Molecular Subclasses of Clear Cell Ovarian Carcinoma and Their Impact on Disease Behavior and Outcomes

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ABSTRACT

Purpose: To identify molecular subclasses of clear cell ovarian carcinoma (CCOC) and assess their impact on clinical presentation and outcomes.

Experimental Design: We profiled 421 primary CCOCs that passed quality control using a targeted deep sequencing panel of 163 putative CCOC driver genes and whole transcriptome sequencing of 211 of these tumors. Molecularly defined subgroups were identified and tested for association with clinical characteristics and overall survival.

Results: We detected a putative somatic driver mutation in at least one candidate gene in 95% (401/421) of CCOC tumors including ARID1A (49% of tumors), PIK3CA (49%), TERT (20%), and TP53 (16%). Clustering of cancer driver mutations and RNA expression converged upon two distinct subclasses of CCOC. The first was dominated by ARID1A-mutated tumors with enriched expression of canonical CCOC genes and markers of platinum resistance; the second was largely comprised of tumors with TP53 mutations and enriched for the expression of genes involved in extracellular matrix organization and mesenchymal differentiation. Compared with the ARID1A-mutated group, women with TP53-mutated tumors were more likely to have advanced-stage disease, no antecedent history of endometriosis, and poorer survival, driven by their advanced stage at presentation. In women with ARID1A-mutated tumors, there was a trend toward a lower rate of response to first-line platinum-based therapy.

Conclusions: Our study suggests that CCOC consists of two distinct molecular subclasses with distinct clinical presentation and outcomes, with potential relevance to both traditional and experimental therapy responsiveness.

See related commentary by Lheureux, p. 4838

Introduction

Historically, tumor treatment approaches have been dictated by tissue site, but large-scale molecular profiling efforts have shown that remarkable heterogeneity exists in the landscape of cancer driver genes and pathways within tumor types and even within histologic subtypes. This has been well characterized for many common tumors through multi-omic profiling and characterization of the genetic determinants of tumor behavior and outcome has led to the development of personalized therapeutic approaches. Indeed, for some cancers, prognosis and therapeutic strategies are based primarily on their presence of genetic driver mutations identified in the tumor (2–7). For several rare cancer types such as ovarian clear cell carcinoma (CCOC), no strong associations between molecular profiles and clinical presentation or outcomes are known and broad-acting platinum-based chemotherapy remains the standard of care.

When diagnosed at an advanced stage, CCOC has a worse outcome than other invasive ovarian cancers including the more common high-grade serous ovarian carcinoma (HGSOC; median overall survival of 10 months; refs. 8, 9) presents at a younger age (10), and is less responsive to platinum-based therapy (11). Relatedly small studies suggest that CCOC possesses several driver events that

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Translational Relevance

Clear cell ovarian cancer (CCOC) is the second most common subtype of epithelial ovarian cancer and when diagnosed at an advanced stage, has a poor prognosis. The relationship between molecular profiles and clinical presentation or outcomes is still unknown but could help guide the development of personalized therapeutic approaches for CCOC. Here, we profiled 421 primary CCOCs using deep targeted sequencing and whole transcriptome sequencing on a subset of 211. Clustering of cancer driver mutations and RNA expression converged upon two distinct subclasses of CCOC. The first was dominated by ARID1A-mutated tumors with enriched expression of canonical CCOC genes and markers of platinum resistance; the second was largely comprised of tumors with TP53 mutations and enriched for the expression of genes involved in extracellular matrix organization and mesenchymal differentiation. These two distinct molecular subclasses showed distinct clinical presentation and outcomes, with potential relevance to therapeutic responsiveness.

are distinct from HGSOC. CCOC is thought to arise from endometriotic lesions with recurrent somatic mutations in PIK3CA and ARID1A, which are rare in HGSOC (12–15). In addition, the existing data suggests that CCOCs are commonly TP53-wild-type (whereas HGSOC ubiquitously harbors TP53 mutations) and exhibits fewer structural rearrangements than HGSOC (13). However, it is not known whether clinically meaningful molecular subtypes of CCOC exist.

In the current study, we performed comprehensive targeted sequencing and transcriptomic profiling of a large, multi-ethnic cohort of 421 primary CCOCs to identify disease subclasses with distinct biology and clinical behavior, which in turn may provide avenues for personalized therapeutic approaches.

Materials and Methods

Study participants

Clinical data and therapy-naïve fresh frozen tumor material were utilized from women diagnosed with invasive CCOC and enrolled into research studies from the following sites: Memorial Sloan Kettering Cancer Center Gynecology Tissue Bank (MSK), Mayo Clinic (MAY), Addenbrooks Hospital (ADD), Cedars-Sinai Medical Center (WCP; Los Angeles, CA), University of Pittsburgh (PIT; Pittsburgh, PA), Gynaecological Oncology Biobank (GynBiobank) at Westmead Hospital (WMH, Sydney, Australia), University of Edinburgh (SCOT; Scotland), Canadian Ovarian Experimental Unified Resource (COEUR; multiple sites), Brigham and Women’s Hospital (BWH; Boston, MA), and University of Pennsylvania (UPA; Philadelphia, PA). Participants provided written informed consent. The studies were conducted in accordance with recognized ethical guidelines (e.g., Declaration of Helsinki, CIOMS, Belmont Report, U.S. Common Rule), and approved by local institutional review boards. Extraction of DNA/RNA was performed centrally at MSK (for cases from MSK, WCP, PIT, BWH, and UPA) or locally (for cases from MAY, ADD, WMH, and COEUR). For the cases which were extracted centrally at MSK, slides from frozen tissue sections were reviewed by a pathologist (R. Murali) and extraction of DNA/RNA was performed from tumor sections, selected based on high content (>80%) of clear cell carcinoma. In total, tumors from 447 women diagnosed with CCOC were analyzed. Race and menstruation status (pre vs. postmenopausal) was obtained through participant self-report. History of endometriosis was also obtained through self-report except at MSK where endometriosis was only available if mentioned on the pathology report. Tumor characteristics and clinical outcomes were obtained through medical record review.

Targeted DNA sequencing and analysis

We performed targeted sequencing of 163 putative CCOC driver genes (Supplementary Table S1) in DNA samples from the 447 tumor and blood-derived DNA from 16 unmatched controls using a custom Nimblegen capture-based panel. Genes were selected based on a combined analysis of 105 clear cell somatic sequencing studies including: (i) whole genome sequencing of 31 CCOCs from Wang and colleagues (13); (ii) whole-exome sequencing of eight cases from Jones and colleagues (12); (iii) targeted sequencing of 26 CCOCs using a panel of 465 known cancer drivers (MSK-IMPACT; ref. 16); and targeted or whole exome sequencing of 40 CCOCs from project GENIE (17). Included in our panel were 119 genes where somatic mutations have been identified in two or more CCOCs; 41 established cancer driver genes based on the COSMIC Cancer Gene Census (18) mutated in one CCOC and three genes in the SWI/SNF complex (SMARCBI, SMARCCI, SMARCC2) (14) that have been implicated in CCOC biology (Supplementary Table S1; ref. 19). We also included on the sequencing panel highly polymorphic single nucleotide variants distributed every 3 MB throughout the genome to capture large copy number deletions/amplifications.

Of 447 tumor samples, 421 (94%) passed quality control. As a technical set of normal samples (n = 10) we used 10 putative normal samples extracted from the blood of 10 healthy, cancer-free individuals. Two tumor samples failed due to low coverage, 12 due to sample contamination and 12 due to duplication. The median sequencing coverage per sample was 539x. Raw sequence data were aligned to the human genome (NCBI build 37) using BWA (20). Variant calling for single nucleotide variants was performed using Mutect2 (21), Strelka (22), and CaVEMan (23) and for insertions/deletions using Pindel (24), Mutect2 (21), and Strelka (22). We considered mutations to be true if they: (i) passed at least two variant callers; (ii) were present at a variant allele fraction of greater than 2%; (iii) were present in gNOMAD (25) whole-exome sequencing data with a maximum population frequency of less than 0.001; (iv) had a variant allele frequency (VAF) at least two times greater than the median VAF in a panel of normal samples; and (v) were present in none of the panel of normal samples at a VAF of 2% or greater. We further excluded mutations in low complexity regions [DUST (26) score >7]. Mutations in known cancer hotspots that met all other requirements but failed due to low complexity or to only being passed by one variant caller were retained for consideration. We calculated a microsatellite instability score for each tumor using MSI sensor (27). We used Bayesian Dirichlet processes to establish classification rules that partitioned tumors into subgroups, minimizing overlap between categories. The Dirichlet process defines an infinite prior distribution for the number and proportions of clusters in a mixture model, fitted with the use of the Markov chain Monte Carlo method (28). Our method was based on an implementation of the Dirichlet process mixture model available at https://github.com/nicolaoloberti/bdp using a non-hierarchical Dirichlet process. We used 5,000 burnin iterations and subsequently sampled 10,000 realizations at intervals of 20 iterations. From this collection of data, we computed the optimal number of clusters, requiring that 90% of the samples were assigned a cluster.
Whole transcriptome sequencing and analysis

RNA sequencing (RNA-Seq) libraries were prepared for 211 cases from total RNA derived from the same tumor sections using poly(A) enrichment of the mRNA. One hundred bp paired-end libraries were sequenced on Illumina’s HiSeq at a targeted depth of 40 million reads per sample. We performed alignment using STAR (version STAR_2.5.1b; ref. 29) against the reference genome hg38 (GENCODE v26). Reads were summarized using featureCounts (version 1.5.0-p1; ref. 30). RNA clusters were defined using hierarchical clustering using the top 500 most variable protein coding genes (clustering parameters: method = ward, D2, distance = canberra). Differentially expressed genes between RNA cluster 1 and RNA cluster 2 samples were obtained using the R package DESeq2 (version 1.28.1; ref. 31) with collection site ref. 30). RNA clusters were de

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**Table 1. Clinical characteristics of CCOC cases sequenced using targeted panel.**

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**Data availability**

The somatic variant calls and normalized RNA-seq intensity data, code, and deidentified clinical data are available here: https://github.com/bolton-lab/Bolton_COC. This will enable all the figures and tables to be re-generated and also provide data for others for future analyses. We will also make the BAMs/FASTQs available to researchers through contacting Kelly Bolton (bolton@wustl.edu).

**Results**

**Clinical characteristics**

Key characteristics, other than race, of the 421 participants included in the study did not vary between study sites (Table 1). Compared with clinical characteristics reported in the literature for women with HGSOC (10, 33), women with CCOC in this cohort were more likely to be of Asian ancestry (12% of individuals with non-missing race), have a history of endometriosis (13%), and present with early-stage disease (69%).

**Targeted DNA sequencing of candidate CCOC driver genes**

In 163 candidate CCOC driver genes we identified 6,361 mutations. Of these, 1,488 mutations were classified as potentially pathogenic based upon annotation on OncoKB (34), frequency in COSMIC, frequency in previously published CCOC sequencing data (12, 13, 16), predicted pathogenicity based on PolyPhen (35) and SIFT (36), and prior evidence in the literature (Supplementary Table S2). At least one putative driver mutation was identified in 401 of 421 tumors (95%) (mean number of mutations 3, range 1–25; Fig. 1A and C). The most commonly mutated genes were ARID1A (49%, N = 205), PIK3CA (45%, N = 188), and the TERT promoter (20%, N = 84). The most frequently recurrent mutations were clonally dominant with a VAF >35% (e.g., ARID1A and TP53) suggesting that they represented early events while others (e.g., CREBBP) were more often subclonal, possibly representing secondary events (Fig. 1B). We detected a higher proportion (16%, N = 71) of tumors with TP53 mutations than has been
described by some (9%–15%; refs. 13, 37) but not all NGS studies (18%; ref. 38). This raises the possibility that some of the CCOCs in this cohort were misdiagnosed high-grade serous or endometrioid ovarian cancers. We explored this possibility in detail. First, we noted that 10 of 71 TP53 mutations (14%) were deeply subclonal (VAF<10%); previous studies may not have detected these mutations as they used lower-depth sequencing (Fig. 1B). Second, we performed additional pathologic review to verify clear cell histology for a subset of the cases where formalin-fixed paraffin-embedded (FFPE) tissue sections were available. On the basis of morphology combined with immunohistochemical staining of Napsin A, p53, and WT1 (markers of HGSOC) and not CCOC; ref. 39), it was determined that four of 14 TP53-mutant cases and 4 of 71 TP53-mutant/ARID1A-mutant cases were misclassified high-grade serous or endometrioid ovarian cancers. We explored this possibility in detail. First, we noted that 10 of 71 TP53 mutations (14%) were deeply subclonal (VAF<10%); previous studies may not have detected these mutations as they used lower-depth sequencing (Fig. 1B). Second, we performed additional pathologic review to verify clear cell histology for a subset of the cases where formalin-fixed paraffin-embedded (FFPE) tissue sections were available. On the basis of morphology combined with immunohistochemical staining of Napsin A, p53, and WT1 (markers of HGSOC and not CCOC; ref. 39), it was determined that four of 14 TP53-mutant cases (28%; three endometrioid carcinomas and one HGSOC) were misclassified as CCOC. None of the BRCA1/2-mutated cases were misclassified. Thus, by extrapolation we estimate that approximately 19 of our 71 TP53-mutant tumors in this cohort were misclassified.

A subset of tumors (N = 20) bore mutations in SMARCA4, a gene that is the sole driver mutation in ovarian small cell carcinoma hypercalcemic type (OSCCHT; refs. 40–42). However, unlike OSCCHT, in our CCOC cases we observed SMARCA4 to be most commonly comutated with either ARID1A (50%) or PIK3CA (35%). Similar to our analysis of TP53 mutated cases, we performed central pathology review of a subset (N = 8) of the SMARCA4 mutated cases. All of these cases showed typical CCOC morphology and were positive for clear cell markers such as PAX8 (8/8 diffuse), and Napsin A (5/8 diffuse, 2/8 focal), or HNF1B (5/5 diffuse). We conclude that there was no evidence for these cases being misclassified OSCCHT. Whether SMARCA4 has a similar driver capacity in CCOC compared with OSCCHT requires further study.

Most cases (75%) had at least one large-scale copy number event with the most frequently recurrent events reflecting common cancer-driver aneuploidies including 8q amplification (Supplementary Fig. S1; ref. 19). Cases with TP53 mutations had more whole chromosome or arm-level aneuploidies (mean = 12) compared with wild-type tumors (mean = 8; Supplementary Fig. S2). TP53-mutant/ARID1A-mutant tumors showed less genomic instability (mean number of aneuploidies = 7) compared with TP53-mutant/ARID1A-wild type tumors (mean number of aneuploidies = 13). We detected recurrent fusions in TGM7 (N = 5) as previously shown by Earp and colleagues (43). In addition, recurrent fusions involving BCAR4 (N = 6), ITCH (N = 6), and DCAF12 (N = 5) were observed. These are known...
We evaluated mutation status with respect to clinical and epidemiological factors including age, race, tumor, and history of endometriosis. Compared with ARID1A–mutated tumors, patients with KRAS mutations were older at presentation (median age 53 vs. 67, \( p = 0.03 \); Fig. 2A). Individuals with a history of endometriosis were more likely to have ARID1A–mutated tumors (72% and 47% of patients with and without endometriosis respectively, \( P = 2 \times 10^{-4} \); Fig. 2B). Advanced stage tumors were more likely to harbor TP53 mutations than early-stage tumors (27% vs. 11% respectively, \( P = 2 \times 10^{-2} \); Fig. 2C). Among TP53 mutant tumors, a similar proportion (50% and 51%, respectively) were advanced stage with or without co-occurring ARID1A mutations. There was a trend toward a higher frequency of ARID1A–mutated tumors in women of east Asian descent but this was not significant (Fig. 2D).

We next examined the relationship between mutational burden, cancer driver genes, and patterns of genetic cooccurrence. Several genes harbored recurrent mutations within the same tumor (Supplementary Fig. S4). This was seen for both tumor suppressor genes (e.g., ARID1A) and specific oncogenes including PIK3R1 and PIK3CA. Among tumors with multiple PIK3CA mutations, variants were more likely to occur in nonhotspot locations within the gene (Supplementary Fig. S5; ref. 44). MSIsensor score was higher among individuals more than 10 driver mutations (Supplementary Fig. S6). We observed a statistically significant co-occurrence between mutations in ARID1A, PIK3CA, TP53 and BRCA1/BRCA2. Mutual exclusivity between somatic mutations of ARID1A, TP53, PIK3CA and PIK3R1 (Supplementary Fig. S7) suggests that these may represent distinct pathways to oncogenesis. The exclusivity between TP53 and ARID1A mutation was stronger in the setting of multiple ARID1A mutations (OR = 0.21; 95% CI, 0.07–0.54; \( P = 2 \times 10^{-4} \)) compared with a single ARID1A mutations (OR = 0.68; 95% CI, 0.32–1.34; \( P = 0.28 \)).

Because we observed clear patterns of exclusivity and cooccurrence between gene drivers, we used unsupervised clustering approaches to define nonoverlapping subgroups of COCOC based on their mutational spectrum. We defined seven subgroups (Supplementary Fig. S8) and compared the frequency of mutations between subgroups. Four clusters were characterized by having an ARID1A mutation; the first cluster (cluster A) was characterized by a single ARID1A mutation in combination with another disease defining mutation (e.g., PIK3CA, TERT, TP53, KRAS, PTEN, PPP2R1A, PIK3R1, CREBBP, or SPOP; \( N = 86 \)); the second (cluster B) with a single ARID1A mutation alone or in combination with non-disease defining mutation (\( N = 19 \)); the third (cluster C) with multiple ARID1A mutations combined with a PIK3CA mutation (\( N = 81 \)); and a forth (cluster D) with multiple ARID1A mutations and PIK3CA wild-type (\( N = 25 \)). Two clusters were ARID1A wildtype: Cluster E was defined by a TP53 mutation (\( N = 50 \)); and cluster F by other non-TP53 disease-defining mutations (\( N = 104 \)). A final cluster (cluster G) was characterized by mutations in SMARCA4 (\( N = 13 \)); a mutation typically observed in small cell ovarian carcinoma (23). The remaining tumors were undefined (\( N = 57 \)).

**Figure 2.**
Frequency of somatic mutations by clinical characteristics including age at diagnosis (A), endometriosis (B), stage (C), and race (D). Genes that were mutated in at least 20 individuals with nonmissing values for the clinical characteristic were included. Shown are q-values (FDR corrected \( P \) values) based on Fisher exact test. \( * \), \( q < 0.05 \); \( ** \), \( q < 0.01 \).
Similar to the patterns we observed when studying the association between individual mutations and clinical features, the TP53-mutated, ARID1A wild-type cluster showed an enrichment of advanced stage disease while tumors belonging to the ARID1A-mutant clusters were more likely in individuals of Asian ancestry and those with a history of endometriosis (Supplementary Fig. S9). Individuals in cluster G (SMARCA4-mutant tumors) had a nonsignificant trend towards a younger age at diagnosis ($P = 0.32$).

**Transcriptomic profiling of CCOC**

Transcriptomic profiles were generated for 212 CCOC tumors in which targeted sequencing was also performed. Using unsupervised clustering informed by expression of the 500 most variable genes, we identified two main RNA clusters (Supplementary Fig. S10): Expression cluster 1 showed higher expression of genes previously reported as highly expressed in CCOC including ANXA4 and GPX3, both of which are linked to platinum resistance (45, 46). Among the most highly expressed genes in cluster 1 compared with 2 also included GPX3 (47), which is known to be overexpressed in endometriosis compared to normal endometrial tissue, and EEF1A2, known to be overexpressed in CCOC associated endometriosis but not benign endometriosis (48). Genes that characterized this cluster were enriched in metabolic pathways including flavonoid glucuronidation ($P = 10^{-12}$) and monocarboxylic acid metabolism ($P = 10^{-13}$). Expression cluster 2 showed enriched expression of genes involved in extracellular matrix (ECM) organization ($P = 10^{-22}$) and mesenchymal differentiation, including genes such as ADGR2 and PDCH19 (Supplementary Fig. S10 and Fig. 3B). Compared to cluster 1, expression cluster 2 also showed higher expression of WT1 and lower expression of CCOC marker HNF1B, which are features classically associated with high-grade serous ovarian cancer (Fig. 3B; ref. 9). Expression cluster 2 was enriched with TP53-mutant tumors (55% of cases in cluster 2 compared with 10% in cluster 1). When comparing RNA expression and mutation clusters, cluster 2 was largely comprised of tumors belonging to mutation cluster E, that is, TP53-mutant ARID1A-wild-type tumors (45% of cluster 2) and the undefined mutation cluster (33% of cluster 2; Fig. 3A).

**Clinical outcomes**

There was no statistically significant association between overall survival and CCOC mutations when examined on a per-gene level in Cox proportional hazards models stratified by study site (Supplementary Table S3). We observed a nonsignificant trend toward improved survival for patients with ARID1A (HR = 0.82; 95% CI, 0.58–1.15; $P = 0.24$) and PTEN (HR = 0.52; 95% CI, 0.24–1.12; $P = 0.10$) mutant tumors. Because of the similarity of the ARID1A-mutant clusters in regards to clinical presentation and outcome, we combined these clusters for the purpose of survival analysis. Women with TP53-mutant, ARID1A-wild-type tumors had worse overall survival compared to those with ARID1A-mutant tumors (HR = 1.72; 95% CI, 1.06–2.81; $P = 0.03$; Fig. 4A). Similarly, RNA-seq cluster 2 showed an increased risk of death compared with RNA-seq cluster 1 (Fig. 4B). Tumor Cluster 2 vs. Tumor Cluster 1 HR 2.8; 95% CI, 1.66–4.84; $P = 10^{-7}$). Covariate adjustment for age, race, stage, and residual disease attenuated the estimated mutation and cluster-associated risk (Supplementary Table S4). To explore how these subgroups might influence therapy outcome, we studied the relationship between mutation status and response to first line therapy with platinum/taxane combination therapy. We limited this to women with advanced stage disease who successfully underwent debulking surgery followed by combination platinum/taxane therapy ($N = 36$). Women with ARID1A wild-type, TP53-mutant tumors were more likely to have a complete response 75% ($N = 11$) compared to ARID1A-mutant tumors (55%), although this was not statistically significant ($P = 0.33$) in this small sample size.

**Discussion**

Our results have several clinical implications. First, the results of both genomic and transcriptomic cluster associations with clinical presentation and outcome converged, suggesting two main subgroups of CCOC: The first subtype included ARID1A-mutant tumors (particularly double-mutant tumors) and other common CCOC mutations (e.g., PIK3CA, TERT, etc.) that showed enriched expression of metabolic pathways, presented with early-stage disease and were more likely to have a history of endometriosis. We denote this group as “classic-CCOC”, which represented 83% of our cohort. The second CCOC subtype was dominated by TP53-mutant tumors that showed enriched expression of genes involved in extracellular matrix organization, mesenchymal differentiation and immune-related pathways. These cases presented with advanced disease and had worse survival. Interestingly, TP53 mutations either in the presence or absence of cooccurring ARID1A mutations were associated with a higher degree of genomic instability and aggressive, advanced stage tumors. The worse survival for tumors in this “HGSOC-like” subgroup was largely explained by advanced stage and higher burdens of residual disease.

Within both the “classic-CCOC” and “HGSOC-like” subgroups we noted a subset of individuals had tumor with mutations in genes known to be both somatic drivers of ovarian cancer and germline susceptibility genes including PMS2, MSH6, MSH2, BRCA1, and BRCA2. Due to the absence of matched normal samples, we were unable to fully distinguish whether these represented somatic or germline events and is a limitation of our study. Future studies estimating the frequency of CCOC cases that arise in women with strong hereditary predisposition and who may be considered for risk reducing bilateral salpingo-oophorectomy should be prioritized (49). There is increasing recognition that other histologic types of ovarian carcinoma, including HGSOC and endometrioid carcinoma, can contain areas with clear cell change complicating the histologic diagnosis (50). While a subset of cases in the “HGSOC-like” cluster are misclassified HGSOC, and is a weakness of our study, it is unlikely that this alone explains our findings. Firstly, all of our cases were morphologically diagnosed by expert gynecological pathologists and at some centers, this morphologic review was supplemented by immunohistochemistry for histotype-specific markers. Secondly, in a subset of TP53-mutant cases, we reconfirmed the diagnosis of CCOC using a combination of morphologic and immunohistochemical features. Thus, our results suggest that a subset of bona fide CCOCs with HGSOC-like features exist. Our results also emphasize that expert histologic review of CCOC cases, particularly those who present with TP53-mutant, ARID1A-wild-type tumors, is warranted given similarities to the biology and behavior of HGSOC.

Gene expression profiles of the “classic-CCOC” and “HGSOC-like” CCOC subtypes we observed are similar to those reported by Tan and colleagues (51) which also reported two clusters, the first enriched for genes in metabolic pathways and the second, a less common mesenchymal-like subgroup associated with late-stage disease. However, unlike Tan and colleagues, we observed differences in the frequency of TP53-mutated tumors across clusters. The source of this discrepancy is unclear and may include differences in sequencing technology (Tan and colleagues performed targeted sequencing using Ion Torrent) and patient characteristics (Tan and colleagues, included only...
women of Asian ancestry which trend towards lower frequencies of TP53-mutated tumors in our analysis and which are known to have lower frequencies of endometrial ovarian cancer). The overlap between genes highly expressed in our “classic-CCOC” subgroup and those enriched in endometriosis provide further support for the likely transition from endometriosis to carcinoma in CCOC.

The greatest translational impact from these molecular CCOC subtypes is expected to lie in the development of therapeutic...
approaches tailored to the vulnerabilities of each group. Interestingly, despite being aggressive on presentation, a trend was seen towards the “HGSOCC-like” CCOC subgroup having higher response rates to first line platinum-based chemotherapy. Future studies are warranted to further explore whether genomic subtypes of OCOC predict response to platinum-based and other therapies as treatment data were limited here. The “classic-CCOC” subgroup dominated by mutations in the SWI/SNF pathway and markers linked to chemo-resistance may be of particular relevance to target for investigational first-line therapies. Recent data suggests that the SWI/SNF pathway plays a novel role in the regulation of antitumor immunity, and that SWI/SNF deficiency can be therapeutically targeted by immune checkpoint blockade (19). Several studies are currently evaluating the role of immune check point inhibitors in CCOC including NCT03405454, NCT03425565. While a limitation of our study was that we were unable to assess MMR functional status, we did note a rare subset of tumors (3%) with higher mutational burden (>10 drivers) and MSIsensor score. The extent to which the subset of CCOCs with higher total mutation and with MMR deficiency show improved responsiveness to immune checkpoint blockade in ongoing clinical trials will be an important avenue of investigation. Additional targeted therapeutic strategies have been explored in preclinical settings including epigenetic synthetic lethality, some of which are entering into clinical trials. The PI3K inhibitor, alpelisib, is now FDA approved for HR-positive breast cancer and ongoing trials in additional PIK3CA-mutated cancers including CCOC are underway. Double PIK3CA mutations appear to hyperactivate PI3K signaling and enhance tumor growth and may confer increased responsiveness to PI3K inhibitors than those with a single mutation (52). Thus, for CCOC cases harboring multiple PIK3CA mutations, PI3K inhibitors either alone or in combination with other agents may represent a promising approach.

The strengths of this study include the large sample size, use of multiple study sites, inclusion of women of European and non-European ancestry, and integration of genetic and transcriptomic markers of disease behavior and outcome. While this is the most extensive genomic study of CCOC to date, greater sample size with additional follow-up data will allow improved assessment and validation of these clinically relevant subtypes. Although future analyses would benefit from larger patient collections, our current results suggest that genomic classification may inform the future development of targeted therapeutics in CCOC.

Authors’ Disclosures

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Authors’ Contributions

K.L. Bolton: Conceptualization, resources, data curation, formal analysis, funding acquisition, writing–original draft, writing–review and editing. D. Chen: Resources, data curation, investigation, writing–original draft, project administration, writing–review and editing. R. Corona de la Fuente: Formal analysis, writing–original draft, writing–review and editing. Z. Fu: Data curation, writing–original draft, writing–review and editing. R. Murali: Data curation, validation, investigation, writing–
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