history of violence, crime and conflict; alcohol and drugs; neglect, mistreatment and abuse; inadequate supervision and monitoring practices; and delinquent peers. Thus, early prevention efforts are crucial, particularly for groups that present risk factors for juvenile delinquency or that already show behavioral problems. **Objectivos:** Understand the main risk factors for juvenile delinquency and raise awareness for its prevention. Material and Methods: Bibliographic research of scientific articles, books, and internationally recognized studies. Main search engine: PubMed. **Material and Methods:** Literature revision. **Results:** Literature indicates that preventing juvenile delinquency can have clinical and societal benefits, reducing the clinical burden for both offenders and victims as well as the costs associated with criminal justice systems resources. The Perry Preschool Project is an example of successful delinquency prevention program. The project involved 123 children aged 3 and 4 from a disadvantaged social background. Two groups of children were created, one group benefited from the program and the other group did not. Each child received 12 hours of preschool education per week for 2 years, and children's families received weekly 90-minute home visits. The focus was on children's socio-emotional and cognitive development and the promotion of parenting practices and skills. The children were followed up and studied until they were 40 years old. It was found that only 28% of the participants of the prevention group served a prison sentence, while 52% of controls were convicted.
Conclusions: Knowing and understanding risk factors for juvenile delinquency helps us to know when and where to intervene. Preventing juvenile delinquency has more benefits than trying to correct it later.

Keywords: juvenile delinquency; prevention; risk facts.

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POSTER 43

Current perspective on the relevance of bacterial communities to estimate post-mortem intervals – how far are we?

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Resumo

Introduction: The relevance of postmortem microbiological examinations is controversial for decades, but the boom in advanced sequencing techniques over the last decade is increasingly demonstrating their usefulness, including for determination of the postmortem interval (PMI; time since death). This is an emerging field with a growing number of studies unveiling the feasibility of using microbial community changes to track the progression of decomposition if reliably quantified by high-throughput DNA sequencing [1]. **Objective:** We aimed to provide an overview of current knowledge about the role and utility of bacterial populational shifts in PMI calculations. **Methods:** A bibliographic research was conducted in PubMed database using the keywords

forensic research, post mortem interval, bacteria and microbiology. We selected five recent articles (2020-2021) offering novel/broad overviews of the topic. **Results:** Most microbial forensic studies focus on gut samples, whereas microbial communities from the skin, mouth and intimate areas are underexplored, with the recent ones applying advance sequencing tools reaching different taxonomic levels until genus [2,3]. An approach to estimate PMI is the study of microbes colonizing internal organs/orifices after death, the thanatomicrobiome. Studies analyzing the sequences of bacterial 16S rRNA genes on model animals and humans, respectively, indicated a high accuracy (>94%) and that class or phylum taxonomic levels models provided the most accurate PMI predictions [1]. Different studies in internal organs reported a shift in microbial communities from dominant aerobic (e.g., *Staphylococcus/ Enterobacterales*) to more facultative/obligate anaerobic bacteria (e.g., *Enterococcus/Clostridium*) [1,2]. However, thanatomicrobiome composition may be affected by other factors, including post-mortem translocation or sample contamination [4]. Recent studies applying machine learning models have identified particular bacterial species (e.g.*Enterococcus faecalis*) as the most informative in the decomposition process [3,5]. **Conclusions:** Several limitations preclude the current use of bacteria in PMI estimations. Even when applied to healthy humans, the lack of uniformization in methods/databases makes the interpretation of microbiome studies debatable. Given the complexity in identifying unique post-mortem microbial signatures to generate robust databases, a deeper knowledge on individual bacterial species/strains that can act as PMI indicators during body decomposition is warranted – ideally, they could be included in routine analysis for PMI estimation.

Keywords: rorensic research; decomposition; bacteria; microbiology; thanatomicrobiome.

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POSTER 44

Estudo dos biomarcadores de toxicidade decorrente da exposição ao opioide tapentadol

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Resumo

Introdução: O tapentadol é um opioide utilizado no tratamento da dor moderada a severa [1]. Atua como agonista do recetor opioide μ e inibindo a recaptação da noradrenalina, maximizando o efeito analgésico [2]. Estudos in vitro e in vivo, demonstraram toxicidade após exposição a tapentadol. Este parece ter efeito na diminuição da atividade metabólica e da biomassa celular [2]. Foram também reportadas alterações na expressão génica, o aumento do stress oxidativo e de inflamação [3]. Contudo, não foram ainda reportados estudos relativamente a genotoxicidade do tapentadol. No entanto, estudos realizados no tramadol, um opioide com algumas similaridades com o tapentadol, demonstram genotoxicidade dependente da dose, afetando a capacidade de reparação do DNA [4]. **Objetivos:** Este trabalho teve como objetivo a pesquisa de biomarcadores de toxicidade decorrente da exposição de opioides.**Material e Métodos:** Foi realizada uma pesquisa bibliográfica em diversos artigos científicos publicados na PubMed, onde se pesquisaram biomarcadores de toxicidade decorrente da exposição a opioides. **Resultados:** Os estudos realizados, demonstraram a presença de toxicidade quando administradas doses, acima 800 mg de