

抑郁症神经生理机制研究进展

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摘要

抑郁症是一种常见的精神障碍疾病, 是以显著而持久的情绪低落为主要特征的精神障碍。其主要表现是以情感低落、思维迟缓和精神运动性抑制三大症状为基本特征。部分抑郁症患者伴有严重的焦虑症状, 出现自杀观念及行为, 给全球带来沉重的疾病负担。抑郁症的病因十分复杂, 迄今仍未完全阐明。近年来, 国内外对抑郁症的研究从未停止, 在抑郁症发病机制的研究上取得了重要进展。本文通过对以往基因遗传学研究, 脑结构和功能研究, 神经炎症以及神经内分泌的研究进行阐述, 以拓展对抑郁症的认识。

关键词

抑郁症, 神经生理机制, 下丘脑, HPA

Progress in Neurophysiological Mechanisms of Depression

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Abstract

Depression is a common mental disorder that is characterized by significant and persistent depressed mood. It is characterized by low emotion, slow thinking and psychomotor inhibition. Some patients with depression have serious anxiety symptoms, suicidal ideas and behaviors, which bring heavy disease burden to the world. The etiology of depression is very complex and has not yet been fully elucidated. In recent years, the research on depression has never stopped at

home and abroad, and important progress has been made in the pathogenesis of depression. In this paper, the past genetic studies, brain structure and function studies, neuroinflammation and neuroendocrine studies are briefly described in order to expand the understanding of depression.

Keywords

Depression, Neurophysiological Mechanisms, Hypothalamic, HPA

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1. 引言

抑郁症是最常见的精神疾病之一,主要表现为情绪低落、思维迟缓、活动减少,常同时伴有焦虑情绪,及饮食、睡眠等障碍。其不仅影响患者的正常工作和生活,严重者甚至导致患者自杀。2018年3月,世界卫生组织(WHO)公布,全球约有3亿人遭受抑郁症的困扰,每年约有80万人因抑郁症而自杀身亡。抑郁症是自杀的头号杀手,其死亡率高达15%~25% (Sokero et al., 2005)。随着抑郁症的发病率呈逐年上升趋势,不仅给患者和家属带来痛苦,也给社会带来巨大的负担。但令人遗憾的是,抑郁症的病因至今尚不完全清楚,并且对于抑郁症的诊断还是以临床表现及量表作为其主要的诊断依据,尚缺乏实验诊断等客观指标。但关于抑郁症生理机制的研究却不曾停止。本文列举了一些最近有关抑郁症的神经生理机制研究,包括基因遗传学研究,脑结构和功能研究,神经炎症以及神经内分泌的研究,以增进对抑郁症的了解。

2. 基因遗传研究与抑郁症

通过家庭和双胞胎的研究,发现遗传因素在抑郁症的致病过程中起着十分重要的作用(McGuffin et al., 2007)。与遗传力较高程度的自闭症,双相情感障碍和精神分裂症相比,抑郁症的遗传力更大,介于31%和42%之间(Sullivan et al., 2000)。

2.1. MDD 候选基因研究

候选基因的选取一般与疾病的病理生理机制和药物作用机制来确定。根据以往的研究,抑郁症的候选基因主要集中在神经递质系统,下丘脑-垂体-肾上腺轴(HPA)和脑源性神经营养因子(BDNF)上。

研究发现,承受压力和抑郁能力低的人的5-羟色胺转运蛋白(5-HTT)基因,同时,这些人的单胺氧化酶A(MAOA)基因,COMT基因的表达水平有出现异常(Azadmarzabadi et al., 2018),这些特质都与抑郁症的发病有关。Bustamante et al. (2018)发现,HPA轴中涉及的FKBP5基因表达水平与抑郁症的发病史有关,存在抑郁症发病史的人FKBP5基因表达水平更高。Van Der Auwera (2018)通过荟萃分析得到,FKBP5、5-HTT基因,色氨酸羟化酶2(TPH2)基因,多巴胺D2受体(DADR2)基因,BDNF基因以及其他候选基因和抑郁症患者的儿童期创伤经历显著相关,具有儿童创伤经历的患者存在更高水平的该候选基因。通过药物的作用机制也能得出相似的结论,Fischer et al. (2018)对HPA轴的荟萃分析发现,促肾上腺皮质激素释放激素结合蛋白(CRHBP)基因,促肾上腺皮质激素释放激素受体1(CRHR1)基因和促黑素皮质激素(POMC)基因座可以预测抗抑郁药的治疗效果。另外,聂容荣等人通过对脑卒中后抑郁症患者针灸治疗也发现患者血清5-HT、NE和BDNF水平比对照组显著降低(聂容荣等, 2017)。

2.2. MDD 基因突变研究

常见突变在抑郁症的遗传力中所占的比例约为 4%，因此这种遗传变异吸引了大量学者进行相关研究。

对于大样本基因的分析表明，与抑郁症相关的变异基因与肥胖，HPA 轴的慢性过度激活，突触前分化，神经免疫，神经元钙通道，多巴胺能神经递质和谷氨酸能神经递质有关(Li et al., 2018)。分析还发现，这些突变位于大脑皮层，涉及神经元并且没有发生显著的子序列变化富集，这表明涉及外显子序列变化的遗传变异对抑郁的意义不大(Wray et al., 2018)。

具有不同抑郁特征或不同抑郁特征的人可能具有不同的遗传结构，减少异质性将有助于更好地揭示抑郁的遗传特征(Ostergaard et al., 2011)。Howard et al. (2018)根据表型将 322,580 例英国抑郁症患者分为三个亚组，发现 17 个位点与三种亚型显著相关，表明兴奋性突触可能与抑郁症有关。Peterson et al. (2017)针对汉族妇女严重抑郁症患者进行研究，不仅发现与抑郁症相关的常见 SNP (单核苷酸多态性)，而且还发现该选择位点已定位在蛋白质编码区中。Hall et al. (2018)发现 3p22.3 基因在苏格兰和英国的男性抑郁症患者中有一定的作用。这些发现不仅为抑郁症的现有假设提供了相关证据，而且为进一步了解抑郁症的生物学机制和后续研究提供了线索。

常见突变仍不能完全揭示抑郁症的遗传模型。因此，越来越多的学者将注意力转向稀有突变研究。Pirooznia et al. (2016)使用高通量测序技术对涉及突触的 1742 个基因进行测序和分析，提出抑郁症的病因可能与钙通道和树突的调节有关。此外，研究发现 NKPD1 基因的突变(Amin et al., 2017a)和 LIPG 基因 rs77960347 位点的错义突变(Amin et al., 2017b)与抑郁症状具有一定的关系。

2.3. MDD 的染色体结构变异研究

除了可以解释抑郁症遗传力的突变位点外，一些学者还把诸如短串联重复序列和重复数变异(CNV)等结构突变视为抑郁症的来源之一。Yu et al. (2017)使用全基因组测序的研究发现 CNV 缺失突变与抑郁症相关。并发现墨西哥裔美国人抑郁症患者的 23 条染色体的短串联重复序列明显少于正常对照(Yu et al., 2018)。此外，Gillentine et al. (2018)对候选基因 CHRNA7 的 CNV 研究发现抑郁症和焦虑症患者中该基因的重复数增加，表明该基因调节的神经元烟碱型乙酰胆碱受体可用作治疗抑郁症的靶标。以上表明对染色体结构变异的进一步探索将有助于抑郁症遗传学研究的发展。

3. 神经结构功能异常研究与抑郁症

在过去的几十年中，大量的神经影像研究证明了抑郁症中的各种临床症状与特定大脑区域(尤其是那些支持情绪调节，认知控制和奖励的区域)的结构和功能异常改变有关，并进一步将发生异常的脑结构定位于“皮质 - 边缘系统”。

3.1. MDD 中神经结构异常

先前的结构神经影像学研究发现，抑郁的受试者在许多大脑区域都伴有结构异常，包括背阔肌前额叶皮层，眶额叶皮层，前扣带回皮层，海马，纹状体，杏仁核和尾状核(Zhang et al., 2019; Han et al., 2014; Pirnia et al., 2016)。MDD 患者大脑多个区域的皮质厚度和灰质体积减小，表明灰质体积的差异可能会成为 MDD 的鉴别诊断标记(Kambeitz et al., 2017)。Suh et al. (2019)对测量皮质厚度的神经影像学研究进行了全面系统的回顾表明，抑郁的受试者的左钙骨肌裂隙/舌状回，左近颞肌和双侧额回的皮质厚度显著降低，而缘上回的皮质厚度显著增加。另外的一些荟萃分析研究显示，抑郁的受试者在右下纵筋膜，右额枕下部和右后丘脑辐射中显示出分数各向异性变化(Jiang et al., 2017; Wise et al., 2016)。

3.2. MDD 中神经功能异常

神经影像学技术的最新进展发现, 抑郁症中功能性神经的拓扑特征受到破坏。研究表明, MDD 与许多局部脑区域发生改变有关(Qiu et al., 2018)。

大量的神经影像研究表明, MDD 患者在额叶前额叶, 颞叶和边缘系统中观察到了明显的大脑异常(Sheline et al., 2010; Arnone, 2019; Tang et al., 2018)。Gong & He (2015)发现 MDD 患者存在大规模的异常脑连接组。抑郁症中的神经回路受到破坏, 导致各种神经基质发生临床症状, 包括前额皮层下回路, 背外侧前额回路, 眶额前额回路, 前扣带回前额回路, 前额海马回路和额丘脑回路(Zhang et al., 2018; Marchand, 2010; Tekin & Cummings, 2002; Wegener et al., 2015)。国内学者郁仁强等通过静息态功能磁共振研究发现, 与对照组相比, 观察组默认网络(DMN)在左内侧额上回脑区功能连接强度值显著减低(郁仁强等, 2019)。此外, 中央执行网络(CEN)和显著网络(SN)也和抑郁症的发病机制相关(Zhang et al., 2016)。这些异常的功能拓扑与诸如奖励处理, 认知控制和情绪调节之类的认知功能相关联, 因此有可能充当 MDD 的生物标记(Jie et al., 2015)。

4. 神经炎症研究与抑郁症

炎症激活被认为是一种自我保护的生存机制, 它是人体对各种创伤刺激的自我防御反应。越来越多的临床证据表明, 免疫分子和细胞都与 MDD 的病理生理持有关系, 与健康受试者相比, 抑郁者的血浆细胞因子升高(Mao et al., 2018)。

4.1. 免疫细胞

免疫细胞主要包括小胶质细胞、星形细胞、T 细胞、B 细胞。

小胶质细胞是脑细胞的主要成分, 参与许多病理和生理过程。在正常情况下, 小胶质细胞的功能主要有助于大脑发育以及神经元的正常结构和功能过程。但是, 在存在病原体和压力的情况下, 小胶质细胞可以作为中枢神经系统的一种重要效应物和调节剂。最近的证据证实, 过度激活和激活不足的小胶质细胞均可引起抑郁。Wohleb et al. (2018)发现, 在前额叶皮层(PFC)中, 压力使小胶质细胞激活并发生形态和功能变化, 这导致突触缺陷并引发焦虑和抑郁行为。Tong et al. (2017)发现由慢性不可预测的压力(CUS)导致的严重抑郁小鼠, 其海马小胶质细胞数量减少以及激活异常。还有研究表明小胶质细胞活化减少有可能助于 MDD 恢复(Juarez-Orozco et al., 2018)。

星形胶质细胞也被认为是大脑中的主要免疫介质, 在动物模型和人脑中, 星形胶质细胞功能障碍与 MDD 的发病机理有关。在抑郁症中, 星形胶质细胞显示出退化的迹象并且数量减少, 这可能导致神经传递失衡和突触连接异常。最近的一项研究发现, 星形胶质细胞在抑制抑郁症神经炎症方面对脑膜蛋白具有独特的作用(Leng et al., 2018)。另一项研究发现在不服用抗抑郁药的抑郁受试者中, 海马星形胶质细胞的密度显著降低(Cobb et al., 2016)。Monai & Hirase (2018)最近研究发现, 星形胶质细胞钙信号被颅直流电刺激(tDCS)激活, tDCS 是治疗慢性束缚应激诱导的抑郁小鼠所必需的成分。

除此之外, 调节性 T 细胞(Treg)也与抑郁症有关, 某些药物如长期高剂量卡托普利的长期给药可能会通过 Treg 减少和小胶质细胞活化来诱导抑郁样行为(Park et al., 2017)。T 淋巴细胞对 MDD 的抵抗力也至关重要。在抑郁过程中, T 淋巴细胞在平衡适应性和适应不良的免疫反应中, 在神经免疫网络中起着至关重要的作用(Toben and Baune, 2015)。

4.2. 免疫分子

越来越多的证据证实, MDD 患者大脑中趋化因子和细胞因子被激活。

最近的研究表明, MDD 患者趋化因子水平和常人相比较。一项研究表明, IL-1 β (促炎细胞因子)与激活 CNS (中枢神经系统)炎症途径和行为改变有关, 用 IL-4 进行治疗可以调节 IL-1 β 诱导的抑郁样行为并增加社交活动能力(Park et al., 2015)。IL-1 β 是脂多糖(LPS)产生的氧化和神经炎症反应所必需的, 当海马中的 IL-1 β 敲低可显著减轻 LPS 诱导的小鼠的记忆障碍以及焦虑和抑郁样行为时(Li et al., 2017)。IL-6 是一种可以被压力诱导的细胞因子。它可能通过其对 HPA 轴的影响而参与抑郁症的治疗(Girotti et al., 2013)。Kakeda et al. (2018)发现在未接受药物治疗的 MDD 患者的第一个抑郁发作期间, 血清 IL-6 水平显著升高, 并且在 MDD 早期阶段 PFC 的形态变化中起关键作用。Ng et al. (2018)对 34 项相关研究的荟萃分析显示, 患有抑郁症的老年人中仅 IL-6 仍显著较高。研究发现 TNF- α 破坏了血脑屏障的完整性(Cheng et al., 2018)。抑郁症伴随着在 mRNA 和蛋白质水平上 TNF, TNFRSF1A 和 TNFRSF1B 基因的表达增加, 并且 TNF- α , TNFRSF1A 和 TNFRSF1B 的表达升高与认知效率呈负相关(Bobinska et al., 2017)。TNF- α 拮抗剂有助于缓解抑郁症状和改善认知缺陷(Bortolato et al., 2015)。有证据表明干扰素 IFN- α 发现了抑郁症的病理生理学(Su, 2015)。IFN- α 可以诱发抑郁症, 这种抑郁症具有更多的躯体症状, 更少的情绪, 焦虑和负面认知症状(Su et al., 2019)。

总而言之, 了解神经免疫系统的作用和 MDD 中的炎症机制可能有助于解释抑郁症的症状, 识别诊断的生物标志物以及探索新的治疗方法。

5. 神经内分泌研究与抑郁症

5.1. 下丘脑 - 垂体 - 肾上腺素轴(HPA)与抑郁症

以往研究发现 HPA 参与抑郁症的发病机制, 大脑边缘系统与下丘脑之间神经信息传递障碍是抑郁症发病的重要原因之一(龚绍麟, 2010)。

以往研究显示, HPA 轴过度活动对抑郁症的形成和发展起到了重要的影响(Barden, 2004; Holsboer and Ising, 2008)。以往发现高达 80% 的抑郁症患者存在下丘脑 - 垂体 - 肾上腺轴功能亢进的现象(汪道文, 何健, 2010)。有研究表明, 抑郁症患者的唾液、血浆及尿液中皮质激素水平和垂体和肾上腺的体积成显著正相关, 与海马体积成显著负相关; 抑郁症患者的唾液、血浆及尿液中皮质激素水平增高, 垂体和肾上腺的体积增大(Nemeroff and Vale, 2005)、海马的体积缩小(Colla et al., 2007); Ge 通过对小鼠不可预见性温和攻击(CUMS), 发现每当大鼠有 HPA 轴过度活动时, 会产生抑郁样行为(Ge et al., 2013)。近年来发现, 通过对伴有精神病性症状的抑郁患者研究, 发现也存在 HPA 功能轴的活动显著增加的情况(Schatzberg, 2015)。

5.2. 下丘脑 - 垂体 - 甲状腺轴(HPT)与抑郁症

HPT 轴功能紊乱也可能与抑郁的相关症状有关。研究发现, 抑郁症患者血浆甲状腺激素(T3、T4)显著降低(于璟, 2013)。一些研究发现甲状腺功能标记物的变化与产后抑郁症相关(Plaza et al., 2010)。还有研究者更进一步认识到甲状腺功能和抑郁症之间的关系, 发现患有甲状腺功能减退的患者通常表现出抑郁症状(Kvetny et al., 2015)。也有研究发现甲状腺过氧化物酶自身抗体(TPO-Ab)与抑郁症的特征标记存在正相关, TPO-Ab 的出现可能是抑郁症易感性的标志物(Van de Ven et al., 2012)。

5.3. 下丘脑 - 垂体 - 性腺轴(HPG)与抑郁症

当 HPG 功能轴紊乱时, 性激素水平也随之下降, 进而可致机体生理周期紊乱, 性欲减退, 从而产生焦虑、抑郁等症状。Bloch et al. (2011)的研究发现, 对处在体外受精转移周期的女性使用促性腺激素释放激素(GnRH)受体激动剂可以导致她们产生抑郁和焦虑症状; 此外, 研究发现低水平的睾丸酮(testosterone, T)与抑郁症间的因果关系本质虽然不确定, 但是许多性腺机能减退的男性患有抑郁症, 反之有些抑郁症

病人同时患有性腺机能减退(Amore et al., 2012)。还有研究提示, 对某些围绝经期的抑郁症患者进行抗抑郁药治疗, 使用雌激素替代疗法有抗抑郁的效果(Rasgon et al., 2001)。以上这些结果提示抑郁症患者可能存在 HPG 功能轴紊乱。

6. 结语

以上研究提供众多证据, 从不同角度说明抑郁症的神经生理机制。然而, 有关抑郁症生理机制的研究仍有很长的路要走, 未来可以从以下三个方面进行研究。首先, 要扩大样本量, 大样本可以克服某些抑郁症的异质性干扰。其次, 为了减少异质性, 具有不同抑郁特征或不同抑郁特征的人可能具有不同的遗传结构, 减少异质性将有助于更好地揭示抑郁的遗传特征。最后, 需要寻求新技术和分析方法。新的分析方法和新的计算方法是可能的并为抑郁症的基因研究带来新的线索。综上所述, 抑郁症发病机制复杂。明确抑郁症的发病机制, 对于抑郁症的诊治至关重要。随着样本量的不断积累和技术的进步, 抑郁症的发病机制有望取得突破性进展, 以进一步了解抑郁症, 为寻求新的治疗方法提供线索。

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