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Distinct histomorphological features are associated with *IDH1* Mutation in Intrahepatic Cholangiocarcinoma

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Abstract

Intrahepatic cholangiocarcinoma has known histological heterogeneity. Mutations in *IDH1* (m*IDH1*) define a molecular subclass of intrahepatic cholangiocarcinoma and *IDH*-targeted therapies are in development. Characterizing m*IDH1* ICC histomorphology is of clinical interest for efficient identification. Resected ICCs with targeted next generation sequencing by MSK-IMPACT were selected. Clinical data were obtained. By slide review, blinded to *IDH* status, data were collected for histology type, mucin production, necrosis, fibrosis, cytoplasm cell shape (low cuboidal, plump cuboidal/polygonal, and columnar), and architectural pattern (anastomosing, tubular, compact tubular, and solid). A tumor was considered architecturally heterogeneous if no dominant pattern represented ≥75% of the tumor. Parameters were compared between m*IDH1*and *IDH* wild type controls. In the examined cohort (113 ICC: 29 m*IDH1* and 84 *IDH* wild type), all *IDH1* mutant tumors were of small duct type histology, thus analysis was limited to 101 small duct type tumors. m*IDH1*cases were more likely to have plump cuboidal/ polygonal shape (P=.014) and geographic-type fibrosis (P=.005) while *IDH1* wild type were more likely to have low cuboidal shape (P=.005). Both groups were predominantly architecturally heterogeneous with no significant difference in the distribution of architectural patterns. Plump cuboidal/polygonal cell shape and a geographic-type pattern of intra-tumoral fibrosis are more often seen in m*IDH1*compared to *IDH* wild type tumors, however *IDH1* mutation is not associated with a distinct histoarchitectural pattern.

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Keywords

cholangiocarcinoma; histology; liver cancer; genomics; *IDH1*

1. Introduction

Biliary adenocarcinomas are classified as intrahepatic, peri-hilar and extrahepatic based on their anatomical location. Intrahepatic cholangiocarcinoma (ICC) is a rare tumor in western populations with an incidence of approximately 4–10 per 100,000 person years and a 5-year survival rate of around 15%.[1] Surgical resection with curative intent offers a 5-year survival of 20–40%.[2]

Recent genomic studies have shown that neomorphic mutations in isocitrate dehydrogenase 1 (*IDH1*) in cholangiocarcinoma is highly associated with intrahepatic origin, with a prevalence of approximately 20% in North American studies. [3, 4] IDH1 is an enzyme in the tricarboxylic acid cycle that catalyzes the oxidative decarboxylation of isocitrate to alpha-ketoglutarate. Neomorphic mutations in this enzyme, which also occur in acute myeloid leukemia, gliomas, and chondrosarcoma, typically lead to altered activity that results in the increased production of (R)-2-hydroxyglutarate, which interferes with histone and DNA demethylases, as well as several other alpha-ketoglutarate-consuming processes. [5, 6, 7, 8] An additional consequence of this mutation in myeloid neoplasms and glioma is interference with tumor differentiation.[9] Mutations in *IDH1* tend to occur in hotspots such as R132, and in ICC the most common mutations are R132C, R132G, and R132L, which are distinct from the R132H mutation found in gliomas and not detected by commercially available immunohistochemical stains. [5, 10] Nonetheless, these activating mutations have been shown to increase the serum level of (R)-2-hydroxyglutarate in cholangiocarcinoma. [11] In cholangiocarcinoma, the effects of interference with phenotypic or functional differentiation are of great interest.

Given the singular metabolic disruption of *IDH1*-mutated neoplasms, it is logical to consider whether this molecular subtype produces a recognizable phenotype. Intrahepatic cholangiocarcinoma has been subclassified by both gross and histological configuration with varying acceptance. Grossly, ICC occurs in mass forming, periductal infiltrating, and intraductal subtypes. [12] Histologic subtyping has gained less widespread acceptance and clinical significance is less substantiated. On the one hand, the neoplasms have been separated into “peripheral” and “hilar” subtypes. [13, 14] Alternatively, the neoplasms have been divided into groups based on resemblance to large bile duct cells (large duct) versus cholangiolar cells (small duct type).[15] Additional patterns such as ductal plate malformation have been described. [16]

While the prognostic relevance of *IDH1* mutation is uncertain, it is expected to be of therapeutic relevance. Survival analysis of *IDH* mutant ICC have shown conflicting results and are often limited in power because the mutation is present only in a subset of the populations studied.[3, 5, 10, 17, 18] Nonetheless, mutant *IDH1* represents a promising actionable target for small molecule therapy in leukemia, glioma, and cholangiocarcinoma and clinical trials are in progress.[19, 20, 21] This study aims to comprehensively evaluate

the cytological and architectural features of *IDH1* mutated (m*IDH1*) ICC in comparison to ICC lacking hotspot mutations in *IDH1* and *IDH2* which could aid in the identification of *IDH1* mutant tumors.

2. Materials and Methods

This study was approved by the Institutional Research Ethics Board of Memorial Sloan Kettering Cancer Center. Surgically resected ICCs from 1993 to 2017 which had undergone targeted next generation sequencing by MSK-IMPACT either on a clinical basis or as a part of retrospective, investigational testing (based on the availability of archived tumor and normal control tissue availability). MSK-IMPACT was clinically validated for the detection of mutations of *IDH1* exon 4 (41–138) and *IDH2* exon 4 (125–178) inclusive of hotspot mutations observed in intrahepatic cholangiocarcinoma. [22] Cases were stratified by the mutation status of *IDH1*. Tumors with *IDH2* mutations were excluded, therefore the wild type *IDH* (wt*IDH*) was defined by lacking alterations in *IDH1* and *IDH2* as detected by MSK-IMPACT. The frequency of alterations was grouped by signaling pathways as determined using the Reactome open-source pathway database.

2.1 Clinical and pathologic variables

Clinical data including age at diagnosis, sex, ethnicity, history of autoimmune disease, chronic viral hepatitis, smoking, and clinical cirrhosis were obtained by review of electronic medical records. Pathology slides and reports were reviewed to assess characteristics of tumor size, grade, presence of perineural invasion, lymphovascular invasion, periductal infiltration, satellite nodules, presence of mucin, and intraductal precursor lesions. Small duct versus large duct types, results of albumin mRNA in situ hybridization, Arginase-1, and HepPar-1 immunohistochemistry were determined using methods and criteria from a prior publication.[15] Tumor grading was performed by applying the Bloom-Richardson system commonly used in breast carcinoma. [23] Clinical stage and lymph node status was assigned using the AJCC 8th edition using the available pathological and clinical information at the time of resection.[24]

Tumor architecture was classified into four patterns as shown in Figure 1A–D. The anastomosing pattern consisted of anastomosing small ductular structures like the ductular reaction. The simple tubular pattern consisted of non-anastomosing tubules with stroma between glands. The compact tubular pattern had lumens or slit-like spaces, but the glands were compressed together without intervening stroma. The solid pattern was confluent with minimal lumens. Architecturally heterogeneous comprised no one pattern ≥ 75% of the tumor across all reviewed slides. Percent of necrosis and fibrosis were evaluated by semiquantitative estimation of volume involving tumor on each reviewed tumor slide with average across the aggregate of all tumor slides. Geographic-type fibrosis was defined as a discrete region of fibrosis without intervening viable tumor glands (Figure 1I). The cell shape was categorized as low cuboidal, plump cuboidal/polygonal, and columnar as illustrated in Figure 1. Low cuboidal had less than 1 nuclear diameter of apical cytoplasmic length, plump cuboidal/polygonal had between 1 to 2 nuclear diameters of apical cytoplasm or has cytoplasm which exceeds 2x the width of the nuclei, and columnar cells had more

than 2 nuclear diameters of apical cytoplasm with or without mucin. Clear cell features were recorded as present if seen in >10% of tumor cells (Figure 1H)

2.2 Statistical Methods

Statistical comparisons were performed by Fisher's exact test for categorical variables. For histological comparisons, tumors that underwent neoadjuvant therapy were excluded from the analysis, and only small duct type tumors were included. For sensitivity and specificity, we tested *IDH1* mutation predictions from logistic regression models against observed *IDH1* mutation and used *IDH1* mutation prevalence as the prediction threshold cut-off. We analyzed for associations between *IDH1* mutation status for clinical and histological characteristics for all tumors, and then repeated the analysis for small duct type tumors only. Tumors with slides reviewed from recurrence were included in *IDH1* morphology analysis. Statistical significance for all comparisons was set as $P \leq 0.05$.

3. Results

We identified 29 m*IDH1* ICC and a control population of 84 wt*IDH* ICC. The somatic alterations in *IDH1* exon 4 consisted of p.R132C in n=23 (79.3%), p.R132L in n=3 (10.3%), and p.R132G in n=3 (10.3%). All mIDH1 were of small duct type whereas large duct (n=9) and indeterminate types (n=3) comprised a minority of the wt*IDH* group. Since large duct and indeterminate were exclusively in the wt*IDH* group, they were excluded from clinico-pathological analysis. For the clinical variables, only autoimmune disease was significantly associated with m*IDH1* (Table 1). The six patients with autoimmune diseases in the m*IDH1* group had Hashimoto's thyroiditis (n=2), rheumatoid arthritis (n=2), scleroderma (n=1), and Crohn's colitis (n=1). Patients with small duct type wt*IDH* small duct type had primary sclerosing cholangitis (n=1), Bell's palsy (n=1), and multiple sclerosis (n=1).

Significant differences in cell shape and fibrosis pattern were detected (Table 2). Plump cuboidal/polygonal shape and geographic fibrosis were significant associated with m*IDH1* while low cuboidal shape was significantly associated with wt*IDH1* while. The presence of plump cuboidal/polygonal shape had a sensitivity of 60% and specificity of 71% for identifying *IDH1* mutation. Geographic-type fibrosis had a sensivitity 44% and specificity of 86% for identifying *IDH1* mutation. The presence of both features (plump cuboidal/polygonal shape and geographic fibrosis) had a sensitivity of 72% and specificity of 60% for identifying *IDH1* mutation.

IDH mutation status was not associated with an architectural pattern (Table 2). Examples of *IDH1* mutant histology are shown in Figure 2. The compact tubular pattern was the most common dominant pattern for both groups (14–15%). The volumes for the patterns were similar for both groups (Table 2).

Necrosis and fibrosis were limited in all untreated tumors. The identification of mucin, intra- or extracellular, did not distinguish m*IDH1* from wt*IDH,* but was notably present in both groups, albeit in a very low percentage of tumors and generally focal (Figure 2H–I).

Staining for albumin mRNA by in situ hybridization did not show a statistically significant difference in the groups. Of 26 m*IDH1* tested, 17 (65%) were albumin positive and of the 56 wt*IDH* tested, 47 (83%) were albumin positive (P=0.084). The results for immunohistochemistry for markers of hepatocellular differentiation was: Arginase-1: positive in 0/23 tested m*IDH1*, 1/74 tested wt*IDH*; HepPar1: positive in 0/24 m*IDH1*, 1/74 tested wt*IDH*.

FGFR2 rearrangements, and the corresponding signaling pathway (MAPK), were the only two significant other genomic differences between the wt*IDH* and m*IDH1* groups (Table 3).

4. Discussion

IDH1 mutated intrahepatic cholangiocarcinoma has uniquely altered cellular biology known to affect cellular differentiation on a molecular level. Our study systematically classified the phenotype of a large cohort of ICC with prior targeted sequencing analysis and comparatively analyzed the histoarchitectural patterns of untreated tumors with the aim to detect phenotypic characteristics associated with this mutation. After our initial observation that all m*IDH1* ICC were small duct type, subsequent analysis excluded large duct and indeterminate types in the wild type group. By comparing m*IDH1* and wt*IDH* control groups, we determined that m*IDH1* tumors have a significantly higher proportion of cells with plump cuboidal/polygonal shape (60% vs 29%, P=0.014) and geographic fibrosis (44% versus 14%, p=0.005).

Prior comparisons between m*IDH1* and non*IDH* mutant ICC have described a higher proportion of clear cell change and lower proportion of poor differentiation in m*IDH* tumors. [4, 10] We did not confirm these differences, however our methodology differed from other studies, for instance we included small duct histology only. There is no criteria-based system for grading differentiation for ICC and we experimentally applied a system borrowed from breast cancer grading to allow contributions to grade from mitotic activity and architecture. If we consider that our assessment of dominant (>75%) solid architecture is a surrogate marker of poor differentiation based on architecture only, there is no detectable difference between the groups.

Since complexity of histoarchitecture is a component of most criteria of tumor differentiation at various anatomic sites, another aim of this study was to determine whether m*IDH1*-related altered cellular differentiation would have an observable histoarchitectural association. Examining this question is of considerable interest, because intrahepatic cholangiocarcinoma has distinctive architectural patterns and several investigators have attempted to subclassify them based on the premise that the patterns may have potential clinical or biological significance.[25, 26] Recently, for example, the ductal plate malformation pattern was shown to have an association with *ARID1A* mutation [27]. We discovered that m*IDH1* and wt*IDH* ICCs are equally architecturally heterogeneous with a strikingly similar distribution of dominant architectural patterns. As noted, instead of an architectural difference, a distinctive cytomorphological appearance was recognized. We find it especially interesting that the plump cuboidal/polygonal morphology resemble oncocytes and hepatocytes given metabolic and gene expression changes in these neoplasms.

IDH1 mutants accumulate the metabolite (R)-2-hydroxyglutarate, show high expression of mitochondrial genes by integrative genomic analysis, and high mitochondrial DNA copy number.[5] Increased mitochondria are a feature of oncocytes, which typically have plump/polygonal shape. [5] In vitro models and mouse studies have also shown that mutant *IDH* blocks hepatocyte differentiation and *IDH* mutant ICC express a liver progenitor cell gene signature.[28].

Among the clinical variables we assessed, only autoimmune disease had a significant association with *IDH1* mutation status. Notably, none of the m*IDH1* patients had autoimmune diseases directly associated with biliary disease such as primary sclerosing cholangitis. Worldwide, there are regional differences in risk factors for cholangiocarcinoma and molecular subtypes have been shown to cluster with clinical factors such as liver fluke infection.[29] This study of ICC was performed in a population lacking liver fluke infection, hepatolithiasis, biliary cysts, and with a lower prevalence of chronic hepatitis (18%) compared to other published ICC cohorts.[13, 30]

A potentially confounding factor is the possibility of increased biologic heterogeneity in the wt*IDH* group. Removing the large duct and indeterminate types from our analysis was intended to mitigate biological heterogeneity within the wt*IDH* group because they are morphologically distinct from small duct type and there is some evidence that the large duct type has distinct biology and molecular associations.[13] We explored for potential genomic heterogeneity by comparing the mutation profiles of the two groups. Except for *FGFR2* rearrangements, we found no significant differences between the two groups in the proportions of the most common mutations in ICC. Analysis that compared the detected mutations by grouping into signaling pathway only showed a significant difference in the MAPK pathway that includes FGFR2 rearrangements.

In summary, our findings indicate that m*IDH1* intrahepatic cholangiocarcinoma are small duct type and have significant differences in cell shape (plump cuboidal/polygonal) and fibrosis (geographic) pattern compared to wt*IDH.* The tumor architectural patterns we studied do not distinguish m*IDH1* and wt*IDH1* intrahepatic cholangiocarcinoma.

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Highlights

- *IDH1* mutant intrahepatic cholangiocarcinomas are small duct histologic type
- *IDH1* mutant intrahepatic cholangiocarcinomas tend to have plump cuboidal/polygonal cell shape and geographic fibrosis
- *IDH1* and *IDH* wild type intrahepatic cholangiocarcinomas are predominantly architecturally heterogeneous with no significant difference in the distribution of tubular, anastomosing, compact tubular, and solid architectural patterns

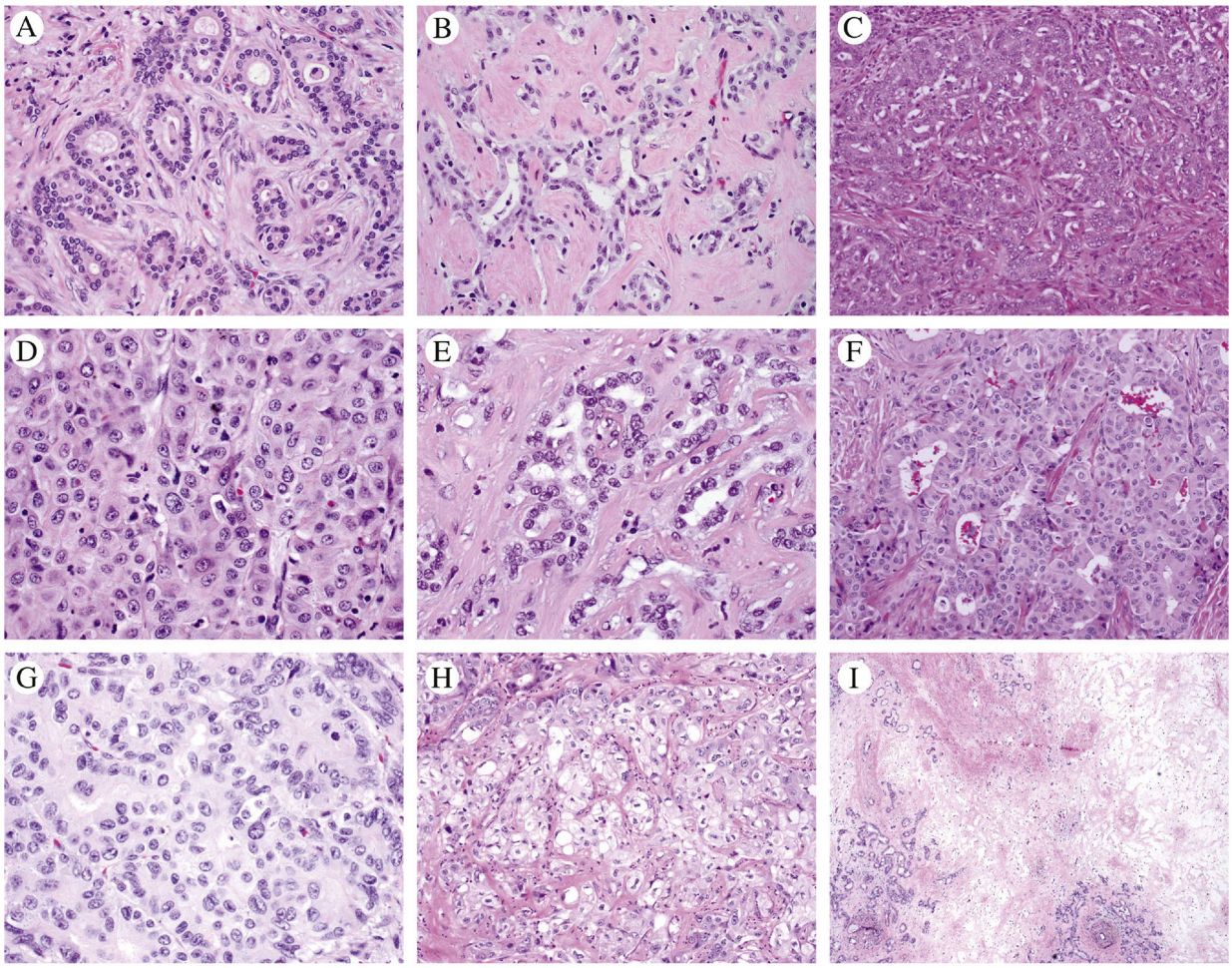

Figure 1.

The various architectural patterns and cell shapes evaluated in this study are illustrated using *IDH1* mutant intrahepatic cholangiocarcinomas. A) Simple tubular pattern; B) Anastomosing pattern; C) Compact tubular pattern; D) Solid pattern; E) Low cuboidal shape; F-G) Plump cuboidal shapes line lumens and polygonal cells are seen in crowded or solid areas; H) Clear cell features; I) Geographic fibrosis.

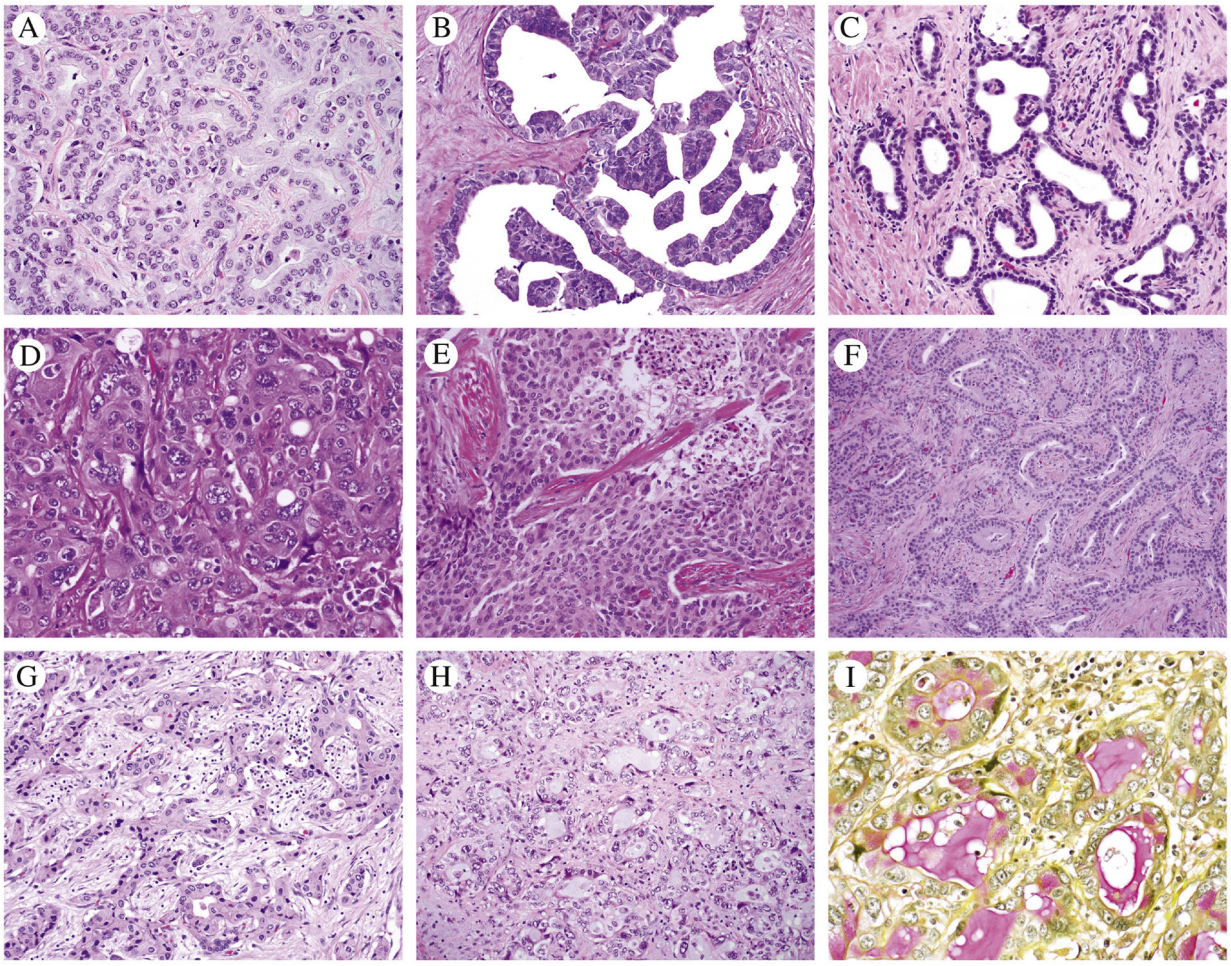

Figure 2.

A-I) Diverse histology and cell shape patterns are seen in *IDH1* mutants; A) Anastomosing glands with plump cuboidal cells; B) micropapillary; C) low cuboidal cells with dilated tubules; D) pleomorphic nuclei in polygonal cells, solid pattern; E) Solid pattern; F) Tubular and anastomosing glands, plump cuboidal; G) Anastomosing glnads plump cuboidal; H-I) tubules cuboidal cells and focal with intra and extracellular mucin highlighted by mucicarmine stain.

Table 1:

Clinical characteristics of Patients with *IDH1* Mutant and *IDH* Wild Type Intrahepatic Cholangiocarcinoma, small duct type

Variable	Wild type *IDH*	Mutant *IDH1*	p-value
	N = 72	N = 29	
Age (Median, IQR)	67 (58, 73)	73 (65, 78)	0.052
Sex			0.7
F	42 (58%)	15 (52%)	
M	30 (42%)	14 (48%)	
Ethnicity			0.3
Asian	6 (8.3%)	2 (6.9%)	
Black	6 (8.3%)	0 (0%)	
White	60 (83%)	27 (93%)	
Autoimmune disease	3 (4.2%)	6 (21%)	0.016
Chronic viral hepatitis B/C	9 (19%)	3 (14%)	0.7
Unknown	25	8	
Smoking	29 (40%)	14 (50%)	0.5
Unknown	0	1	
Clinical cirrhosis	7 (9.7%)	1 (3.6%)	0.4
Unknown	0	1	
Frequent alcohol	3 (4.2%)	3 (11%)	0.3
Unknown	0	1	
Steatosis	4 (5.6%)	3 (11%)	0.4
Unknown	0	2	
Neoadjuvant chemotherapy (systemic or intrahepatic)			>0.9
Any chemo	7 (9.7%)	3 (11%)	
No chemo	65 (90%)	25 (89%)	
Unknown	0	1	

Table 2:

Histopathological Characteristics of *IDH1* Mutant and *IDH* Wild Type Intrahepatic Cholangiocarcinoma, small duct type[a]

Variable	Wild type *IDH* N = 65	Mutant *IDH1* N = 25	p-value
Median tumor size (cm, range)	6.0 (4.2, 8.4)	5.5 (3.8,6.5)	0.14
Unknown	2	0	
Heterogeneous histology	44 (68%)	18 (72%)	0.9
Homogeneous: Anastomosing	6 (9.2%)	0	0.2
Homogeneous: Compact tubular	11 (17%)	4 (16%)	>0.9
Homogeneous: Solid	2 (3.1%)	2 (8.0%)	0.3
Homogeneous: Simple tubular	2 (3.1%)	1 (4.0%)	>0.9
% Anastomosing (Median, range)	15 (0,35)	18 (5,40)	0.7
% Tubular (Median, range)	0 (0,20)	10 (0,20)	0.10
% Compact (Median, range)	40 (25,70)	35 (23,64)	0.5
% Solid (Median, range)	10 (0,30)	8 (0,26)	0.4
Necrosis (mean % volume)	3 (0, 0)	2 (0,11)	0.6
Necrosis >25%	7 (11%)	0	0.2
Necrosis (any)	39 (60%)	14 (56%)	>0.9
Fibrosis (mean % volume)	14 (10,20)	20 (15,26)	**0.009**
Geographic-type fibrosis	9 (14%)	11 (44%)	**0.005**
Low cuboidal cell shape	58 (89%)	15 (60%)	**0.005**
Plump cuboidal/polygonal shape	19 (29%)	15 (60%)	**0.014**
Columnar cell shape	2 (3.1%)	0	>0.9
Variable cytoplasm pattern	19 (29%)	8 (32%)	>0.9
Intracellular mucin	8 (12%)	1 (4.0%)	0.4
Extracellular mucin	17 (26%)	2 (8.0%)	0.11
Clear cell features	24 (37%)	15 (60%)	0.082
Grade			0.8
1	32 (49%)	14 (56%)	
2	24 (37%)	9 (36%)	
3	9 (14%)	2 (8.0%)	
Perineural invasion	15 (24%)	7 (30%)	0.8
Unknown	3	2	
Lymphovascular invasion	16 (25%)	4 (16%)	0.6
Periductal infiltration	6 (9.2%)	2 (8.0%)	>0.9
Satellite nodules	16 (25%)	4 (16%)	0.6
AJCC 8th ed. Primary tumor Stage			0.5
1	24 (37%)	13 (54%)	
2	32 (49%)	10 (42%)	
3	8 (12%)	1 (4.2%)	
4	1 (1.5%)	0 (0%)	

Variable	Wild type *IDH* N = 65	Mutant *IDH1* N = 25	p-value
Unknown	0	1	
Regional lymph nodes (at resection)			0.4
pN0	22 (34%)	5 (20%)	
pNx	8 (12%)	5 (20%)	
pNl	35 (54%)	15 (60%)	

[a]Tumors with neoadjuvant chemotherapy were excluded.

Table 3:

Mutations and Genetic Pathways in IDH1 Mutant and IDH1 Wild Type Small Duct Intrahepatic Cholangiocarcinoma

Variable	Wild type *IDH*	Mutant *IDH1*	p-value
	N = 72	N = 29	
Gene			
ARID1A	18 (25%)	6 (21%)	0.8
BAP1	11 (15%)	7 (25%)	0.3
FGFR2	13 (18%)	0 (0%)	0.017
KRAS	7 (9.7%)	0 (0%)	0.2
PBRM1	14 (19%)	4 (14%)	0.8
TP53	11 (15%)	5 (18%)	0.8
Pathway			
SWI/SNF[a]	32 (44%)	9 (31%)	0.3
DNA damage[b]	27 (38%)	14 (48%)	0.4
MAPS[c]	29 (40%)	4 (14%)	0.011
PI3FC[d]	2 (2.8%)	3 (10%)	0.14

[a] SWI/SNF: *ARID1A, PBRM1, ATRX*

[b] DNA Damage: *BAP1, TP53, ATM, BRCA1, BARD1, KMT2A, KMT2C*

[c] MAPK: *KRAS, FGFR2, NF1, ARAF, BRAF, RASA1, MAP2K1, MAPK3, PDGFRA, GRIN2A*

[d] PI3K: *PTEN, PIK3R2, RPTOR*