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中国森林生物多样性监测网络：二十年群落构建机制探索的回顾与展望

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摘要: 中国森林生物多样性监测网络(CForBio)目前已经沿纬度梯度从寒温带带到热带布设23个大型森林动态样地, 监测1,893种木本植物, 代表我国木本植物种类的近1/6。CForBio的主要目标之一是研究森林群落的构建机制。本文综述了近20年来CForBio在群落构建机制探索方面取得的进展, 包括生物多样性时空格局、生境过滤、生物相互作用、局域扩散和区域因素以及利用新技术取得的新认知等。CForBio研究发现: (1)生境过滤和扩散限制共同决定种-面积关系及 β 多样性等多多样性格局, 但二者的相对作用在不同样地及不同尺度存在差异; (2)生境过滤对局域群落构建的作用广泛存在, 但很难量化其对群落构建的重要性; (3)同种负密度制约在不同气候带样地普遍存在, 负密度制约的强度主要由植物菌根类型介导, 并随植物生活史类型、功能性状及环境变化而变化; (4)扩散限制在局域群落构建中发挥关键作用, 而区域因素如区域地质历史、区域物种库大小等塑造不同生物地理区群落之间的生物多样性差异; (5)宏观和微观两个方面的新技术促进群落构建机制的研究。在宏观方面, 遥感技术以低成本使大范围、多尺度的连续群落生物多样性监测和时空比较研究成为可能; 另一方面, 叶绿体基因技术和代谢组学等微观技术能促进推导群落构建的分子机制。同时, 本文还总结了以往研究的不足, 并展望了基于森林动态样地开展群落构建机制研究的未来发展, 特别强调了: (1)关注群落构建研究中的尺度问题; (2)深入开展多维度(物种、功能和系统发育)、多营养级生物互作相关的研究; (3)拓展全球变化对群落构建影响的研究; (4)融合观测-实验-模型多种手段开展群落构建机制的研究; (5)连结“群落构建理论研究”和“森林管理实践”。总之, 中国森林生物多样性监测网络的长期监测和联网研究是森林群落构建机制研究的重要基础, 也是推动群落构建理论、解决森林管理难题的重要平台。

关键词: 森林生物多样性; 群落构建; 格局; 生境过滤; 生物相互作用; 局域扩散

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Chinese Forest Biodiversity Monitoring Network (CForBio): Twenty years of exploring community assembly mechanisms and prospects for future research

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ABSTRACT

Background & Aim: Since 2004, the Chinese Forest Biodiversity Monitoring Network (CForBio) has established 23 large forest dynamics plots along a latitude gradient ranging from cold temperate forests to tropical forests in China. The forest dynamics plots include about 1,893 species, representing one-sixth of the known tree diversity in China. With > 700 papers and > 400 papers published in international journals, CForBio researchers have made significant contributions toward understanding mechanisms of forest community assembly. This review summarizes the progresses achieved by CForBio researchers, including knowledge of the spatiotemporal patterns of plant communities, the roles of habitat filtering, biotic interactions, effects of dispersal limitation and regional effects in structuring plant communities, and the application of new technologies in understanding community assembly.

Review Results: (1) Habitat filtering and dispersal limitation jointly affect the diversity patterns such as species–area relationship and β diversity, but their relative effects vary among plots and across scales. (2) Habitat filtering generally plays an important role in forest community assembly. However, it is difficult to quantify its relative importance. (3) Conspecific negative density dependence (CNDD) is prevalent in these CForBio plots across latitudes. In addition, the strength of CNDD is found to be mediated by plant mycorrhizal type, and varies with life history, functional traits and environmental change. (4) Dispersal limitation predominantly shapes community structure at local scales, whereas regional effects, such as regional pool size and geological history, strongly determine spatial patterns of biodiversity among communities over broader biogeographic regions. (5) New technologies provide novel ways to advance studies of community assembly from both macro and micro-perspectives. On one hand, remote sensing enables us to monitor forest community biodiversity from local to large scales in a cost-effective way. On the other hand, transcriptomics and metabolomics enable us to precisely infer molecular mechanisms of community assembly.

Perspectives: This review also discusses the limitations in current community assembly studies and proposes some issues and potential topics to be considered for future studies. We discuss the vital role of CForBio in promoting the application and future development of community assembly studies, including (1) the spatiotemporal scale problem; (2) the multi-dimensional (taxonomic, functional, and phylogenetic diversity) and multi-trophic biotic interactions; (3) the advantages of interdisciplinary and multipath approaches such as the “observational evidence-controlled experiment-ecosystem model” methodology; (4) the effect of global change on community assembly; and (5) the applications of community assembly findings for addressing forest management challenges. In conclusion, the long-term forest biodiversity monitoring is fundamental for a comprehensive understanding of community assembly and serves as an important platform for bridging studies on theories of assembly and on forest management challenges.

Key words: forest biodiversity; community assembly; pattern; habitat filtering; biotic interaction; dispersal limitation

森林生态系统具有最丰富的植物多样性, 同时也是最主要的陆地碳汇(Pan et al, 2011)。一方面, 随着人口、经济剧增以及城市化的加速, 我国森林生物多样性遭到破坏, 高等植物受威胁物种的比例达11% (覃海宁和赵莉娜, 2017); 另一方面, 政府实施的退耕还林(草)、天然林保护等重大生态工程改善了生态环境, 使我国森林生物多样性得到了较好的保护; 第九次全国森林资源清查(2014–2018年)结

果表明, 我国森林覆盖面积已经从第一次清查时的12.69%增加到22.96% (国家林业和草原局, 2019)。在我国不同森林区生物多样性破坏和保护并存的同时, 建立国家水平的监测网络来观测森林生物多样性的变化趋势、研究不同区域森林生物多样性变化的驱动和维持机制, 在全球变化背景下提出森林生物多样性的适应性管理策略显得非常迫切。

作为国家尺度的生物多样性监测网络之一, 中国森林生物多样性监测网络 (Chinese Forest Biodiversity Monitoring Networks, CForBio) 自2004年开始, 沿纬度梯度在不同气候带(从寒温带到热带北缘; 附录1)建设大型森林动态样地(面积不少于15 ha), 目前已经建成了23个, 总面积665.6 ha, 监测1,893种木本植物。自第一个大型森林样地建设完成至今, CForBio已历经近20年发展, 研究人员围绕森林群落构建机制这一主题累计发表论文700多篇, 其中国际刊物论文400多篇。本文回顾了CForBio的发展历程, 系统梳理了CForBio在群落构建机制探索方面取得的研究进展、存在的研究空缺和潜在发展方向, 以期明晰CForBio未来在群落构建机制研究的发展重点。

1 森林生物多样性研究与CForBio的发展历程

传统的森林生物多样性研究通常基于小型样地进行观测和理论分析, 存在样地面积小、监测时间短等问题, 无法涵盖群落中众多稀有物种, 难以反映群落生物多样性在多个尺度上的长期变化趋势, 不足以深入认识群落构建机制(米湘成等, 2016; 马克平等, 2019)。针对这些问题, 建立大型森林动态样地长期监测中国主要森林类型的生物多样性变化, 研究变化的驱动机制及群落构建机制十分必要。2004年2月, 中国科学院生物多样性委员会在北京香山召开森林生物多样性监测研讨会 (Mapping Plot—Beijing Workshop)。会上, 全球森林生物多样性监测网络主任Stuart Davis博士与加拿大阿尔伯特大学何芳良教授梳理了当前森林动态样地网络发展现状和发展趋势, 台湾东海大学孙义方教授对样地建立方法进行了介绍。中国科学院生物多样性委员会决定启动中国森林生物多样性监测网络建设项目, 按照CTFS (Center of Tropical Forest Science, 现改为Forest Global Earth Observatory, ForestGEO)样地建设的技术规范(Condit, 1998)建设森林动态大样地, 投入经费150万元。项目于2004年正式启动(附录1), 首先在长白山地区建成了一个25 ha温带森林样地, 这是我国第一个大型森林动态样地, 也是全球第一个温带森林样地。2005年在浙江古田山建立了24 ha中亚热带森林样地、在广东

鼎湖山建立了20 ha南亚热带森林样地; 2007年在云南西双版纳建立了20 ha热带季节雨林样地。此后, 又陆续建成了亚热带高海拔的八大公山25 ha样地、喀斯特季雨林的弄岗15 ha样地、暖温带中部的东灵山20 ha样地、暖温带南部的宝天曼25 ha样地等。同时, 联合高校和其他研究单位建立了若干大型森林动态样地, 如: 小兴安岭丰林和凉水的红松阔叶林样地、浙江天童的常绿阔叶林样地、大兴安岭的寒温带针叶林样地等(米湘成等, 2016; 马克平等, 2019)。

在推动大型森林动态样地建设的同时, CForBio也通过举办系列专题培训班和研讨会加强研究能力建设。CForBio邀请了一批国内外生物多样性监测和研究方面的知名教授对CForBio研究人员进行专题培训和指导, 如: 加拿大阿尔伯特大学何芳良教授讲授空间统计学并培养了大量年轻学者; 加拿大蒙特利尔大学Pierre Legendre教授、台湾东海大学孙义方教授、ForestGEO科学家Richard Condit、Joseph Wright、Nathan Swenson、Liza Comita和Helene Muller-Landau等, 为CForBio研究人员举办了“数量生态学”“种子生态学与植物功能性状”“R语言”“群落系统发育生态学”“种内密度制约”以及“动态样地数据管理”等培训, 极大地提升了CForBio研究人员的数据分析与研究能力。同时, CForBio也举办了一系列研讨会, 如: 2007–2016年共举办了10届海峡两岸森林动态样区研讨会, 两岸学者在动态样地的建设和研究方面进行了广泛而深入的学术交流; 2011–2017年, 获中美双方国家基金委员会资助, CForBio和ForestGEO每年在美国或中国举办一次问题讨论和数据分析研讨班, 加强我国学者的能力提升, 加深与ForestGEO各样地的交流。

经过监测和分析方法的培训, 采用统一的监测标准和标准的分析方法, 各样地研究人员主要聚焦在生物多样性静态格局的分析, 围绕物种的空间分布格局、生态位过程和中性过程在群落构建中的相对作用、种内和种间相互作用等主题开展研究。近年来进一步开展多样地之间的比较研究, 以及长时序群落生物多样性动态研究, 推进了我国森林群落构建机制的研究(米湘成等, 2016; 马克平等, 2019)。

2 森林生物多样性格局和群落构建机制研究进展

2.1 生物多样性时空格局

生物多样性格局是生物多样性在地理空间上的分布，能够直观地反映生物及环境因素对物种分布的影响(Gaston, 2000)，研究生物多样性格局及其驱动机制是生物多样性保护研究的重要基础(Kratochwil & Okologie, 1999)。

种群个体的分布一直是生态学理论的中心问题，但是由于传统的样方调查方法没有个体的坐标数据，不能进行空间格局分析。在具备了个体详细坐标信息的动态监测大样地中，利用空间点格局的方法可以分析群落物种个体的空间分布格局，从而推断物种分布的影响因素。依托CForBio平台，研究人员发现不同植被类型的群落中物种以聚集分布为主(Jin et al, 2007; Li et al, 2009; Lan et al, 2011; Guo et al, 2013)，随空间尺度增加而聚集程度降低，且稀有种的聚集程度较优势种和常见种更高(张健等, 2007; Wang et al, 2010; 毛子昆等, 2020)。在较平坦的生境中，生境异质性的影响比其他非生境聚集过程要小，地形复杂的生境则相反(Shen et al, 2013)。

在群落水平上，研究生物多样性格局最常用到的指标有 β 多样性、种-面积关系、个体种-面积曲线等。 β 多样性衡量群落物种组成的空间转换(Kraft et al, 2011)，在CForBio多个森林动态样地中都进行了其空间格局的研究，结果表明确定性过程和随机过程共同决定了树木 β 多样性的变化格局(Legendre et al, 2009; Qiao et al, 2015; Wang et al, 2015; Guo et al, 2018)，但确定性过程和随机性过程在不同样地中的相对重要程度存在差异(Feng et al, 2016)。如在古田山和八大公山样地中两种作用重要程度相当(Legendre et al, 2009; Qiao et al, 2015)，而在弄岗喀斯特森林中环境异质性非常大，因此确定性作用的影响更加强烈(Guo et al, 2018))。Yang等(2015)在西双版纳热带季节雨林动态样地还开展了功能性状和系统发育 β 多样性研究，发现在该样地环境距离对功能性状或系统发育 β 多样性的解释力度均比空间距离大，且环境距离的解释力度随空间尺度的增大而增大。不同过程对 β 多样性的影响还存在明显

的尺度依赖性，通常在大尺度上生境过滤起主要作用，中尺度上扩散限制作用最强，而种间关系仅在小空间尺度上起作用(Wang et al, 2015)。种-面积关系描述了物种数随面积增加的规律(Lomolino, 2000)，也在CForBio得到广泛的关注。Shen等(2009)在古田山运用不同空间分布模型分析种-面积关系，发现生态位过程和中性过程共同决定了群落结构。Ren等(2022)进一步研究了不同空间尺度上种-面积关系的变化规律，发现古田山亚热带森林的种-面积关系在小尺度上符合幂函数并且在30 m尺度处存在明显的转换。Wang等(2013)在长白山样地首次将系统发育和功能多样性引入到种-面积关系的研究，探讨了随机分布、环境异质性、扩散限制对群落结构的影响，结果表明系统发育多样性和功能多样性也随着面积增加而增加，环境异质性和扩散限制均能影响系统发育和功能多样性与面积的关系，其中扩散限制的作用较大。

近年来，随着样地间合作增加，区域内和区域间生物多样性格局变化的研究也随之增加。如Wang等(2011)以长白山温带森林样地和美国威斯康辛温带森林样地为研究平台，探讨环境异质性、扩散限制及这二者共同作用对种-面积关系和 β 多样性的影响，发现二者的共同作用能较好解释物种分布格局。Yang等(2013)利用全球9个大型森林动态样地的树种分布数据分析了个体系统发育多样性-面积关系，发现系统发育的累积种(accumulator)和排斥种(repeller)均表现出显著的系统发育信号，且主要在较小的邻域尺度内起作用。Wang等(2018)以8个温带森林动态样地为研究平台，探讨 β 多样性的格局及其组分的影响因子，发现温带森林群落物种周转所占比例高于嵌套格局，扩散限制和生境过滤对二者的相对作用不同：扩散限制对物种周转的作用强于生境过滤，而对嵌套格局的作用与生境过滤相当。Qiao等(2021)基于CForBio 12个大型动态样地基础物种的研究发现，中国森林基础物种对群落物种多样性格局存在强烈的影响，且基础物种数存在显著的纬度梯度格局。

虽然生物多样性格局，如种-面积曲线、 β 多样性、物种-多度分布曲线等都是反映群落统计规律的，但是不同的生态学过程可能产生非常相似的格局，因此解释格局的各个假说很难得到排他性的检

验(Gaston et al, 2008)。近20年来, 研究人员越来越清楚这些格局反映了一些基本生态格局的不同方面, 是密切关联且数学上可相互推导的, 如物种的聚集程度和不同尺度上的物种-多度分布等(Storch et al, 2008), 因此May等(2015)建议同时检验多个生物多样性格局来推断生态学过程。另一方面, 仅从这些格局似乎难以推断物种共存机制。最近一项研究中, Wiegand等(2021)利用树种的空间分布数据、空间统计和动力学理论, 揭示了空间格局与种间相互作用系数的关系及其对多物种动态和共存的影响。他们发现, 只有当类似动物传播的机制存在, 更新的个体在远离母树的位置产生聚集时, 才能产生稀有种优势并与其他中性的竞争物种共存。因此, 将这些静态的空间格局与群落动态共同进行分析, 可能是未来生物多样性格局研究的发展方向之一。

2.2 生境过滤

生境过滤指非生物环境筛选特定性状物种进入局域群落的过程。它常被称为“环境筛”(Keddy, 1992), 与扩散限制和生物互作一起, 被认为是群落构建的三大过程(HilleRisLambers et al, 2012)。生境过滤的核心观点是: 在不同的环境中, 物种常常具备不同的适合度, 因此就会形成不同的种群数量。这一认知已被总结为检验生境过滤的第一个期望: 物种多度、分布和存活状态等会随着非生物环境梯度发生变化。由于森林动态样地内详细记录了环境数据和每个物种的个体分布, CForBio平台由此成为了检验该期望的绝佳平台, 并为该期望的检验做出了突出贡献。例如在热带、亚热带、暖温带和温带森林中, 多数树种的分布(胸径大于1 cm的个体)受地形和土壤等环境因子的显著影响(谢玉彬等, 2012; Wang et al, 2014; Qiao et al, 2015; Fang et al, 2017; Guo et al, 2016; Song et al, 2016; Liu Q et al, 2018; Shi et al, 2019; 朱文婷等, 2021)。许多研究还发现环境因子对林下植物幼苗的存活、生长、分布(田锴等, 2013; 赵雪等, 2013; Pu et al, 2017; Xia et al, 2019; Xu et al, 2019; Martini et al, 2020), 林下灌木的分布(Chen et al, 2016)及林下土壤种子库(Martini et al, 2020; Zou et al, 2021)等都存在显著影响, 甚至依赖其他树木生长的藤本植物的分布也受地形、土壤养分等环境因子的影响(Liu & He, 2021)。除了植物之外, Wang等(2016)、Gao等(2017)

和Shang等(2021)还发现环境因子对土壤微生物的物种组成也有很大影响, Chen等(2019)证明了环境因子对鸟类分布有显著影响。环境因子还能影响食果动物的平均访果时间和取食量(Tongkok et al, 2020)、陆生甲虫的物种组成(Gao et al, 2020)。但是, 生境过滤对不同生活型物种、不同生活史阶段的种群作用不同(刘海丰, 2013; 陈云等, 2014; 韩大校和金光泽, 2017)。例如, Bai等(2012)和Lu等(2015)发现地形条件对幼苗生长的影响较弱; Yang等(2016)发现生境过滤对树木分布的影响广度和强度随着生活史阶段从小树到成树而增强, 可能与生境过滤的累积效应、不同生活史阶段资源分配和利用策略的差异有关。此外, Oktavia和Jin (2019)发现在种群个体数较多的生境中, 小树的相对生长量反而更低, 个体死亡率更高, 可能与生境过滤导致种群密度变化后引起的其他生态过程(如同种密度制约, 详见第4节)强度变化有关(Lu et al, 2015)。

由于功能性状直接决定植物对环境的适应, 有许多研究从功能性状角度探讨生境过滤。一般认为, 如果生境过滤在局域自然群落起较大作用, 那么群落功能性状均值和性状权衡会随着非生物环境梯度发生变化。这是生境过滤的第二个期望, 且得到大样地观测结果的基本证实。例如, Liu等(2012)和刘志理等(2017)发现土壤肥力与叶面积、叶面积指数和木材密度显著相关。Liu等(2014)和Zhang等(2020)发现地形因子能显著影响植物种子质量、干材密度、最大树高、木质部对于干旱引起栓塞的抵御能力等。蒋裕良等(2016)发现地形等环境因子还显著影响植物的花色。除了这些表型或生理性状外, 植物的一些其他性状也表现出强烈的环境相关性。例如, Zhang等(2016)和Zhu等(2017b)发现环境因子能影响树木的生长速率和死亡率, 且对不同菌根类型的树木生长影响不同(Ren et al, 2021), 但Wu等(2017)没有发现类似规律。郭屹立等(2016)发现植物群落胸高断面面积之和与环境因子显著相关。Lin DM等(2012)、Xu等(2015)、Liu等(2020)发现地形条件显著影响种群生物量, 且这种影响在物种间具有较大差异。Yang等(2014)和Asefa等(2017)还发现环境因子能影响不同物种间的性状权衡。此外, 同一物种的叶面积、木材密度、叶干物质含量、叶氮含量甚至是遗传结构等也随环境而发生变化(马金等,

2015; Oktavia & Jin, 2020; Qadir, 2021)。同时, 种内功能性状分化也通过影响群落中物种的存活率、生长率和死亡率以及对环境的响应来调节群落的物种共存(Yang et al, 2018), 如采用个体水平功能性状的树木生长模型要优于常用的物种水平性状模型(Liu et al, 2016; Yang et al, 2021, 2022)。

此外, 性状的离散程度也能检验生境过滤对群落构建的影响。如果生境过滤在局域自然群落中起较大作用, 那么群落内某一非生物环境中的功能性状会更加相似, 从而降低功能性状多样性。这一逻辑衍生了生境过滤研究中的第三期望: 不同物种的性状在相同环境下具有趋同性。当系统发育距离相近的物种具有更相似的功能性状时, 生境过滤会导致某一非生物环境中存在系统发育格局聚集(phylogenetic clustering), 同时降低系统发育多样性; 不同环境则驱使系统发育格局发散, 系统发育多样性增加。例如Liu等(2013)、Li等(2019)、Wei等(2020)发现环境因子对物种间性状发散程度有很大影响, 但不同生活史阶段会有变化。Asefa等(2019)通过点格局过程建模方法, 证明了环境因子对系统发育 β 多样性有显著影响。进一步研究发现, 不同环境能显著增加群落间的系统发育 β 多样性(Shi et al, 2021), 同一环境能显著降低系统发育 β 多样性(王薇等, 2014)。不过, 以往研究也出现了不支持生境过滤期望的结果。例如, Xu等(2016)发现单一的低磷环境能够促使植物物种系统发育结构发散; 王薇等(2014)发现生境过滤能增加单一环境中幼苗的系统发育 α 多样性。这些结果表明, 通过系统发育格局检验生境过滤的作用存在诸多不确定性; 其他生态过程, 如邻体尺度的密度制约(王薇等, 2014)和扩散限制(Asefa et al, 2019)等, 都会干扰生境过滤对群落系统发育结构的作用。

生境过滤对群落的作用也存在尺度依赖性(Kraft et al, 2015)。不同空间尺度下生境过滤对群落的作用存在差异(Yuan et al, 2016), 且不同环境因子形成的过滤效应也具有不同的尺度特征(Zhu et al, 2017b)。但多数研究发现, 随空间尺度的增加, 生境过滤的影响会增加。例如, Lin等(2013)发现环境因子对群落物种分布的解释度随着取样方尺度的增加而增加。类似的尺度规律也适用于群落功能特征(Li et al, 2019)。土壤磷含量对叶面积的影响也随

着尺度的增加而增加(Liu et al, 2021)。这些尺度依赖的生境过滤作用说明, 不同空间尺度上主导群落构建的过程可能存在较大差异。

上述有关生境过滤的4类研究极大加深了对森林群落构建机制的理解, 但也出现了较多不符合预期的观测结果。多数生态学家已逐渐认识到, 上述推论都只是生境过滤的必要非充分条件(Kraft et al, 2015)。其他诸如扩散限制、种间竞争等都可能产生或干扰上述的期望格局。例如当种间竞争受适合度差异主导时, 竞争也会形成生境过滤所期望的功能性状或系统发育结构聚集的格局(Mayfield & Levine, 2010)。扩散限制也会限制部分物种无法到达某一局域群落, 因此它能改变检验生境过滤的物种库组成, 进而影响检测生境过滤的能力。虽然已有理论工作在剥离扩散限制的作用后仍观测到了非生物环境对物种分布的显著影响(Shen et al, 2013; Asefa et al, 2020), 但缺乏基于实际物种扩散数据的研究工作。基于观测数据的研究很难剥离这些干扰因素, 但可以通过同时检验多个生境过滤的期望来降低该类错误发生的概率(Cadotte & Tucker, 2017)。

为严格检验生境过滤对群落构建的影响, Kraft等(2015)提出了通过控制实验排除生物因素的影响。不过这种方式也存在一些问题, 例如多数植物不仅受环境的影响, 同时也能改变其周围的非生物环境, 进而影响自身及其他物种对非生物环境的适应能力。例如, 桂旭君等(2019)展示了由林冠结构导致的林下不同高度上光照、空气温度等微环境的变化。其他研究也发现地形因子对叶凋落量(Guo et al, 2019; 贾梦可等, 2020)、地表凋落物层(Wang et al, 2019)有显著影响, 而植物凋落叶的多少又会进一步显著影响土壤养分含量(Xia et al, 2015, 2016)。不同的森林结构也能显著改变到达地面的光照强度, 进而改变林下土壤呼吸速率(Shi et al, 2016; Han et al, 2020), 调节林下幼苗生长存活(Lin et al, 2014), 改变林下幼苗多样性(徐耀粘等, 2020)。同时, 林窗密度也能显著影响林下幼苗更新(Jin et al, 2018)。Li等(2021)还发现树木种类对根际真菌物种组成存在很大影响。这些生物对微环境的改变最终会影响到生境过滤对群落的作用, 因此, Thakur和Wright(2017)提议生境过滤中要考虑生物对非生物环境的改造作用。

总之, 上述基于CForBio平台的研究表明, 生境过滤对局域群落构建的作用广泛存在, 但严格检验生境过滤并非易事。由于非生物环境与某些生物互作往往交织在一起, 是否要剥离生境过滤和生物互作各自的效应, 非生物环境究竟如何影响物种的种群动态等值得进一步探讨。这些问题的答案将能帮助我们理解和预测人类活动和气候变化干扰下局域森林群落的结构和动态。

2.3 生物相互作用

2.3.1 密度制约机制

同种密度制约效应(*conspecific negative density dependence*)是森林群落构建和物种多样性维持的重要生态学过程(Wright, 2002; 祝燕等, 2009; Chen et al, 2019)。由于同种个体间的资源竞争、天敌侵害(比如病原微生物、植食动物捕食)等相互损害的行为, 导致在较小的空间尺度内, 同种个体密度高的情况下个体生长率低, 死亡率高, 从而为其他物种的生存提供空间和资源, 促进物种共存。国际同行围绕同种密度制约效应开展了大量研究工作(Basset et al, 2019; Comita & Stump, 2020; Hülsmann et al, 2020; Terborgh, 2020), 过去20年间我国学者基于森林动态样地也开展了大量密度制约效应的群落学研究(Chen et al, 2010; Zhu et al, 2010; Lu et al, 2015; Wu et al, 2016; Kuang et al, 2017; Pu & Jin, 2018; Song et al, 2020)。

尽管大部分关于密度制约效应的研究都来自热带地区(祝燕等, 2009), 但这一机制在我国许多高纬度生态系统(如温带森林中)同样得到了许多研究证据的支持(Jia et al, 2020)。通过比较热带(海南霸王岭)、亚热带(广东黑石顶)和温带(吉林长白山)的样地调查数据(Xiao et al, 2012), 也发现专一性病原菌驱动的密度制约机制和群落补偿效应对植物群落结构的调节作用是热带和温带地区都存在的一种普遍现象。树种间邻体的相互作用具有系统发育依赖性, 即系统发育距离近的树种间具有更强烈的负效应(Pu & Jin, 2018)。然而, 这一系统发育密度制约效应在西双版纳热带森林中并不明显, 并且受到了生境过滤效应的掩盖(Wu et al, 2016)。最新的研究证据显示, 密度制约效应不仅在不同植物类群间不同(Lu et al, 2015; Jiang et al, 2020), 还具有种内变异, 不同基因型的种群间抵抗天敌的能力不同,

聚集的病原菌群落也存在差异(Liu XB et al, 2015; Shao et al, 2018; Wang et al, 2022)。

同种密度制约效应的种间变化也受到植物生活型、叶片物候型、种子扩散类型的影响(Lu et al, 2015)。同种密度制约效应还与植物性状有关, 例如丛枝菌根(*arbuscular mycorrhiza*, AM)树种和耐阴树种更容易受到病原菌的影响, 而不耐阴的树种更容易受到植食动物的侵害(Jia et al, 2020)。树种防御能力相关的功能性状可以预测同种密度制约效应的种间变化(Song et al, 2021)。植物受到密度制约效应的强度与植物生活史阶段(Zhu et al, 2015)及其生长防御策略相关(Zhu et al, 2018)。相比于丛枝菌根植物, 外生菌根(*ectomycorrhiza*, EM)可以减少病原菌对植物的侵害(Marx, 1972), 其受到同种密度制约效应的影响较弱(Chen et al, 2019; Jiang et al, 2020)。由于引起同种密度制约效应的天敌类群存在显著的种间变化, 因此在群落水平上针对不同天敌类群进行综合研究十分必要。

进入人类世以来, 森林生态系统正经历着快速且剧烈的环境变化, 受到日益严峻的高温和干旱威胁(Brodribb et al, 2020; McDowell et al, 2020)。在此大背景下, 环境(特别是气候变化)与密度制约的相互作用对物种共存机制的影响应给予更多的关注, 以利于预测森林群落未来的结构、功能和动态(Valladares et al, 2015)。在我国亚热带常绿阔叶林中, 密度制约效应和生境的相互作用共同制约幼苗群落的更新(Chen et al, 2010), 在我国温带针叶林的研究也显示密度制约和环境作用的重要性具有强烈的种间变异(Zhu et al, 2017a)。同时, 同种密度制约效应具有显著的季节动态(Lin LX et al, 2012)和年际动态(Song et al, 2018)。在西双版纳热带季节雨林, 幼苗间的同种密度制约效应在旱季强于雨季(Lin LX et al, 2012), 且该地区年均温的增加增强了同种密度制约效应(Song et al, 2018), 温带地区的研究也报道了密度制约效应的年际波动性(Kuang et al, 2017)。密度制约响应气候变化的生态学过程和机理尚不明确。控制实验结果表明, 增温加强了病原菌引起的同种密度制约效应可能是原因之一(Liu & He, 2021)。

虽然似乎森林群落的负密度制约促进物种共存已经成为共识(Adler et al, 2018), 但Detto等(2019)

指出前人的调查研究中普遍存在统计偏差。而关于该效应的早期实验研究则多集中在物种水平及报道该效应是否存在(Comita et al, 2014), 针对该效应发生机制的实验研究近年来才有所增加。在群落水平针对该效应发生和调控机制开展的系统性研究工作则更加缺乏(Jia et al, 2020; Hazelwood et al, 2021), 对该效应的种间变化规律和时空特征仍然缺乏足够的研究(Song et al, 2021)。不同的森林群落中, 密度制约机制是否促进以及在多大程度上促进物种共存, 仍然是群落生态学一个有待回答的重要问题。

2.3.2 植物与微生物互作机制

植物与土壤微生物之间的相互作用被认为是森林群落中物种共存的重要驱动因素, 特别是由专一性土壤病原真菌驱动的密度和距离制约效应对植物群落结构有重要的调节作用(Bever et al, 2012; Liu Y et al, 2015)。研究人员通过长期幼苗动态监测揭示了同种成树密度制约现象, 利用高通量测序阐明了寄主植物密度与土壤病原菌浓度之间的正相关关系, 并进一步运用控制实验证明土壤病原菌是成树密度制约效应的重要驱动者(Liu Y et al, 2015; Liang et al, 2016), 揭示了成树密度制约在群落水平和种群水平上促进幼苗补偿的现象, 进而从土壤微生物群落结构动态的角度阐明了密度制约机制的形成过程(Liang et al, 2016)。

植物-土壤反馈作用中的另外一个主要驱动因子为菌根真菌(mycorrhizal fungi)。菌根真菌能够与93%以上的陆生植物形成共生体, 是自然界中普遍存在的互利共生现象(Smith & Read, 2008)。森林群落中最主要的两个菌根真菌类型分别是丛枝菌根真菌和外生菌根真菌。其中, 丛枝菌根真菌能与绝大多数树种形成共生关系, 而外生菌根真菌的寄主则只限于少数植物类群。菌根真菌能够降低病原菌对植物的侵害, 提高植物抵御恶劣环境的能力, 促进寄主在贫瘠土地上的定植, 提高植物群落的生产力等。正是由于植物与菌根真菌之间的这些正反馈作用, 菌根真菌普遍被认为能够提高寄主植物在与其他物种共存时的竞争优势, 抵消土壤病原菌的负反馈作用(Liang et al, 2015)。因此, 传统上认为菌根真菌与植物的互利共生不利于森林群落的物种共存。另一方面, 菌根真菌可以通过地下菌丝网络

(common mycelial network, CMN)实现不同植物个体间的物理连接, 进而形成遍布林下土壤的物质和信号传输的高速通路。野外调查发现, AM植物的根际土壤和根系内聚集了相对更多的病原真菌(Chen et al, 2019; Liang et al, 2020)。因而, 植物幼苗在连接不同类型菌根菌丝网络时, 其密度制约方向与强度如何被调节成为本领域关注的热点问题之一。其中, 利用0.5 μm 或35–50 μm 孔径尼龙网制作的原位内生长环控制幼苗与外部菌根菌丝网络的连接, 可以直观地分离土壤病原真菌和菌根真菌的不同作用。Liang等利用该装置分别在AM树种和EM树种占优势的生境中进行不同菌根类型幼苗交互移栽实验(Liang et al, 2020)和密度梯度实验(Liang et al, 2021), 揭示了菌根菌丝网络在抵消密度制约强度、调节幼苗更新动态中的关键作用, 并阐明了AM和EM树种两大类群间植物-土壤反馈强度差异的形成机制。

菌根真菌与高等植物根系形成的共生体中, 菌丝能够为寄主植物吸收矿物营养特别是磷元素, 而寄主植物则将光合作用产物碳水化合物及其他营养物质输送给菌根真菌(Smith & Read, 2008)。在马来西亚婆罗洲热带雨林和华南地区亚热带森林的幼苗盆栽实验证实了植物-土壤正反馈作用驱动的限制性磷资源分割利用机制(Liu XB et al, 2018)。群落中共存的寄主植物通过与不同类别的菌根真菌合作, 实现了对土壤中限制性营养元素不同形态化合物的差异化利用, 其中EM植物对复杂的有机磷化合物有显著偏好, 而AM植物则只能利用简单的有机磷和无机磷, 最终促进了热带亚热带树种间的生态位分化和稳定共存。

因为EM树种的幼苗在母树下通常具有正的密度依赖效应, 同时利用土壤中复杂有机营养物质的能力更强, 能够在土壤较为贫瘠的生境斑块中拥有更高的适合度(Mao et al, 2019), 进而形成了一定的竞争优势, 提高了该类群在森林群落中的相对多度甚至形成EM植物的局部单优群落, 而AM植物则因聚集了相对更多的病原菌而具有更强的密度制约效应, 对群落多样性有更大的影响(Mao et al, 2019)。这些植物与土壤微生物的相互作用最终塑造了从热带到寒温带森林群落的外貌和结构, 在空间结构复杂、层次多样的热带雨林和亚热带常绿阔叶

林中, 能够长得更高、占据冠层优势地位的往往是营养获取能力强、具有正反馈的EM树种, 包括龙脑香科和壳斗科等, 而下层则是物种丰富、多样性极高的AM树种(图1), 不同类型的菌根植物在生境异质性条件下占据各自的更新生态位, 共同组成了森林群落的生物多样性。

2.4 局域扩散和区域因素

除了生境过滤和生物之间相互作用, 局域尺度的扩散限制是另外一个影响森林生物多样性与群落构建的重要局域过程, 也是CForBio研究的主要问题之一(Shen et al, 2009; Feng et al, 2016; Chen et al, 2019)。植物群落中的扩散限制主要指由于传播者数量或种类的不足和限制, 阻碍了种子到达适合的萌发地点(饶米德等, 2013; Dent & Estrada-Villegas, 2021)。扩散限制的重要作用已经在CForBio中得到了广泛验证, 包括不同森林类型(温带、亚热带、热带)、不同生物多样性维度(物种多

样性、系统发育多样性、功能多样性)、不同生物类群等(Legendre et al, 2009; Gao et al, 2015; Yang et al, 2015; Wang et al, 2018)。例如, 在古田山亚热带森林的研究发现, 与生境过滤相比较, 扩散限制与生境过滤对植物群落物种多样性与系统发育多样性格局具有相似的解释能力, 且扩散限制在小尺度上的作用更大, 而随着尺度的增大生境过滤的作用逐渐变大(Legendre et al, 2009b; 饶米德等, 2013)。同时, 扩散限制也能更好地解释中国北方与北美温带森林动态样地的植物群落物种组成(Wang et al, 2018)。此外, 研究表明扩散限制也能显著影响森林土壤微生物群落组成, 并且影响的强度随森林演替阶段的不同而发生变化(Gao et al, 2015; Wang et al, 2016)。

更为重要的是, 越来越多的研究表明在区域地质历史过程、物种库和环境等区域因素与局域生态因子共同作用下形成了局域群落生物多样性、物种组成与结构(Ricklefs, 1987; Mittelbach et al, 2007;

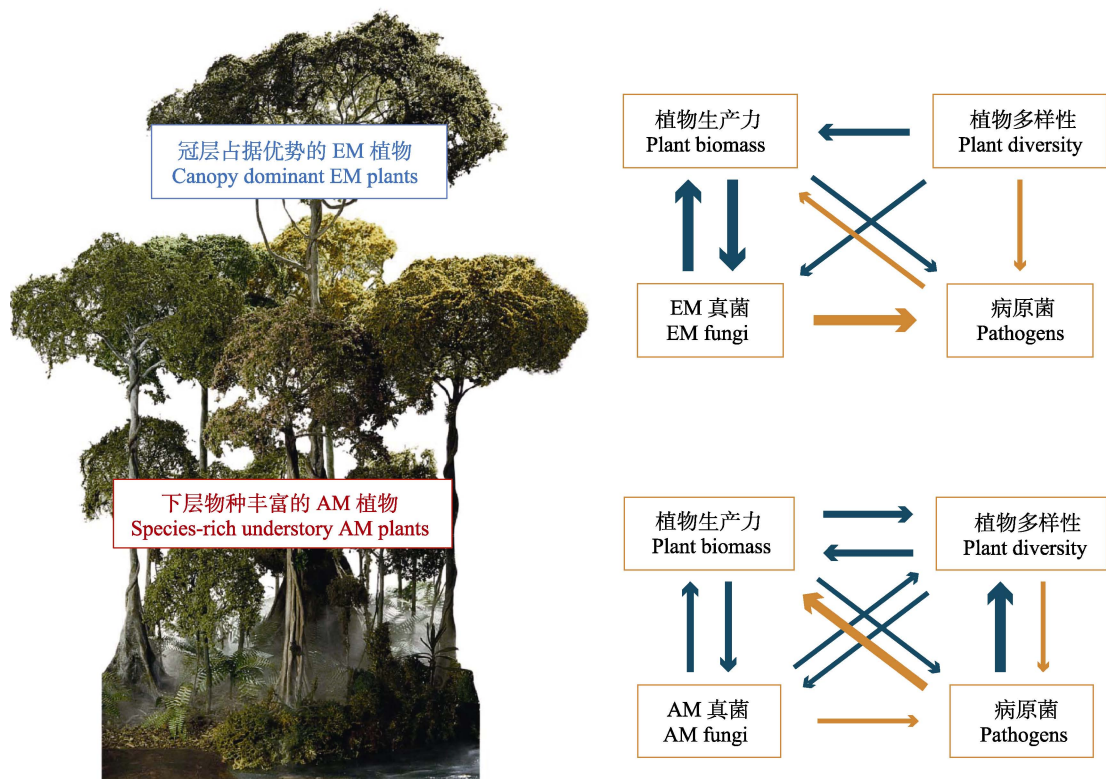


图1 植物-土壤反馈作用下不同类型菌根植物的更新生态位差异塑造了森林群落的物种组成和空间结构。右图改自Tedersoo等(2020), 蓝色和橙色箭头分别代表促进和抑制作用, 箭头宽度代表相应作用过程的相对重要性。
Fig.1 Plant-soil feedback effects and relative regeneration niches among tree species with different mycorrhizal types regulating the species composition and spatial structure of forest communities. AM, Arbuscular mycorrhiza; EM, Ectomycorrhiza. Right panel is modified from Tedersoo et al (2020), blue and orange arrows indicate positive and negative effects, respectively; arrow width depicts the relative importance of the effect.

Harrison & Cornell, 2008)。基于CForBio的样地, 研究人员也初步探讨了区域因素对我国森林生物多样性与群落结构的影响(Feng et al, 2014, 2015; Cao et al, 2021; Wang et al, 2021)。例如, 基于11个中国森林样地的研究表明冰期间冰期的气候变化显著影响中国森林群落的系统发育结构(Feng et al, 2014)。而最近的一项研究发现冰期间冰期的气候变化对我国东北地区森林群落的木本植物多样性和草本植物多样性影响相反, 即冰期间冰期的温度变化促进了木本植物丰富度, 但降低了草本植物丰富度(Wang et al, 2021)。此外, 通过比较基于不同物种库(东亚物种库与全球物种库)的系统发育结构的差异, 发现洲际迁徙和局部种化均显著影响我国森林群落的系统发育结构(Feng et al, 2014)。近期基于东亚地区森林动态监测网络21个大型森林动态样地的数据研究分析了 β 多样性的纬度梯度格局, 发现在控制了地形和 γ 多样性的影响后, 热带地区仍比温带地区拥有更高的 β 多样性, 表明热带地区更稳定的气候条件和更高的生产力允许物种产生更高的生境专一性以及利用稀有资源和空间的能力(Cao et al, 2021)。Zhong等(2021)利用全球45个森林动态样地的数据评估了丛枝菌根和外生菌根对 β 多样性及其组成的贡献, 结果发现纬度梯度上 β 多样性格局高度依赖于菌根类型的变化, 主要受到丛枝菌根的影响。Chu等(2019)利用全球23个森林动态样地的数据分析了大尺度生物多样性格局, 发现气候显著影响树木多样性, 其直接影响明显大于间接影响, 可能是热带气候造成的更快的进化速率和更窄的生态位宽度所引起的。

目前基于CForBio的扩散限制影响的相关研究大多是简单地将样方之间的距离或空间排列作为扩散限制的度量, 并未开展实际的扩散限制相关的调查、观测与实验。而样方之间的距离或空间排列与环境因子的分布密切相关, 如利用土壤和地形数据共同分析时, 扩散限制对群落构建的影响就小于仅用地形数据所得到的结果, 因为加入土壤数据后其空间结构减少了空间结构代表的扩散限制的作用(Chang et al, 2013)。同时, 随着当前全球变化的影响日趋加剧, 全球森林的大中型哺乳动物及鸟类等植物种子传播者的种群数量下降或灭绝(Emer et al, 2019; Fricke et al, 2022), 理解传播对群落构建的

作用对预测群落多样性的变化十分重要。未来应该利用CForBio的数十个大型或面积不等的长期森林动态样地, 通过长时间系统的观测与实验, 采用先进的追踪技术与分子分析方法更深入地探讨局域扩散限制的影响(Dent & Estrada-Villegas, 2021)。同时, 结合基因组学等新技术手段, 深入探讨揭示区域过程对森林生物多样性与群落构建的影响。

2.5 新技术应用带来新的认知

现代技术的发展从宏观和微观两个方面促进群落构建机制的研究。在宏观方面, 随着激光雷达、高光谱在森林生物多样监测研究上的应用, 克服了目前典型样地监测面积小、覆盖森林类型有限、监测成本高的缺陷, 使大范围、多尺度、低成本的连续群落生物多样性监测和时空比较研究成为可能(徐岩等, 2021)。同时, 叶绿体基因组(plastid genome)技术和代谢组学(metabolomics)等微观技术的利用能更好地推导群落构建的分子机制(Han et al, 2017; Jin et al, 2022), 并预测将来的生物多样性变化。这些技术提供了新的视角, 将进一步推动生物多样性监测和研究的发展。

随着新一代测序技术的发展, 叶绿体基因组技术已用于重建更精确的种间系统发育关系。同时, 转录组学(transcriptomics)方法也被引入群落生态学中, 根据种间决定关键功能的数十至数百个同源基因的相似性来推导关键的群落生态过程。如Jin等(2022)采用叶绿体基因组79种蛋白编码基因重建了中国亚热带地区6个样地580个物种的系统树, 并用这个系统树与DNA条形码(*rbcL* + *matK* + *trnH* - *psbA*)所重建的系统树和由全球74,533个维管植物生成的系统发育骨架所产生的名录系统树进行了比较。结果发现, 利用叶绿体基因组构建的群落系统树, 其建树效果要明显优于DNA条形码片段, 尤其在同属种比例较高的群落中, 应尽可能使用分辨率较高的叶绿体基因组树, 以得到更为准确的指数和生态推断结果。Han等(2017)通过转录组学手段检测了物种间与光相关的同源基因相似性对古田山85种木本植物幼苗存活的影响, 发现与光相关的15个基因本体中有3个是与幼苗存活相关的, 反映了光环境的过滤作用。

代谢组学利用植物代谢过程产生的代谢产物组分的差异, 能够从更深层次揭示植物群落的构建

机制。植物次生代谢物(plant secondary metabolite, PSM)由一些分子量较低的化合物组成(Wink, 2004), 它们通过对抗环境压力、防御食草动物和病原体形成植物防御的综合体系, 调控植物对环境的适应以及与群落成员的互作, 从而影响植物的适合度、群落组成和生态系统功能(Richards et al, 2015; Wink, 2018)。与植物的形态性状如木质密度和比叶面积等及少数生理性状相比, 植物次生代谢物能更好地推导产生生态学格局的生理生态过程, 并预测将来的生物多样性变化。在群落学水平上, 次生代谢产物更相似的物种更容易共享自然天敌, 由此产生的密度制约效应为稀有种提供了生存空间, 这也是森林植物共存的主要驱动因素(Janzen, 1970; Connell, 1971)。基于代谢组学可以从数千个候选化合物中识别出与特定天敌相关的化合物类型, 能够从生产者-消费者维度揭示影响植物群落构建的因素。使用标准化代谢组学可以研究不同生物地理区域中次生代谢物的差异, 进而推断不同区域物种组成差异的潜在原因。例如, 通过对西双版纳样地中大戟科26个树种次生代谢产物和其他功能性状的比较研究, 证实树种基于次生代谢产物的化学防御轴上的生态位分化是促进近缘种共存的机制之一(Wang et al, 2022)。

随着激光雷达、高光谱在森林生物多样监测研究中的应用, 基于地面监测, 激光雷达技术能提供高分辨率的单木和样地的冠层结构参数, 同时高光谱技术能反演冠层重要的功能性状, 如冠层的叶绿素、氮、水分和干物质等含量, 能以低成本方法进行大范围、多尺度的连续监测, 为森林生物多样性监测与研究开辟了新的前景(郭庆华等, 2016)。Zhang等(2016)发现, 在南亚热带森林鼎湖山样地, 无人机近地面遥感获得的高分辨率林冠参数可以很好地揭示森林群落结构和生物多样性的关系。Yi等(2022)利用激光雷达技术量化了亚热带9个不同演替阶段的1 ha森林样地的冠层结构多样性, 与以往大多数研究结论相反, 该研究发现冠层结构多样性对生产力存在负效应, 这种负效应可能源于上层和下层树冠对光资源的不对称竞争, 林下层叶面积与总体生产力之间的负相关关系为不对称竞争机制提供了进一步的证据。Wang等(2022)采用激光雷达量化了8个20–30 ha森林动态样地的冠层最大高

度, 发现地形导致的水分差异比辐射差异更能影响群落尺度冠层结构中最大冠层高度的变化, 验证了最大树高的“水分限制假说”; 同时, 从温带到热带森林, 最大冠层高度的主要影响因素呈现由辐射主导到水分限制主导的变化, 暗示了全球气候变化背景下降水变化可能会改变群落结构。

3 问题与展望

3.1 森林群落构建的尺度问题

森林群落构建过程存在明显的时空尺度效应。Wang等(2015)通过对2个25 ha温带森林动态样地多样性格局的研究, 发现生境过滤主要在150–250 m尺度发挥作用, 扩散过程则在< 150 m尺度发挥作用, 而种间互作在< 20 m尺度起关键作用。另外, 森林群落多样性、生态系统功能及两者的关系也随空间尺度发生变化(Chisholm et al, 2013; Gonzalez et al, 2020)。因此, 多空间尺度的对比研究不仅代表着未来森林群落构建机制的重要发展方向(例如密度制约机制)(Hülsmann et al, 2021), 也是运用群落构建理论解决森林管理难题的必然趋势(Manning et al, 2019)。另一方面, 群落构建机制也会随森林演替(长时间尺度)和干扰(短时间尺度)发生变化, 并对森林多样性和生态系统功能造成影响(Gonzalez et al, 2020)。例如, 近期样地研究发现, 林分结构复杂性及其驱动的种间竞争作用会随森林演替发生变化, 是决定受干扰森林生产力等多功能恢复的重要因素(Yuan et al, 2021; Yi et al, 2022)。未来工作应该侧重长期数据的运用, 从气候变化、干扰作用、森林群落构建过程等综合角度研究森林生物多样性、碳汇功能等的动态变化规律(Finzi et al, 2020)。

3.2 多维度、多营养级生物互作

生物互作是森林群落构建的重要驱动过程, 长期以来备受关注, 当代物种共存理论更是格外强调种内和种间关系在物种长期稳定共存中的核心地位(Chesson, 2000; 储诚进等, 2017)。然而, 目前相关研究主要集中于单营养级(植物)、单一维度(物种)生物互作, 研究结论比较局限。在多维度研究方面, 生物多样性不仅包括物种丰富度, 还包括功能性状和系统发育多样性(Swenson & Enquist, 2009), 综合考虑物种在功能和系统发育等其他维度的信息, 可以深入揭示驱动生物互作规律的关键机制(Webb et

al, 2002; Jia et al, 2020)。另外, 近年来的森林群落研究在植物菌根(Tedersoo et al, 2020; Chaudhary et al, 2022)、光谱特征(Cavender-Bare et al, 2020)等方面取得了一系列新的进展。在此基础上, 依托CForBio平台的研究发现了这些植物特征对植物间关系乃至群落多样性和生态系统功能的影响机制(Mao et al, 2019; Zhong et al, 2021), 极大丰富了生物互作的研究维度。未来的生物互作研究应该结合植物学、生态学新进展(如地下功能性状), 从新角度揭示生物互作的驱动机制及其对森林群落构建的影响过程(Wiegand et al, 2021)。

在多营养级互作方面, 针对森林群落内植物-动物-微生物等多营养级生物关系的研究相对薄弱, 由于跨营养级的生物关系是生物互作的关键组成部分(王晴晴等, 2021), 这将导致对生物互作的认识较为片面并低估其对群落构建机制的贡献。近年来, 随着高通量测序等方法的不断成熟, 大量研究开始关注植物-微生物关系, 发现土壤微生物是决定森林群落多样性的关键因素之一(Chen et al, 2019; Liang et al, 2020), 极大推动了群落构建理论的更新发展。另一方面, 借助红外相机、采样调查、围栏实验等方法, 陆续有研究揭示昆虫、动物、鸟类等在森林中的活动规律及其对植物群落的影响过程(谢文华, 2014; Zou et al, 2015; Jia et al, 2018; Wang et al, 2022)。然而, 目前关于多营养级生物互作的驱动机制及其对生物多样性维持和生态系统多功能的影响过程仍然存在诸多挑战(Eisenhauer et al, 2019)。例如, 近期研究通过实验 + 模型的方式, 探讨了多营养级物种对生物多样性-生态系统功能关系的驱动作用(王少鹏, 2020; Albert et al, 2022), 然而这些实验和模型结果多适用于物种较少的生态系统, 很难揭示物种异常丰富的森林生态系统的真实情况。未来的森林研究需要发展多类型、长时间的多营养级生物监测平台, 构建“野外观测 + 实验模拟 + 模型预测”的一体化综合研究体系, 深入回答以下科学问题: (1)多营养级物种共存网络: 自然森林群落内, 不同营养级生物如何实现稳定共存? (2)多营养级群落稳定性: 多营养级生物互作随环境条件(空间)和群落演替(时间)如何变化? (3)多营养级群落功能性: 各营养级生物如何决定森林群落构建过程和生态系统功能?

3.3 全球变化与森林群落构建机制

近百年来, 受到人类干扰和全球变化(如气温升高、降水改变、土地利用变化等)的持续影响, 全球森林遭受了极大破坏, 生物多样性和生态系统功能不断变化(McDowell et al, 2020)。全球变化通过调控生物与生物、生物与环境之间的关系, 进而改变森林群落的构建过程并决定森林的动态变化(McDowell et al, 2020; Collins et al, 2022)。然而, 考虑到生物的多样性(植物、动物、微生物等)和生物关系的复杂性(竞争、互惠、寄生等), 未来的研究需要结合森林地上-地下的群落特征, 从多维度(如物种、功能性状、系统发育)、多营养级角度揭示全球变化对生物关系的驱动机制(Davies et al, 2021; 贺强, 2021)。例如, Schleuning等(2020)提出了基于“响应性状(response traits)、匹配性状(matching traits)和扩散性状(dispersal traits)”的植物-动物互作研究框架, 这不仅为研究多营养级生物互作对全球变化的响应机制提供了新思路, 同时也强调了长期、多类型的森林监测数据对全球变化研究的重要意义。

另外, 全球变化可改变森林局域环境(水热条件、光照、土壤等), 并通过生境过滤和生物-环境互馈等过程影响森林群落的构建过程(HilleRisLambers et al, 2012)。因此, 在全球变化背景下, 森林局域环境的长期监测和局域环境-生物互馈的研究越来越重要, 但这方面工作仍很欠缺(de Frenne et al, 2021)。近年来, 森林动态样地结合长期监测数据发现局域环境和年际气象条件对森林幼苗更新具有重要作用, 显著影响森林群落构建过程(Uriarte et al, 2018; Xu et al, 2022)。此外, 由于森林结构和环境条件具有高度的时空变异性, 未来工作应该更加关注多时空尺度对比研究, 发展多尺度普适的森林群落构建规律和机制, 并在全球变化背景下, 为森林生物多样性保护和森林管理实践提供切实可信的参考依据。

3.4 观测-实验-模型融合研究揭示群落构建机制

由于森林群落构建规律十分复杂且随环境和时间变异明显, 因此未来应该采取“野外观测 + 实验模拟 + 模型预测”的多途径综合手段开展研究, 揭示群落构建的复杂规律并模拟构建过程以确定关键机制。其中, 实验模拟 + 模型方法可以模拟复杂过程: 例如生物多样性与生态系统功能(BEF)研

究运用大型控制实验结合邻域模型方法, 验证了邻域交互作用对森林群落多样性和生产力关系的驱动作用(Fichtner et al, 2018), 确定了生物互作在BEF理论体系中的关键地位。另外, 野外观测 + 模型方法可以揭示复杂规律: 森林动态样地可以为模型提供详细的森林结构、过程、动态以及环境参数, 为准确预测森林未来变化提供巨大帮助(McDowell et al, 2020)。近期研究通过整合森林动态样地观测数据和森林动态模型, 成功将个体、物种水平的空间过程与群落水平的多样性动态进行联系, 结果发现远离母树的聚集性分布(对应动物传播和埋藏种子、林窗下的更新过程等)有利于树种之间的稳定共存, 实现了群落构建理论的新突破(Wiegand et al, 2021)。最后, 野外观测 + 实验模拟可以确定关键机制: 近期的密度制约研究通过长期的野外幼苗调查数据及菌根实验方法, 发现EM真菌可以提高幼苗的存活率和生长速率, 造成EM树种没有密度制约效应并成为群落优势种, 从而确定了EM树种获得优势的关键途径(Liang et al, 2020)。在全球变化背景下, 这种多途径融合的研究方式将变得越来越重要, 而集中全球性的森林监测网络(如ForestGEO; Davies et al, 2021)、实验平台(如TreeDivNet; <https://treedivnet.ugent.be>)和大型地球系统模型(McDowell et al, 2020)开展整合研究, 是准确预测未来全球森林变化趋势、制定森林管理策略的重要科学基础。

3.5 群落构建机制的应用前景

随着森林群落构建机制研究的不断积累, 目前已经对森林更新、生长、死亡动态变化(McDowell et al, 2020)、群落多样性维持机制(HilleRisLambers et al, 2012)以及生物量、生产力等碳积累过程(Muller-Landau et al, 2021)有了较为深入的认识。然而, 由于目前的森林群落构建机制研究多集中于局域和邻域尺度(例如, 密度制约机制, Hülsmann et al, 2021)、实验和观测研究经常发现相悖结论(Hagan et al, 2021)、理论研究与管理实践的关注点不同(Coll et al, 2018)等, 导致群落构建理论研究难以直接解决森林管理实践中面临的难题(例如, 如何调整群落结构以提高森林固碳能力, 抚育造林中的物种选择等; Manning et al, 2019)。近年来, 依托CForBio平台, 结合长期积累的森林调查数据和树种特性数据

(例如, 功能性状), 通过量化不同树种在维持森林群落多样性、提高生态系统功能的作用潜力(原作强等 2022), 在不同环境条件下(如土壤肥力条件)提出了具体的树种管理方式(例如, 不同菌根类型树种的混合比例; Mao et al, 2019), 可以为植树造林和森林管理过程中的树种选择及群落结构优化提供科学参考。

综上所述, CForBio作为森林动态样地长期监测平台, 以其时间长、尺度大、对整个生活史全面监测的独特优势, 可以作为“天然试金石”, 检验和发展森林群落构建理论, 并连结森林群落构建理论和森林管理实践(Coll et al, 2018)。另外, 森林动态样地可以为生态系统模型提供详细的森林结构、过程、动态以及环境参数, 是森林模型研究的“天然百宝箱”, 为准确预测森林未来变化提供巨大帮助(McDowell et al, 2020)。因此, 森林动态样地的长期监测工作是实现多营养级结合、多方法融合、多时空尺度整合的森林群落构建机制研究体系的重要基础。未来森林群落构建机制研究应该特别重视积累长期的观测证据, “尝试回答森林长期管理面临的急迫难题”, 推动相关研究从“理论探究”到“实践应用”的转变, 为森林生物多样性保护和应对全球变化等做出重要贡献。

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附录 Supplementary Material

附录1 中国森林生物多样性监测网络样地基本信息

Appendix 1 Basic information of forest dynamic plots in Chinese Forest Biodiversity Monitoring Network (CForBio)

<https://www.biodiversity-science.net/fileup/PDF/2022504-1.pdf>