Evaluation of Treatment Outcomes in Patients with Testicular Cancer

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INTRODUCTION

Testicular Cancer Significance

- In 2015, an estimated 9000 men were expected to be diagnosed with testicular cancer, the second leading cause of death and the most common malignancy in young men 20 to 40 years of age.[1,2,3]
- 95% of all testis cancer malignancies are comprised of testicular germ cell tumors (TGCT), and over the past four decades, incidence of germ cell tumors has been increasing not only in the United States but also worldwide.[1,2]
- Current treatment options include radical orchiectomy, retroperitoneal lymph node dissection, chemotherapy, radiation, and active surveillance.[1,3]

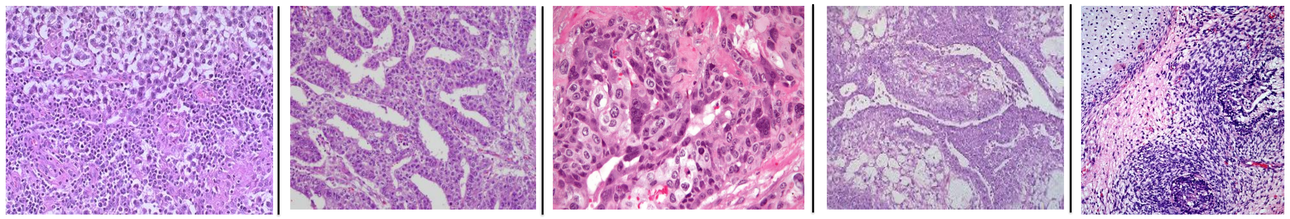

Figure 1: Seminomatous GCT (left). Non-seminomatous Embryonal carcinoma GCT (left middle), Choriocarcinoma GCT (middle), Yolk sac GCT (right middle), and Teratoma GCT (right).

Research objectives

- To develop a comprehensive testicular cancer database for:
  - Evaluation of clinical outcomes.
  - Assessment of different treatment modalities, disease-specific outcomes, and toxicities.
  - Correlation of clinical and pathologic data in search of translational research opportunities.

STUDY DESIGN

Type of Study

- IRB approved protocol for retrospective and prospective chart review from January 2010-present using CERNER EMR chart system.

Study Population

- CoPath search algorithms utilized to identify study population in order to most effectively find each patient who has presented to Carolinas Health Care system with testicular cancer since January 2010 (Table 1).
- 279 patients found

CoPath search algorithm	Type of text in Pathology report	Number of patients collected	Date Range
radical orchiectomy, tumor ALL	Final diagnosis	193	1/1/10-present
radical orchiectomy, seminoma ALL	Final diagnosis	43	1/1/10-present
radical orchiectomy ALL; embryonal carcinoma, choriocarcinoma, yolk sac	Final diagnosis	2	1/1/10-present
radical orchiectomy, teratoma ALL	Final diagnosis	2	1/1/10-present
orchiectomy, tumor ALL; exclude radical	Final diagnosis	28	1/1/10-present
Leydig cell tumor; Sertoli cell tumor ANY	Final diagnosis	2	1/1/10-present
metastatic seminoma	Final diagnosis	8	1/1/10-present

Table 1. CoPath search algorithms and their respective patients.

DATABASE MANAGEMENT

Definition of Variables

- A preliminary set of variables was defined while writing the IRB protocol.
- All variables, considered to impact disease-specific outcomes using Research Electronic Data Capture software, or REDCap software, were organized into 5 different “subject buckets,” according to their timeline with a testis cancer patient.

Testicular treatment collection tool paradigm

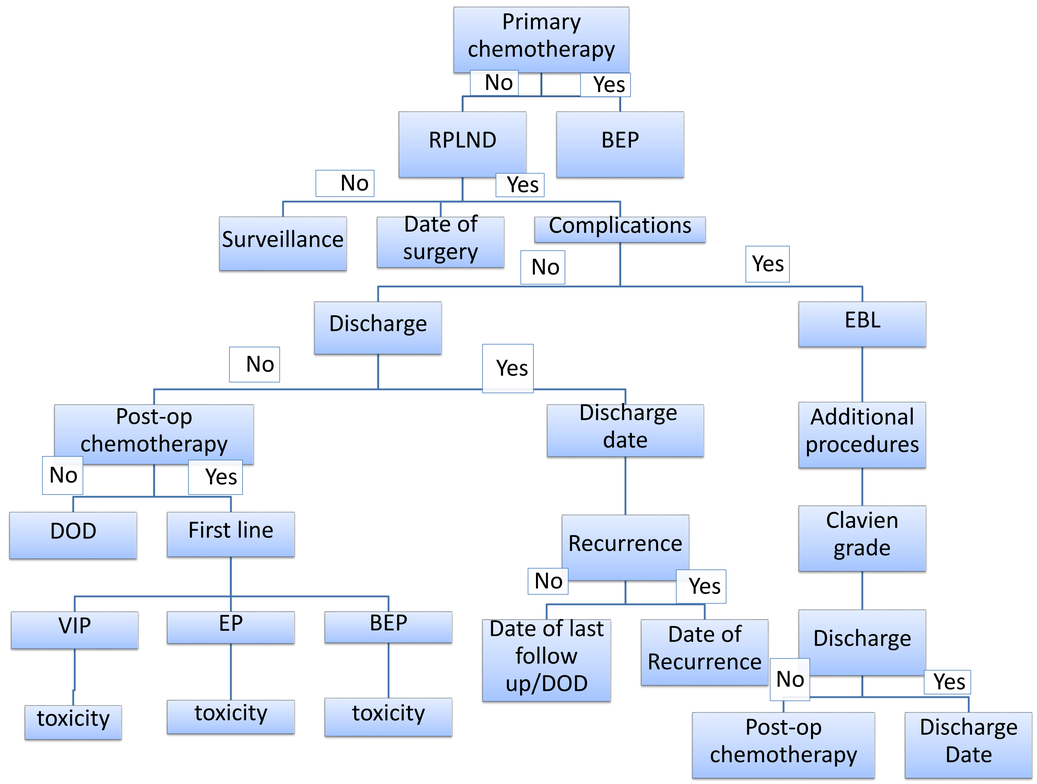

Figure 2. Part of REDCap treatment bucket depicted in a flowchart.

CURRENT AND FUTURE WORK

- Pilot the use of CERNER to navigate patient charts and enhance the REDCap project’s network of variables.
- Significant amount of testing the project is paramount prior to data collection. Optimizing the project’s variable organization will allow me to collect data encompassing all treatment paradigms from the study population.

Data Analysis

- The data will be analyzed using standard statistical methods in collaboration with the Levine Cancer Institute Department of Biostatistics.
- Frequencies and proportions will be used to summarize categorical variables; other descriptive statistical measures, including means, medians, standard deviations, and ranges, will be calculated for quantitative variables. Conclusions will then be drawn from the summation of the descriptive statistical analysis.

ACKNOWLDEGEMENTS

I am thankful to Dr. Riggs for the plethora of knowledge that I have gained on testicular cancer, treatment paradigms, and clinical aspects. I also appreciate his guidance throughout the writing and submission of the IRB protocol, and Joanna Ramirez for teaching me how to navigate patient charts in CERNER, pathology reports in CoPath, and REDCap software. Lastly, I am thankful to Dr. Mamoon for her guidance as a mentor and for educating me on the molecular aspects of cancer ranging from the roles of DNA hypermethylation and hypomethylations in regulation of gene expression to molecular aberrations and their roles in tumorigenesis.

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