

CHAPTER 51 – REFERENCES

1. El-Serag HB. Epidemiology of viral hepatitis and hepatocellular carcinoma. *Gastroenterology* 2012;142:1264–1273.e1.
2. El-Serag HB. Hepatocellular carcinoma. *N Engl J Med* 2011;365:1118–1127.
3. Bruix J, Sherman M, American Association for the Study of Liver D. Management of hepatocellular carcinoma: an update. *Hepatology* 2011;53:1020–1022.
4. Marquardt JU, Galle PR, Teufel A. Molecular diagnosis and therapy of hepatocellular carcinoma (HCC): an emerging field for advanced technologies. *J Hepatol* 2012;56:267–275.
5. Bruix J, Boix L, Sala M, et al. Focus on hepatocellular carcinoma. *Cancer Cell* 2004;5:215–219.
6. Thorgerisson SS, Grisham JW. Molecular pathogenesis of human hepatocellular carcinoma. *Nature Genet* 2002;31:339–346.
7. Zender L, Villanueva A, Tovar V, et al. Cancer gene discovery in hepatocellular carcinoma. *J Hepatol* 2010;52:921–929.
8. Quackenbush J. Microarray analysis and tumor classification. *N Engl J Med* 2006;354:2463–2472.
9. Hood L, Heath JR, Phelps ME, et al. Systems biology and new technologies enable predictive and preventative medicine. *Science* 2004;306:640–643.
10. McDermott U, Downing JR, Stratton MR. Genomics and the continuum of cancer care. *N Engl J Med* 2011;364:340–350.
11. Vogelstein B, Papadopoulos N, Velculescu VE, et al. Cancer genome landscapes. *Science* 2013;339:1546–1558.
12. Meyerson M, Gabriel S, Getz G. Advances in understanding cancer genomes through second-generation sequencing. *Nat Rev Genet* 2010;11:685–696.
13. Krawczyk M, Mullenbach R, Weber SN, et al. Genome-wide association studies and genetic risk assessment of liver diseases. *Nat Rev Gastroenterol Hepatol* 2010;7:669–681.
14. Kumar V, Kato N, Urabe Y, et al. Genome-wide association study identifies a susceptibility locus for HCV-induced hepatocellular carcinoma. *Nat Genet* 2011;43:455–458.
15. Moinzadeh P, Breuhahn K, Stutzer H, et al. Chromosome alterations in human hepatocellular carcinomas correlate with aetiology and histological grade—results of an explorative CGH meta-analysis. *Br J Cancer* 2005;92:935–941.
16. Poon TC, Wong N, Lai PB, et al. A tumor progression model for hepatocellular carcinoma: bioinformatic analysis of genomic data. *Gastroenterology* 2006;131:1262–1270.
17. Su WH, Chao CC, Yeh SH, et al. OncoDB.HCC: an integrated oncogenomic database of hepatocellular carcinoma revealed aberrant cancer target genes and loci. *Nucleic Acids Res* 2007;35:D727–D731.
18. Woo HG, Park ES, Lee JS, et al. Identification of potential driver genes in human liver carcinoma by genomewide screening. *Cancer Res* 2009;69:4059–4066.
19. Lamb J. The Connectivity Map: a new tool for biomedical research. *Nat Rev Cancer* 2007;7:54–60.
20. Roessler S, Long EL, Budhu A, et al. Integrative genomic identification of genes on 8p associated with hepatocellular carcinoma progression and patient survival. *Gastroenterology* 2012;142:957–966.e12.
21. Feinberg AP. Phenotypic plasticity and the epigenetics of human disease. *Nature* 2007;447:433–440.
22. Feinberg AP, Ohlsson R, Henikoff S. The epigenetic progenitor origin of human cancer. *Nat Rev Genet* 2006;7:21–33.
23. Calvisi DF, Ladu S, Gorden A, et al. Mechanistic and prognostic significance of aberrant methylation in the molecular pathogenesis of human hepatocellular carcinoma. *J Clin Invest* 2007;117:2713–2722.
24. Hernandez-Vargas H, Lambert MP, Le Calvez-Kelm F, et al. Hepatocellular carcinoma displays distinct DNA methylation signatures with potential as clinical predictors. *PLoS One* 2010;5:e9749.
25. Lambert MP, Paliwal A, Vaisiere T, et al. Aberrant DNA methylation distinguishes hepatocellular carcinoma associated with HBV and HCV infection and alcohol intake. *J Hepatol* 2011;54:705–715.
26. Andersen JB, Factor VM, Marquardt JU, et al. An integrated genomic and epigenomic approach predicts therapeutic response to zebularine in human liver cancer. *Sci Transl Med* 2010;2:54ra77.
27. Lee JS, Heo J, Libbrecht L, et al. A novel prognostic subtype of human hepatocellular carcinoma derived from hepatic progenitor cells. *Nat Med* 2006;12:410–416.
28. Um TH, Kim H, Oh BK, et al. Aberrant CpG island hypermethylation in dysplastic nodules and early HCC of hepatitis B virus-related human multistep hepatocarcinogenesis. *J Hepatol* 2011;54:939–947.
29. Revill K, Wang T, Lachenmayer A, et al. Genome-wide methylation analysis and epigenetic unmasking identify tumor suppressor genes in hepatocellular carcinoma. *Gastroenterology* 2013;145:1424–1435.e1–25.
30. Esteller M. Epigenetics in cancer. *N Engl J Med* 2008;358:1148–1159.
31. Hoshida Y, Toffanin S, Lachenmayer A, et al. Molecular classification and novel targets in hepatocellular carcinoma: recent advancements. *Semin Liver Dis* 2010;30:35–51.
32. Lujambio A, Lowe SW. The microcosmos of cancer. *Nature* 2012;482:347–355.
33. Coulouarn C, Factor VM, Andersen JB, et al. Loss of miR-122 expression in liver cancer correlates with suppression of the hepatic phenotype and gain of metastatic properties. *Oncogene* 2009;28:3526–3536.
34. Mott JL. MicroRNAs involved in tumor suppressor and oncogene pathways: implications for hepatobiliary neoplasia. *Hepatology* 2009;50:630–637.
35. Ladeiro Y, Couachy G, Balabaud C, et al. MicroRNA profiling in hepatocellular tumors is associated with clinical features and oncogene/tumor suppressor gene mutations. *Hepatology* 2008;47:1955–1963.
36. Toffanin S, Hoshida Y, Lachenmayer A, et al. MicroRNA-based classification of hepatocellular carcinoma and oncogenic role of miR-517a. *Gastroenterology* 2011;140:1618–1628.e16.
37. Ji J, Shi J, Budhu A, et al. MicroRNA expression, survival, and response to interferon in liver cancer. *N Engl J Med* 2009;361:1437–1447.
38. Ji J, Yu L, Yu Z, et al. Development of a miR-26 companion diagnostic test for adjuvant interferon-alpha therapy in hepatocellular carcinoma. *Int J Biol Sci* 2013;9:303–312.
39. Arzumanyan A, Reis HM, Feitelson MA. Pathogenic mechanisms in HBV- and HCV-associated hepatocellular carcinoma. *Nat Rev Cancer* 2013;13:123–135.
40. Teufel A, Marquardt JU, Galle PR. Next generation sequencing of HCC from European and Asian HCC cohorts. Back to p53 and Wnt/beta-catenin. *J Hepatol* 2013;58:622–624.
41. Fujimoto A, Totoki Y, Abe T, et al. Whole-genome sequencing of liver cancers identifies etiological influences on mutation patterns and recurrent mutations in chromatin regulators. *Nat Genet* 2012;44:760–764.
42. Guichard C, Amadeo G, Imbeaud S, et al. Integrated analysis of somatic mutations and focal copy-number changes identifies key genes and pathways in hepatocellular carcinoma. *Nat Genet* 2012;44:694–698.
43. Li M, Zhai H, Zhang X, et al. Inactivating mutations of the chromatin remodeling gene ARID2 in hepatocellular carcinoma. *Nat Genet* 2011;43:828–829.
44. Totoki Y, Tatsuno K, Yamamoto S, et al. High-resolution characterization of a hepatocellular carcinoma genome. *Nat Genet* 2011;43:464–469.
45. Toffanin S, Cornell H, Harrington A, et al. Next-generation sequencing: path for driver discovery in hepatocellular carcinoma. *Gastroenterology* 2012;143:1391–1393.
46. Cleary SP, Jeck WR, Zhao X, et al. Identification of driver genes in hepatocellular carcinoma by exome sequencing. *Hepatology* 2013;58:1693–1702.
47. Kan Z, Zheng H, Liu X, et al. Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. *Genome Res* 2013;23:1422–1433.
48. Nault JC, Mallet M, Pilati C, et al. High frequency of telomerase reverse-transcriptase promoter somatic mutations in hepatocellular carcinoma and preneoplastic lesions. *Nat Commun* 2013;4:2218.
49. Huang Q, Lin B, Liu H, et al. RNA-Seq analyses generate comprehensive transcriptomic landscape and reveal complex transcript patterns in hepatocellular carcinoma. *PLoS One* 2011;6:e26168.
50. Chen L, Li Y, Lin CH, et al. Recoding RNA editing of AZIN1 predisposes to hepatocellular carcinoma. *Nat Med* 2013;19:209–216.
51. Kaposi-Novak P, Libbrecht L, Woo HG, et al. Central role of c-Myc during malignant conversion in human hepatocarcinogenesis. *Cancer Res* 2009;69:2775–2782.
52. Marquardt JU, Seo D, Andersen JB, et al. Sequential transcriptome analysis of human liver cancer indicates late stage acquisition of malignant traits. *J Hepatol* 2014;60:346–353.
53. Hernandez-Gea V, Toffanin S, Friedman SL, et al. Role of the microenvironment in the pathogenesis and treatment of hepatocellular carcinoma. *Gastroenterology* 2013;144:512–527.
54. Karin M. Nuclear factor-kappaB in cancer development and progression. *Nature* 2006;441:431–436.
55. Luedde T, Schwabe RF. NF-kappaB in the liver—linking injury, fibrosis and hepatocellular carcinoma. *Nat Rev Gastroenterol Hepatol* 2011;8:108–118.
56. He G, Dhar D, Nakagawa H, et al. Identification of liver cancer progenitors whose malignant progression depends on autocrine IL-6 signaling. *Cell* 2013;155:384–396.
57. Hoshida Y, Villanueva A, Kobayashi M, et al. Gene expression in fixed tissues and outcome in hepatocellular carcinoma. *N Engl J Med* 2008;359:1995–2004.
58. Thorgerisson SS. Genomic decoding of hepatocellular carcinoma. *Gastroenterology* 2006;131:1344–1346.
59. Schirmacher P, Calvisi DF. Molecular diagnostic algorithms in hepatocellular carcinoma: dead-end street or light at the end of the tunnel? *Gastroenterology* 2013;145:49–53.
60. Farazli PA, DePinho RA. Hepatocellular carcinoma pathogenesis: from genes to environment. *Nat Rev Cancer* 2006;6:674–687.
61. Villanueva A, Hoshida Y, Battiston C, et al. Combining clinical, pathology, and gene expression data to predict recurrence of hepatocellular carcinoma. *Gastroenterology* 2011;140:1501–1512.e2.
62. Gerlinger M, Rowan AJ, Horswill S, et al. Intratumor heterogeneity and branched evolution revealed by multiregion sequencing. *N Engl J Med* 2012;366:883–892.
63. Teufel A, Marquardt JU, Galle PR. Novel insights in the genetics of HCC recurrence and advances in transcriptomic data integration. *J Hepatol* 2012;56:279–281.

64. Nault JC, De Reynies A, Villanueva A, et al. A hepatocellular carcinoma 5-gene score associated with survival of patients after liver resection. *Gastroenterology* 2013;145:176–187.
65. Oikawa T, Kamiya A, Zeniya M, et al. Sal-like protein 4 (SALL4), a stem cell biomarker in liver cancers. *Hepatology* 2013;57:1469–1483.
66. Yong KJ, Gao C, Lim JS, et al. Oncofetal gene SALL4 in aggressive hepatocellular carcinoma. *N Engl J Med* 2013;368:2266–2276.
67. Marquardt JU, Thorgeirsson SS. Sall4 in “stemness”-driven hepatocarcinogenesis. *N Engl J Med* 2013;368:2316–2318.
68. Marquardt JU, Raggi C, Andersen JB, et al. Human hepatic cancer stem cells are characterized by common stemness traits and diverse oncogenic pathways. *Hepatology* 2011;54:1031–1042.
69. Yamashita T, Forgues M, Wang W, et al. EpCAM and alpha-fetoprotein expression defines novel prognostic subtypes of hepatocellular carcinoma. *Cancer Res* 2008;68:1451–1461.
70. Andersen JB, Thorgeirsson SS. Genetic profiling of intrahepatic cholangiocarcinoma. *Curr Opin Gastroenterol* 2012;28:266–272.
71. Andersen JB, Spee B, Blechacz BR, et al. Genomic and genetic characterization of cholangiocarcinoma identifies therapeutic targets for tyrosine kinase inhibitors. *Gastroenterology* 2012;142:1021–1031.e15.
72. Sia D, Hoshida Y, Villanueva A, et al. Integrative molecular analysis of intrahepatic cholangiocarcinoma reveals 2 classes that have different outcomes. *Gastroenterology* 2013;144:829–840.
73. Woo HG, Lee JH, Yoo JH, et al. Identification of a cholangiocarcinoma-like gene expression trait in hepatocellular carcinoma. *Cancer Res* 2010;70:3034–3041.
74. Lee JS, Choi IS, Heo J, et al. Classification and prediction of survival in hepatocellular carcinoma by gene expression profiling. *Hepatology* 2004;40:667–676.
75. Lee JS, Thorgeirsson SS. Comparative and integrative functional genomics of HCC. *Oncogene* 2006;25:3801–3809.
76. Marquardt JU, Thorgeirsson SS. Stem cells in hepatocarcinogenesis: evidence from genomic data. *Semin Liver Dis* 2010;30:26–34.
77. Marquardt JU, Factor VM, Thorgeirsson SS. Epigenetic regulation of cancer stem cells in liver cancer: current concepts and clinical implications. *J Hepatol* 2010;53:568–577.