This finding, and its cost-effectiveness, should be validated in a clinical study.

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SAT0117 THE IMPACT OF DIFFERENT CRITERIA SETS ON EARLY REMISSION AND IDENTIFYING ITS PREDICTORS IN RHEUMATOID ARTHRITIS: RESULTS FROM AN OBSERVATIONAL COHORT (2009–2018)

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Background: Currently, with increased awareness of early diagnosis and intervention and the identified association of early remission with a better clinical outcome in patients with rheumatoid arthritis (RA), shorter time to remission appears to be a more attractive goal. There are several studies reported the prevalence of early remission, no study so far has demonstrated the issue in Chinese population. Moreover, further investigative studies need to be performed due to limited and conflicting predictors of early remission in previous studies.

Objectives: To assess rates of early remission and investigate the concordance across different remission definitions, and to identify predictors of early remission in Chinese patients with RA.

Methods: For this study, clinical records were retrospectively reviewed for RA patients at rheumatologic clinic in Peking University First Hospital from 2009 to 2018. Disease activity and remission were determined according to DAS28-ESR, CDAI, SDAI, and Boolean criteria. Early remission was defined as time to remission ≤ 6 months. A secondary definition evaluated early remission as ≤ 3 months. Logistic-regression analyses were performed to identify determinants of early remission.

Results: 869 consecutive patients contributing 8,640 clinic visits were studied. Early remission rates were respectively 42.0% (DAS28-ESR), 25.0% (CDAI), 29.4% (SDAI), and 26.1% (Boolean). Notably, patients achieving remission within 6 months more frequently attained sustained remission by contrast to those not achieving early remission (68.7-75.1% vs. 31.2-33.1%, $P < 0.0001$). Further logistic-regression analyses revealed male (OR=1.42-1.74, $p < 0.05$), early RA (OR=1.64-2.22, $p < 0.05$), as well as initial hydroxychloroquine treatment (OR=1.41-1.81, $p < 0.05$) were independently associated higher probability of early remission, as demonstrated by nearly all definitions, while a higher baseline disease activity (DAS28-ESR, CDAI, and SDAI) lowered the possibility of early remission in corresponding remission indices. However, the significant associations of treatment-naïve, serological features with early remission were not confirmed.

Conclusion: Early remission was strongly associated with sustained remission, however infrequently achievable in real-life practice. Male, early RA, a low baseline disease activity, and initial hydroxychloroquine treatment were stable independent predictors of early remission.

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SAT0118 PRETREATMENT PREDICTION OF INDIVIDUAL OUTCOME OF RHEUMATOID ARTHRITIS PATIENTS TO INFliximab THERAPY USING SERUM BIOMARKERS AND CLINICAL DATA

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Background: Infliximab (IFX), is a most effective b-DMARD, and results in a 60% remission rate on average in rheumatoid arthritis (RA) patients. The remaining 40% of patients undergo other biologics treatments that follow a 'treat-to-target method' until they achieve remission. Predicting in advance that a patient cannot achieve clinical remission with IFX, would allow doctors to start such patients on treat-to-target treatments sooner. Unfortunately, no reliable method has yet been found to predict patient-response.

Objectives: We tried to establish a prediction method using the serum of individual patient with RA related biomarkers present in varying amounts before they underwent IFX.

Methods: This study uses an observational retrospective study with 85 patients. 22 clinical data were used as explanation variables, such as, disease duration, combination of c-DMARDs, DAS 28-ESR, and day 0 laboratory data. 84 biomarkers in patients' pretreatment serum were measured using Multi-Plex Human Cytokine Chemokine beads array. DAS-28-ESR after 24 weeks was used as an objective variable. Patients administered IFX with regular method were divided into two groups: complete remission (DAS 28-ESR < 2.6) and non-remission (DAS 28-ESR ≥ 2.6) at 24 weeks. The log-transformed value of all parameters were used for the statistical analysis. We used the least absolute shrinkage and selection operator (Lasso) approach to select combination markers that were most predictive of remission. In the process of multi-marker prognostic model building, to avoid over fitting, leave-one-out cross validation (LOOCV) was used to evaluate the performance of the multi-marker model.

The receiver operating characteristic (ROC) analysis was used to evaluate the ability of the models to predict the 24-week outcome of patients. The area under the ROC curve is the product of the cross validation procedure.

Results: We selected a combination from 104 markers. 3 to 5 combinations were most predictive of remission with 1.405 Cohen's d and at 0.85 AUC, 0.826 PPV, 0.882 NPV, and 0.689 ACC. On the contrary, using 22 clinical parameters, AUC, PPV, NPV and ACC were 0.726, 0.713, 0.649 and 0.673, respectively.

Conclusion: Using the pre-treatment serum, we were able to predict with high accuracy patients who would achieve remission. Our method is stable and economical; therefore, it may be applicable as a way of identifying individual patients who are resistant to IFX therapy, so as to avoid treating them with IFX in the first place. The next step is to confirm these results in larger scale retrospective and prospective studies. The first highly accurate method identified for predicting remission and non-remission in individual RA patients who are targeted for IFX treatment.

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CREATE RISK PREDICTION MODELING AND DRUG WITHDRAWAL ROAD MAP THROUGH PATTERN EXTRACTION AND DATA MINING: A MASTER ALGORITHM DEVELOPMENT FROM THE SMART SYSTEM OF DISEASE MANAGEMENT (SSDM)

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Background: Combination therapy with DMARDs for treating RA is standard of care. However, certain rates of adverse events (AEs) are unavoidable. The stigmas are how to predict the risk and how to define drug withdraw sequence if AEs persist for optimal risk reductions. The decisions made are always empirically.

Objectives: To develop a risk prediction model and an algorithm for drug withdrawal sequence based on data mining from the SSDM.

Methods: SSDM is an interactive mobile disease management tool, including two application systems (APPs) for both the doctors and the patients. The patients can input medical records (including medication and laboratory test results) and perform self-evaluation (DAS28, HAQ) via App. The data synchronizes to mobiles of authorized rheumatologists through cloud and advices could be delivered. In previous studies, we demonstrated that patients could master SSDM after training.

In order to develop a prediction model and the master algorithm, abnormal white blood cell counts (WBC) and alanine aminotransferase (ALT) elevation were targeted. Data was collected, extracted, validated, and Bayesian networking, data mining, modeling were performed. WBC under 4k/ml is defined as leukocytopenia (LP), over 10k/ml as infection predisposing (IP), and ALT > 40 U/L as ALT elevation.

Results: From Jun 2014 to Jan 2019, 44,533 RA patients from 587 centers registered in SSDM. 135 different drugs and 882 combination therapies are identified. LP happens at 317 and IP at 286, ALT at 322 cases in 641 treatment regimens. Among them, MTX based regimens are 257 types, and the risk ratio (RR) are profiled as prediction model by comparing each AE rate of combination regimen with that of MTX monotherapy (Fig 1). The RR ranges from 0.28 to 6.28. The highest risk combination of prednisone (Pred), leflunomide (LEF), methotrexate (MTX), hydroxychloroquine (HCQ) and Celecoxib is selected (RR=6.28) to develop a master algorithm. Figure 2 shows Bayesian network, in which, quartet correlates with 31 different regimens. Based on Bayesian method, the probabilities of LP, IP and ALT are plotted through 64 modeling, and the algorithm for drug withdraws strategies is generated. Drug withdrawing sequence for LP is HCQ, then Cel, then LEF, then Pre, the risks of LP are reduced by 41%, 22% 36% and 15%, respectively. For IP, withdraw sequence is Pred, then LEF, then Cel, then HCQ, the risks of IP are reduced by 45%, 28%, 23% and 4%, respectively. For ALT, withdraw sequence is MTX, then Pred, LEF, then Cel, the risks of ALT are reduced by 48%, 8%, 7% and 6%.

Conclusion: Through patterns extraction, data mining, modeling, and Bayesian networking, a risk prediction model and a master algorithm for drug withdraw strategy in reduction of AEs are developed, which are expendable and replicatable. Via continuing data inputs and machine learning, an artificial intelligent system in assisting clinical forecast and decision-making may be achieved with SSDM.

MPEP Motif	Number of combinations
Celecoxib_Pref_HQ2_MTX	6.28
AZA_HQ2_MTX	4.93
Pref_CA_MTX	4.19
BioD_Pref_HQ2_MTX	4.19
NMTH_MTX	4.19
Meloxicam_Pref_MTX	4.19
TW_Pref_HQ2_MTX	2.73
Pref_SS2_MTX	2.70
Pref_AZA_HQ2_MTX	2.62
Meloxicam_Pref_HQ2_MTX	2.42
TW_Pref_LEF_MTX	2.39
Pref_LEF_Aspirin_MTX	2.09
Celecoxib_TW_HQ2_MTX	2.09
Celecoxib_Pref_SS2_MTX	2.09
Celecoxib_BioD_MTX	2.09
diGloirac_HQ2_MTX	2.09
TW_Pref_LEF_MTX	2.09
Aspirin_MTX	2.09
Pref_TW_HQ2_MTX	2.01
Pref_Aspirin_MTX	1.99
TW_LEF_SS2_MTX	1.75
Lornoxicam_LEF_MTX	1.75
Pref_MTX	1.75
Pref_TW_MTX	1.75
Pref_LEF_HQ2_MTX	1.71
Meloxicam_Pref_LEF_HQ2_MTX	1.54
CA_MTX	1.50
Celecoxib_BioD_SS2_HQ2_MTX	1.50
Gloirac_SS2_MTX	1.50
Meloxicam_HQ2_MTX	1.46
TW_LEF_MTX	1.38
TW_HQ2_MTX	1.37
SS2_MTX	1.31
diGloirac_MTX	1.31
TW_Aspirin_MTX	1.31
TW_Pref_MTX	1.27
SS2_MTX	1.26
Celecoxib_Pref_HQ2_MTX	1.16
CA_HQ2_MTX	1.16
Aspirin_Pref_HQ2_MTX	1.16
Pref_HQ2_MTX	1.16
Pref_CA_HQ2_MTX	1.05
Celecoxib_Aspirin_MTX	1.05
Celecoxib_MTX	1.02
TW_MTX	1.02
MTX	1.00

Figure 1

Figure 2. Bayesian network and data processing: Patients number (black as blow) and the rate of LP, IP and ALT elevation in 31 regiments.

Figure 2

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