Scores were considered useful if AUROC was >0.7 and excellent if >0.8.

Results: 332 patients with severe AH were treated with prednisolone 40 mg/day. At first day of treatment, patients had the following characteristics (results in medians): male gender 55.9%, ascites 74.2%, encephalopathy 24.3%, age 50.5years (95% CI: 49.2–51.7), alcohol consumption 100 g/day (80–100), prothrombin time 20.9sec (20.3–21.8), INR 1.9 (1.85–2), AST 109 IU/l (102–117), albumin 25 g/l (24.1–26), bilirubin 15.6 mg/dl (13.4–18), creatinine 0.86 mg/dl (0.8–0.9). At first day of treatment with steroids, median of prognostic functions were: ABIC 8.3 (8–8.5), Glasgow 9 (8–9), Lille 0.31 (0.25–0.37), Maddrey 60.3 (56.2–63.4) and MELD 22.5 (21.2–23.6). The AUROC (0.84) of the Lille score was significantly higher than the AUROC of other scores: ABIC (0.76, $p = 0.008$), Glasgow (0.68, $p = 0.0004$), Maddrey (0.65, $p < 0.00001$) and MELD (0.7, $p = 0.0002$). The AUROC for ABIC score was higher than for Glasgow ($p = 0.003$), Maddrey ($p < 0.0001$) and MELD ($p = 0.002$). The diagnostic accuracy of the scores using baseline variables was not improved by their evolution between 1st and 7th day of treatment: ABIC 0.68, Glasgow 0.65, Maddrey 0.65, MELD 0.64. We compared the ability of the Lille, Glasgow and ABIC scores to classify patients according to their proposed cut-offs (9 for the ABIC and Glasgow scores, 0.45 for the Lille score). Percentage of patients correctly classified by these cut-offs was higher for the Lille score than for the ABIC (79.2% vs. 72%, $p = 0.01$) and of the Glasgow scores (62.8%, $p < 0.01$).

Conclusion: In a prospective cohort of more than 300 patients, the ABIC and the MELD scores are clinically useful and the Lille score has an excellent diagnostic accuracy for predicting deaths at 6 months. In addition, the 0.45 cut-off of Lille score is superior in terms of patients correctly classified.

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A RETROSPECTIVE AUDIT OF ALCOHOLIC CARDIOMYOPATHY DIAGNOSES AT A LARGE AUSTRALIAN HOSPITAL

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Background: Endstage alcoholic liver disease is generally treated in terms of the complications of portal hypertension but alcohol also causes cardiac myopathy and this may complicate the management of the liver disease. Excess daily alcohol ingestion for 5 years can lead to alcoholic cardiomyopathy (AC) which can have a long asymptomatic phase and so can be under diagnosed. An audit was formulated to assess this potential disease burden within Western Health, a community based hospital system with 800 inpatient beds.

Method: 2 patient cohorts were selected to compare and contrast the potential for missed diagnoses. One cohort consisted of 17 gastroenterology in-patients under the care of our in unit on a single day. The other retrospective cohort consisted of 50 consecutive recent admissions with alcohol abuse. All case histories were reviewed for significant alcohol intake, clinical evidence consistent with AC and whether or not they had been assessed with an echocardiogram. All chest x-rays (CXR) were reviewed for evidence of cardiomegaly and signs of cardiac failure.

Results: Of the in-patient cohort of 17, there were 5 (29%) alcoholics with cardiomegaly. There were 4 (24%) cases of at least early AC, 2 of which were symptomatic. All patients with cardiomegaly or AC had a diagnosis of cirrhosis. Of the recent admission cohort of 50 patients, 25 (50%) had significant alcohol intake and cardiomegaly on the CXR. 9 (36%) of these 25 had symptoms or signs of cardiac failure, 8 (32%) had echocardiograms and 3 had diagnosed AC. The majority (76%) of this second cohort with cardiomegaly had cirrhosis.

Conclusion: Half the recent admissions to our unit, with a significant history of alcohol intake, had cardiomegaly but most had not had an echocardiogram. The majority of those with cardiomegaly have cirrhosis. The presence of cardiomyopathy has implications for management, in particular for fluid replacement and suitability for liver transplant. Continued alcohol consumption will worsen cardiac function in addition to also damaging the liver. Abstinence has been shown previously to improve prognosis. A prospective study is underway to confirm the initial data and explore the impact on disease management.

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ALLELIC VARIANTS OF CYP2E1 GENE IN HEPATOCARCINOMA PATIENTS AND IN HEPATIC TUMOR CELL LINES

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Background and Aims: Hepatic enzyme CYP2E1 is involved in the metabolism of a number of exogenous and endogenous substances (i.e. ethanol, drugs and chemical carcinogens). Being polymorphic, CYP2E1 gene can give different xeno-metabolic capabilities in a population and it is well known that inadequate or no enzymatic deactivation of xenobiotics could induce an increased susceptibility to disease and cancer. In particular, one of the 5′-flanking region polymorphisms, able to differentiate CYP2E1 gene transcriptional activity, is caused by the appearance/disappearance of RsaI and PstI restriction sites, which generates two different alleles, namely *C1(Rsa+/Pst−) and *C2(Rsa−/Pst+) respectively, reported to be in complete linkage disequilibrium.

Methods: To confirm the existence of a correlation between some particular CYP2E1 genotypes/haplotypes and hepatocarcinoma, we determined CYP2E1 PstI/RsaI genotypes/haplotypes by RFLP-PCR in a cohort of central western Sicily hepatocarcinoma patients and in a population of healthy students from the same geographic area.

Results: In hepatocarcinoma patients, modal genotype association was Rsa++/Pst−−, corresponding to CYP2E1 *C1/*C1 haplotype, whereas the Rsa+−/Pst−+ association, equivalent to CYP2E1 *C1/*C2 haplotype, resulted to have the lowest frequency both in patients and in controls. Moreover, both in patients and in controls, non-canonical genotype associations were frequent and arose from a no-linkage disequilibrium between the two polymorphic sites. Other authors reported this finding as a rare occurrence. Thus, from analysis of only one restriction site, Rsa++ genotype was approximately 1.5-fold more frequent in patients than in controls, and the non-canonical Rsa+− genotype was found relatively frequent in patients. Moreover, HuH7 and HA22T transformed hepatocarcinoma cell lines also showed the Rsa+− genotype.

Conclusions: These results suggest that the presence in CYP2E1 genotype of at least one allele with an Rsa I restriction site is correlated with hepatocarcinoma. As this site is known a consensus sequence for some specific CYP gene transcription factors, like HNF-1, it may be supposed that a single nucleotide polymorphism can alter the possibility of HNF-1 to bind CYP2E1 promoter. This could determine a marked change in the transcriptional activity of the gene, incompetence in xenobiotic metabolism or in toxic substance deactivation and an increased susceptibility to neoplastic diseases, such as hepatocarcinoma.