our own personal journey to believe. The book of Deuteronomy begins with a striking verse. In parentheses between verses 1 and 3, verse 2 reads, “(There are eleven days' journey from Horeb by the way of mount Seir unto Kadesh-barnea)” (Deuteronomy 1:2).

Why did God choose Canaan as the Promised Land? Its location created a physical climate of faith in which God taught Abraham's descendants about Himself and called upon them to live in obedience to Him. The land of Canaan lay at the strategic land bridge connecting the continents of Asia and Africa.

How many Israelites walked to reach the Promised Land? “Numbers 26:51 says there were 601,730 family men ready to enter the Promised Land, suggesting a total population of at least two and a half million, including women and children: These were the numbers of the children of Israel, six hundred thousand and a thousand seven hundred and thirty.”

What is the summary of the Israelites' journey? Moses was tasked with leading the Israelites to the "Promised Land" Yahweh had promised them: the land of Israel. For decades, the Israelites journeyed toward Israel and encountered many hardships, which Moses, enabled by Yahweh, remedied with miracles like getting water from a rock and providing bread from heaven.

How long was the trip from Egypt to the promised land? In other words, it took the children of Israel 40 years to travel the distance they could have traveled in 11 days.

What happened in the promised land in the Bible? The land was ultimately a place where God could dwell with humans—the place where God's space and humans' space overlapped. In the garden, humans walked with God in the cool of the day, experiencing his gracious gifts and ruling over creation with him.

Why did it take 40 years to get from Egypt to Israel? “The 40 year Wilderness wandering” refers to the plight of the Israelites due to their disobedience and unbelief in God. Nearly 3,500 years ago, God delivered His people from Egyptian bondage as described in Exodus, chapters 1–12.

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